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(54) Titre : ACTIVITE ENZYMATIQUE HETEROLOGUE FE-S AUGMENTEE CHEZ LA LEVURE
(54) Title: INCREASED HETEROLOGOUS FE-S ENZYME ACTIVITY IN YEAST

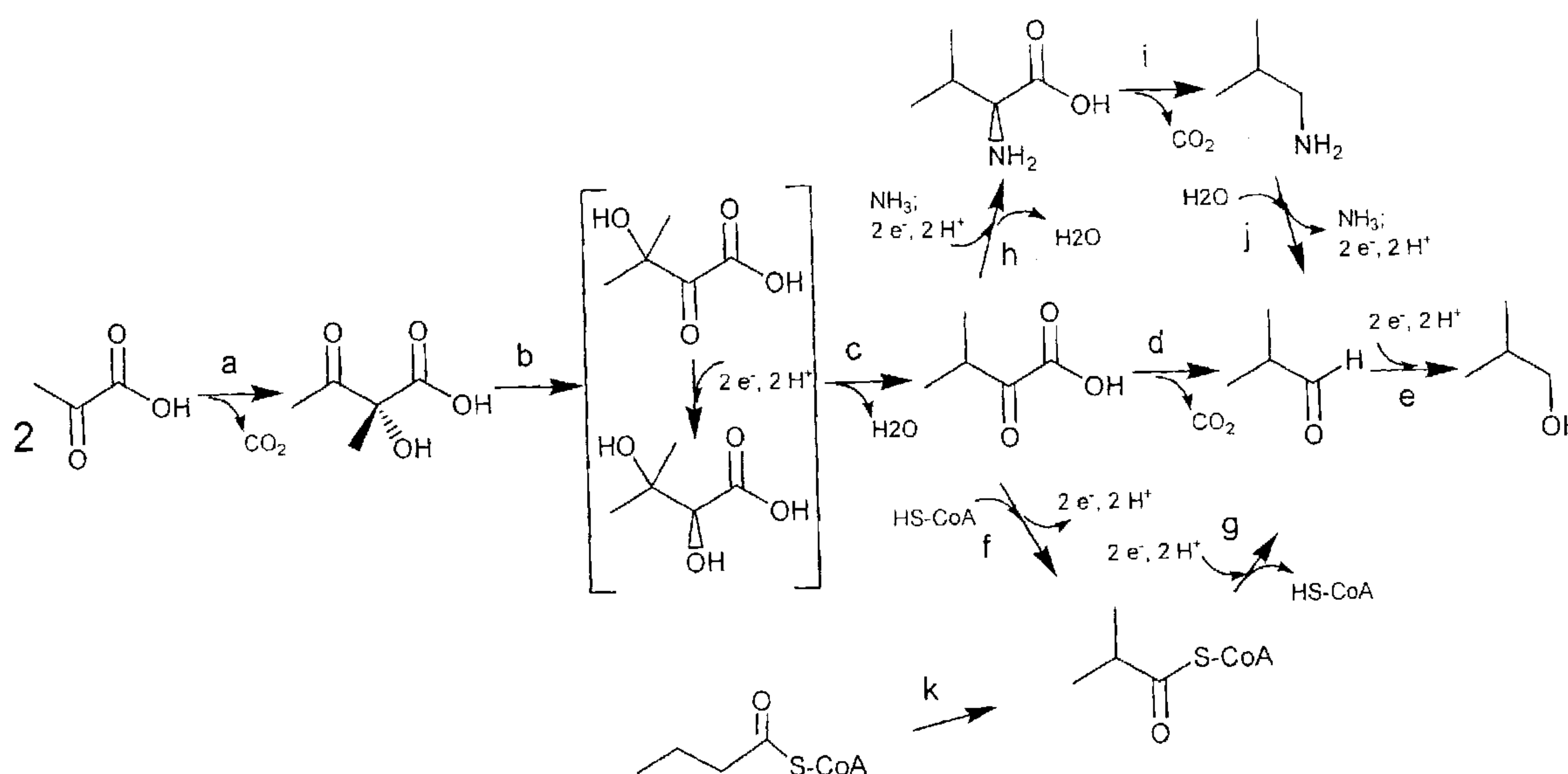


FIG. 1

(57) **Abrégé/Abstract:**

Yeast strains were engineered that have increased activity of heterologous proteins that require binding of an Fe-S cluster for their activity. The yeast strains have reduced activity of an endogenous Fe-S protein. Activities of heterologous fungal or plant 2Fe-2S dihydroxy-acid dehydratases and Fe-S propanediol dehydratase reactivase were increased for increased production of products made using biosynthetic pathways including these enzymes, such as valine, isoleucine, leucine, pantothenic acid (vitamin B5), isobutanol, 2-butanone and 2-butanol.



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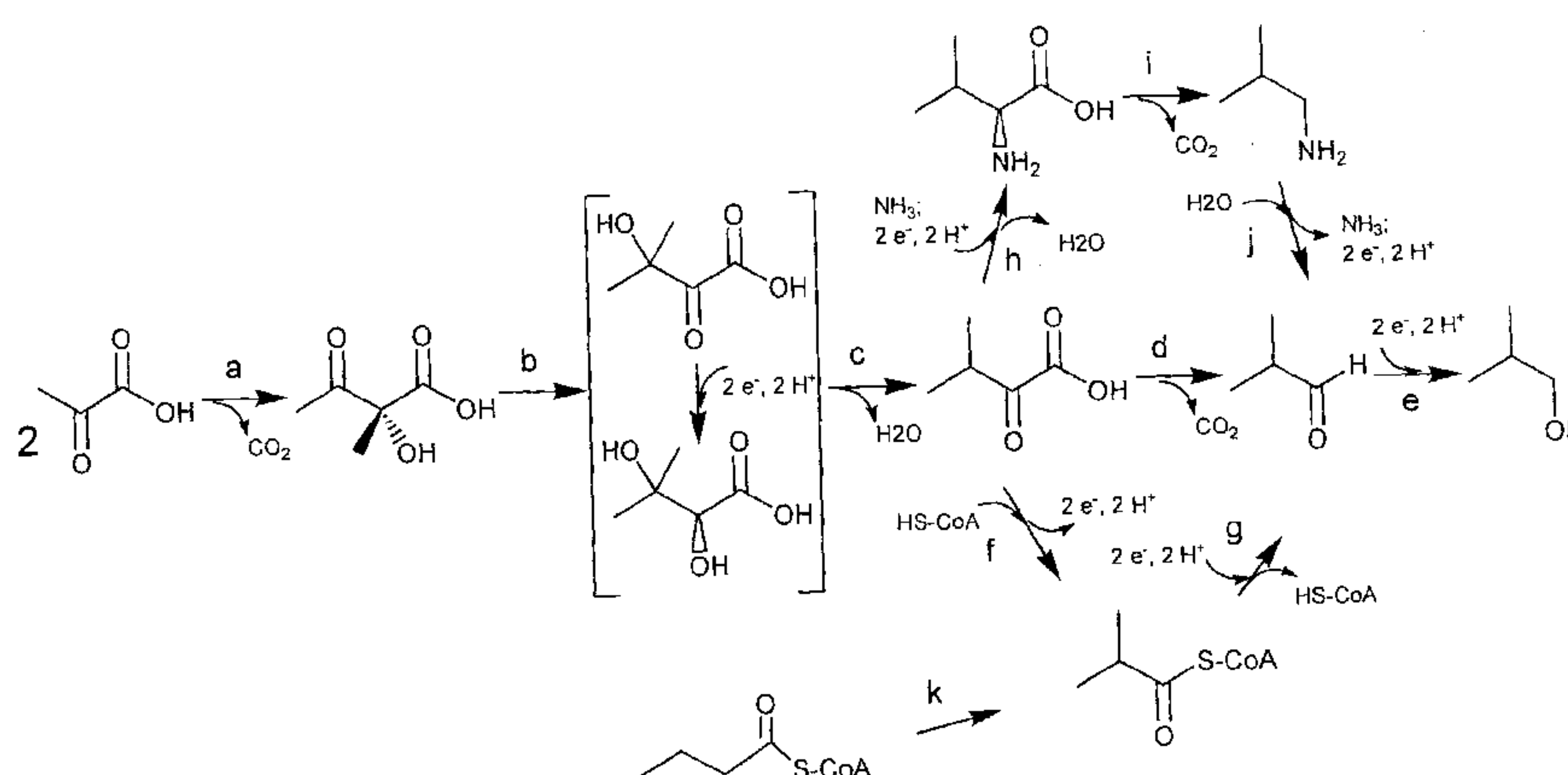


FIG. 1

(57) Abstract: Yeast strains were engineered that have increased activity of heterologous proteins that require binding of an Fe-S cluster for their activity. The yeast strains have reduced activity of an endogenous Fe-S protein. Activities of heterologous fungal or plant 2Fe-2S dihydroxy-acid dehydratases and Fe-S propanediol dehydratase reactivase were increased for increased production of products made using biosynthetic pathways including these enzymes, such as valine, isoleucine, leucine, pantothenic acid (vitamin B5), isobutanol, 2-butanone and 2-butanol.

TITLE

INCREASED HETEROLOGOUS Fe-S ENZYME ACTIVITY IN YEAST

CROSS REFERENCE TO RELATED APPLICATIONS

5 This application is related to and claims the benefit of priority to U.S. Provisional Application Nos. 61/100,801 filed September 29, 2008 and 61/100,806 filed September 29, 2008. The entirety of each is hereby incorporated by reference.

FIELD OF THE INVENTION

10 The invention relates to the field of industrial microbiology and the expression of proteins that require an iron-sulfur cluster for activity. More specifically, expression of heterologous Fe-S protein activity in yeast cells is improved through specific host gene inactivation.

BACKGROUND OF THE INVENTION

15 Engineering of yeast for fermentative production of commercial products is an active and growing field. Enzymatic pathways engineered for biosynthesis of some products include enzymes that require binding of an iron-sulfur (Fe-S) cluster for activity. Dihydroxy-acid dehydratase (DHAD) is one example. DHAD is part of naturally occurring biosynthetic
20 pathways producing valine, isoleucine, leucine and pantothenic acid (vitamin B5). Increased expression of DHAD activity is desired for enhanced microbial production of branched chain amino acids or of pantothenic acid. In addition, DHAD catalyzed conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate is a common step in the multiple
25 isobutanol biosynthetic pathways that are disclosed in co-pending US Patent Pub No. US 20070092957 A1. Disclosed therein is engineering of recombinant microorganisms for production of isobutanol, which is useful as a fuel additive and whose availability may reduce the demand for petrochemical fuels.

30 Diol dehydratase provides an enzyme activity in a biosynthetic pathway for production of 2-butanone and 2-butanol that is disclosed in co-pending US Patent Pub No. US 2007-0292927A1. Disclosed in US Patent Pub No. US20090155870 is a butanediol dehydratase that is

useful for expression in this pathway due to its coenzyme B-12 independence. A diol dehydratase reactivase that is an Fe-S cluster protein required for activity of the B12-independent butanediol dehydratase, is also disclosed in US Patent Pub No. US20090155870. 2-
5 Butanone, also referred to as methyl ethyl ketone (MEK), is a widely used solvent, extractant and activator of oxidative reactions, as well as a substrate for chemical synthesis of 2-butanol. 2-butanol is useful as a fuel additive, whose availability may reduce the demand for petrochemical fuels.

10 For improved production of compounds synthesized in pathways including an Fe-S cluster containing enzyme, it is desirable to provide a host cell capable of expressing high levels of this enzymatic activity in the production host of interest. Whereas a number of commercially relevant bacteria and yeast can express activity of Fe-S cluster containing proteins,
15 this activity is at levels far below what is commercially useful for enhancing introduced biosynthetic pathways. Consequently a need exists for the discovery of host cells capable of expressing activity of Fe-S cluster containing proteins at levels high enough to enhance introduced pathways that have Fe-S requirements. Obtaining high functional expression of
20 heterologous Fe-S cluster containing enzymes is problematic due to the Fe-S cluster requirement, which involves availability and proper loading of the cluster into the apo-protein.

SUMMARY OF THE INVENTION

Provided herein are recombinant yeast host cells comprising at
25 least one heterologous Fe-S cluster protein wherein the yeast host has reduced expression of at least one endogenous Fe-S cluster protein.

The recombinant yeast cell may be grown under suitable conditions for the production of products including isobutanol, 2-butanol and 2-butanone.

30 In one aspect, the recombinant yeast cell comprises a disruption in the gene encoding the at least one endogenous Fe-S cluster protein.

In another aspect, the endogenous Fe-S cluster protein is selected from the group consisting of dihydroxy-acid dehydratase, isopropylmalate

dehydratase, sulfite reductase, glutamate dehydrogenase, biotin
 synthase, aconitase, homoaconitase, lipoate synthase, ferredoxin
 maturation, NADH ubiquinone oxidoreductase, succinate dehydrogenase,
 ubiquinol-cytochrome-c reductase, ABC protein Rli1, NTPase Nbp35,
 5 and hydrogenase-like protein.

In another aspect, the yeast is selected from the group consisting of
Saccharomyces, *Schizosaccharomyces*, *Hansenula*, *Candida*,
Kluyveromyces, *Yarrowia* and *Pichia*.

In another aspect, the endogenous Fe-S protein is expressed in the
 10 mitochondria, and in another embodiment, the endogenous Fe-S cluster
 protein has an activity selected from the group consisting of: dihydroxy-
 acid dehydratase and isopropylmalate dehydratase activity.

In another aspect, the host cell is *Saccharomyces* expressing a
 gene encoding a polypeptide having the amino acid sequence as set forth
 15 in SEQ ID NO:114.

In some embodiments, the at least one heterologous Fe-S cluster
 protein is selected from the group consisting of fungal 2Fe-2S dihydroxy-
 acid dehydratases and plant 2Fe-2S dihydroxy-acid dehydratases. In one
 embodiment, the heterologous fungal or plant 2Fe-2S cluster dihydroxy-
 20 acid dehydratase is expressed in the cytosol. In one embodiment, the
 heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is
 a polypeptide having an amino acid sequence that matches the Profile
 HMM of table 9 with an E value of $< 10^{-5}$ wherein the polypeptide
 additionally comprises all three conserved cysteines, corresponding to
 25 positions 56, 129, and 201 in the amino acids sequences of the
Streptococcus mutans DHAD enzyme corresponding to SEQ ID NO:179.
 In one embodiment, the heterologous fungal or plant 2Fe-2S cluster
 dihydroxy-acid dehydratase is a polypeptide having an amino acid
 sequence that has at least about 95% sequence identity to an amino acid
 30 sequence selected from the group consisting of SEQ ID NOs:46, 48, 50,
 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88,
 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120,
 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150

and 152. In one embodiment, the heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is a polypeptide having an amino acid sequence that is at least about 90% identical to SEQ ID NO:114 using the Clustal W method of alignment using the default parameters of GAP

5 PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

In another aspect, a method for the conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate is provided, said method comprising:

10 a) providing (1) a recombinant yeast host cell comprising at least one heterologous gene encoding a 2Fe-2S dihydroxy-acid dehydratase wherein the recombinant yeast host cell has reduced activity of at least one endogenous Fe-S cluster protein; and (2) a source of 2,3-dihydroxyisovalerate; and

15 b) growing the recombinant host cell of (a) with said source of 2,3-dihydroxyisovalerate under conditions where the 2,3-dihydroxyisovalerate is converted by the host cell to α -ketoisovalerate.

In another aspect, a method for the conversion of 2,3-butanediol to 2-butanone is provided, said method comprising:

20 a) providing (1) a recombinant yeast host cell comprising at least one heterologous gene encoding a Fe-S propanediol dehydratase reactivase wherein the recombinant yeast host cell has reduced activity of at least one endogenous Fe-S cluster protein; and (2) a source of 2,3-butanediol; and

25 b) growing the recombinant host cell of (a) with said source of 2,3-butanediol under conditions where 2,3-butanediol is converted by the host cell to 2-butanone.

Also provided is a method for the production of isobutanol comprising growing a recombinant yeast host cell disclosed herein under
30 conditions wherein isobutanol is produced.

In other embodiments, the at least one heterologous Fe-S cluster protein has Fe-S propanediol dehydratase reactivase activity. In some embodiments, the at least one heterologous Fe-S cluster protein having

Fe-S propanediol dehydratase reactivase activity is a propanediol dehydratase reactivase having an amino acid sequence that is at least about 90% identical to the amino acid sequence as set forth in SEQ ID NO:44 using the Clustal W method of alignment using the default
5 parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

In some embodiments, the cell produces 2-butanol, and in some embodiments the cell produces 2-butanone. In some embodiments, the
10 cell comprises a 2-butanol biosynthetic pathway, and in some embodiments, the cell comprises a 2-butanone biosynthetic pathway.

BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE DESCRIPTIONS

The invention can be more fully understood from the following
15 detailed description, figures, and the accompanying sequence descriptions, which form a part of this application.

Figure 1 shows biosynthetic pathways for isobutanol production.

Figure 2 shows a biosynthetic pathway for 2-butanone and 2-butanol production.

20 Table 9 is a table of the Profile HMM for dihydroxy-acid dehydratases based on enzymes with assayed function prepared as described in Example 1. Table 9 is submitted herewith electronically and is incorporated herein by reference.

The following sequences conform with 37 C.F.R. 1.821-1.825
25 ("Requirements for Patent Applications Containing Nucleotide Sequences and/or Amino Acid Sequence Disclosures - the Sequence Rules") and are consistent with World Intellectual Property Organization (WIPO) Standard ST.25 (1998) and the sequence listing requirements of the EPO and PCT (Rules 5.2 and 49.5(a-bis), and Section 208 and Annex C of the
30 Administrative Instructions). The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

Table1. Inactivation target Fe-S protein encoding genes

Organism and gene	SEQ ID NO: Nucleic Acid	SEQ ID NO: Peptide
<i>Saccharomyces cerevisiae</i> LEU1	1	2
<i>Schizosaccharomyces pombe</i> LEU1	3	4
<i>Candida glabrata</i> CBS 138 LEU1	5	6
<i>Candida albicans</i> SC 5314 LEU1	7	8
<i>Kluyveromyces lactis</i> LEU1	9	10
<i>Yarrowia lipolytica</i> LEU1	11	12
<i>Pichia stipitis</i> LEU1	13	14
<i>Saccharomyces cerevisiae</i> YJM789 ILV3	111	112
<i>Schizosaccharomyces pombe</i> ILV3	93	94
<i>Candida glabrata</i> CBS 138 ILV3	107	108
<i>Candida albicans</i> SC5314 ILV3	101	102
<i>Kluyveromyces lactis</i> ILV3	113	114
<i>Yarrowia lipolytica</i> ILV3	105	106
<i>Pichia stipitis</i> CBS 6054 ILV3	103	104
<i>Saccharomyces cerevisiae</i> ACO1	153	154
<i>Schizosaccharomyces pombe</i> (chromosome II) ACO1	155	156
<i>Schizosaccharomyces pombe</i> (chromosome I) ACO1	157	158
<i>Kluyveromyces lactis</i> NRRL Y-1140 ACO1	159	160
<i>Candida albicans</i> SC5314 ACO1	161	162
<i>Yarrowia lipolytica</i> CLIB122 ACO1	163	164
<i>Pichia stipitis</i> CBS 6054 ACO1	165	166
<i>Candida glabrata</i> CBS138 (chromosome F) ACO1	167	168
<i>Candida glabrata</i> CBS138 (chromosome D) ACO1	169	170
<i>Candida glabrata</i> CBS138 (chromosome K) ACO1	171	172

Table 2. Fungal and plant 2Fe-2S DHADs in addition to those in Table 1

Description	SEQ ID NO: Nucleic acid	SEQ ID NO: Peptide
<i>Chlamydomonas reinhardtii</i>	45	46
<i>Ostreococcus lucimarinus</i> CCE9901	47	48
<i>Vitis vinifera</i> (Unnamed protein product: CAO71581.1)	49	50
<i>Vitis vinifera</i> (CAN67446.1)	51	52
<i>Arabidopsis thaliana</i>	53	54
<i>Oryza sativa</i> (indica cultivar-group)	55	56
<i>Physcomitrella patens</i> subsp. <i>patens</i>	57	58
<i>Chaetomium globosum</i> CBS 148.51	59	60
<i>Neurospora crassa</i> OR74A	61	62
<i>Magnaporthe grisea</i> 70-15	63	64
<i>Gibberella zeae</i> PH-1	65	66
<i>Aspergillus niger</i>	67	68
<i>Neosartorya fischeri</i> NRRL 181 (XP_001266525.1)	69	70
<i>Neosartorya fischeri</i> NRRL 181 (XP_001262996.1)	71	72
<i>Aspergillus niger</i> (An03g04520)	73	74
<i>Aspergillus niger</i> (An14g03280)	75	76
<i>Aspergillus terreus</i> NIH2624	77	78
<i>Aspergillus clavatus</i> NRRL 1	79	80
<i>Aspergillus nidulans</i> FGSC A4	81	82
<i>Aspergillus oryzae</i>	83	84
<i>Ajellomyces capsulatus</i> NAm1	85	86
<i>Coccidioides immitis</i> RS	87	88

<i>Botryotinia fuckeliana</i> B05.10	89	90
<i>Phaeosphaeria nodorum</i> SN15	91	92
<i>Pichia guilliermondii</i> ATCC 6260	95	96
<i>Debaryomyces hansenii</i> CBS767	97	98
<i>Lodderomyces elongisporus</i> NRRL YB-4239	99	100
<i>Vanderwaltozyma polyspora</i> DSM 70294	109	110
<i>Ashbya gossypii</i> ATCC 10895	115	116
<i>Laccaria bicolor</i> S238N-H82	117	118
<i>Coprinopsis cinerea okayama7#130</i>	119	120
<i>Cryptococcus neoformans</i> var. <i>neoformans</i> JEC21	121	122
<i>Ustilago maydis</i> 521	123	124
<i>Malassezia globosa</i> CBS 7966	125	126
<i>Aspergillus clavatus</i> NRRL 1	127	128
<i>Neosartorya fischeri</i> NRRL 181 (Putative)	129	130
<i>Aspergillus oryzae</i>	131	132
<i>Aspergillus niger</i> (An18g04160)	133	134
<i>Aspergillus terreus</i> NIH2624	135	136
<i>Coccidioides immitis</i> RS (CIMG_04591)	137	138
<i>Paracoccidioides brasiliensis</i>	139	140
<i>Phaeosphaeria nodorum</i> SN15	141	142
<i>Gibberella zeae</i> PH-1	143	144
<i>Neurospora crassa</i> OR74A	145	146
<i>Coprinopsis cinerea okayama 7#130</i>	147	148
<i>Laccaria bicolor</i> S238N-H82	149	150
<i>Ustilago maydis</i> 521	151	152

Table 3. Expression genes

<i>Description</i>	SEQ ID NO: Nucleic acid	SEQ ID NO: Peptide
Roseburia inulinivorans (RdhtA)	15	43
Roseburia inulinivorans (RdhtB)	16	44
Bacillus subtilis (alsS)	27	28
<i>Vibrio cholerae</i> (KARI)	35	36
<i>Pseudomonas aeruginosa</i> PAO1 (KARI)	37	38
<i>Pseudomonas fluorescens</i> PF5 (KARI)	39	40
<i>Achromobacter xylosoxidans</i> (sadB)	41	42
B12-independent glycerol dehydratase from <i>Clostridium butyricum</i>	190	191
B-12 independent butanediol dehydratase reactivase from <i>Clostridium butyricum</i>	192	193

SEQ ID NO:17 is a synthetic rdhtAB sequence.

SEQ ID NOs:18-21 and 30-33 are primers for PCR, cloning or sequencing analysis used as described in the Examples herein.

5 SEQ ID NO:22 is a dual terminator sequence.

SEQ ID NO:23 is the *Saccharomyces cerevisiae* ADH terminator.

SEQ ID NO:24 is the *Saccharomyces cerevisiae* CYC1 terminator.

SEQ ID NO:25 is the *Saccharomyces cerevisiae* FBA promoter.

SEQ ID NO:26 is the *Saccharomyces cerevisiae* GPM promoter.

10 SEQ ID NO:29 is the pNY13 vector.

SEQ ID NO:34 is the *Saccharomyces cerevisiae* CUP1 promoter.

SEQ ID NO:173 is the codon optimized coding region for *ILV3* DHAD from *Kluyveromyces lactis*.

15 Table 4. Functionally verified DHADs used for Profile HMM

<i>Organism</i>	SEQ ID NO: Nucleic acid	SEQ ID NO: Peptide
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Nitrosomonas europaea ATCC 19718	174	175
Synechocystis sp. PCC 6803	176	177
Streptococcus mutans UA159	178	179
Streptococcus thermophilus LMG 18311	180	181
Ralstonia metallidurans CH34	182	183
Ralstonia eutropha JMP134	184	185
Lactococcus lactis subsp. cremoris SK11	186	187
Flavobacterium johnsoniae UW101	188	189

DETAILED DESCRIPTION OF THE INVENTION

Disclosed herein is the discovery that introduced Fe-S containing proteins in yeast host cells have high activity levels when expression of endogenous Fe-S containing proteins is inhibited or disrupted. The present invention relates to recombinant yeast cells engineered to provide expression of at least one heterologous protein that is an Fe-S cluster protein, and engineered for reduced expression of at least one endogenous Fe-S cluster protein. In these cells the activity of the heterologous Fe-S cluster protein is improved, such that there is improved production of a product made in a biosynthetic pathway that includes the enzyme activity. Examples of commercially useful products from a pathway including an Fe-S protein include valine, isoleucine, leucine, pantothenic acid, isobutanol, 2-butanone and 2-butanol.

The following abbreviations and definitions will be used for the interpretation of the specification and the claims.

As used herein, the terms “comprises,” “comprising,” “includes,” “including,” “has,” “having,” “contains” or “containing,” or any other variation thereof, are intended to cover a non-exclusive inclusion. For example, a composition, a mixture, process, method, article, or apparatus that comprises a list of elements is not necessarily limited to only those elements but may include other elements not expressly listed or inherent to such composition, mixture, process, method, article, or apparatus.

Further, unless expressly stated to the contrary, “or” refers to an inclusive or and not to an exclusive or. For example, a condition A or B is satisfied by any one of the following: A is true (or present) and B is false (or not present), A is false (or not present) and B is true (or present), and both A
5 and B are true (or present).

Also, the indefinite articles “a” and “an” preceding an element or component of the invention are intended to be nonrestrictive regarding the number of instances (i.e. occurrences) of the element or component. Therefore “a” or “an” should be read to include one or at least one, and the
10 singular word form of the element or component also includes the plural unless the number is obviously meant to be singular.

The term “invention” or “present invention” as used herein is a non-limiting term and is not intended to refer to any single embodiment of the particular invention but encompasses all possible embodiments as
15 described in the specification and the claims.

As used herein, the term “about” modifying the quantity of an ingredient or reactant of the invention employed refers to variation in the numerical quantity that can occur, for example, through typical measuring and liquid handling procedures used for making concentrates or use
20 solutions in the real world; through inadvertent error in these procedures; through differences in the manufacture, source, or purity of the ingredients employed to make the compositions or carry out the methods; and the like. The term “about” also encompasses amounts that differ due to different equilibrium conditions for a composition resulting from a particular initial
25 mixture. Whether or not modified by the term “about”, the claims include equivalents to the quantities. In one embodiment, the term “about” means within 10% of the reported numerical value, preferably within 5% of the reported numerical value

The term “Fe-S cluster protein” is a protein that binds an iron-sulfur
30 cluster and requires the binding of the cluster for its activity.

The term “2Fe-2S DHAD” refers to DHAD enzymes requiring a bound [2Fe-2S]²⁺ cluster for activity.

The term "Fe-S propanediol dehydratase reactivase" refers to propanediol dehydratase reactivases requiring a bound Fe-S cluster for activity.

5 The term "isobutanol biosynthetic pathway" refers to an enzyme pathway to produce isobutanol from pyruvate.

The term "2-butanol biosynthetic pathway" refers to an enzyme pathway to produce 2-butanol from pyruvate.

The term "2-butanone biosynthetic pathway" refers to an enzyme pathway to produce 2-butanone from pyruvate.

10 There term "Dihydroxy-acid dehydratase", also abbreviated DHAD , will refer to an enzyme that converts 2,3-dihydroxyisovalerate to α -ketoisovalerate.

The term "butanediol dehydratase", also known as "diol dehydratase" or "propanediol dehydratase" refers to a polypeptide (or
15 polypeptides) having an enzyme activity that catalyzes the conversion of 2,3-butanediol to 2-butanone. Butanediol dehydratases that do not utilize the cofactor adenosyl cobalamin (also known as coenzyme B12, or vitamin B12; although vitamin B12 may refer also to other forms of cobalamin that are not coenzyme B12) are coenzyme B12-independent
20 diol dehydratases that require association with a diol dehydratase reactivase that is a Fe-S cluster protein. Examples of B12-independent diol dehydratases include those from *Clostridium glycolicum* (Hartmanis et al. (1986) *Arch. Biochem. Biophys.* 245:144-152), *Clostridium butyricum* (protein SEQ ID NO:191; coding region SEQ ID NO:190; O'Brien et al.
25 (2004) *Biochemistry* 43:4635-4645), and *Roseburia inulinivorans* (coding: SEQ ID NO:15; protein: SEQ ID NO:43; disclosed in co-pending US Patent Pub No. US20090155870.

The term "propanediol dehydratase reactivase" , also known as "diol dehydratase reactivase" or "butanediol dehydratase reactivase" refers
30 to a reactivating factor for diol dehydratase, an enzyme which undergoes suicide inactivation during catalysis. Diol dehydratase reactivases associated with coenzyme B12-independent diol dehydratases may be Fe-S cluster proteins. Examples include those from *Clostridium glycolicum*

(Hartmanis et al. (1986) *Arch. Biochem. Biophys.* 245:144-152),
Clostridium butyricum (protein SEQ ID NO:193; coding region SEQ ID
NO:192; O'Brien et al. (2004) *Biochemistry* 43:4635-4645), and *Roseburia*
inulinivorans (coding: SEQ ID NO:16; protein: SEQ ID NO:44; disclosed in
5 commonly owned and co-pending US Patent Pub No. US20090155870).

The term "reduced expression" as it applies to the expression of a
protein in a cell host will include those situations where the activity of the
protein is diminished as compared with a wildtype form (as with antisense
technology for example) or substantially eliminated as with gene
10 disruption, deletion or inactivation for example.

The term "carbon substrate" or "fermentable carbon substrate"
refers to a carbon source capable of being metabolized by host organisms
of the present invention and particularly carbon sources selected from the
group consisting of monosaccharides, oligosaccharides, polysaccharides,
15 and one-carbon substrates or mixtures thereof.

The term "gene" refers to a nucleic acid fragment that is capable of
being expressed as a specific protein, optionally including regulatory
sequences preceding (5' non-coding sequences) and following (3' non-
coding sequences) the coding sequence. "Native gene" refers to a gene
20 as found in nature with its own regulatory sequences. "Chimeric gene"
refers to any gene that is not a native gene, comprising regulatory and
coding sequences that are not found together in nature. Accordingly, a
chimeric gene may comprise regulatory sequences and coding sequences
that are derived from different sources, or regulatory sequences and
25 coding sequences derived from the same source, but arranged in a
manner different than that found in nature. "Endogenous gene" refers to a
native gene in its natural location in the genome of an organism. A
"foreign gene" or "heterologous gene" refers to a gene not normally found
in the host organism, but that is introduced into the host organism by gene
30 transfer. "Heterologous gene" includes a native coding region, or portion
thereof, that is reintroduced into the source organism in a form that is
different from the corresponding native gene. For example, a heterologous
gene may include a native coding region that is a portion of a chimeric

gene including non-native regulatory regions that is reintroduced into the native host. Also a foreign gene can comprise native genes inserted into a non-native organism, or chimeric genes. A “transgene” is a gene that has been introduced into the genome by a transformation procedure.

5 As used herein the term “coding region” refers to a DNA sequence that codes for a specific amino acid sequence. “Suitable regulatory sequences” refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing
10 or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters, translation leader sequences, introns, polyadenylation recognition sequences, RNA processing site, effector binding site and stem-loop structure.

 The term “promoter” refers to a DNA sequence capable of
15 controlling the expression of a coding sequence or functional RNA. In general, a coding sequence is located 3' to a promoter sequence. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. It is understood by
20 those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental or physiological conditions. Promoters which cause a gene to be expressed in most cell types at most times are commonly referred to as “constitutive promoters”.
25 It is further recognized that since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

 The term “operably linked” refers to the association of nucleic acid sequences on a single nucleic acid fragment so that the function of one is
30 affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of effecting the expression of that coding sequence (i.e., that the coding sequence is under the

transcriptional control of the promoter). Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation.

The term “expression”, as used herein, refers to the transcription and stable accumulation of sense (mRNA) or antisense RNA derived from the nucleic acid fragment of the invention. Expression may also refer to translation of mRNA into a polypeptide.

As used herein the term “transformation” refers to the transfer of a nucleic acid fragment into a host organism, resulting in genetically stable inheritance. Host organisms containing the transformed nucleic acid fragments are referred to as “transgenic” or “recombinant” or “transformed” organisms.

The terms “plasmid” and “vector” as used herein, refer to an extra chromosomal element often carrying genes which are not part of the central metabolism of the cell, and usually in the form of circular double-stranded DNA molecules. Such elements may be autonomously replicating sequences, genome integrating sequences, phage or nucleotide sequences, linear or circular, of a single- or double-stranded DNA or RNA, derived from any source, in which a number of nucleotide sequences have been joined or recombined into a unique construction which is capable of introducing a promoter fragment and DNA sequence for a selected gene product along with appropriate 3' untranslated sequence into a cell.

As used herein the term “codon degeneracy” refers to the nature in the genetic code permitting variation of the nucleotide sequence without effecting the amino acid sequence of an encoded polypeptide. The skilled artisan is well aware of the “codon-bias” exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a gene for improved expression in a host cell, it is desirable to design the gene such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

The term “codon-optimized” as it refers to genes or coding regions of nucleic acid molecules for transformation of various hosts, refers to the alteration of codons in the gene or coding regions of the nucleic acid

molecules to reflect the typical codon usage of the host organism without altering the polypeptide encoded by the DNA.

As used herein, an “isolated nucleic acid fragment” or “isolated nucleic acid molecule” will be used interchangeably and will mean a polymer of RNA or DNA that is single- or double-stranded, optionally
5 containing synthetic, non-natural or altered nucleotide bases. An isolated nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

A nucleic acid fragment is “hybridizable” to another nucleic acid
10 fragment, such as a cDNA, genomic DNA, or RNA molecule, when a single-stranded form of the nucleic acid fragment can anneal to the other nucleic acid fragment under the appropriate conditions of temperature and solution ionic strength. Hybridization and washing conditions are well known and exemplified in Sambrook, J., Fritsch, E. F. and Maniatis, T.
15 Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory: Cold Spring Harbor, NY (1989), particularly Chapter 11 and Table 11.1 therein (entirely incorporated herein by reference). The conditions of temperature and ionic strength determine the “stringency” of the hybridization. Stringency conditions can be adjusted to screen for
20 moderately similar fragments (such as homologous sequences from distantly related organisms), to highly similar fragments (such as genes that duplicate functional enzymes from closely related organisms). Post-hybridization washes determine stringency conditions. One set of preferred conditions uses a series of washes starting with 6X SSC, 0.5%
25 SDS at room temperature for 15 min, then repeated with 2X SSC, 0.5% SDS at 45 °C for 30 min, and then repeated twice with 0.2X SSC, 0.5% SDS at 50 °C for 30 min. A more preferred set of stringent conditions uses higher temperatures in which the washes are identical to those above except for the temperature of the final two 30 min washes in 0.2X
30 SSC, 0.5% SDS was increased to 60 °C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65 °C. An additional set of stringent conditions include hybridization at 0.1X

SSC, 0.1% SDS, 65 °C and washes with 2X SSC, 0.1% SDS followed by 0.1X SSC, 0.1% SDS, for example.

Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (see Sambrook et al., *supra*, 9.50-9.51). For hybridizations with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see Sambrook et al., *supra*, 11.7-11.8). In one embodiment the length for a hybridizable nucleic acid is at least about 10 nucleotides. Preferably a minimum length for a hybridizable nucleic acid is at least about 15 nucleotides; more preferably at least about 20 nucleotides; and most preferably the length is at least about 30 nucleotides. Furthermore, the skilled artisan will recognize that the temperature and wash solution salt concentration may be adjusted as necessary according to factors such as length of the probe.

A “substantial portion” of an amino acid or nucleotide sequence is that portion comprising enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to putatively identify that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Altschul, S. F., et al., *J. Mol. Biol.*, 215:403-410 (1993)). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as

homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises enough of the sequence to specifically identify and/or isolate a nucleic acid fragment comprising the sequence. The instant specification teaches the complete amino acid and nucleotide sequence encoding particular proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

The term "complementary" is used to describe the relationship between nucleotide bases that are capable of hybridizing to one another. For example, with respect to DNA, adenosine is complementary to thymine and cytosine is complementary to guanine.

The term "percent identity", as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in: 1.) Computational Molecular Biology (Lesk, A. M., Ed.) Oxford University: NY (1988); 2.) Biocomputing: Informatics and Genome Projects (Smith, D. W., Ed.) Academic: NY (1993); 3.) Computer Analysis of Sequence Data, Part I (Griffin, A. M., and Griffin, H. G., Eds.) Humana: NJ (1994); 4.) Sequence Analysis in

Molecular Biology (von Heinje, G., Ed.) Academic (1987); and
5.) Sequence Analysis Primer (Gribskov, M. and Devereux, J., Eds.)
Stockton: NY (1991).

Preferred methods to determine identity are designed to give the
5 best match between the sequences tested. Methods to determine identity
and similarity are codified in publicly available computer programs.
Sequence alignments and percent identity calculations may be performed
using the MegAlign™ program of the LASERGENE bioinformatics
computing suite (DNASTAR Inc., Madison, WI). Multiple alignment of the
10 sequences is performed using the “Clustal method of alignment” which
encompasses several varieties of the algorithm including the “Clustal V
method of alignment” corresponding to the alignment method labeled
Clustal V (described by Higgins and Sharp, *CABIOS*. 5:151-153 (1989);
Higgins, D.G. et al., *Comput. Appl. Biosci.*, 8:189-191 (1992)) and found in
15 the MegAlign™ program of the LASERGENE bioinformatics computing
suite (DNASTAR Inc.). For multiple alignments, the default values
correspond to GAP PENALTY=10 and GAP LENGTH PENALTY=10.
Default parameters for pairwise alignments and calculation of percent
identity of protein sequences using the Clustal method are KTUPLE=1,
20 GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. For nucleic
acids these parameters are KTUPLE=2, GAP PENALTY=5, WINDOW=4
and DIAGONALS SAVED=4. After alignment of the sequences using the
Clustal V program, it is possible to obtain a “percent identity” by viewing
the “sequence distances” table in the same program. Additionally the
25 “Clustal W method of alignment” is available and corresponds to the
alignment method labeled Clustal W (described by Higgins and Sharp,
CABIOS. 5:151-153 (1989); Higgins, D.G. et al., *Comput. Appl. Biosci.*
8:189-191(1992)) and found in the MegAlign™ v6.1 program of the
LASERGENE bioinformatics computing suite (DNASTAR Inc.). Default
30 parameters for multiple alignment (GAP PENALTY=10, GAP LENGTH
PENALTY=0.2, Delay Divergen Seqs(%)=30, DNA Transition Weight=0.5,
Protein Weight Matrix=Gonnet Series, DNA Weight Matrix=IUB). After
alignment of the sequences using the Clustal W program, it is possible to

obtain a “percent identity” by viewing the “sequence distances” table in the same program.

It is well understood by one skilled in the art that many levels of sequence identity are useful in identifying polypeptides, from other species, wherein such polypeptides have the same or similar function or activity. Useful examples of percent identities include, but are not limited to: 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%, or any integer percentage from 55% to 100% may be useful in describing the present invention, such as 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%. Suitable nucleic acid fragments not only have the above homologies but typically encode a polypeptide having at least 50 amino acids, preferably at least 100 amino acids, more preferably at least 150 amino acids, still more preferably at least 200 amino acids, and most preferably at least 250 amino acids.

The term “sequence analysis software” refers to any computer algorithm or software program that is useful for the analysis of nucleotide or amino acid sequences. “Sequence analysis software” may be commercially available or independently developed. Typical sequence analysis software will include, but is not limited to: 1.) the GCG suite of programs (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, WI); 2.) BLASTP, BLASTN, BLASTX (Altschul et al., *J. Mol. Biol.*, 215:403-410 (1990)); 3.) DNASTAR (DNASTAR, Inc. Madison, WI); 4.) Sequencher (Gene Codes Corporation, Ann Arbor, MI); and 5.) the FASTA program incorporating the Smith-Waterman algorithm (W. R. Pearson, *Comput. Methods Genome Res.*, [Proc. Int. Symp.] (1994), Meeting Date 1992, 111-20. Editor(s): Suhai, Sandor. Plenum: New York, NY). Within the context of this application it will be understood that where sequence analysis software is used for analysis, that the results of the analysis will be based on the “default values” of the program referenced, unless otherwise specified. As used herein “default values”

will mean any set of values or parameters that originally load with the software when first initialized.

Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter "Maniatis"); and by Silhavy, T. J., Bennis, M. L. and Enquist, L. W., *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1984); and by Ausubel, F. M. et al., *Current Protocols in Molecular Biology*, published by Greene Publishing Assoc. and Wiley-Interscience (1987). Additional methods used here are in *Methods in Enzymology*, Volume 194, *Guide to Yeast Genetics and Molecular and Cell Biology* (Part A, 2004, Christine Guthrie and Gerald R. Fink (Eds.), Elsevier Academic Press, San Diego, CA).

15 Discovery of improved Fe-S cluster protein activity in yeast

Proteins that contain a bound iron-sulfur cluster (Fe-S) that is required for their activity may have low activity when used in heterologous expression systems. Formation of Fe-S clusters and their transfer to apo-proteins is a multistep process involving at least several proteins including cysteine desulfurase, a scaffold protein and a chaperone. Thus a heterologous Fe-S protein may not be effectively composed by the endogenous host system. Applicants have discovered a way to increase activity of an Fe-S protein expressed as a heterologous protein in a yeast host cell. Applicants have found that by reducing production of an endogenous Fe-S protein in the yeast host cell, an improvement in activity of an expressed heterologous Fe-S cluster protein can be achieved. Expression in yeast of either heterologous fungal or plant 2Fe-2S dihydroxy-acid dehydratase (DHAD) or Fe-S propanediol dehydratase reactivase (RdhtB) was improved when an endogenous gene encoding isopropylmalate dehydratase (LEU1) or an endogenous gene encoding dihydroxy-acid dehydratase (ILV3) was inactivated in the yeast host cells.

In yeast host cells with inactivation of a gene encoding an endogenous Fe-S protein, the activity of the expressed heterologous Fe-S

protein may be increased to at least about 1.4 fold of the activity in a yeast host cell with no inactivation of Fe-S protein encoding gene. For example, the *Kluyveromyces lactis* DHAD had 1.4 fold activity in a LEU1 deletion host as compared to a host without the deletion; the *Roseburia*
 5 *inulinivorans* RdhtB had 1.7 fold comparative activity in a LEU deletion host as measured by the activated RdhtA protein activity (described below); *Saccharomyces cerevisiae* DHAD expressed in the cytosol had 1.5 fold comparative activity in a mitochondrial ILV3 deletion host; and
 10 *Kluyveromyces lactis* DHAD expressed in the cytosol had 7.4 fold comparative activity in a mitochondrial ILV3 deletion host.

Yeast host cells with reduced expression of endogenous Fe-S protein

Reduced endogenous Fe-S protein expression may be engineered in any yeast cell that is amenable to genetic manipulation. Examples include yeasts of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*,
 15 *Candida*, *Kluyveromyces*, *Yarrowia* and *Pichia*. Suitable strains include, but are not limited to, *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis*, *Kluyveromyces thermotolerans*, *Candida glabrata*, *Candida albicans*, *Pichia stipitis* and *Yarrowia lipolytica*. Particularly suitable is *Saccharomyces cerevisiae*.

20 In any of these yeasts, any endogenous Fe-S protein may be a target for reduced expression. Fe-S proteins in yeast that may be targeted for reduced expression include, for example, the following proteins (with encoding gene): aconitase (ACO1), homoaconitase (LYS4), DHAD (ILV3), lipoate synthase (LIP5), biotin synthase (BIO2), ferredoxin maturation
 25 (YAH1), NADH ubiquinone oxidoreductase (NDI1), succinate dehydrogenase (SDH2), ubiquinol-cytochrome-c reductase (RIP1), isopropylmalate isomerase (LEU1), sulfite reductase (ECM17), glutamate dehydrogenase (GLT1), ABC protein Rli1 (RLI1), NTPase Nbp35 (NBP35), and hydrogenase-like protein (NARI1). Yeast cells with reduced
 30 expression of individual Fe-S proteins may require special conditions for growth such as supplementation of the growth medium with a particular nutrient, as is well known to one skilled in the art. For example, a strain with disruption of LEU1 is supplemented with leucine, a strain with

disruption of DHAD is supplemented with leucine, isoleucine, and valine, and a strain with disruption of LYS4 is supplemented with lysine. Some strains with a disruption require no supplementation for growth.

Particularly suitable Fe-S proteins that may be targeted for reduced expression include Isopropylmalate isomerase (LEU1), Dihydroxyacid dehydratase (ILV3), Sulfite reductase (ECM17), Glutamate dehydrogenase (GLT1), and Biotin synthase (BIO2). Reduced expression is engineered for at least one endogenous Fe-S protein, and two or more endogenous Fe-S proteins may be reduced.

LEU1 encodes isopropylmalate dehydratase, an enzyme belonging to EC 4.2.1.33 that is involved in branched chain amino acid biosynthesis, specifically synthesis of leucine. Any gene encoding an isopropylmalate dehydratase, which is an enzyme requiring a 4Fe-4S cluster for activity, may be inactivated in a yeast host cell of this disclosure. Examples of yeast LEU1 inactivation target genes and their encoded proteins are those from *Saccharomyces cerevisiae* (coding SEQ ID NO:1; protein SEQ ID NO:2), *Schizosaccharomyces pombe* (coding SEQ ID NO:3; protein SEQ ID NO:4), *Candida glabrata* strain CBS 138 (coding SEQ ID NO:5; protein SEQ ID NO:6), *Candida albicans* SC5314 (coding SEQ ID NO:7; protein SEQ ID NO:8), *Kluyveromyces lactis* (coding SEQ ID NO:9; protein SEQ ID NO:10), *Yarrowia lipolytica* (coding SEQ ID NO:11; protein SEQ ID NO:12) and *Pichia stipitis* (coding SEQ ID NO:13; protein SEQ ID NO:14).

Similarly in any of the yeast hosts described herein, an endogenous ILV3 gene may be inactivated to reduce endogenous Fe-S protein expression. ILV3 encodes mitochondrial DHAD that is involved in branched chain amino acid biosynthesis. Mitochondrial DHAD is encoded by a nuclear gene, and has a mitochondrial targeting signal sequence so that it is transported to and localized in the mitochondrion. Any ILV3 gene may be inactivated in a yeast host cell of this disclosure. Examples of yeast ILV3 inactivation target genes and their encoded proteins are those from *Saccharomyces cerevisiae* YJM78 (coding SEQ ID NO:111; protein SEQ ID NO:112), *Schizosaccharomyces pombe* (coding SEQ ID NO:93; protein SEQ ID NO:94), *Candida glabrata* strain CBS 138 (coding SEQ ID

NO:107; protein SEQ ID NO:108), *Candida albicans* SC5314 (coding SEQ ID NO:101; protein SEQ ID NO:102), *Kluyveromyces lactis* (coding SEQ ID NO:113; protein SEQ ID NO:114), *Yarrowia lipolytica* (coding SEQ ID NO:105; protein SEQ ID NO:106) and *Pichia stipitis* CBS 6054 (coding
5 SEQ ID NO:103; protein SEQ ID NO:104).

Because genes encoding isopropylmalate dehydratases and DHAD enzymes genes are well known, and because of the prevalence of genomic sequencing, additional suitable species of these enzymes can be readily identified by one skilled in the art on the basis of sequence
10 similarity using bioinformatics approaches. Typically BLAST (described above) searching of publicly available databases with known isopropylmalate dehydratase amino acid sequences, such as those provided herein, is used to identify these enzymes and their encoding sequences that may be targeted for inactivation in the present strains. For
15 example, endogenous yeast isopropylmalate dehydratase and DHAD proteins having amino acid sequence identities of at least about 70-75%, 75%-80%, 80-85%, 85%- 90%, 90%- 95% or 98% sequence identity to any of the isopropylmalate dehydratase proteins of SEQ ID NOs:2, 4, 6, 8, 10, 12 and 14 and the DHAD proteins of SEQ ID NOs:94, 102, 104, 106,
20 108, 112, and 114 may have reduced expression in the present strains. Identities are based on the Clustal W method of alignment using the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix.

Additionally, the sequences of LEU1 coding regions and ILV3
25 provided herein may be used to identify other homologs in nature. For example each of the coding regions described herein may be used to isolate genes encoding homologous proteins. Isolation of homologous genes using sequence-dependent protocols is well known in the art. Examples of sequence-dependent protocols include, but are not limited to:
30 1.) methods of nucleic acid hybridization; 2.) methods of DNA and RNA amplification, as exemplified by various uses of nucleic acid amplification technologies [e.g., polymerase chain reaction (PCR), Mullis et al., U.S. Patent 4,683,202; ligase chain reaction (LCR), Tabor, S. et al., *Proc.*

Acad. Sci. USA 82:1074 (1985); or strand displacement amplification (SDA), Walker, et al., *Proc. Natl. Acad. Sci. U.S.A.*, 89:392 (1992)]; and 3.) methods of library construction and screening by complementation.

For example, genes encoding similar proteins or polypeptides to the isopropylmalate dehydratase and DHAD encoding genes provided herein could be isolated directly by using all or a portion of the instant nucleic acid fragments as DNA hybridization probes to screen libraries from any desired organism using methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the disclosed nucleic acid sequences can be designed and synthesized by methods known in the art (Maniatis, *supra*). Moreover, the entire sequences can be used directly to synthesize DNA probes by methods known to the skilled artisan (e.g., random primers DNA labeling, nick translation or end-labeling techniques), or RNA probes using available *in vitro* transcription systems. In addition, specific primers can be designed and used to amplify a part of (or full-length of) the instant sequences. The resulting amplification products can be labeled directly during amplification reactions or labeled after amplification reactions, and used as probes to isolate full-length DNA fragments by hybridization under conditions of appropriate stringency.

Typically, in PCR-type amplification techniques, the primers have different sequences and are not complementary to each other. Depending on the desired test conditions, the sequences of the primers should be designed to provide for both efficient and faithful replication of the target nucleic acid. Methods of PCR primer design are common and well known in the art (Thein and Wallace, "The use of oligonucleotides as specific hybridization probes in the Diagnosis of Genetic Disorders", in *Human Genetic Diseases: A Practical Approach*, K. E. Davis Ed., (1986) pp 33-50, IRL: Herndon, VA; and Rychlik, W., In Methods in Molecular Biology, White, B. A. Ed., (1993) Vol. 15, pp 31-39, PCR Protocols: Current Methods and Applications. Humana: Totowa, NJ).

Generally two short segments of the described sequences may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The

polymerase chain reaction may also be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the described nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding microbial genes.

Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow the RACE protocol (Frohman et al., *PNAS USA* 85:8998 (1988)) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (e.g., BRL, Gaithersburg, MD), specific 3' or 5' cDNA fragments can be isolated (Ohara et al., *PNAS USA* 86:5673 (1989); Loh et al., *Science* 243:217 (1989)).

Alternatively, the provided isopropylmalate dehydratase and DHAD encoding sequences can be employed as hybridization reagents for the identification of homologs. The basic components of a nucleic acid hybridization test include a probe, a sample suspected of containing the gene or gene fragment of interest, and a specific hybridization method. Probes are typically single-stranded nucleic acid sequences that are complementary to the nucleic acid sequences to be detected. Probes are "hybridizable" to the nucleic acid sequence to be detected. The probe length can vary from 5 bases to tens of thousands of bases, and will depend upon the specific test to be done. Typically a probe length of about 15 bases to about 30 bases is suitable. Only part of the probe molecule need be complementary to the nucleic acid sequence to be detected. In addition, the complementarity between the probe and the target sequence need not be perfect. Hybridization does occur between imperfectly complementary molecules with the result that a certain fraction of the bases in the hybridized region are not paired with the proper complementary base.

Hybridization methods are well defined. Typically the probe and sample must be mixed under conditions that will permit nucleic acid hybridization. This involves contacting the probe and sample in the presence of an inorganic or organic salt under the proper concentration and temperature conditions. The probe and sample nucleic acids must be in contact for a long enough time that any possible hybridization between the probe and sample nucleic acid may occur. The concentration of probe or target in the mixture will determine the time necessary for hybridization to occur. The higher the probe or target concentration, the shorter the hybridization incubation time needed. Optionally, a chaotropic agent may be added. The chaotropic agent stabilizes nucleic acids by inhibiting nuclease activity. Furthermore, the chaotropic agent allows sensitive and stringent hybridization of short oligonucleotide probes at room temperature (Van Ness and Chen, *Nucl. Acids Res.* 19:5143-5151 (1991)). Suitable chaotropic agents include guanidinium chloride, guanidinium thiocyanate, sodium thiocyanate, lithium tetrachloroacetate, sodium perchlorate, rubidium tetrachloroacetate, potassium iodide and cesium trifluoroacetate, among others. Typically, the chaotropic agent will be present at a final concentration of about 3 M. If desired, one can add formamide to the hybridization mixture, typically 30-50% (v/v).

Various hybridization solutions can be employed. Typically, these comprise from about 20 to 60% volume, preferably 30%, of a polar organic solvent. A common hybridization solution employs about 30-50% v/v formamide, about 0.15 to 1 M sodium chloride, about 0.05 to 0.1 M buffers (e.g., sodium citrate, Tris-HCl, PIPES or HEPES (pH range about 6-9)), about 0.05 to 0.2% detergent (e.g., sodium dodecylsulfate), or between 0.5-20 mM EDTA, FICOLL (Pharmacia Inc.) (about 300-500 kdal), polyvinylpyrrolidone (about 250-500 kdal) and serum albumin. Also included in the typical hybridization solution will be unlabeled carrier nucleic acids from about 0.1 to 5 mg/mL, fragmented nucleic DNA (e.g., calf thymus or salmon sperm DNA, or yeast RNA), and optionally from about 0.5 to 2% wt/vol glycine. Other additives may also be included, such as volume exclusion agents that include a variety of polar water-

soluble or swellable agents (e.g., polyethylene glycol), anionic polymers (e.g., polyacrylate or polymethylacrylate) and anionic saccharidic polymers (e.g., dextran sulfate).

Nucleic acid hybridization is adaptable to a variety of assay formats.

- 5 One of the most suitable is the sandwich assay format. The sandwich assay is particularly adaptable to hybridization under non-denaturing conditions. A primary component of a sandwich-type assay is a solid support. The solid support has adsorbed to it or covalently coupled to it immobilized nucleic acid probe that is unlabeled and complementary to
10 one portion of the sequence.

Protein and nucleic acid encoding sequences for any of the other Fe-S proteins that may be targeted for reduced activity in a yeast cell of the invention may be identified using bioinformatics and other methods well known to one skilled in the art. For example, aconitase sequences are
15 identified by keyword searching in bioinformatics databases. Several sequences identified by this method are those from *Saccharomyces cerevisiae* (coding SEQ ID NO:153; protein SEQ ID NO:154), *Schizosaccharomyces pombe* on chromosome II (coding SEQ ID NO:155; protein SEQ ID NO:156), *Schizosaccharomyces pombe* on chromosome I
20 (coding SEQ ID NO:157; protein SEQ ID NO:158), *Kluyveromyces lactis* (coding SEQ ID NO:15; protein SEQ ID NO:160), *Candida albicans* SC5314 (coding SEQ ID NO:161; protein SEQ ID NO:162), *Yarrowia lipolytica* (coding SEQ ID NO:163; protein SEQ ID NO:164), *Pichia stipitis* CBS 6054 (coding SEQ ID NO:165; protein SEQ ID
25 NO:166), *Candida galbrata* CBS 138 chromosome F (coding SEQ ID NO:167; protein SEQ ID NO:168), *Candida galbrata* CBS 138 chromosome D (coding SEQ ID NO:169; protein SEQ ID NO:170), and *Candida galbrata* CBS 138 chromosome K (coding SEQ ID NO:171; protein SEQ ID NO:172).

- 30 Genes encoding Fe-S proteins, for example LEU1, ILV3, or ACO1 may be disrupted in any yeast cell using genetic modification. Many methods for genetic modification of target genes are known to one skilled in the art and may be used to create the present yeast strains.

Modifications that may be used to reduce or eliminate expression of a target protein are disruptions that include, but are not limited to, deletion of the entire gene or a portion of the gene, inserting a DNA fragment into the gene (in either the promoter or coding region) so that the protein is not
5 expressed or expressed at lower levels, introducing a mutation into the coding region which adds a stop codon or frame shift such that a functional protein is not expressed, and introducing one or more mutations into the coding region to alter amino acids so that a non-functional or a less enzymatically active protein is expressed. In addition, expression of a
10 gene may be blocked by expression of an antisense RNA or an interfering RNA, and constructs may be introduced that result in cosuppression. In addition, the synthesis or stability of the transcript may be lessened by mutation. Similarly the efficiency by which a protein is translated from mRNA may be modulated by mutation. All of these methods may be
15 readily practiced by one skilled in the art making use of the known or identified coding sequences such as LEU1 or ILV3.

DNA sequences surrounding a LEU1, ILV3, or ACO1 coding sequence are also useful in some modification procedures and are available for yeasts such as for *Saccharomyces cerevisiae* in the complete
20 genome sequence coordinated by Genome Project ID9518 of Genome Projects coordinated by NCBI (National Center for Biotechnology Information) with identifying GOPID 13838. Additional examples of yeast genomic sequences include that of *Yarrowia lipolytica*, GOPIC 13837, and of *Candida albicans*, which is included in GPID 10771, 10701 and 16373.
25 Additional genomes have been completely sequenced and annotated and are publicly available for the following yeast strains *Candida glabrata* CBS 138, *Kluyveromyces lactis* NRRL Y-1140, *Pichia stipitis* CBS 6054, and *Schizosaccharomyces pombe* 972h-.

In particular, DNA sequences surrounding a target coding
30 sequence, such as LEU1 or ILV3, are useful for modification methods using homologous recombination. For example, in this method flanking sequences are placed bounding a selectable marker gene to mediate homologous recombination whereby the marker gene replaces the target

gene. Also partial target gene sequences and flanking sequences
bounding a selectable marker gene may be used to mediate homologous
recombination whereby the marker gene replaces a portion of the target
gene. In addition, the selectable marker may be bounded by site-specific
5 recombination sites, so that following expression of the corresponding site-
specific recombinase, the resistance gene is excised from the target gene
without reactivating the latter. The site-specific recombination leaves
behind a recombination site which disrupts expression of the target gene
encoded protein. The homologous recombination vector may be
10 constructed to also leave a deletion in the target gene following excision of
the selectable marker, as is well known to one skilled in the art.

Deletions may be made using mitotic recombination as described in
Wach et al. ((1994) *Yeast* 10:1793-1808). This method involves preparing
a DNA fragment that contains a selectable marker between genomic
15 regions that may be as short as 20 bp, and which bound a target DNA
sequence. This DNA fragment can be prepared by PCR amplification of
the selectable marker gene using as primers oligonucleotides that
hybridize to the ends of the marker gene and that include the genomic
regions that can recombine with the yeast genome. The linear DNA
20 fragment can be efficiently transformed into yeast and recombined into the
genome resulting in gene replacement including with deletion of the target
DNA sequence (as described in *Methods in Enzymology*, v194, pp 281-
301 (1991)).

Moreover, promoter replacement methods may be used to
25 exchange the endogenous transcriptional control elements allowing
another means to modulate expression such as described in Mnaimneh et
al. ((2004) *Cell* 118(1):31-44) and in Example 12 herein.

In addition, a target gene in any yeast cell may be disrupted using
random mutagenesis, which is followed by screening to identify strains
30 with reduced target gene encoded activity. Using this type of method, the
DNA sequence of for example the LEU1, ILV3, or any other region of the
genome affecting expression of a target Fe-S protein, need not be known.

Methods for creating genetic mutations are common and well known in the art and may be applied to the exercise of creating mutants. Commonly used random genetic modification methods (reviewed in *Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) include spontaneous mutagenesis, mutagenesis caused by mutator genes, chemical mutagenesis, irradiation with UV or X-rays, or transposon mutagenesis.

Chemical mutagenesis of yeast commonly involves treatment of yeast cells with one of the following DNA mutagens: ethyl methanesulfonate (EMS), nitrous acid, diethyl sulfate, or N-methyl-N'-nitro-N-nitroso-guanidine (MNNG). These methods of mutagenesis have been reviewed in Spencer et al (Mutagenesis in Yeast, 1996, *Yeast Protocols: Methods in Cell and Molecular Biology*. Humana Press, Totowa, NJ). Chemical mutagenesis with EMS may be performed as described in *Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. Irradiation with ultraviolet (UV) light or X-rays can also be used to produce random mutagenesis in yeast cells. The primary effect of mutagenesis by UV irradiation is the formation of pyrimidine dimers which disrupt the fidelity of DNA replication. Protocols for UV-mutagenesis of yeast can be found in Spencer et al (Mutagenesis in Yeast, 1996, *Yeast Protocols: Methods in Cell and Molecular Biology*. Humana Press, Totowa, NJ). Introduction of a mutator phenotype can also be used to generate random chromosomal mutations in yeast. Common mutator phenotypes can be obtained through disruption of one or more of the following genes: *PMS1*, *MAG1*, *RAD18* or *RAD51*. Restoration of the non-mutator phenotype can be easily obtained by insertion of the wildtype allele. Collections of modified cells produced from any of these or other known random mutagenesis processes may be screened for reduced Fe-S protein activity.

Heterologous Fe-S proteins

Any fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase (DHAD) and any Fe-S propanediol dehydratase reactivase may be expressed as a heterologous protein in a yeast host cell engineered as

disclosed herein for reduced endogenous Fe-S cluster protein expression, and increased activity may be obtained. A heterologous protein includes one that is expressed in a manner differently from expression of a corresponding endogenous protein. For example in yeast, endogenous

5 DHAD is encoded by ILV3 in the nucleus and the expressed DHAD protein has a mitochondrial targeting signal sequence such that the protein is localized in the mitochondrion. An Fe-S cluster is added to the DHAD protein in the mitochondrion for its activity in branched chain amino acid biosynthesis. It is desirable to express DHAD activity in the cytosol for

10 participation in biosynthetic pathways that are localized in the cytosol. Cytosolic expression of DHAD in yeast is heterologous expression since the native protein is localized in the mitochondrion. For example, heterologous expression of the *Saccharomyces cerevisiae* DHAD in *S. cerevisiae* is obtained by expressing the *S. cerevisiae* DHAD coding

15 region with the mitochondrial targeting signal removed, such that the protein remains in the cytosol. 2Fe-2S DHADs that may be used in the present disclosure include those from fungi and plants. Representative fungal or plant 2Fe-2S DHADs are listed in Tables 1 and 2. Fungal or plant 2Fe-2S DHADs with amino acid sequence identities of 95% or greater

20 were removed from the analysis providing this list for simplification. However, any sequences with 95% or greater amino acid identities to any of these sequences are useful in the present invention. The analysis used to obtain 2Fe-2S DHADs is described in commonly owned and co-pending US Patent Application 61/100792, which is herein incorporated by

25 reference. The analysis is as follows: Therein a Profile Hidden Markov Model (HMM) was prepared based on amino acid sequences of eight functionally verified DHADs. These DHADs are from *Nitrosomonas europaea* (DNA SEQ ID NO:174; Protein SEQ ID NO:175), *Synechocystis* sp. PCC6803 (DNA SEQ ID:176; Protein SEQ ID NO:177), *Streptococcus mutans* (DNA SEQ ID NO:178; Protein SEQ ID NO:179), *Streptococcus thermophilus* (DNA SEQ ID NO:180; protein SEQ ID No:181), *Ralstonia metallidurans* (DNA SEQ ID NO:182; protein SEQ ID NO:183), *Ralstonia eutropha* (DNA SEQ ID NO:184; protein SEQ ID NO:185), and

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Lactococcus lactis (DNA SEQ ID NO:186; protein SEQ ID NO:187). In addition the DHAD from *Flavobacterium johnsoniae* (DNA SEQ ID NO:188; protein SEQ ID NO:189) was found to have dihydroxy-acid dehydratase activity when expressed in *E. coli* and was used in making the Profile. The Profile HMM is prepared using the HMMER software package (The theory behind profile HMMs is described in R. Durbin, S. Eddy, A. Krogh, and G. Mitchison, Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998; Krogh et al., 1994; J. Mol. Biol. 235:1501–1531), following the user guide which is available from HMMER (Janelia Farm Research Campus, Ashburn, VA). The output of the HMMER software program is a Profile Hidden Markov Model (HMM) that characterizes the input sequences, given in Table 9.

Any protein that matches the Profile HMM with an E value of $< 10^{-5}$ is a DHAD related protein, which includes 4Fe-4S DHADs, 2Fe-2S DHADs, arabonate dehydratases, and phosphogluconate dehydratases. Sequences matching the Profile HMM are then analyzed for the presence of the three conserved cysteines, corresponding to positions 56, 129, and 201 in the *Streptococcus mutans* DHAD. The presence of all three conserved cysteines is characteristic of proteins having a $[2Fe-2S]^{2+}$ cluster. Proteins having the three conserved cysteines include arabonate dehydratases and 2Fe-2S DHADs. The 2Fe-2S DHADs may be distinguished from the arabonate dehydratases by analyzing for signature conserved amino acids found to be present in the 2Fe-2S DHADs or in the arabonate dehydratases at positions corresponding to the following positions in the *Streptococcus mutans* DHAD amino acid sequence. These signature amino acids are in 2Fe-2S DHADs or in arabonate dehydratases, respectively, at the following positions (with greater than 90% occurrence): 88 asparagine vs glutamic acid; 113 not conserved vs glutamic acid; 142 arginine or asparagine vs not conserved; 165: not conserved vs glycine; 208 asparagine vs not conserved; 454 leucine vs not conserved; 477 phenylalanine or tyrosine vs not conserved; and 487 glycine vs not conserved.

The proteins identified by this process that have a fungal or plant origin, such as SEQ ID NOs:46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 5 134, 136, 138, 140, 142, 144, 146, 148, 150 and 152 may be used in the present invention, as well as any protein with amino acid identity of at least about 95%, 96%, 97%, 98%, or 99% to any of these sequences.

Particularly suitable is the DHAD from *Kluyveromyces lactis* (SEQ ID NO:114) and DHADs with at least about 90% amino acid sequence 10 identity to SEQ ID NO:114 using the Clustal W method of alignment using the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

In addition, fungal or plant 2Fe-2S DHADs that may be used in the 15 present invention may be identified by their position in a fungal or plant 2Fe-2S DHAD branch of a phylogenetic tree of DHAD related proteins. In addition, 2Fe-2S DHADs that may be used may be identified using sequence comparisons with any of the fungal or plant 2Fe-2S DHADs whose sequences are provided herein, where sequence identity may be at 20 least about 80%-85%, 85%-90%, 90%-95% or 95%-99%.

Additionally, the sequences of fungal or plant 2Fe-2S DHADs provided herein may be used to identify other homologs in nature. For example each of the DHAD encoding nucleic acid fragments given herein as SEQ ID NOs:45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 25 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149 and 151 may be used to isolate genes encoding homologous proteins as described above for the LEU1 coding region.

The coenzyme B12-independent propanediol dehydratase reactivase 30 of *Roseburia inulinivorans* is a protein requiring an Fe-S cluster for activity. This protein, RdhtB, is disclosed in co-pending US Patent Pub No. US20090155870, which is herein incorporated by reference. RdhtB reactivates a coenzyme B12-independent propanediol dehydratase of

Roseburia inulinivorans, which is named RdhtA and is also disclosed in commonly owned and co-pending US Patent Pub No. US20090155870. The activity of RdhtB may be assessed by assaying the activity of RdhtA, since RdhtB is required for RdhtA activity. Activity of RdhtB, and therefore
5 of RdhtA, is improved by expressing in a yeast host with reduced endogenous Fe-S protein expression disclosed herein. Heterologous expression of any coenzyme B12-independent propanediol dehydratase reactivase that requires an Fe-S cluster for activity may be improved in a yeast strain having reduced endogenous Fe-S protein expression. A
10 coenzyme B12-independent propanediol dehydratase reactivase may be readily identified by one skilled in the art by assessing propanediol dehydratase activity of the associated propanediol dehydratase enzyme in the presence or absence of coenzyme B12. An example is a diol dehydratase reactivase of *Clostridium butyricum* (coding region SEQ ID
15 NO:192; protein SEQ ID NO:193).

Other coenzyme B12-independent propanediol dehydratase reactivases that may be used may be identified through bioinformatics analysis of sequences as compared to that of RdhtB SEQ ID NO:44 by one skilled in the art. Proteins with coenzyme B12-independent
20 propanediol dehydratase reactivase activity and sequence identity to SEQ ID NO:44 of at least about 80%-85%, 85%-90%, 90%-95% or 95%-99% may be used. Particularly suitable are those that are at least about 90% identical to the amino acid sequence as set forth in SEQ ID NO:44 using the Clustal W method of alignment using the default parameters of GAP
25 PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

In addition, other coenzyme B12-independent propanediol dehydratase reactivase homologs that may be used may be identified using the RdhtB coding region (SEQ ID NO:16) by methods as described above
30 for the LEU1 coding region.

Expression of Heterologous Fe-S proteins

Expression is achieved by transforming with a sequence encoding an Fe-S protein. The coding region to be expressed may be codon

optimized for the target host cell, as well known to one skilled in the art. Methods for gene expression in yeast are known in the art (see for example *Methods in Enzymology*, Volume 194, *Guide to Yeast Genetics and Molecular and Cell Biology* (Part A, 2004, Christine Guthrie and Gerald R. Fink (Eds.), Elsevier Academic Press, San Diego, CA).

Expression of genes in yeast typically requires a promoter, operably linked to a coding region of interest, and a transcriptional terminator. A number of yeast promoters can be used in constructing expression cassettes for genes in yeast, including, but not limited to promoters derived from the following genes: *CYC1*, *HIS3*, *GAL1*, *GAL10*, *ADH1*, *PGK*, *PHO5*, *GAPDH*, *ADC1*, *TRP1*, *URA3*, *LEU2*, *ENO*, *TPI*, *CUP1*, *FBA*, *GPD*, *GPM*, and *AOX1*. Suitable transcriptional terminators include, but are not limited to FBA_t, GPD_t, GPM_t, ERG10_t, GAL1_t, *CYC1*, and *ADH1*.

Suitable promoters, transcriptional terminators, and coding regions may be cloned into *E. coli*-yeast shuttle vectors, and transformed into yeast cells. These vectors allow strain propagation in both *E. coli* and yeast strains. Typically the vector used contains a selectable marker and sequences allowing autonomous replication or chromosomal integration in the desired host. Typically used plasmids in yeast are shuttle vectors pRS423, pRS424, pRS425, and pRS426 (American Type Culture Collection, Rockville, MD), which contain an *E. coli* replication origin (e.g., pMB1), a yeast 2 μ origin of replication, and a marker for nutritional selection. The selection markers for these four vectors are His3 (vector pRS423), Trp1 (vector pRS424), Leu2 (vector pRS425) and Ura3 (vector pRS426). Construction of expression vectors with a chimeric gene encoding the described Fe-S protein coding regions may be performed by either standard molecular cloning techniques in *E. coli* or by the gap repair recombination method in yeast.

The gap repair cloning approach takes advantage of the highly efficient homologous recombination in yeast. Typically, a yeast vector DNA is digested (e.g., in its multiple cloning site) to create a "gap" in its sequence. A number of insert DNAs of interest are generated that contain a ≥ 21 bp sequence at both the 5' and the 3' ends that sequentially overlap

with each other, and with the 5' and 3' terminus of the vector DNA. For example, to construct a yeast expression vector for "Gene X", a yeast promoter and a yeast terminator are selected for the expression cassette. The promoter and terminator are amplified from the yeast genomic DNA, and Gene X is either PCR amplified from its source organism or obtained from a cloning vector comprising Gene X sequence. There is at least a 21 bp overlapping sequence between the 5' end of the linearized vector and the promoter sequence, between the promoter and Gene X, between Gene X and the terminator sequence, and between the terminator and the 3' end of the linearized vector. The "gapped" vector and the insert DNAs are then co-transformed into a yeast strain and plated on the medium containing the appropriate compound mixtures that allow complementation of the nutritional selection markers on the plasmids. The presence of correct insert combinations can be confirmed by PCR mapping using plasmid DNA prepared from the selected cells. The plasmid DNA isolated from yeast (usually low in concentration) can then be transformed into an *E. coli* strain, e.g. *TOP10*, followed by mini preps and restriction mapping to further verify the plasmid construct. Finally the construct can be verified by sequence analysis.

Like the gap repair technique, integration into the yeast genome also takes advantage of the homologous recombination system in yeast. Typically, a cassette containing a coding region plus control elements (promoter and terminator) and auxotrophic marker is PCR-amplified with a high-fidelity DNA polymerase using primers that hybridize to the cassette and contain 40-70 base pairs of sequence homology to the regions 5' and 3' of the genomic area where insertion is desired. The PCR product is then transformed into yeast and plated on medium containing the appropriate compound mixtures that allow selection for the integrated auxotrophic marker. For example, to integrate "Gene X" into chromosomal location "Y", the promoter-coding regionX-terminator construct is PCR amplified from a plasmid DNA construct and joined to an autotrophic marker (such as *URA3*) by either SOE PCR or by common restriction digests and cloning. The full cassette, containing the promoter-coding

regionX-terminator-*URA3* region, is PCR amplified with primer sequences that contain 40-70 bp of homology to the regions 5' and 3' of location "Y" on the yeast chromosome. The PCR product is transformed into yeast and selected on growth media lacking uracil. Transformants can be
5 verified either by colony PCR or by direct sequencing of chromosomal DNA.

Any coding regions expressed in the present yeast cells may be codon optimized for expression in the specific host yeast cell being engineered as is well known to one skilled in the art. For
10 example, for expression of the *K. lactis* and *P. stipitis* ILV3 coding regions in *S. cerevisiae*, each was codon optimized for *S. cerevisiae* expression in Example 1 herein.

Product Biosynthesis with improved heterologous Fe-S protein activity

Production of any product that has an Fe-S protein contributing to
15 its biosynthetic pathway may benefit from the improved activity disclosed herein of a heterologous expressed Fe-S protein in a yeast host with reduced endogenous Fe-S protein expression. For example, DHAD provides a step in pathways for biosynthesis of isobutanol, and RdhtB contributes to a biosynthetic pathway to produce 2-butanone or 2-butanol.

20 Biosynthetic pathways including a step performed by DHAD for synthesis of isobutanol are disclosed in commonly owned and co-pending US Patent Application publication US 20070092957 A1, which is herein incorporated by reference. A diagram of the disclosed isobutanol biosynthetic pathways is provided in Figure 1. Production of isobutanol in
25 a strain disclosed herein benefits from increased DHAD activity. As described in US Patent Pub No. US20070092957 A1, steps in an example isobutanol biosynthetic pathway include conversion of:

- pyruvate to acetolactate (Fig.1 pathway step a) as catalyzed for example by acetolactate synthase;
- 30 - acetolactate to 2,3-dihydroxyisovalerate (Fig. 1 pathway step b) as catalyzed for example by acetohydroxy acid isomeroreductase;

- 2,3-dihydroxyisovalerate to α -ketoisovalerate (Fig. 1 pathway step c) as catalyzed for example by acetohydroxy acid dehydratase also called DHAD;

- α -ketoisovalerate to isobutyraldehyde (Fig. 1 pathway step d) as catalyzed for example by branched-chain α -keto acid decarboxylase ;and

- isobutyraldehyde to isobutanol (Fig. 1 pathway step e) as catalyzed for example by branched-chain alcohol dehydrogenase.

The substrate to product conversions, and enzymes involved in these reactions, for steps f, g, h, i, j, and k of alternative pathways are described in US 20070092957 A1.

Genes that may be used for expression of the enzymes for the isobutanol pathways are described in US 20070092957 A1, and additional genes that may be used can be identified by one skilled in the art through bioinformatics or experimentally as described above. The preferred use in all three pathways of ketol-acid reductoisomerase (KARI) enzymes with particularly high activities are disclosed in commonly owned and co-pending US Patent Pub No. US20080261230. Examples of high activity KARIs disclosed therein are those from *Vibrio cholerae* (DNA: SEQ ID NO:35; protein SEQ ID NO:36), *Pseudomonas aeruginosa* PAO1, (DNA: SEQ ID NO:37; protein SEQ ID NO:38), and *Pseudomonas fluorescens* PF5 (DNA: SEQ ID NO:39; protein SEQ ID NO:40).

Additionally described in US 20070092957 A1 are construction of chimeric genes and genetic engineering of yeast, exemplified by *Saccharomyces cerevisiae*, for isobutanol production using the disclosed biosynthetic pathways.

A biosynthetic pathway including propanediol dehydratase for synthesis of 2-butanone and 2-butanol is disclosed in commonly owned and co-pending US Patent Pub No. US20070292927A1, which is herein incorporated by reference. A diagram of the disclosed 2-butanone and 2-butanol biosynthetic pathway is provided in Figure 2. 2-Butanone is the product made when the last depicted step of converting 2-butanone to 2-butanol is omitted. Production of 2-butanone or 2-butanol in a strain disclosed herein benefits from increased coenzyme B12-independent

propanediol dehydratase reactivase activity. As described in US Patent Pub No. US20070292927A1, steps in the disclosed biosynthetic pathway include conversion of:

- pyruvate to acetolactate (Fig 2 step a) as catalyzed for example by acetolactate synthase;
- acetolactate to acetoin (Fig. 2 step b) as catalyzed for example by acetolactate decarboxylase;
- acetoin to 2,3-butanediol (Fig. 2 step i) as catalyzed for example by butanediol dehydrogenase;
- 2,3-butanediol to 2-butanone (Fig. 2 step j) as catalyzed for example by diol dehydratase glycerol dehydratase, or propanediol dehydratase; and
- 2-butanone to 2-butanol (Fig. 2 step f) as catalyzed for example by butanol dehydrogenase.

Genes that may be used for expression of these enzymes are described in US Patent Pub No. US20070292927A1. The use in this pathway in yeast of the butanediol dehydratase from *Roseburia inulinivorans*, *RdhtA*, (protein SEQ ID NO:43, coding region SEQ ID NO:15) is disclosed in commonly owned and co-pending US Patent Pub No. US20090155870. This enzyme is used in conjunction with the butanediol dehydratase reactivase from *Roseburia inulinivorans*, *RdhtB*, (protein SEQ ID NO:44, coding region SEQ ID NO:16). This butanediol dehydratase is desired in many hosts because it does not require coenzyme B₁₂.

Additionally described in US Patent Pub No. US20090155870 are construction of chimeric genes and genetic engineering of yeast for 2-butanol production using the US 20070292927A1 disclosed biosynthetic pathway.

Fermentation Media

Yeasts disclosed herein may be grown in fermentation media for production of a product having an Fe-S protein as part of the biosynthetic pathway. Fermentation media must contain suitable carbon substrates.

Suitable substrates may include but are not limited to monosaccharides such as glucose and fructose, oligosaccharides such as lactose or sucrose, polysaccharides such as starch or cellulose or mixtures thereof and unpurified mixtures from renewable feedstocks such as cheese whey permeate, cornsteep liquor, sugar beet molasses, and barley malt.

5 Additionally the carbon substrate may also be one-carbon substrates such as carbon dioxide, or methanol for which metabolic conversion into key biochemical intermediates has been demonstrated. In addition to one and two carbon substrates methylotrophic organisms are also known to utilize
10 a number of other carbon containing compounds such as methylamine, glucosamine and a variety of amino acids for metabolic activity. For example, methylotrophic yeast are known to utilize the carbon from methylamine to form trehalose or glycerol (Bellion et al., *Microb. Growth C1 Compd.*, [Int. Symp.], 7th (1993), 415-32. Editor(s): Murrell, J. Collin; Kelly, Don P. Publisher: Intercept, Andover, UK). Similarly, various
15 species of *Candida* will metabolize alanine or oleic acid (Sulter et al., *Arch. Microbiol.* 153:485-489 (1990)). Hence it is contemplated that the source of carbon utilized in the present invention may encompass a wide variety of carbon containing substrates and will only be limited by the choice of
20 organism.

Although it is contemplated that all of the above mentioned carbon substrates and mixtures thereof are suitable in the present invention, preferred carbon substrates are glucose, fructose, and sucrose.

In addition to an appropriate carbon source, fermentation media
25 must contain suitable minerals, salts, cofactors, buffers and other components, known to those skilled in the art, suitable for the growth of the cultures and promotion of the enzymatic pathway necessary for production of the desired product.

Culture Conditions

30 Typically cells are grown at a temperature in the range of about 20 °C to about 37 °C in an appropriate medium. Suitable growth media in the present invention are common commercially prepared media such as broth that includes yeast nitrogen base, ammonium sulfate, and dextrose

as the carbon/energy source) or YPD Medium, a blend of peptone, yeast extract, and dextrose in optimal proportions for growing most *Saccharomyces cerevisiae* strains. Other defined or synthetic growth media may also be used and the appropriate medium for growth of the particular microorganism will be known by one skilled in the art of microbiology or fermentation science.

Suitable pH ranges for the fermentation are between pH 3.0 to pH 7.5, where pH 4.5.0 to pH 6.5 is preferred as the initial condition.

Fermentations may be performed under aerobic or anaerobic conditions, where anaerobic or microaerobic conditions are preferred.

The amount of butanol produced in the fermentation medium can be determined using a number of methods known in the art, for example, high performance liquid chromatography (HPLC) or gas chromatography (GC).

15 Industrial Batch and Continuous Fermentations

The present process employs a batch method of fermentation. A classical batch fermentation is a closed system where the composition of the medium is set at the beginning of the fermentation and not subject to artificial alterations during the fermentation. Thus, at the beginning of the fermentation the medium is inoculated with the desired organism or organisms, and fermentation is permitted to occur without adding anything to the system. Typically, however, a "batch" fermentation is batch with respect to the addition of carbon source and attempts are often made at controlling factors such as pH and oxygen concentration. In batch systems the metabolite and biomass compositions of the system change constantly up to the time the fermentation is stopped. Within batch cultures cells moderate through a static lag phase to a high growth log phase and finally to a stationary phase where growth rate is diminished or halted. If untreated, cells in the stationary phase will eventually die. Cells in log phase generally are responsible for the bulk of production of end product or intermediate.

A variation on the standard batch system is the Fed-Batch system. Fed-Batch fermentation processes are also suitable in the present

invention and comprise a typical batch system with the exception that the substrate is added in increments as the fermentation progresses.

Fed-Batch systems are useful when catabolite repression is apt to inhibit the metabolism of the cells and where it is desirable to have limited

5 amounts of substrate in the media. Measurement of the actual substrate concentration in Fed-Batch systems is difficult and is therefore estimated on the basis of the changes of measurable factors such as pH, dissolved oxygen and the partial pressure of waste gases such as CO₂. Batch and Fed-Batch fermentations are common and well known in the art and
10 examples may be found in Thomas D. Brock in *Biotechnology: A Textbook of Industrial Microbiology*, Second Edition (1989) Sinauer Associates, Inc., Sunderland, MA., or Deshpande, Mukund V., *Appl. Biochem. Biotechnol.*, 36:227, (1992), herein incorporated by reference.

Although the present invention is performed in batch mode it is
15 contemplated that the method would be adaptable to continuous fermentation methods. Continuous fermentation is an open system where a defined fermentation medium is added continuously to a bioreactor and an equal amount of conditioned media is removed simultaneously for processing. Continuous fermentation generally maintains the cultures at a
20 constant high density where cells are primarily in log phase growth.

Continuous fermentation allows for the modulation of one factor or any number of factors that affect cell growth or end product concentration. For example, one method will maintain a limiting nutrient such as the carbon source or nitrogen level at a fixed rate and allow all other
25 parameters to moderate. In other systems a number of factors affecting growth can be altered continuously while the cell concentration, measured by media turbidity, is kept constant. Continuous systems strive to maintain steady state growth conditions and thus the cell loss due to the medium being drawn off must be balanced against the cell growth rate in the
30 fermentation. Methods of modulating nutrients and growth factors for continuous fermentation processes as well as techniques for maximizing the rate of product formation are well known in the art of industrial microbiology and a variety of methods are detailed by Brock, *supra*.

The present invention may be practiced using either batch, fed-batch or continuous processes and known modes of fermentation are suitable. Additionally, it is contemplated that cells may be immobilized on a substrate as whole cell catalysts and subjected to fermentation conditions for 1-butanol production.

Methods for Butanol Isolation from the Fermentation Medium

Bioproducted butanol may be isolated from the fermentation medium using methods known in the art. For example, solids may be removed from the fermentation medium by centrifugation, filtration, decantation, or the like. Then, the butanol may be isolated from the fermentation medium, which has been treated to remove solids as described above, using methods such as distillation, liquid-liquid extraction, or membrane-based separation. Because butanol forms a low boiling point, azeotropic mixture with water, distillation can only be used to separate the mixture up to its azeotropic composition. Distillation may be used in combination with another separation method to obtain separation around the azeotrope. Methods that may be used in combination with distillation to isolate and purify butanol include, but are not limited to, decantation, liquid-liquid extraction, adsorption, and membrane-based techniques. Additionally, butanol may be isolated using azeotropic distillation using an entrainer (see for example Doherty and Malone, *Conceptual Design of Distillation Systems*, McGraw Hill, New York, 2001).

The butanol-water mixture forms a heterogeneous azeotrope so that distillation may be used in combination with decantation to isolate and purify the butanol. In this method, the butanol containing fermentation broth is distilled to near the azeotropic composition. Then, the azeotropic mixture is condensed, and the butanol is separated from the fermentation medium by decantation. The decanted aqueous phase may be returned to the first distillation column as reflux. The butanol-rich decanted organic phase may be further purified by distillation in a second distillation column.

The butanol may also be isolated from the fermentation medium using liquid-liquid extraction in combination with distillation. In this method, the butanol is extracted from the fermentation broth using liquid-liquid

extraction with a suitable solvent. The butanol-containing organic phase is then distilled to separate the butanol from the solvent.

Distillation in combination with adsorption may also be used to isolate butanol from the fermentation medium. In this method, the fermentation broth containing the butanol is distilled to near the azeotropic composition and then the remaining water is removed by use of an adsorbent, such as molecular sieves (Aden et al. *Lignocellulosic Biomass to Ethanol Process Design and Economics Utilizing Co-Current Dilute Acid Prehydrolysis and Enzymatic Hydrolysis for Corn Stover*, Report NREL/TP-510-32438, National Renewable Energy Laboratory, June 2002).

Additionally, distillation in combination with pervaporation may be used to isolate and purify the butanol from the fermentation medium. In this method, the fermentation broth containing the butanol is distilled to near the azeotropic composition, and then the remaining water is removed by pervaporation through a hydrophilic membrane (Guo et al., *J. Membr. Sci.* 245, 199-210 (2004)).

EXAMPLES

The present invention is further defined in the following Examples. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various uses and conditions.

General Methods

Standard recombinant DNA and molecular cloning techniques used in the Examples are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, NY

(1989) (Maniatis) and by T. J. Silhavy, M. L. Bannan, and L. W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1984) and by Ausubel, F. M. *et al.*, *Current Protocols in Molecular Biology*, pub. by Greene Publishing Assoc. and
5 Wiley-Interscience (1987), and by *Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

Materials and methods suitable for the maintenance and growth of bacterial cultures are well known in the art. Techniques suitable for use in the following Examples may be found as set out in *Manual of Methods for*
10 *General Bacteriology* (Phillipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds), American Society for Microbiology, Washington, DC. (1994)) or by Thomas D. Brock in *Biotechnology: A Textbook of Industrial Microbiology*, Second Edition, Sinauer Associates, Inc., Sunderland, MA
15 (1989). All reagents, restriction enzymes and materials used for the growth and maintenance of microbial cells were obtained from Aldrich Chemicals (Milwaukee, WI), BD Diagnostic Systems (Sparks, MD), Life Technologies (Rockville, MD), or Sigma Chemical Company (St. Louis, MO) unless otherwise specified. Microbial strains were obtained from The
20 American Type Culture Collection (ATCC), Manassas, VA, unless otherwise noted. All the oligonucleotide primers were synthesized by Sigma-Genosys (Woodlands, TX) or Integrated DNA Technologies (Coralsville, IA).

Synthetic complete medium is described in Amberg, Burke and
25 Strathern, 2005, *Methods in Yeast Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

HPLC

Analysis for fermentation by-product composition is well known to those skilled in the art. For example, one high performance liquid
30 chromatography (HPLC) method utilizes a Shodex SH-1011 column with a Shodex SH-G guard column (both available from Waters Corporation, Milford, MA), with refractive index (RI) detection. Chromatographic separation is achieved using 0.01 M H₂SO₄ as the mobile phase with a

flow rate of 0.5 mL/min and a column temperature of 50 °C. Isobutanol retention time is 47.6 minutes.

The meaning of abbreviations is as follows: “s” means second(s), “min” means minute(s), “h” means hour(s), “psi” means pounds per square inch, “nm” means nanometers, “d” means day(s), “μL” means microliter(s), “mL” means milliliter(s), “L” means liter(s), “mm” means millimeter(s), “nm” means nanometers, “mM” means millimolar, “M” means molar, “mmol” means millimole(s), “μmol” means micromole(s), “g” means gram(s), “μg” means microgram(s) and “ng” means nanogram(s), “PCR” means
10 polymerase chain reaction, “OD” means optical density, “OD₆₀₀” means the optical density measured at a wavelength of 600 nm, “kDa” means kilodaltons, “g” means the gravitation constant, “bp” means base pair(s), “kbp” means kilobase pair(s), “% w/v” means weight/volume percent, % v/v” means volume/volume percent, “wt %” means percent by weight,
15 “HPLC” means high performance liquid chromatography, and “GC” means gas chromatography. The term “molar selectivity” is the number of moles of product produced per mole of sugar substrate consumed and is reported as a percent.

Example 1

Expression of DHAD from *K. lactis* in *LEU1* deletion strain of *S. cerevisiae*

The yeast *LEU1* gene encodes isopropylmalate dehydratase, an enzyme that requires an Fe-S cluster for its function. The impact of *LEU1* deletion on DHAD activity expressed from the *Kluyveromyces lactis* DHAD coding region was examined in this example. For gene expression in yeast, the shuttle vector pNY13 (SEQ ID NO:29) derived from pRS423 was used. This shuttle vector contained an F1 origin of replication (1423 to 1879) for maintenance in *E. coli* and a 2 micron origin (nt 7537 to 8881) for replication in yeast. The vector has an FBA promoter (nt 2111 to 3110) and FBA terminator (nt 4316 to 5315). In addition, it carries the *HIS3* marker (nt 504 to 1163) for selection in yeast and ampicillin resistance marker (nt 6547 to 7404) for selection in *E. coli*. pNY9 is the same vector with a *URA3* marker replacing the *HIS3* marker.

The *ILV3* coding region for DHAD from *Kluyveromyces lactis* was synthesized with codon-optimization for expression in *S. cerevisiae* by DNA 2.0 (Menlo Park, CA). The cloned synthesized sequence was PCR amplified. During amplification, a portion of the mitochondrial signal peptide for the DHAD at the N-terminus was deleted by using *ilv3(K)(0)-F(delet)* as the forward primer with *ilv3(K)(o)-R* as the reverse primer, resulting in a coding region for cytoplasmic expression (SEQ ID NO:173). In addition, an *SphI* site was incorporated in the forward primer, while a *NotI* site was included in the reverse primer. The PCR product was cloned into the shuttle vectors pNY9 and pNY13 so that the *ILV3* coding region was under the control of the FBA promoter. Both PCR product and each vector (pNY9, pNY13) were digested with *SphI* and *NotI*. After digestion, the components were ligated, and the ligation mixture was transformed into TOP10 competent cells (Invitrogen). Transformants were selected in LB agar plates supplemented with 100 µg/ml of ampicillin. Positive clones were screened by PCR with the forward and reverse primers described above. The resulting plasmids were designated as pRS423::FBAp-*ILV3*(KL) and pRS426::FBAp-*ILV3*(KL), derived from plasmids pNY13 and pNY9, respectively.

To study the expression of the DHAD from *K. lactis* in *S. cerevisiae* the expression vector pRS423::FBAP-*ILV3*(KL) along with an empty vector pRS426 were transformed into strains BY4743 and BY4743 *leu1::kanMX4* (ATCC 4034377). The competent cell preparation and transformation were based on the Frozen Yeast Transformation kit from Zymo Research. The transformants were selected on agar plates with yeast synthetic medium lacking histidine and uracil (Teknova). For enzymatic assays, the strains carrying the expression construct and the empty vector pRS426 were first grown overnight in 5 ml synthetic complete yeast medium lacking histidine and uracil. The 5 ml overnight cultures were transferred into 100 ml of medium in a 250 ml flask. The cultures were harvested when they reached 1 to 2 O.D. at 600 nm. The samples were washed with 10 ml of 20 mM Tris (pH 7.5) and then resuspended in 1 ml of the same Tris buffer. The samples were transferred into 2.0 ml tubes containing 0.1 mm silica (Lysing Matrix B, MP biomedical). The cells were then broken in a bead-beater (BIO101). The supernatant was obtained by centrifugation in a microfuge at 13,000 rpm at 4°C for 30 minutes. Typically, 0.06 to 0.1 mg of crude extract protein was used in a DHAD assay. Protein in the crude extracts was determined by Bradford assay with Coomassie stain.

Dihydroxy-acid dehydratase enzyme assay

The *in vitro* DHAD enzyme assay is a variation on the assay described in Flint et al. (J. Biol. Chem. (1993) 268:14732–14742.). The assay was performed in a 1.6 ml total volume and consisted of: 800 µl 2X buffer (100mM Tris pH 8.0, 20mM MgCl₂), 160 µl 10X substrate (15.6 mg/ml dihydroxyisovalerate), crude extract (typically 50-200 µg protein), and water. The reaction was incubated at 37°C. At 0, 30, 60, and 90 minute time intervals, 350 µl aliquots of the reaction were removed and incubated with 350 µl of 0.05% dinitrophenylhydrazine in 1N HCl for 30 minutes at 25°C. To quench the reaction, 350 µl of 4N sodium hydroxide was added to the reaction mixture, and the reaction was centrifuged at 15,000 x g for 2 minutes. The supernatant was transferred to a plastic

disposable cuvette and absorbance at 540 nm was measured in a spectrophotometer. The amount of α -ketoisovalerate (KIV) produced was determined by entering the absorbance into the linear regression equation obtained from a standard curve of α -ketoisovalerate. The amount of KIV
5 produced at each time point was plotted to determine the rate of production. The slope of the linear regression was then used to calculate specific activity using the formula:

Specific activity calculation = (slope of KIV production/1000) / mg
protein per 1.6 mL reaction = mmol/min * mg

10 The dehydratase from *K. lactis* had a specific activity in the range of 0.2 to 0.35 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ when expressed in yeast strain BY4743 (Δleu1). In contrast, this enzyme had a specific activity in the range of only 0.14 $\mu\text{mol min}^{-1} \text{mg}^{-1}$ when expressed in the parent yeast strain BY4743. Strains BY4743 (Δleu1) and wildtype BY4743 containing empty
15 vectors pRS423 or pRS426 had a background of activity in the range of 0.03 to 0.1 $\mu\text{mol min}^{-1} \text{mg}^{-1}$.

Example 2

Expression of diol dehydratase in *LEU1* deletion strain of *S. cerevisiae*

20 A coenzyme B12-independent propanediol dehydratase is disclosed in commonly owned and co-pending US Patent Pub No. US20090155870. The sequences encoding this coenzyme B12-independent (S-adenosylmethionine (SAM)-dependent) propanediol dehydratase (SEQ ID NO:15) and its putative associated reactivase (SEQ
25 ID NO:16) in the bacterium *Roseburia inulinivorans* [Scott *et al.*(2006) *J. Bacteriol.*188:4340-9], hereafter referred to as *rdhtA* and *rdhtB*, respectively, were synthesized as one DNA fragment (SEQ ID NO:17) by standard methods and cloned into an *E. coli* vector (by DNA2.0, Inc., Menlo Park, CA). This clone was used as a PCR template to prepare
30 separate RdhtA and RdhtB coding region fragments. The RdhtA coding region for the diol dehydratase was amplified by PCR using primers N695 and N696 (SEQ ID NOs:18 and 19). The RdhtB coding region for the diol dehydratase activase, was amplified by PCR using primers N697 and

N698 (SEQ ID NOs:20 and 21). The two DNA fragments were combined with a dual terminator DNA fragment (SEQ ID NO:22) that has an ADH terminator (SEQ ID NO:23) and a CYC1 terminator (SEQ ID NO:24) adjacent to each other in opposing orientation using SOE PCR (Horton et al. (1989) Gene 77:61-68). The dual terminator fragment was isolated as a 0.6 kb fragment following *PacI* digestion of pRS426::FBA-ILV5+GPM-kivD (described in co-owned and co-pending US Patent Publication 20070092957 A1, Example 17). The resulting 4 kb DNA fragment had the RdhtA and RdhtB coding regions in opposing orientation on either side of the dual terminator, with the 3' end of each coding region adjacent to the dual terminator sequence. This DNA fragment was then cloned by gap repair methodology (Ma et al. (1987) Genetics 58:201-216) into the *S. cerevisiae* shuttle vector pRS426::FBA-ILV5+GPM-kivD that was prepared by digestion with *BbvCI* to remove the *ILV5* and *kivD* coding regions and dual terminator sequence between their 3' ends. The resulting plasmid, pRS426::RdhtAB (below), contained the RdhtA gene under the control of the *S. cerevisiae* FBA promoter (SEQ ID NO:25) and the RdhtB gene under control of the *S. cerevisiae* GPM promoter (SEQ ID NO:26).

Plasmids pRS426 and pRS426::RdhtAB were introduced into *S. cerevisiae* strains BY4743 (ATCC 201390) and BY4743 *leu1::kanMX4* (ATCC 4034377) by standard techniques (*Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 201-202). Cells were plated on synthetic complete medium lacking uracil to select for transformants. Transformants were tested for diol dehydratase activity using an *in vivo* assay as follows. Patched cells grown on solid medium were used to inoculate liquid media (20 ml) in petri plates. Media used were synthetic complete minus uracil with and without addition of 5 g/L 1,2-propanediol 9Aldrich Cat. No. 398039). The petri plates were transferred to an Anaeropack™ System jar (Mitsubishi Gas Chemical Co. Cat. No.50-70). An anaerobic environment (<0.1% oxygen) was generated using Pack-Anaero sachets (Mitsubishi Gas Chemical Co. Cat. No. 10-01). After 48 hours, culture supernatants were sampled, filtered and analyzed by HPLC as described in General Methods.

Propanol, which has a retention time of 38.8 minutes, was observed in culture supernatants of strains carrying pRS426::RdhtAB when 1,2-propanediol was provided in the medium. The results given in Table 5 show that more propanol was produced in the supernatants of the strain also carrying the LEU1 deletion than in the strain without the LEU1 deletion. Statistical analysis gave a P score of less than 0.0005.

Table 5. Propanol production with propanediol dehydratase/reactivase expression in yeast with and without LEU1 knockout.

Strain	1,2-propanediol Added	Propanol Peak Area
BY4743 Δ leu1::kanMX4/pRS426::RdhtAB	5 g/L	19472 $\pm$ 1403 (n=6)
BY4743 Δ leu1::kanMX4/pRS426::RdhtAB	0 g/L	2478 (n=1)
BY4743 /pRS426::RdhtAB	5 g/L	11830 $\pm$ 1963 (n=6)
BY4743 /pRS426::RdhtAB	0 g/L	2369 (n=1)
BY4743 Δ leu1::kanMX4/pRS426	5 g/L	2633 (n=1)
BY4743 /pRS426	5 g/L	2841 (n=1)

10

Example 3:

Improving cytosolic dihydroxy-acid dehydratase (DHAD) activity in *S. cerevisiae* through a disruption of mitochondrial *ILV3*

Vector/host construction

15 In *S. cerevisiae* *ILV3* encodes the mitochondrial dihydroxy-acid dehydratase that is involved in branched chain amino acid biosynthesis. To reduce background from endogenous *ILV3* expression for *in vitro* enzymatic assays in *S. cerevisiae*, an *ilv3::URA3* disruption cassette was constructed by PCR amplification of the *URA3* marker from pRS426
20 (ATCC No. 77107) with primers "ILV3::URA3 F" and "ILV3::URA3 R", given as SEQ ID NO:30 and 31. These primers produced a 1.4 kb *URA3* PCR product that contained 70 bp 5' and 3' extensions identical to

sequences upstream and downstream of the *ILV3* chromosomal locus for homologous recombination. The PCR product was transformed into BY4741 cells (ATCC 201388) using standard genetic techniques (*Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 201-202) and resulting transformants were maintained on synthetic complete media lacking uracil and supplemented with 2% glucose at 30°C. Transformants were screened by PCR using primers "ILV3 F Check" and "URA3 REV Check", given as SEQ ID NOs:32 and 33, to verify integration at the correct site and disruption of the endogenous *ILV3* locus. The correct transformants had the genotype: BY4741 *ilv3::URA3*.

Construction of plasmid pRS423::FBAP-*ILV3*(KL) and pRS426::FBAP-*ILV3*(KL) were described in Example 1. Construction of pRS423::CUP1-*alsS*+FBA-*ILV3* has been described in co-owned and co-pending US Patent Publication US20070092957 A1, Example 17 which is herein incorporated by reference. pRS423::CUP1-*alsS*+FBA-*ILV3* is the same plasmid as pRS423::CUP1p-*alsS*-FBAP-*ILV3*. This construction contains a chimeric gene containing the *S. cerevisiae* CUP1 promoter (SEQ ID NO:34), *alsS* coding region from *Bacillus subtilis* (SEQ ID NO:27), and CYC1 terminator (SEQ ID NO:24); and also a chimeric gene containing the *S. cerevisiae* FBA promoter (SEQ ID NO:25), *ILV3* coding region from *S. cerevisiae* lacking the mitochondrial targeting signal coding sequence (SEQ ID NO:111) and ADH1 terminator (SEQ ID NO:23).

Preparation of samples

Plasmid vectors pRS423::CUP1p-*alsS*-FBAP-*ILV3* and pRS423::FBAP-*ILV3*(KL) were transformed into strain BY4741 *ilv3::URA3* using standard genetic techniques (*Methods in Yeast Genetics*, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) and maintained on synthetic complete media lacking histidine. Plasmid vectors pRS423::CUP1p-*alsS*-FBAP-*ILV3* and pRS426::FBAP-*ILV3*(KL) were also transformed into strain BY4741. Aerobic cultures were grown in 1000 ml flasks containing 200 ml synthetic complete media lacking histidine and supplemented with 2% glucose in an Innova4000 incubator (New

Brunswick Scientific, Edison, NJ) at 30°C and 225 rpm. Cultures were harvested at OD600 measurements of 1.0-2.0 and pelleted by centrifugation at 6000 x *g* for 10 minutes. Cell pellets were washed with 10 mM Tris-HCl, pH 8.0 and pellets were stored at -80°C until assayed for activity. Cell free extracts were prepared by standard bead beating method using 1 ml of 0.5 mm beads and 1.5 ml of yeast cell suspension. Protein concentration in the extracts was determined by Bradford assay with Coomassie stain. DHAD enzyme assays and specific activity calculations were performed as described in Example 1. The results given in Table 6 show that there was higher DHAD activity in the *ILV3* deletion cells than in cells without the *ILV3* deletion.

Table 6. DHAD activity in yeast with and without *ILV3* deletion.

Strain	Specific Activity ($\mu\text{mol}/\text{min}\cdot\text{mg}$)	Average Specific Activity ($\mu\text{mol}/\text{min}\cdot\text{mg}$)
BY4741	0.018	0.013
	0.014	
	0.008	
BY4741 pRS423::CUP1p- <i>alsS</i> -FBAP- <i>ILV3</i>	0.018	0.019
	0.020	
BY4741 pRS426::FBAP- <i>ILV3</i> (KL)	0.040	0.038
	0.036	
BY4741 <i>ilv3</i> :: <i>URA3</i>	0.00006	0.00041
	0.00075	
BY4741 <i>ilv3</i> :: <i>URA3</i> pRS423::CUP1p- <i>alsS</i> -FBAP- <i>ILV3</i>	0.030	0.029
	0.028	
BY4741 <i>ilv3</i> :: <i>URA3</i> pRS423::FBAP- <i>ILV3</i> (KL)	0.317	0.281
	0.244	

15 Verification of alpha-ketoisovalerate formation by HPLC

Formation of alpha-ketoisovalerate from the *in vitro* DHAD enzyme assays was accomplished using HPLC and semicarbizide derivatization. DHAD enzyme assays were performed in a 1.6 ml total volume and consisted of: 800 μl 2X buffer (100mM Tris pH 8.0, 20mM MgCl_2), 160 μl 10X substrate (15.6 mg/ml dihydroxyisovalerate), crude extract (typically 50-200 μg protein), and water. The reactions were incubated at 37°C. At

time intervals of zero and 90 minutes 350 μ l aliquots of the reactions were removed, transferred to ice, and centrifuged at 13,000 x *g* for 2 minutes at 4°C to remove precipitated protein. The supernatants were transferred to ice-chilled Microcon YM-10 (Sigma) spin columns and centrifuged at

5 13,000 x *g* for 20 minutes at 4°C to remove enzymes and soluble proteins. The flowthroughs were mixed with 100 μ l derivatizing reagent (1% semicarbazide hydrochloride and 1.5% sodium acetate trihydrate) and incubated at room temperature for 15 minutes. The reactions were spun through CoStar spin filters (CoStar, 0.22 μ m filter) at 13,000 x *g* for 5

10 minutes at 4°C to remove any precipitates. The flowthroughs were transferred to HPLC vials for analysis.

Analysis of derivatized alpha-ketoisovalerate was conducted using reverse phase chromatography on a Supelco LC-18 column with Superguard LC-18-DB guard column (Supelco; 25 cm x 4.6 mm, 5 μ m).

15 Injection volumes were 10 μ l. Mobile phases were methanol (A) and 50 mM NaOAc pH 7.2. The gradient program utilized is given in Table 7, with detection at 250 nm.

Table 7. Gradient used for derivatized alpha-ketoisovalerate HPLC assay

Time (min)	Flow (ml/min)	% NaOAc (50mM)	% MEOH	Curve
Initial	1.0	95	5	
5	1.0	95	5	6
20	1.0	70	30	6
21	1.0	0	100	6
25	1.0	0	100	6
26	1.0	95	5	6
35	1.0	95	5	6

20 The retention time of semicarbazide-derivatized alpha-ketoisovalerate was 11.5 minutes.

The results, which are given in Table 8, confirmed that KIV was produced in the cells, as detected in the indirect assay for specific activity

25 above. The amount of KIV listed in the DHAD Assay column is the amount determined indirectly in the 90 min sample for the activity assay described

above in determining the specific activity. This amount of KIV correlates well with the amount detected in the HPLC assay.

Table 8. Comparison of KIV detected in DHAD activity assay and by HPLC.

Strain	keto-isovalerate production (μ M)	
	DHAD Assay	HPLC
BY4741 <i>ilv3::URA3</i> pRS423::FBAP- <i>ILV3</i> (KL)	256	256
BY4741 <i>ilv3::URA3</i> pRS423::FBAP- <i>ILV3</i> (KL)	162	163

5

Table 9

HMMER2.0 [2.2g]
NAME dhad_for_hmm
LENG 564
ALPH Amino
MAP yes
COM /app/public/hmmer/current/bin/hmmbuild -F dhad-exp_hmm dhad_for_hmm.aln
COM /app/public/hmmer/current/bin/hmmcalibrate dhad-exp_hmm
NSEQ 8
DATE Tue Jun 3 10:48:24 2008
XT -8455 -4 -1000 -1000 -8455 -4 -8455 -4
NULT -4 -8455

Program name and version
Name of the input sequence alignment file
Length of the alignment: include indels
Type of residues
Map of the match states to the columns of the alignment
Commands used to generate the file: this one means that hmmbuild (default parameters) was applied to the alignment file
Commands used to generate the file: this one means that hmmcalibrate (default parameters) was applied to the hmm profile
Number of sequences in the alignment file
When was the file generated

The transition probability distribution for the null model (single G state).
The symbol emission probability distribution for the null model (G state); consists of K (e.g. 4 or 20) integers. The null probability
The extreme value distribution parameters μ and λ respectively; both floating point values. Lambda is positive and nonzero. These
values are set when the model is calibrated with hmmcalibrate.

NULE 595 -1558 85 338 -294 453 -1158 197 249 902 -1085 -142 -21 -313 45 531 201 384 -195 used to convert these back to model probabilities is 1/K.

EVD -499.650970 0.086142

values are set when the model is calibrated with hmmcalibrate.

HMM	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	Position in alignment
	m->m	m->i	m->d	i->m	i->i	d->m	d->d	b->m	m->e												
	-538 *		-1684																		
1(M)	-233	-1296	99	1223	-1477	-1132	89	-1122	420	-1248	1757	1553	-1296	464	-24	-190	-188	-838	-1578	-985	6
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378	-538 *													
2(E)	-220	-1288	232	1356	-1807	1016	-70	-1474	190	-1584	-775	132	-1298	300	-282	-183	1140	-1092	-1872	-1262	7
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378 *	*													
3(K)	-448	-1932	1558	658	-2220	-1048	40	-1983	1569	-1938	-1091	1558	-1319	450	-193	-278	-419	-1552	-2121	-1397	8
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378 *	*													
4(V)	-404	-498	-1497	-939	-588	-1810	-640	1591	914	-127	335	-962	-1866	-562	-767	-868	-357	1720	-1169	-763	9
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378 *	*													
5(E)	-265	-1340	-52	1376	-1572	-1189	113	-1125	1345	-1287	-496	99	-1321	505	198	-218	-205	597	-1598	-1032	10
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378 *	*													
6(S)	256	-397	-1014	-830	-1841	-646	-862	-1443	-767	-1740	-963	-568	-1249	-651	-1007	2267	1586	-862	-2080	-1672	11
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-29	-6203	-7245	-894	-1115	-701	-1378 *	*													
7(M)	-990	-889	-2630	157	-513	-2514	-1346	1309	-1767	820	3683	-1898	-2491	-1496	-1799	-1589	-925	150	-1336	-1041	12
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378 *	*													
8(E)	588	-1875	-194	1536	-2188	-1373	-59	-1931	957	-1890	-977	904	292	393	-162	483	-372	-1495	-2070	-1391	13
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378 *	*													

Table 9

9(N)	-514	-1116	1207	-315	447	-1650	-304	-778	-224	825	-277	1457	-1738	-123	-618	-627	-454	-603	-1186	763	14
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
10(N)	-815	-1190	-1360	-922	-904	-1967	-797	-442	-670	381	1700	3009	-2099	-654	-934	-1051	-791	-445	-1490	-979	15
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
11(K)	-1530	-2498	-1722	-855	-3141	-2246	-428	-2627	2828	-2404	-1656	-927	662	-2	2047	-1421	-1337	-2324	-2357	-2081	16
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
12(Y)	-872	-1887	-861	-290	-1369	-1801	1662	-1797	325	-1793	-1031	893	-1876	56	2219	-812	-780	-1514	-1565	2287	17
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
13(S)	-830	-1586	-1471	-1099	-2717	-1642	-1010	-2479	-266	-2518	-1746	-1065	-2069	-676	1822	2748	-1000	-1950	-2597	-2189	18
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
14(Q)	-851	-2131	-775	-153	-2554	-1735	-211	-2205	1908	-2094	-1244	-386	-1802	2254	974	1001	-747	-1819	-2181	-1667	19
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
15(T)	-405	-1258	-618	-100	-1490	-1466	1158	-1121	1	-1299	-514	578	-1607	65	-433	960	1849	343	-1677	-1143	20
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
16(I)	-1772	-1325	-4307	-3877	-1405	-3993	-3383	2935	-3705	820	-217	-3632	-3761	-3400	-3682	-3260	-1742	2033	-2838	-2525	21
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
17(T)	-1018	-1329	-2004	-1771	-409	-1993	-1000	-1256	-1512	-1464	-966	-1543	-2367	-1428	-1638	-1257	3050	-1090	-1012	2448	22
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
18(Q)	-1509	-3056	1970	44	-3310	-1666	-896	-3242	-877	-3158	-2439	-322	-2123	3562	-1493	-1259	-1550	-2779	-3260	-2446	23
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
19(D)	-1006	-2199	2178	-88	-3159	1997	-936	-2974	-948	-2977	-2174	-382	-1960	-589	-1571	1295	-1157	-2369	-3178	-2430	24
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
20(M)	445	-796	-1082	-521	-841	-1643	-412	-403	-370	-692	2213	-646	536	1166	-698	-830	660	831	-1204	-767	25
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

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Table 9

221(Q)	741	-990	-1025	-507	-1249	-1551	-519	-720	-357	-1062	-345	-635	-1739	1770	-713	-589	1576	1129	-1559	-1097	26
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
22(R)	-1753	-2648	-2072	-1047	-3365	-2405	-452	-2782	1989	-2495	-1773	-1062	-2379	2402	2643	-1629	-1506	-2504	-2397	-2190	27
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
23(S)	-330	-1010	-1820	-1628	-2778	-1229	-1652	-2481	-1592	-2691	-1841	-1273	2130	-1426	-1834	2449	1034	-1716	-2961	-2594	28
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
24(P)	1882	-1119	-2231	-2302	-3062	-1360	-2209	-2710	-2339	-3013	-2243	-1676	3304	-2117	-2409	-742	-918	-1916	-3263	-3022	29
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
25(N)	969	-1230	-1066	-915	-2593	-1313	-1196	-2242	-1033	-2447	-1626	3197	-1850	-898	-1392	-582	1155	-1644	-2736	-2256	30
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
26(R)	-1847	-2640	-2014	-1161	-3282	-2428	-579	-2818	687	-2553	-1869	-1165	-2462	2447	3181	-1746	-1630	-2555	-2447	-2228	31
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
27(A)	3048	-932	-2480	-2533	-3075	-1200	-2274	-2765	-2501	-3071	-2221	-1658	-1948	-2205	-2512	1225	-739	-1842	-3322	-3078	32
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
28(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	33
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
29(Y)	-1674	-1506	-2863	-2464	596	-2872	2251	-972	-2024	2197	-552	-1986	-2876	-1739	-1988	-1987	-1601	-1002	-95	2332	34
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
30(Y)	-2013	-2305	-2428	-1781	-328	-2709	-654	-2240	-258	-2064	-1626	-1631	-2788	-899	2789	-2017	-1896	-2130	-857	3434	35
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
31(A)	2822	-1031	-2418	-2539	-3226	1898	-2364	-2941	-2626	-3229	-2379	-1722	-2026	-2302	-2634	-654	-848	-1983	-3415	-3226	36
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
32(I)	-1247	-941	-3569	-3039	-1082	-3101	-2185	2227	-2763	766	-76	-2700	-3050	-2469	-2697	-2253	1322	1974	-1988	-1633	37
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
33(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	38
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

[illegible]

Table 9

46(U)	-1759	-1303	-4330	-3968	-1751	-4051	-3743	3027	-3837	-597	-528	-3729	-3875	-3688	-3910	-3369	-1751	2438	-3259	-2819	51
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
47(V)	1736	-1012	-3546	-3078	-1377	-3073	-2434	2052	-2843	-608	-331	-2754	-3122	-2619	-2855	-2270	-1277	2193	-2333	-1941	52
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
48(N)	-686	-1511	-702	-806	-2927	-1386	-1339	-2841	-1264	-2950	-2137	2702	-1979	-1062	-1648	2444	-971	-2105	-3054	-2475	53
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
49(M)	-411	-857	-1800	-1434	-1528	1914	-1202	-1029	-1247	-1347	2989	-1217	-1912	-1119	-1444	-676	1550	-767	-1922	-1539	54
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
50(W)	-782	-1258	793	-683	1193	346	2051	-932	-556	-1092	-441	-798	-1993	-426	-909	-904	-720	-779	3163	1546	55
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
51(W)	1009	-798	-1470	-935	-463	-1773	-545	-460	-751	-736	-66	-943	-1904	-606	-1002	1604	-507	-322	2535	1521	56
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
52(D)	-1137	-2711	2125	1647	-2995	-1523	-617	-2786	-528	-2743	-1933	-150	-1897	-234	-1165	-924	2117	-2331	-2948	-2141	57
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
53(I)	-599	-1102	-1031	-829	-1522	1429	-927	2119	-880	-1369	-699	1692	-1938	-759	-1188	-799	-698	-689	-1887	-1419	58
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
54(T)	-666	-1412	-954	-984	-2702	-1428	-1357	-2418	-1208	-2650	-1886	2293	-2000	-1101	-1519	-787	2967	-1835	-2866	-2360	59
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
55(P)	-632	-1230	-2074	-2144	-2996	-1453	-2116	-2631	-2128	-2928	-2213	-1658	3610	-2006	-2221	-852	1302	-1931	-3185	-2917	60
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
56(C)	-2476	5735	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3464	-3718	61
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
57(N)	-2171	-2655	-1458	-1748	-3334	-2364	-2267	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	62
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
58(M)	672	-918	-3119	-2578	-742	-2668	-1734	1807	-2263	16	3713	-2271	-2704	-1960	-2216	-1806	-1058	493	-1612	-1306	63
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

71(V)	-1760	-1333	-4244	-3789	-1262	-3902	-3190	1495	-3588	1270	-96	-3536	-3677	-3238	-3534	-3148	-1725	2865	-2654	-2373	76
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
72(W)	-1054	-2172	-1112	-403	-2566	-1917	-286	-2196	2516	-2095	-1292	1183	-1958	140	1333	-959	-922	-1867	2591	-1720	77
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
73(D)	611	-1995	1525	937	-2295	-1400	-148	-2043	211	-2006	-1106	-37	-1553	1420	-312	-408	1235	-1609	-2193	-1499	78
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
74(A)	2716	-902	-2380	-2205	-2799	-1197	-1975	-2459	-2081	-2736	-1895	-1520	-1895	-1844	-2201	1191	1299	-1669	-3045	-2758	79
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
75(G)	-1709	-2833	2424	-409	-3781	2819	-1457	-3777	-1728	-3733	-3076	-739	-2389	-1180	-2441	-1557	-1893	-3158	-3660	-3038	80
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-212	-2909	-8150	-273	-2534	-701	-1378*	*													
76(A)	2529	-1119	-2614	-2330	-1245	-1983	-1829	-377	-2042	1435	-341	-1937	-2411	-1873	-2088	-1266	-1059	-397	-2063	-1713	82
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
77(W)	-472	-361	-2421	-1812	-298	-1979	-826	1164	-1486	-143	2485	873	-2028	-1185	-1426	-1048	-412	1116	2999	-454	83
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
78(P)	-1198	-1737	-2187	-2394	-3665	2006	-2550	-3630	-2743	-3756	-3008	-2052	3474	-2495	-2835	-1401	-1593	-2736	-3511	-3519	84
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
79(Q)	-999	-1075	-2106	-1568	-726	-2370	-1175	83	-1185	1373	218	-1566	-2400	2445	-1340	-1445	-946	1441	-1501	-1146	85
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
80(Q)	-885	-779	-2609	-2018	-481	-2414	-1253	1645	-1736	799	1924	-1827	-2405	2262	-1752	-1484	-821	802	-1240	-935	86
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
81(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	87
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
82(G)	-998	-2100	-120	-175	-2567	2528	2174	-2558	-587	-2583	-1806	1422	-1966	-461	-1038	-925	-1088	-2095	-2657	-1948	88
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
83(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	89
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

96(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	102
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
97(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	103
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
98(R)	-2097	-2786	-2688	-1415	-3622	-2625	-555	-2964	2585	-2627	-1957	-1318	-2577	-137	3015	-1979	-1791	-2732	-2469	-2363	104
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
99(Y)	-3615	-2706	-4169	-4413	2626	-4044	-396	-2535	-3993	-1939	-1985	-2747	-3930	-2852	-3446	-3296	-3494	-2686	347	4252	105
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
100(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	106
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
101(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	107
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
102(V)	-1381	-1065	-3714	-3252	-1453	-3300	-2646	1872	-3023	-615	-373	-2949	-3287	-2816	-3039	-2506	1346	2750	-2489	-2087	108
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
103(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	109
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
104(R)	-2957	-3022	-3318	-2735	-3796	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	110
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
105(E)	-1719	-3572	2596	2779	-3767	-1632	-993	-3700	-1241	-3578	-2920	-234	-2167	-666	-2090	-1380	-1789	-3182	-3742	-2756	111
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
106(V)	-1746	-1296	-4308	-3946	-1757	-4020	-3712	2190	-3811	-614	-539	-3702	-3858	-3667	-3884	-3336	-1740	3098	-3250	-2803	112
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
107(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	113
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
108(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	114
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

121(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	127
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
122(G)	2142	-930	-2334	-2298	-3100	2237	-2139	-2842	-2302	-3074	-2187	-1557	-1909	-2010	-2397	1136	-701	-1871	-3308	-3053	128
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
123(V)	-1514	-1144	-3950	-3459	1821	-3487	-2577	2274	-3208	-209	-87	-3112	-3362	-2864	-3118	-2680	-1476	2426	-2194	-1786	129
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
124(V)	-1743	-1294	-4292	-3873	-1511	-3988	-3433	2287	-3712	598	-319	-3626	-3774	-3456	-3716	-3260	-1717	2790	-2931	-2577	130
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
125(A)	2911	-954	-2808	-2665	-2115	-1577	-2196	-575	-2445	-1646	-1202	-1906	-2208	-2218	-2451	-901	-876	1294	-2727	-2394	131
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
126(I)	-1764	-1323	-4298	-3936	-1668	-3994	-3655	3337	-3783	-508	-462	-3689	-3838	-3608	-3835	-3311	-1759	1847	-3164	-2747	132
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
127(G)	-1157	-1705	-2169	-2375	-3654	3021	-2534	-3611	-2730	-3741	-2984	-2024	2418	-2475	-2826	-1361	-1555	-2705	-3513	-3509	133
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
128(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	134
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
129(C)	-2476	-5735	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3464	-3718	135
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
130(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	136
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
131(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	137
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
132(N)	-2171	-2655	-1458	-1748	-3334	-2364	-2267	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	138
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
133(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	139
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

146(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	152
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
147(S)	1568	-940	-2267	-2192	-3082	1101	-2068	-2826	-2185	-3049	-2159	-1515	-1901	-1915	-2313	2603	-694	-1866	-3279	-3006	153
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
148(I)	-1880	-1492	-4195	-3728	-963	-3841	-2991	3272	-3425	246	2277	-3490	-3613	-3014	-3317	-3092	-1841	628	-2385	-2163	154
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
149(F)	-2204	-1797	-3724	-3473	3206	-3383	-628	-1077	-3092	-746	3167	-2502	-3309	-2372	-2792	-2535	-2120	-1245	28	2460	155
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
150(V)	1265	-1028	-3200	-2994	-1833	-2150	-2480	417	-2771	-1122	-818	-2349	-2640	-2559	-2766	-1464	-1118	3028	-2700	-2325	156
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
151(N)	-3482	-2868	-3701	-3919	238	-3552	-1112	-3000	-3638	-2516	-2526	-3027	-3772	-3101	-3341	-3418	-3527	-3071	-441	4711	157
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
152(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	158
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
153(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	159
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
154(T)	-359	-976	-2225	-2229	-2900	-1242	-2074	-2560	-2170	-2875	-2064	-1561	-1958	-1969	-2247	1110	3375	-1760	-3152	-2850	160
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
155(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	161
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
156(H)	861	-1924	-384	1010	-2260	-1477	1787	-1974	1769	-1918	-1022	-120	-1566	362	697	-417	-459	-1557	-2073	-1446	162
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
157(P)	-655	-1502	-711	-557	-2204	-1463	2143	-2122	-586	-2233	-1445	-688	2941	-560	-941	855	-805	-1657	-2369	-1763	163
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
158(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	164
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													

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Table 9

171(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	177
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
172(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	178
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
173(A)	2966	-1031	-2429	-2551	-3222	1544	-2368	-2934	-2633	-3225	-2377	-1727	-2028	-2309	-2637	-656	-850	-1980	-3412	-3224	179
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
174(V)	-1769	-1342	-4255	-3793	-1216	-3901	-3162	1633	-3589	1486	-51	-3537	-3667	-3214	-3518	-3143	-1731	2692	-2609	-2345	180
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
175(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	181
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
176(Q)	-729	-2116	-413	1096	-2484	-1587	1599	-2186	1695	-2094	-1219	-223	-1698	2418	90	-599	-649	-1770	-2213	-1615	182
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
177(W)	-1652	-1707	-2340	-1879	1996	-2733	2013	-1398	1758	-1386	-938	-1641	-2751	-1364	-1762	-1780	-1577	-1325	3577	2136	183
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
178(T)	-421	-753	-1251	-704	-846	-1670	-535	894	-548	-690	-1	1376	-1791	-421	-846	373	1461	858	-1236	-812	184
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
179(H)	1498	-1593	-504	15	-1895	-1484	2279	-1559	1119	-1640	-810	-242	-1611	194	-171	-462	815	-1231	-1914	-1340	185
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
180(G)	-1515	-2130	-1298	-1450	-2658	3285	2212	-3276	-1691	-3291	-2638	-1524	-2562	-1662	-1925	-1600	-1764	-2713	-2804	-2234	186
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
181(K)	-528	-2010	1346	1082	-2329	-1408	-118	-2080	1475	-2018	-1108	1161	-1543	331	1052	-394	-471	-1632	-2181	-1494	187
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
182(M)	-1894	-1521	-4170	-3679	-840	-3793	-2866	2827	-3360	375	3445	-3437	-3555	-2902	-3223	-3028	-1846	470	-2249	-2059	188
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
183(T)	-670	-1758	1731	-141	-2591	-1399	-691	-2319	-499	-2384	-1543	-387	-1786	-316	-1016	1576	2044	-1811	-2624	-1981	189
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

196(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	202
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
197(G)	-477	-1115	-1983	-2189	-3315	3154	-2272	-3172	-2506	-3387	-2522	-1599	-2042	-2177	-2583	1217	-905	-2130	-3477	-3225	203
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
198(A)	1653	-1347	-705	-249	-1969	-1385	-477	-1629	-159	-1759	-935	-434	1285	1404	-586	-450	1019	-1243	-2070	-1522	204
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
199(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	205
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
200(S)	1870	-938	-2270	-2183	-3068	1488	-2056	-2810	-2168	-3032	-2144	-1511	-1898	-1901	-2300	2236	-690	-1857	-3265	-2990	206
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
201(C)	-2476	-5235	-4102	-4358	-3712	-2763	-3545	-3518	-4167	-3859	-3569	-3631	-3363	-4030	-3832	-2793	-2860	-3158	-3464	-3718	207
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
202(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	208
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
203(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	209
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
204(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	210
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
205(Y)	-3590	-2700	-4146	-4379	2092	-4028	-404	-2517	-3963	-1928	-1973	-2744	-3921	-2845	-3431	-3284	-3474	-2669	336	4423	211
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
206(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	212
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
207(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	213
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
208(N)	-2171	-2655	-1458	-1748	-3334	-2364	-2267	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	214
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

221(L)	-2631	-2159	-4786	-4228	-462	-4506	-3231	96	-3878	2828	2482	-4157	-3880	-3016	-3541	-3793	-2509	-608	-2134	-2182	227
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
222(P)	-1501	-1778	-2473	-2371	-1710	-2311	-2045	-1321	-2060	827	-1068	-2173	3594	-2082	-2130	-1799	-1699	-1373	-2373	-1942	228
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
223(Y)	-1068	-1670	-865	-836	-631	1198	-767	-1828	-1059	-1914	-1304	692	-2203	-906	-1387	-1136	-1163	-1566	-1185	3670	229
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
224(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	230
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
225(S)	1172	-954	-2367	-2422	-3120	-1204	-2237	-2835	-2426	-3122	-2265	-1621	-1948	-2145	-2467	3107	-748	-1884	-3349	-3092	231
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
226(S)	-342	-975	-2176	-2124	-2912	-1229	-2003	-2594	-2067	-2878	-2048	-1510	-1936	-1866	-2184	2553	2492	-1773	-3143	-2833	232
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
227(M)	-720	-1440	-710	-343	-1228	-1693	2436	-1209	-132	-1364	3099	1904	-1852	-183	-458	-776	-680	-1004	-1540	-890	233
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
228(P)	2240	-1100	-2241	-2293	-3037	-1346	-2188	-2683	-2317	-2986	-2210	-1663	3041	-2093	-2391	-722	-895	-1893	-3243	-2998	234
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
229(A)	2958	-1235	-1299	-1377	-2868	-1345	-1673	-2580	-1661	-2843	-2054	1555	-1995	-1468	-1921	-715	-888	-1871	-3064	-2630	235
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
230(E)	-509	-1046	-884	1564	-1116	-1669	-441	-485	-283	250	-206	-577	689	-200	-656	-670	-459	1290	-1467	-995	236
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
231(D)	-1203	-2412	2595	-117	-3286	-1536	-1057	-3176	-1165	-3186	-2436	-428	-2068	-736	-1824	2377	-1366	-2578	-3334	-2552	237
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
232(Q)	954	-1983	-100	971	-2337	177	-267	-2067	81	-2060	-1189	-125	-1637	2600	-418	-514	-597	-1649	-2268	-1597	238
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
233(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	239
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

246(V)	-1178	-1448	-1943	-1452	-1776	-2261	-1140	-227	1866	-1260	-816	-1444	-2448	-902	-540	-1496	-1176	2697	-2161	-1764	252
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
247(E)	-508	-1976	840	1547	-2280	-1393	-117	-2029	1400	-1984	-1077	1158	-1531	330	-253	-378	-454	262	-2163	-1471	253
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
248(M)	1703	-991	-2901	-2342	-528	-2567	-1550	166	-2031	1544	2668	-2104	-2591	-1715	-2010	-1685	-1052	-12	-1442	-1177	254
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
249(I)	-1947	-1516	-4385	-3885	-916	-4013	-3118	2193	-3656	2186	257	-3656	-3687	-3109	-3494	-3250	-1889	1383	-2397	-2258	255
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
250(E)	-1322	-2647	-272	2491	-3071	-1811	-576	-2759	2306	-2633	-1854	-464	-2066	-175	-177	-1144	-1256	-2368	-2692	-2140	256
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
251(K)	-1395	-2059	-1711	-1014	-2215	-2218	-641	-1709	3021	-1652	2578	-1075	-2303	-282	287	-1423	-1283	-1603	-2159	-1803	257
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
252(D)	-1285	-2888	2677	176	-3210	1189	-737	-3047	-715	-2977	-2195	-190	-1979	2106	-1379	-1050	-1315	-2564	-3161	-2320	258
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
253(I)	-2073	-1632	-4434	-3975	-911	-4130	-3238	3164	-3706	1451	244	-3779	-3785	-3187	-3557	-3413	-2021	546	-2449	-2273	259
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
254(K)	-1570	-2144	-1887	-1191	-2098	-2363	-750	-1603	3034	938	-1112	-1231	-2436	-408	215	-1616	-1443	-1580	-2166	-1804	260
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
255(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	261
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
256(R)	-928	-1705	-1507	-1055	-2761	-1730	-896	-2490	-44	-2489	-1723	-1042	-2102	-543	2614	2258	-1053	-1998	-2546	-2158	262
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
257(D)	-1280	-2865	3154	175	-3194	-1547	-743	-3034	-728	-2971	-2194	-190	-1979	1342	-1391	553	-1316	-2552	-3161	-2317	263
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
258(I)	-1997	-1562	-4355	-3927	-1042	-4066	-3261	3343	-3654	937	97	-3718	-3783	-3239	-3555	-3364	-1959	702	-2549	-2295	264
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

271(N)	-1404	-1072	-3766	-3305	-1464	-3356	-2696	2276	-3080	-616	-379	-3001	-3325	-2870	-3091	-2563	1344	2521	-2516	-2113	277
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
272(M)	866	-1113	-2656	-2412	-1322	-1920	-1883	-487	-2081	-587	4451	-1950	-2387	-1928	-2078	-1220	-1053	-498	-2134	-1803	278
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
273(A)	2601	-957	-2898	-2711	-1943	-1740	-2211	-165	-2487	-1406	-1001	-2008	-2320	-2260	-2494	-1053	-929	1990	-2626	-2279	279
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
274(L)	-1171	-983	-3266	-2733	-796	-2795	-1888	590	-2418	2001	198	-2418	-2816	-2106	-2362	-1944	965	1777	-1724	-1426	280
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
275(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	281
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
276(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	282
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
277(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2886	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	283
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
278(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	284
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
279(N)	-2171	-2655	-1458	-1748	-3334	-2364	-2267	-3943	-2365	-3936	-3437	4205	-2932	-2205	-2608	-2224	-2439	-3392	-3253	-2909	285
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
280(A)	3134	-934	-2491	-2567	-3083	-1203	-2300	-2766	-2540	-3082	-2237	-1672	-1954	-2240	-2537	874	-747	-1844	-3333	-3093	286
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
281(V)	-984	-1045	-3169	-2909	-1709	-2304	-2404	531	-2643	-988	-697	-2378	-2722	-2480	-2661	-1601	1504	3014	-2588	-2201	287
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
282(L)	-2631	-2159	-4786	-4228	-462	-4506	-3231	96	-3878	2828	2482	-4157	-3880	-3016	-3541	-3793	-2509	-608	-2134	-2182	288
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
283(H)	-3205	-3079	-2723	-2890	-2110	-3046	5295	-4135	-2617	-3813	-3561	-2886	-3482	-2833	-2620	-3291	-3356	-3895	-2397	-1681	289
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

296(T)	-350	-973	-2204	-2178	-2893	-1236	-2035	-2561	-2117	-2862	-2043	-1536	-1946	-1916	-2214	1618	3198	-1758	-3137	-2831	302
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
297(L)	-1443	-1269	-3144	-2576	-528	-3014	-1816	1945	-2155	2102	508	-2422	-2899	1193	-2133	-2129	-1369	-50	-1616	-1384	303
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
298(D)	-1826	-3682	3559	1199	-3883	-1662	-1073	-3846	-1391	-3720	-3110	-272	-2222	-760	-2283	-1471	-1913	-3321	-3864	-2864	304
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
299(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	305
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
300(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	306
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
301(Q)	-1048	-2608	205	2170	-2893	-1535	-505	-2680	-255	-2604	-1769	1814	-1849	2272	-789	-848	-1028	-2228	-2770	-2013	307
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
302(R)	1083	-1687	691	135	-2058	-1406	-178	-1755	214	-1793	-924	-145	-1553	247	1670	-383	1217	-1367	-2031	-1404	308
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
303(I)	-1915	-1536	-4077	-3667	2027	-3678	-2155	3137	-3381	144	94	-3225	-3506	-2848	-3202	-2914	-1871	345	-1522	-791	309
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
304(R)	-689	-2015	-494	24	-2395	-1582	-184	-2087	444	-2020	-1151	1161	-1687	1832	2131	626	-614	-1684	-2156	-1573	310
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
305(D)	387	-1967	1600	1359	-2275	-1391	1561	-2025	282	-1976	-1067	-25	-1525	342	1024	-369	-443	-1584	-2152	-1462	311
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
306(R)	-1460	-2315	-1793	-887	-2832	-2237	-431	-2288	2193	-2199	-1473	-946	-2245	-20	2706	-1394	-1275	591	-2248	-1961	312
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
307(V)	-941	-1027	-3099	-2832	-1692	-2234	-2324	470	-2565	-1003	-695	-2305	-2663	-2399	-2587	-1527	1858	2876	-2536	-2152	313
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
308(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3761	-3695	-3182	-3279	-4087	-3594	-4054	314
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

321(M)	1225	-469	-2256	-1679	1656	-1926	-870	90	-1396	-210	2763	-1424	-2028	-1129	-1411	-1008	712	154	-951	-586	327
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
322(T)	-738	-2094	-84	1704	-2416	-1495	-317	-2135	61	-2127	-1275	-163	-1704	1857	-405	-613	1930	-1734	-2331	-1668	328
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
323(D)	-1746	-3458	3540	90	-3744	-1650	-1081	-3767	-1381	-3662	-3036	1386	-2211	-772	-2239	-1429	-1850	-3226	-3765	-2789	329
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
324(L)	-2451	-1983	-4707	-4186	-582	-4409	-3259	1510	-3884	2778	592	-4069	-3865	-3091	-3590	-3698	-2355	-150	-2226	-2214	330
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
325(H)	-2923	-2573	-2959	-2926	826	-3449	4553	-2508	-2463	-2054	-1948	-2279	-3499	-2191	-2397	-2761	-2855	-2540	123	2920	331
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
326(K)	373	-1957	-342	1025	-2297	-1472	-98	-2018	2111	-1954	-1056	906	-1570	352	685	-424	-473	-1592	-2105	-1469	332
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
327(V)	1739	-1008	-3509	-3043	-1376	-3028	-2406	1765	-2807	-615	-334	-2718	-3093	-2585	-2823	-2226	-1263	2376	-2322	-1931	333
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
328(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	334
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
329(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	335
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
330(I)	-1758	-1302	-4331	-3970	-1756	-4054	-3748	2976	-3840	-603	-533	-3731	-3877	-3693	-3914	-3372	-1750	2505	-3265	-2824	336
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
331(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	337
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
332(Q)	1795	-1440	-730	-492	-2453	682	-812	-2151	-508	-2256	-1426	-624	-1796	2666	-901	-590	-689	-1636	-2510	-1971	338
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
333(V)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	339
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

346(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	352
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
347(C)	774	4452	-2162	-1688	-1962	-1478	-1302	-1474	-944	-1796	-1088	-1351	-1979	-1147	1684	-732	-719	-1116	-2225	-1881	353
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
348(L)	-2387	-1922	-4674	-4155	-617	-4366	-3250	1889	-3865	2650	558	-4023	-3847	-3098	-3586	-3647	-2296	-38	-2247	-2224	354
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
349(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	355
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
350(C)	-1489	2972	-4007	-3563	-1524	-3541	-2939	2612	-3350	-617	-413	-3224	-3470	-3129	-3335	-2770	-1475	2269	-2657	-2248	356
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
351(T)	-364	-979	-2232	-2250	-2904	-1245	-2090	-2559	-2191	-2881	-2075	-1571	-1964	-1991	-2260	905	3428	-1762	-3159	-2858	357
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
352(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	358
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
353(K)	-1716	-2632	-2004	-1008	-3336	-2379	-444	-2764	2775	-2484	-1756	-1035	-2357	2151	1811	-1592	-1477	-2481	-2391	-2172	359
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
354(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	360
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
355(V)	-1771	-1339	-4275	-3816	-1235	-3919	-3194	2139	-3617	1520	-66	-3558	-3681	-3244	-3547	-3164	-1733	2390	-2634	-2369	361
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
356(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	362
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
357(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3583	-3385	363
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*		*												
358(N)	-823	-1917	-96	1188	-2187	-1547	-506	-1711	-265	-1955	-1191	2711	-1815	-144	-747	-757	-815	1140	-2297	-1666	364
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

371(D)	-1275	-2955	2862	1330	-3205	-1556	-670	-3029	1509	-2936	-2141	-158	-1955	-290	-1213	-1025	-1281	-2554	-3111	-2272	377
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
372(V)	-1738	-1298	-4281	-3921	-1737	-3979	-3665	1917	-3774	-601	-528	-3671	-3834	-3628	-3843	-3293	-1735	3205	-3215	-2770	378
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
373(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3521	-3194	-2146	449	-2877	-2493	379
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
374(M)	-584	-1354	-847	-246	-1467	-1659	2505	-1087	212	-374	2571	-449	-1729	1171	1074	-634	-507	-876	-1617	-1128	380
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
375(P)	-910	-2031	-73	1195	-2792	-1488	-794	-2539	-629	-2588	-1788	-401	3005	-439	-1131	612	-1014	-2050	-2815	-2151	381
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
376(W)	-1588	-1300	-3783	-3197	-329	-3245	-1926	2071	-2827	1901	558	-2822	-3072	-2297	-2616	-2381	-1508	-111	3483	-1042	382
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
377(E)	-1024	-2640	1844	2310	-2908	-1498	-505	-2711	-344	-2636	-1791	-107	-1824	1521	-957	207	-1011	-2243	-2817	-2021	383
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
378(N)	-826	-2349	1089	227	-2651	-1487	-341	-2416	1494	-2346	-1475	2601	-1724	1005	-522	-657	-787	-1968	-2511	-1791	384
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
379(P)	1932	-1116	-2232	-2301	-3058	-1358	-2206	-2706	-2336	-3009	-2238	-1674	3274	-2114	-2406	-739	-914	-1913	-3260	-3019	385
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
380(V)	-914	-773	-2713	-2129	-712	-2505	-1388	1452	1084	1324	204	-1926	-2507	-1580	-1808	-1591	-859	1713	-1424	-1081	386
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
381(Y)	-1484	-2331	-1762	-887	-2436	-2254	-420	-2325	2137	-2195	-1475	-949	-2258	-39	1983	-1411	-1295	-2075	-2087	2868	387
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
382(E)	1256	-1890	-206	1353	-2196	-1401	-89	-1930	812	-1898	-996	-45	547	1252	-162	-356	-414	-1507	-2083	-1416	388
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
383(Q)	-752	-2272	1586	1407	-2561	-1448	-308	-2329	-23	-2276	-1396	-71	-1677	1749	-577	-590	1569	-1881	-2459	-1727	389
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

396(E)	-1481	-3230	1425	2936	-3481	751	-843	-3354	-954	-3256	-2520	-187	-2057	-492	-1711	-1193	-1527	-2852	-3445	-2523	402
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
397(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	403
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
398(A)	2847	-932	-2454	-2477	-3066	-1198	-2236	-2763	-2439	-3057	-2202	-1635	-1940	-2152	-2471	1777	-731	-1840	-3306	-3056	404
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
399(V)	-1771	-1603	-3750	-3689	-2037	-3050	-3231	403	-3479	-1154	-1076	-3246	-3399	-3383	-3437	-2628	-1917	3536	-3074	-2677	405
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
400(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	406
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
401(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	407
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
402(I)	-1761	-1312	-4317	-3954	-1713	-4027	-3703	3225	-3814	-556	-498	-3712	-3859	-3653	-3877	-3344	-1754	2110	-3216	-2787	408
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
403(S)	-348	-981	-2200	-2194	-2989	-1227	-2073	-2686	-2157	-2970	-2136	-1541	-1946	-1946	-2253	3060	1398	-1824	-3217	-2916	409
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
404(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	410
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
405(V)	-917	-809	-2556	-1976	-827	-2491	-1367	1339	1455	721	94	-1841	-2501	-1487	-1710	-1570	-863	2038	-1514	-1151	411
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
406(K)	-1386	-2643	-447	1824	-3108	-1893	-570	-2762	2860	-2616	-1848	-552	-2117	-166	-3	-1217	-1300	-2388	-2647	-2154	412
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
407(N)	-537	-1563	-449	-36	-1889	1143	-307	-1529	932	-1655	-844	1794	-1658	73	-356	-518	-516	924	-1962	-1392	413
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*	*												
408(P)	-894	-2181	-369	1705	-2576	-1650	-357	-2268	243	-2210	-1375	-330	2093	63	1619	-774	-835	-1876	-2347	-1769	414
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

421(Q)	-705	-1925	-199	2112	917	-1534	-288	-1824	42	-1842	-1054	-210	-1709	2163	-420	-611	-656	-1502	-1997	-1291	427
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
422(H)	-569	-2048	1450	1526	-2349	-1405	1830	-2103	181	-2058	-1157	-37	-1569	272	-349	713	620	-1662	-2240	-1537	428
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
423(C)	1626	2878	-2671	-2107	1264	-1968	-1091	233	-1777	-334	250	-1672	-2128	-1459	-1691	-1096	-529	1209	-1066	-704	429
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
424(M)	-2042	-1634	-4379	-3826	-659	-3976	-2899	2765	-3546	1204	3085	-3605	-3604	-2896	-3318	-3183	-1961	195	-2135	-2058	430
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
425(E)	412	-2447	1356	2379	-2747	-1477	-445	-2527	-243	-2477	-1622	-107	855	-36	-831	-730	-894	-2073	-2668	-1906	431
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
426(A)	2822	-1031	-2418	-2539	-3226	1898	-2364	-2941	-2626	-3229	-2379	-1722	-2026	-2302	-2634	-654	-848	-1983	-3415	-3226	432
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
427(I)	-1772	-1325	-4307	-3877	-1405	-3993	-3383	2935	-3705	820	-217	-3632	-3761	-3400	-3682	-3260	-1742	2033	-2838	-2525	433
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
428(L)	-875	-1634	-575	959	-1581	-1769	-525	-1179	-135	1884	-625	-547	-1931	1405	-450	-909	-816	-1074	-1883	-1383	434
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
429(A)	1705	-1826	-180	949	-2318	-1410	-359	-2041	-53	-2067	-1204	1001	-1652	52	-561	1232	-595	-1609	-2298	-1643	435
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
430(D)	-1074	-2458	2381	60	-2921	1927	-658	-2710	-463	-2675	-1860	-271	-1918	-276	866	-915	-1100	-2245	-2845	-2124	436
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
431(K)	-688	-2117	785	888	-2469	-1529	-187	-2189	2380	-2106	-1221	-162	-1661	256	1134	-553	-619	-1760	-2240	-1607	437
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
432(I)	-2019	-1582	-4380	-3941	-1000	-4086	-3253	3295	-3671	1100	145	-3736	-3783	-3222	-3556	-3378	-1976	657	-2517	-2289	438
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
433(Q)	-490	-1797	-369	171	-2078	-1457	1762	-1779	1157	-1780	-905	1165	-1550	1798	-48	-396	-422	725	-1986	-1366	439
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

446(K)	-1060	-2058	-1088	-460	-2432	-1917	-357	-1970	2801	-1978	-1220	-632	-1990	1339	367	-999	-946	536	-2145	-1717	452
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
447(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	453
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
448(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	454
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
449(P)	-2931	-2878	-3420	-3706	-4181	-2925	-3468	-4621	-3859	-4490	-4165	-3491	4225	-3781	-3695	-3182	-3279	-4087	-3594	-4064	455
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
450(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	456
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
451(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	457
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
452(P)	-1659	-2241	-2022	-1646	-3185	-2242	-1373	-3000	-450	-2936	-2274	-1624	3435	-1065	2095	-1730	-1750	-2593	-2816	-2613	458
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
453(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	459
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
454(M)	-2406	-2296	-3638	-3594	-1525	-3105	-2824	-1047	-3121	-596	5043	-3293	-3425	-3046	-2996	-2911	-2552	-1398	-2513	-2207	460
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
455(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	461
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
456(K)	1368	-1491	-763	-332	-2319	-1417	-551	-1998	1786	-2068	-1221	-500	-1721	-160	-470	1631	-587	-1532	-2299	-1754	462
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
457(P)	-1500	-1738	-2514	-2380	-1555	-2358	-2022	-1126	-2063	1224	-841	-2189	3436	-2061	-2129	-1822	-1674	-1231	-2290	-1878	463
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*													
458(T)	-351	-974	-2208	-2185	-2894	-1237	-2041	-2561	-2125	-2863	-2046	-1539	-1948	-1923	-2218	1543	3230	-1758	-3139	-2834	464
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

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Table 9

471(A)	2590	-1035	-2404	-2530	-3236	2290	-2365	-2954	-2627	-3240	-2389	-1719	-2027	-2302	-2637	-656	-851	-1991	-3423	-3234	477
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
472(L)	-2632	-2152	-4630	-4185	1767	-4324	-2442	-61	-3879	2789	563	-3833	-3823	-2970	-3513	-3609	-2518	-738	-1527	-945	478
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
473(I)	-2073	-1632	-4434	-3975	-911	-4130	-3238	3164	-3706	1451	244	-3779	-3785	-3187	-3557	-3413	-2021	546	-2449	-2273	479
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
474(T)	-1213	-1674	-2755	-2906	-3163	-1922	-2659	-2698	-2788	-3105	-2612	-2311	-2600	-2708	-2753	-1463	3819	-2197	-3286	-3156	480
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
475(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	-4046	-3710	-3552	481
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
476(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	482
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
477(R)	-2957	-3022	-3318	-2735	-3796	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	483
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
478(F)	-3342	-2776	-4026	-4232	4354	-3545	-1431	-2315	-4038	-1801	-1900	-3299	-3780	-3350	-3645	-3490	-3420	-2566	-739	349	484
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
479(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	485
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
480(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	486
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
481(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3352	-3748	-3779	-2839	-2981	-4004	-3668	-4222	487
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
482(T)	-359	-976	-2225	-2229	-2900	-1242	-2074	-2560	-2170	-2875	-2064	-1561	-1958	-1969	-2247	1110	3375	-1760	-3152	-2850	488
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
483(Y)	-3402	-2632	-3941	-4011	1064	-3924	3388	-2526	-3541	-1896	-1973	-2625	-3821	-2664	-3170	-3135	-3280	-2619	3420	3756	489
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

496(D)	417	-1831	1647	1094	-2065	-1488	-353	-1618	-107	-1820	-1019	-189	-603	-643	1629	-2154	-1520	502
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
497(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3779	-2839	-2981	-4004	-3668	503
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
498(G)	-2594	-2690	-3304	-3623	-4328	3747	-3462	-4761	-3953	-4671	-4212	-3320	-3779	-2839	-2981	-4004	-3668	504
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
499(T)	492	-1190	-706	-181	-1475	311	-333	-1099	-81	71	-509	570	1113	-6	-509	-450	1123	505
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
500(I)	-2091	-1746	-3971	-3840	-1676	-3532	-3289	3684	-3581	-659	-693	-3562	-3674	-3445	-3194	-2146	449	506
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
501(A)	3103	-1036	-2445	-2572	-3222	1051	-2380	-2930	-2650	-3226	-2381	-1739	-2034	-2327	-2648	-664	-857	507
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
502(L)	-2239	-1892	-3711	-3400	301	-3520	-1210	-542	-2948	2564	-35	-2786	-3395	-2438	-2750	-2747	-2165	508
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
503(V)	-1757	-1387	-4101	-3681	-1174	-3714	-3031	880	-3410	1254	-60	-3407	-3585	-3094	-3354	-2984	-1743	509
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
504(Q)	-982	-2251	-866	971	-2711	-1822	-252	-2340	1444	-2194	-1356	-464	-1885	2646	1632	-858	-863	510
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
505(E)	-1162	-2771	2137	2239	-3046	-1526	-626	-2849	-546	-2792	-1983	-145	-1905	-242	-1192	-940	1396	511
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
506(G)	-1707	-2684	1591	-614	-3783	3190	-1613	-3795	-1887	-3775	-3119	-915	-2456	-1358	-2539	-1610	-1924	512
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
507(D)	-2784	-3432	4016	-1200	-4140	-2466	-2197	-4505	-2621	-4365	-3956	-1551	-3014	-2039	-3232	-2593	-2938	513
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*										
508(M)	-473	-522	-1819	-1236	-468	-1879	-687	1519	-996	566	1677	-1154	-1937	836	-1131	1079	-413	514
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	359	117	-369	-294	-249	

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Table 9

521(N)	-723	-2217	958	236	-2518	-1466	1611	-2279	1719	-2217	-1334	2285	-1666	166	-401	-570	-677	-1837	-2382	-1678	527
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
522(V)	-1754	-1297	-4330	-3968	-1770	-4053	-3752	2623	-3841	-620	-545	-3729	-3878	-3699	-3918	-3371	-1746	2846	-3277	-2830	528
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
523(S)	1545	-974	-2003	-1825	-2867	-1206	-1790	-2580	-1788	-2795	-1932	-1362	1826	-1586	-1999	2362	-672	-1755	-3057	-2721	529
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
524(D)	-1776	-3649	3326	1869	-3838	-1642	-1031	-3788	-1322	-3660	-3029	-245	-2192	-711	-2201	-1425	-1855	-3264	-3821	-2816	530
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
525(E)	423	-2950	1944	2696	-3223	-1545	-718	-3047	-715	-2979	-2196	-161	-1968	-347	-1403	-1043	-1314	-2569	-3177	-2316	531
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
526(E)	-2641	-3308	-896	3732	-3966	-2458	-2043	-4105	-2128	-4016	-3555	-1531	-2959	-1842	-2560	-2479	-2750	-3722	-3563	-3385	532
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
527(L)	-2339	-1899	-4618	-4042	1570	-4204	-2849	1440	-3758	2558	676	-3825	-3700	-2902	-3418	-3418	-2226	-382	-1924	-1778	533
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
528(A)	2338	-1990	-241	938	-2395	-1557	-423	-2061	954	-2103	-1286	-301	-1791	-26	-375	-717	-784	-1691	-2330	-1728	534
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
529(R)	524	-2098	-789	-146	-2504	-1729	1632	-2153	1229	-2054	-1204	-379	-1789	1328	2313	-719	-724	-1774	-2150	-1637	535
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
530(R)	-2957	-3022	-3318	-2735	-3796	-2998	-1968	-3912	-846	-3631	-3157	-2611	-3280	-1724	4056	-3026	-2913	-3650	-3096	-3185	536
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
531(R)	-1895	-2713	-2327	-1192	-3484	-2502	-481	-2856	2144	-2544	-1842	-1161	-2458	1393	3023	-1770	-1619	-2598	-2421	-2259	537
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
532(A)	2935	-1714	-553	857	-2769	-1546	-1218	-2333	-1106	-2591	-1873	-809	-2065	-934	-1502	-954	-1103	-1872	-2898	-2374	538
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
533(A)	1291	-1874	-176	1227	-2177	-1392	-109	-1909	277	-1891	-995	1134	-1522	1248	-228	-361	562	-1492	-2090	-1419	539
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

Table 9

546(L)	-2871	-2457	-4231	-4103	-1033	-3803	-3165	-541	-3734	3130	-31	-3935	-3797	-3286	-3484	-3713	-2869	-1136	-2394	-2220	552
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
547(A)	2404	-890	-1926	-1629	-1803	1275	-1415	-1282	-1490	392	-963	-1316	-1930	-1328	-1674	-654	-644	-952	-2187	-1810	553
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
548(K)	-2620	-2961	-2461	-2046	-3743	-2791	-1570	-3603	3784	-3387	-2839	-2048	-3039	-1260	-465	-2604	-2536	-3331	-3001	-2988	554
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
549(N)	-3621	-2707	-4176	-4424	2950	-4049	-394	-2539	-4002	-1942	-1987	-2749	-3933	-2854	-3451	-3299	-3499	-2690	349	4094	555
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
550(A)	3438	-1472	-2846	-3040	-3287	-1726	-2735	-2840	-3028	-3257	-2662	-2236	-2447	-2798	-2944	-1216	-1387	-2183	-3405	-3320	556
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
551(H)	-1741	-2627	-2070	-1046	-3303	-2401	2713	-2751	2478	-2476	-1755	-1061	-2375	-27	2379	-1621	-1497	-2477	-2379	-2161	557
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
552(L)	-1014	-876	-2956	-2408	-582	-2550	-1529	1721	-2079	2042	345	-2114	-2581	-1775	-2028	454	-980	286	-1414	-1096	558
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
553(V)	933	-842	-2818	-2467	-1542	-1870	-1890	154	-2226	-1095	-617	-1932	-2326	-1995	-2259	-1126	1070	2769	-2180	-1826	559
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
554(S)	-787	-1522	-1486	-1172	-2714	-1599	-1112	-2500	-433	-2563	-1791	-1110	-2067	-796	1351	2916	-989	-1943	-2648	-2234	560
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
555(S)	-326	-1010	-1779	-1541	-2691	-1234	-1566	-2386	-1486	-2594	-1749	-1228	1196	-1330	-1747	2396	1967	-1662	-2876	-2496	561
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
556(A)	3121	-934	-2489	-2561	-3081	-1203	-2295	-2766	-2533	-3080	-2234	-1669	-1953	-2234	-2533	936	-746	-1844	-3331	-3090	562
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
557(S)	-897	-1462	-2333	-2543	-3185	-1640	-2474	-3294	-2686	-3497	-2780	-1973	-2360	-2483	-2703	3465	-1316	-2413	-3310	-3025	563
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378*	*													
558(R)	-586	-1873	-516	979	-2188	-1543	-123	-1869	1290	-353	-980	-202	-1622	314	1886	-491	782	-1495	-2024	-1439	564
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	

CLAIMS

What is claimed is

1. A recombinant yeast host cell comprising at least one heterologous
5 Fe-S cluster protein and wherein the yeast host has reduced expression of
at least one endogenous Fe-S cluster protein.
2. The recombinant yeast cell of Claim 1 comprising a disruption in the
gene encoding the at least one endogenous Fe-S cluster protein.
- 10 3. The recombinant yeast host cell of Claim 1 wherein the
endogenous Fe-S cluster protein is selected from the group consisting of
dihydroxy-acid dehydratase, isopropylmalate dehydratase, sulfite
reductase, glutamate dehydrogenase, biotin synthase, aconitase,
15 homoaconitase, lipoate synthase, ferredoxin maturation, NADH
ubiquinone oxidoreductase, succinate dehydrogenase, ubiquinol-
cytochrome-c reductase , ABC protein Rli1, NTPase Nbp35 , and
hydrogenase-like protein.
- 20 4. The recombinant yeast host cell of Claim 1 wherein the yeast is
selected from the group consisting of *Saccharomyces*,
Schizosaccharomyces, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*
and *Pichia*.
- 25 5. The recombinant yeast host cell of Claim 1 wherein the
endogenous Fe-S protein is expressed in the mitochondria.
6. The recombinant yeast host cell of Claim 1 wherein the
endogenous Fe-S cluster protein has an activity selected from the group
30 consisting of: dihydroxy-acid dehydratase and isopropylmalate
dehydratase activity.

7. The recombinant yeast host cell of Claim 6 wherein the host cell is *Saccharomyces* expressing a gene encoding a polypeptide having the amino acid sequence as set forth in SEQ ID NO:114.
- 5 8. The recombinant yeast host cell of Claim 1 wherein the at least one heterologous Fe-S cluster protein is selected from the group consisting of fungal 2Fe-2S dihydroxy-acid dehydratases and plant 2Fe-2S dihydroxy-acid dehydratases.
- 10 9. The recombinant yeast host cell of Claim 8 wherein the heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is expressed in the cytosol.
- 15 10. The recombinant yeast host cell of Claim 8 wherein the heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is a polypeptide having an amino acid sequence that matches the Profile HMM of Table 9 with an E value of $< 10^{-5}$ wherein the polypeptide additionally comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the
- 20 *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:179.
11. The recombinant yeast host cell of Claim 8 wherein the heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is a polypeptide having an amino acid sequence that has at least about 95%
- 25 sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NOs:46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150 and 152.
- 30 12. The recombinant yeast host cell of Claim 8 wherein the heterologous fungal or plant 2Fe-2S cluster dihydroxy-acid dehydratase is a polypeptide having an amino acid sequence that is at least about 90%

identical to SEQ ID NO:114 using the Clustal W method of alignment using the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

5

13. The recombinant host cell of any one of Claims 10-12 wherein the cell comprises an isobutanol biosynthetic pathway.

14. The recombinant host cell of Claim 13 wherein the cell produces
10 isobutanol.

15. A method for the production of isobutanol comprising growing the recombinant yeast host cell of Claim 14 under conditions wherein isobutanol is produced.

15

16. The recombinant yeast host cell of claim 1 wherein the at least one heterologous Fe-S cluster protein has Fe-S propanediol dehydratase reactivase activity.

20 17. The recombinant host cell of Claim 16 wherein the at least one heterologous Fe-S cluster protein having Fe-S propanediol dehydratase reactivase activity is a propanediol dehydratase reactivase having an amino acid sequence that is at least about 90% identical to the amino acid sequence as set forth in SEQ ID NO:44 using the Clustal W method of
25 alignment using the default parameters of GAP PENALTY=10, GAP LENGTH PENALTY=0.1, and Gonnet 250 series of protein weight matrix over the full length of the protein sequence.

18. The recombinant host cell of Claims 16 or 17 wherein the cell
30 produces 2-butanol.

19. The recombinant host cell of Claims 16 or 17 wherein the cell produces 2-butanone.

20. The recombinant host cell of Claim 18 wherein the cell comprises a 2-butanol biosynthetic pathway.

5 21. The recombinant host cell of Claim 19 wherein the cell comprises a 2-butanone biosynthetic pathway.

22. A method for the conversion of 2,3-dihydroxyisovalerate to α -ketoisovalerate comprising:

10 a) providing (1) a recombinant yeast host cell comprising at least one heterologous gene encoding a 2Fe-2S dihydroxy-acid dehydratase wherein the recombinant yeast host cell has reduced activity of at least one endogenous Fe-S cluster protein; and (2) a source of 2,3-dihydroxyisovalerate; and

15 b) growing the recombinant host cell of (a) with said source of 2,3-dihydroxyisovalerate under conditions where the 2,3-dihydroxyisovalerate is converted by the host cell to α -ketoisovalerate.

23. A method for the production of 2-butanone comprising growing the
20 recombinant yeast host cell of claim 21 under conditions wherein 2-butanone is produced.

24. A method for the conversion of 2,3-butanediol to 2-butanone comprising:

25 a) providing (1) a recombinant yeast host cell comprising at least one heterologous gene encoding a Fe-S propanediol dehydratase reactivase wherein the recombinant yeast host cell has reduced activity of at least one endogenous Fe-S cluster protein; and (2) a source of 2,3-butanediol; and

30 b) growing the recombinant host cell of (a) with said source of 2,3-butanediol under conditions where the 2,3-butanediol is converted by the host cell to 2-butanone.

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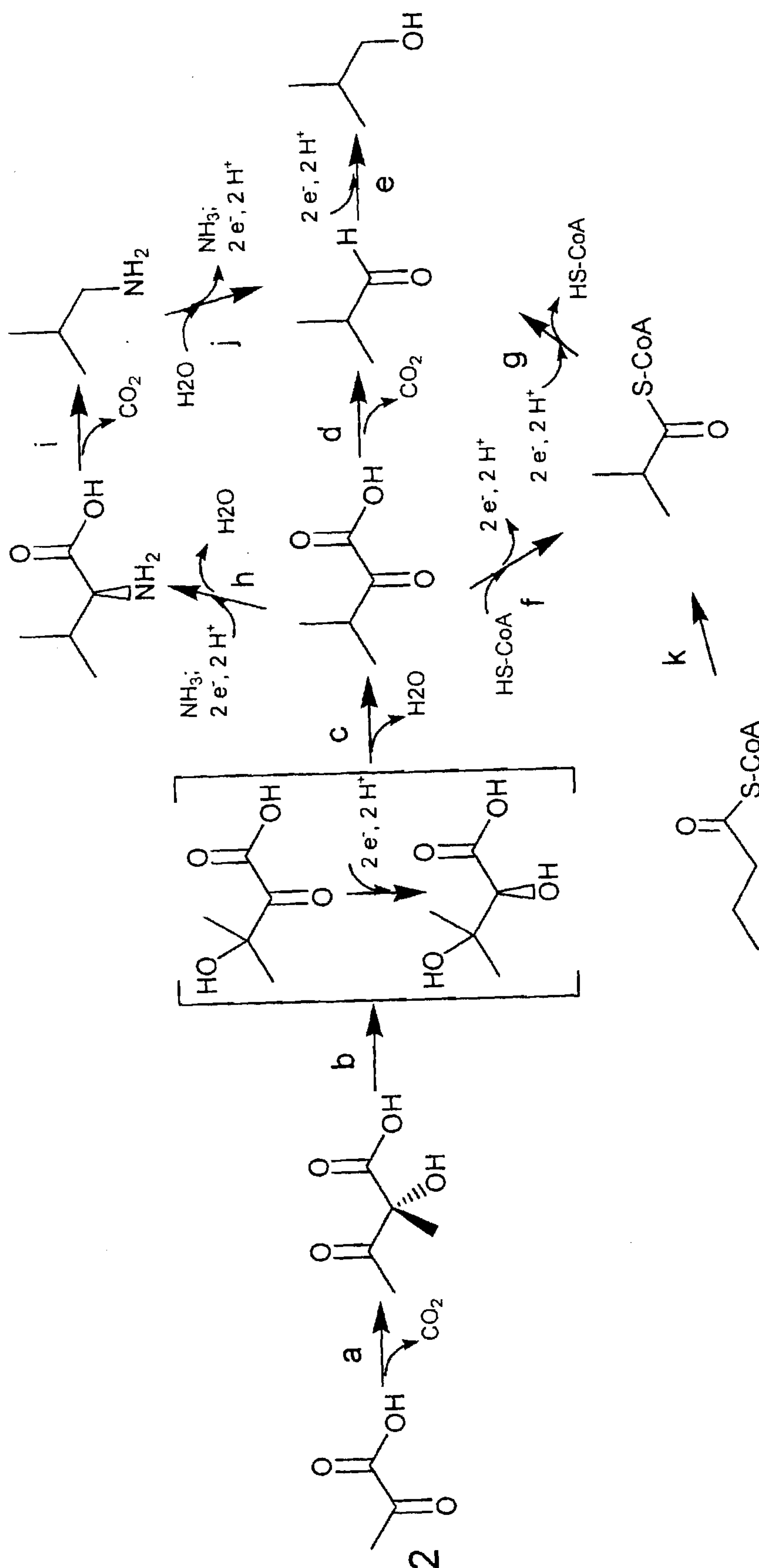


FIG. 1

2/2

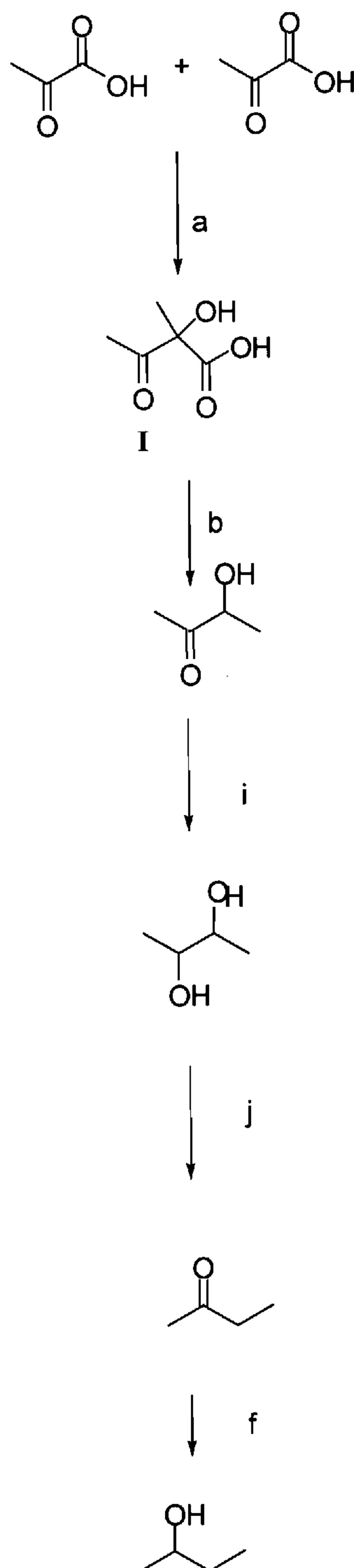


FIG. 2

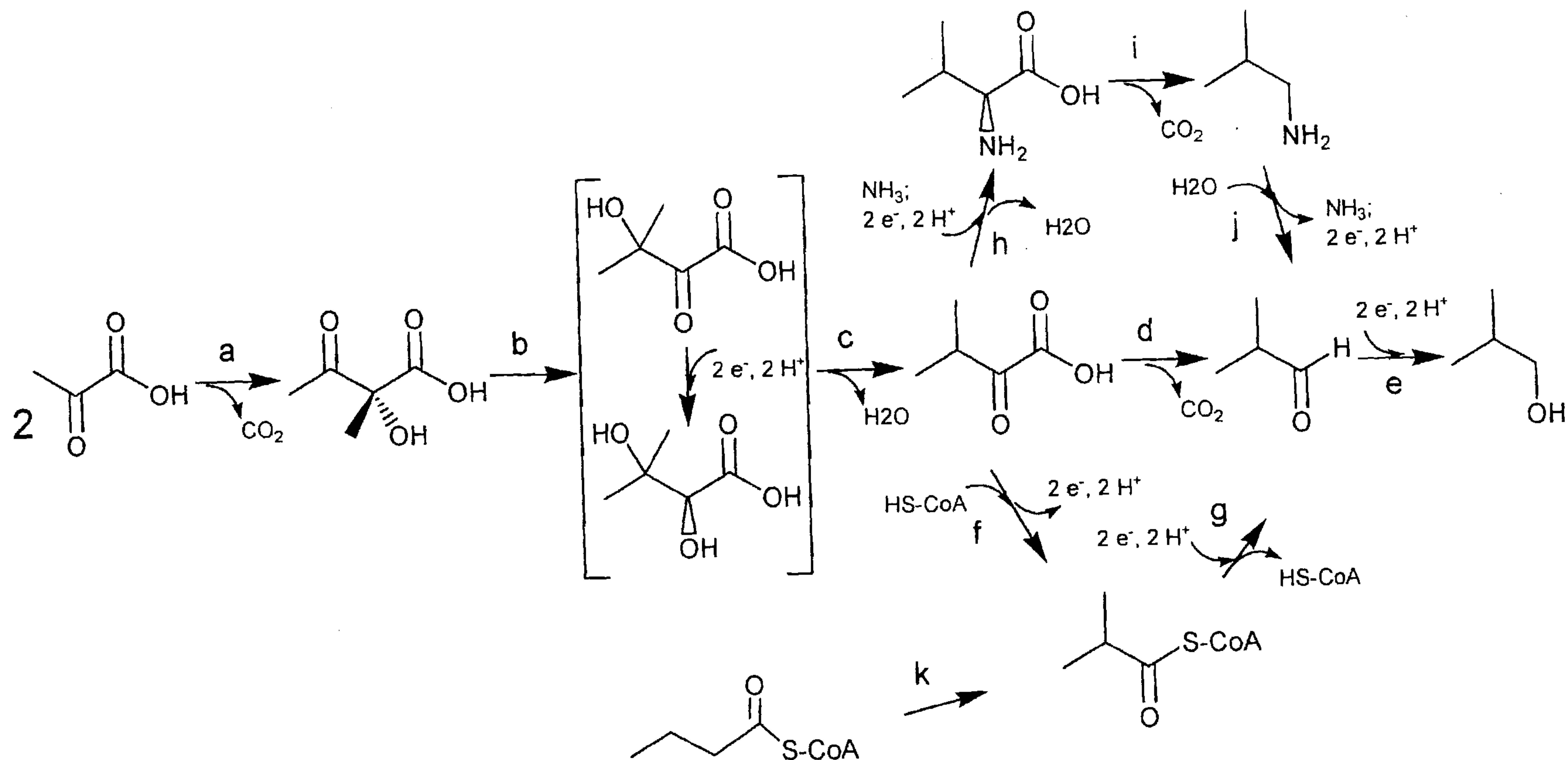


FIG. 1