# IMPROVED ACTIVITY OF FE-S CLUSTER REQUIRING PROTEINS

## BACKGROUND OF THE INVENTION

### Field of the Invention

**[0001]** This invention relates generally to the fields of microbiology and biochemistry. Specifically, the present invention is related to a recombinant host cell, in particular a yeast cell, comprising a dihydroxy-acid dehydratase polypeptide. The invention is also related to a recombinant host cell having increased specific activity of the dihydroxy-acid dehydratase polypeptide as a result of increased expression of the polypeptide, modulation of the Fe-S cluster biosynthesis activity of the cell, or a combination thereof. The present invention also includes methods of using the host cells, as well as methods for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell.

### Background of the Invention

**[0002]** Iron-sulfur (Fe-S) clusters serve as cofactors or prosthetic groups essential for the normal function of the class of proteins that contain them. In the class of Fe-S cluster containing proteins, the Fe-S clusters have been found to play several roles. When proteins of this class are first synthesized by the cell, they lack the Fe-S clusters required for their proper function and are referred to as apoproteins. Fe-S clusters are made in a series of reactions by proteins involved in Fe-S cluster biosynthesis and are transferred to the apo-proteins to form the functional Fe-S cluster containing holoproteins.

**[0003]** One such protein that requires Fe-S clusters for proper function is dihydroxy-acid dehydratase (DHAD) (E.C. 4.2.1.9). DHAD catalyzes the conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate, and of 2,3-dihydroxymethylvalerate to α-ketomethylvalerate. The DHAD enzyme is part of naturally occurring biosynthetic pathways producing the branched chain amino acids, (i.e., valine, isoleucine, leucine), and pantothenic acid (vitamin B5). DHAD catalyzed conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate is also a common step in the multiple isobutanol biosynthetic pathways that are disclosed in U.S. Patent Appl. Pub. No. US 20070092957 A1, incorporated by reference herein. Disclosed therein is, *e.g.*, the engineering of recombinant microorganisms for the production of isobutanol.

**[0004]** High levels of DHAD activity are desired for increased production of products from biosynthetic pathways that include this enzyme activity, including, *e.g.*, enhanced microbial production of branched chain amino acids, pantothenic acid, and isobutanol. Isobutanol, in particular, is useful as a fuel additive, and its ready availability may reduce the demand for petrochemical fuels. However, since all known DHAD enzymes require a Fe-S cluster for their function, they must be expressed in a host having the genetic machinery to provide the Fe-S clusters required by these proteins. In yeast, most of the steps in Fe-S cluster biosynthesis take place in mitochondria. If the DHAD is to be functionally expressed in yeast cytosol, a system to transport the requisite Fe-S precursor from mitochondria and assemble the Fe-S cluster on the cytosolic apoprotein is required. Prior to the work of the present inventors, it was previously unknown whether yeast could provide Fe-S clusters for any DHAD located in the cytoplasm (since native yeast DHAD is located in the mitochondria) and more importantly when the DHAD is expressed at high levels in the cytoplasm

**[0005]** Under certain conditions the rate of synthesis of Fe-S cluster requiring apo-proteins may exceed the cell's ability to synthesize and assemble Fe-S clusters for them. Cluster-less apo-proteins that accumulate under these conditions cannot carry out their normal function. Such conditions can include 1) the expression of a heterologous Fe-S cluster requiring protein especially in high amounts, 2) the expression of a native Fe-S cluster biosynthesis protein at higher levels than normal, or 3) a state where the host cell's ability to synthesize Fe-S clusters is debilitated.

**[0006]** BRIEF SUMMARY OF THE INVENTION

**[0007]** Disclosed herein is the surprising discovery that recombinant host cells expressing a high level of a heterologous Fe-S cluster requiring protein can supply the complement of Fe-S clusters for that protein if the level(s) of at least one Fe uptake, utilization, and/or Fe-S cluster biosynthesis protein are altered.

**[0008]** Provided herein are recombinant host cells comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity wherein said at least one heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated. Also provided are recombinant host cells comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity wherein said at least one heterologous polynucleotide is integrated at least once in the recombinant host cell DNA. Also provided are recombinant host cells comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity, wherein said host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis. Also provided are recombinant host cells comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis.

**[0009]** In embodiments, said heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of the genes in Tables 7, 8 and 9. In embodiments, said heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, FRA2, GRX3, MSN5, and combinations thereof. In embodiments, polypeptide is encoded by a polynucleotide that is constitutive mutant. In embodiments, said constitutive mutant is selected from the group consisting of AFT1 L99A, AFT1 L102A, AFT1 C291F, AFT1 C293F, and combinations thereof. In embodiments said polypeptide affecting Fe-S cluster biosynthesis is encoded by a polynucleotide comprising a high copy number plasmid or a plasmid with a copy number that can be regulated. In embodiments, said polypeptide affecting Fe-S cluster biosynthesis is encoded by a polynucleotide integrated at least once in the recombinant host cell DNA. In embodiments, the at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of FRA2, GRX3, MSN5, and combinations thereof. In embodiments, the at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, and combinations thereof.

**[0010]** In embodiments, said at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity is expressed in multiple copies. In embodiments, said at least one heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated. In embodiments, said at least one heterologous polynucleotide is integrated at least once in the recombinant host cell DNA. In embodiments, said Fe-S cluster biosynthesis is increased compared to a recombinant host cell having endogenous Fe-S cluster biosynthesis.

**[0011]** In embodiments, said host cell is a yeast host cell. In embodiments, said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia* and *Pichia*.

**[0012]** In embodiments, said heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in the cytosol of the host cell. In embodiments, said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168. In embodiments, said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence with at least about 90% identity to SEQ ID NO: 168 or SEQ ID NO: 232. In embodiments said polypeptide having dihydroxy-acid dehydratase activity has a specific activity selected from the group consisting of: greater than about 5-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity, greater than about 8-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity, or greater than about 10-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity. In embodiments, said polypeptide having dihydroxy-acid dehydratase activity has a specific activity selected from the group consisting of: greater than about 0.25 U/mg; greater than about 0.3 U/mg; greater than about 0.5 U/mg; greater than about 1.0 U/mg; greater than about 1.5 U/mg; greater than about 2.0 U/mg; greater than about 3.0 U/mg; greater than about 4.0 U/mg; greater than about 5.0 U/mg; greater than about 6.0 U/mg; greater than about 7.0 U/mg; greater than about 8.0 U/mg; greater than about 9.0 U/mg; greater than about 10.0 U/mg; greater than about 20.0 U/mg; and greater than about 50.0 U/mg.

**[0013]** In embodiments said recombinant host cell produces isobutanol, and in embodiments, said recombinant host cell comprises an isobutanol biosynthetic pathway.

**[0014]** Also provided herein are methods of making a product comprising: providing a recombinant host cell; and contacting the recombinant host cell of with a fermentable carbon substrate in a fermentation medium under conditions wherein said product is produced; and recovering said product, wherein the product is selected from the group consisting of branched chain amino acids, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, isobutanol, and combinations thereof.

**[0015]** Also provided are methods of making isobutanol comprising: providing a recombinant host cell; contacting the recombinant host cell with a fermentable carbon substrate in a fermentation medium under conditions wherein isobutanol is produced; and recovering said isobutanol.

**[0016]** Also provided are methods for the conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate comprising: providing a recombinant host cell; growing the recombinant host cell of under conditions where the 2,3-dihydroxyisovalerate is converted to α-ketoisovalerate.

**[0017]** Also provided are methods for increasing the specific activity of a heterologous polypeptide having dihydroxy-acid dehydratase activity in a recombinant host cell comprising: providing a recombinant host cell; and growing the recombinant host cell of under conditions whereby the heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in functional form having a specific activity greater than the same host cell lacking said heterologous polypeptide.

**[0018]** Also provided are methods for increasing the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising: providing a recombinant host cell; and growing the recombinant host cell under conditions whereby the flux in the Fe-S cluster biosynthesis pathway in the host cell is increased.

**[0019]** Also provide are methods of increasing the activity of an Fe-S cluster requiring protein in a recombinant host cell comprising: providing a recombinant host cell comprising an Fe-S cluster requiring protein; changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis in said host cell; and growing the recombinant host cell under conditions whereby the activity of the Fe-S cluster requiring protein is increased. In embodiments, said increase in activity is an amount selected from the group consisting of: greater than about 10%; greater than about 20%; greater than about 30%; greater than about 40%; greater than about 50%; greater than about 60%;

greater than about 70%; greater than about 80%; greater than about 90%; and greater than about 95%, 98%, or 99%. In embodiments, the increase in activity is in an amount selected from the group consisting of: greater than about 5 fold; greater than about 8 fold; greater than about 10 fold.

**[0020]** A method for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising: changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis; measuring the activity of a heterologous Fe-S cluster requiring protein; and comparing the activity of the heterologous Fe-S cluster requiring protein measured in the presence of the change in expression or activity of a polypeptide to the activity of the heterologous Fe-S cluster requiring protein measured in the absence of the change in expression or activity of a polypeptide, wherein an increase in the activity of the heterologous Fe-S cluster requiring protein indicates an increase in the flux in said Fe-S cluster biosynthesis pathway.

**[0021]** Provided herein are methods for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising: changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis; measuring the activity of a polypeptide having dihydroxy-acid dehydratase activity; and comparing the activity of the polypeptide having dihydroxy-acid dehydratase activity measured in the presence of the change to the activity of the polypeptide having dihydroxy-acid dehydratase activity measured in the absence of change, wherein an increase in the activity of the polypeptide having dihydroxy-acid dehydratase activity indicates an increase in the flux in said Fe-S cluster biosynthesis pathway.

**[0022]** In embodiments, said changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis comprises deleting, mutating, substituting, expressing, up-regulating, down-regulating, altering the cellular location, altering the state of the protein, and/or adding a cofactor. In embodiments, the Fe-S cluster requiring protein has dihydroxy-acid dehydratase activity and wherein said Fe-S cluster requiring protein having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to

SEQ ID NO:168. In embodiments, the polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of the genes in Tables 7, 8 and 9.

**[0023]** Also provided are recombinant host cells comprising at least one polynucleotide encoding a polypeptide identified by the methods provided herein. In embodiments, said host cell further comprises at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity. In embodiments, said heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity is expressed in multiple copies. In embodiments, said heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated. In embodiments, said heterologous polynucleotide is integrated at least once in the recombinant host cell DNA.

**[0024]** In embodiments, said host cell is a yeast host cell. In embodiments, said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia,* and *Pichia*. In embodiments, said heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in the cytosol of the host cell. In embodiments, said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168. In embodiments, said recombinant host cell produces a product selected from the group consisting of branched chain amino acids, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, isobutanol, and combinations thereof. In embodiments, recombinant host cell produces isobutanol. In embodiments, said recombinant host cell comprises an isobutanol biosynthetic pathway. In embodiments said isobutanol biosynthetic pathway comprises at least one polypeptide encoded by a polynucleotide heterologous to the host cell. In embodiments, said isobutanol biosynthetic pathway comprises at least two polypeptides encoded by polynucleotides heterologous to the host cell.

**[0025]** BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

**[0026]** Figure 1A depicts a vector map of a vector for overexpression of the *IlvD* gene from *S. mutans*.

**[0027]** Figure 1B depicts a vector map of an integration vector for overexpression of the *IlvD* gene from *S. mutans* in the chromosome.

**[0028]** Figure 2 depicts a vector map of a centromere vector used to clone *AFT1* or *AFT1* mutants and useful for other genes of interest.

**[0029]** Figure 3 depicts a UV-Vis absorbance spectrum of purified *S. mutans* DHAD.

**[0030]** Figure 4 depicts an EPR spectrum of purified *S. mutans* DHAD.

**[0031]** Figure 5 depicts a biosynthetic pathway for biosynthesis of isobutanol.

**[0032]** Figure 6A depicts a schematic of *Azotobacter vinelandii nif* genes.

**[0033]** Figure 6B depicts a schematic of additional *Azotobacter vinelandii nif* genes.

**[0034]** Figure 6C depicts a schematic of the equation in which NFU acts as a persulfide reductase.

**[0035]** Figure 7 depicts a schematic of *Helicobacter pylori nif* genes.

**[0036]** Figure 8 depicts a schematic of *E. coli isc* genes.

**[0037]** Figure 9 depicts a schematic of *E. coli suf* genes.

Table 12 is a table of the Profile HMM for dihydroxy-acid dehydratases based on enzymes with assayed function prepared as described in U.S. Patent Appl. No. 12/569,636, filed Sept. 29, 2009. Table 12 is submitted herewith electronically and is incorporated herein by reference.

## DETAILED DESCRIPTION OF THE INVENTION

**[0038]** Described herein is a method to increase the fraction of the Fe-S cluster requiring proteins that are loaded with Fe-S clusters. Also described are recombinant host cells that express functional Fe-S cluster requiring proteins, such as DHAD enzymes, and at least one heterologous Fe uptake, utilization, or Fe-S cluster biosynthesis protein, recombinant host cells that express functional DHAD enzymes and comprise at least one deletion, mutation, and/or substitution in a native Fe-S cluster biosynthesis protein, or recombinant host cells comprising combinations thereof. In addition, the present invention describes a method to identify polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell. Also described is a method to identify polypeptides that alter the activity of an Fe-S cluster requiring protein.

**[0039]** <u>Definitions</u>

**[0040]** Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In case of conflict, the present application including the definitions will control. Also, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. All publications, patents and other references mentioned herein are incorporated by reference in their entireties for all purposes.

**[0041]** In order to further define this invention, the following terms and definitions are herein provided.

**[0042]** As used herein, the terms "comprises," "comprising," "includes," "including," "has," "having," "contains" or "containing," or any other variation thereof, will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers. For example, a composition, a mixture, a process, a method, an article, or an 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 and B are true (or present).

**[0043]** As used herein, the term "consists of," or variations such as "consist of" or "consisting of," as used throughout the specification and claims, indicate the inclusion of any recited integer or group of integers, but that no additional integer or group of integers may be added to the specified method, structure, or composition.

**[0044]** As used herein, the term "consists essentially of," or variations such as “consist essentially of” or "consisting essentially of," as used throughout the specification and claims, indicate the inclusion of any recited integer or group of integers, and the optional inclusion of any recited integer or group of integers that do not materially change the basic or novel properties of the specified method, structure or composition.

**[0045]** 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 singular word form of the element or component also includes the plural unless the number is obviously meant to be singular.

**[0046]** 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 described in the application.

**[0047]** 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 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 to 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 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.

**[0048]** The term "isobutanol biosynthetic pathway" refers to an enzyme pathway to produce isobutanol from pyruvate.

**[0049]** The term "a facultative anaerobe" refers to a microorganism that can grow in both aerobic and anaerobic environments.

**[0050]** 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, and one-carbon substrates or mixtures thereof.

**[0051]** The term "Fe-S cluster biosynthesis” refers to biosynthesis of Fe-S clusters, including, *e.g.*, the assembly and loading of Fe-S clusters. The term "Fe-S cluster biosynthesis genes", "Fe-S cluster biosynthesis proteins" or "Fe-S cluster biosynthesis pathway" refers to those polynucleotides/genes and the encoded polypeptides that are involved in the biosynthesis of Fe-S clusters, including, *e.g.*, the assembly and loading of Fe-S clusters.

**[0052]** The term “Fe uptake and utilization” refers to processes which can effect Fe-S cluster biosynthesis such as Fe sensing, uptake, utilization, and homeostasis. “Fe uptake and utilization genes" refers to those polynucleotides/genes and the encoded polypeptides that are involved in Fe uptake, utilization, and homeostasis. Some of these polynucleotides/genes are contained in the "Fe Regulon" that has been described in the literature and is further described hereafter. As used herein, Fe uptake and utilization genes and Fe-S cluster biosynthesis genes can encode a polypeptide affecting Fe-S cluster biosynthesis.

**[0053]** The term "specific activity" as used herein is defined as the units of activity in a given amount of protein. Thus, the specific activity is not directly measured but is calculated by dividing 1) the activity in units/ml of the enzyme sample by 2) the concentration of protein in that sample, so the specific activity is expressed as units/mg. The specific activity of a sample of pure, fully active enzyme is a characteristic of that enzyme. The specific activity of a sample of a mixture of proteins is a measure of the relative fraction of protein in that sample that is composed of the active enzyme of interest. The specific activity of a polypeptide of the invention may be selected from greater than about 0.25 U/mg; greater than about 0.3 U/mg; greater than about 0.4 U/mg; greater than about 0.5 U/mg; greater than about 0.6 U/mg; greater than about 0.7 U/mg; greater than about 0.8 U/mg; greater than about 0.9 U/mg; greater than about 1.0 U/mg; greater than about 1.5 U/mg; greater than about 2.0 U/mg; greater than about 2.5 U/mg; greater than about 3.0 U/mg; greater than about 3.5 U/mg; greater than about 4.0 U/mg; greater than about 5.5 U/mg; greater than about 5.0 U/mg; greater than about 6.0 U/mg; greater than about 6.5 U/mg; greater than about 7.0 U/mg; greater than about 7.5 U/mg; greater than about 8.0 U/mg; greater than about 8.5 U/mg; greater than about 9.0 U/mg; greater than about 9.5 U/mg; greater than about 10.0 U/mg; greater than about 20.0 U/mg; or greater than about 50.0 U/mg. In one embodiment, the specific activity of a polypeptide of the invention is greater than about 0.25 U/mg. In another embodiment, the specific activity is greater than about 1.0 U/mg. In yet another embodiment, the specific activity is greater than about 2.0 U/mg or greater than about 3.0 U/mg.

**[0054]** The term "polynucleotide" is intended to encompass a singular nucleic acid as well as plural nucleic acids, and refers to a nucleic acid molecule or construct, *e.g.*, messeger RNA (mRNA) or plasmid DNA (pDNA). A polynucleotide can contain the nucleotide sequence of the full-length cDNA sequence, or a fragment thereof, including the untranslated 5' and 3' sequences and the coding sequences. The polynucleotide can be composed of any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. "Polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

**[0055]** A polynucleotide sequence may be referred to as "isolated," in which it has been removed from its native environment. For example, a heterologous polynucleotide encoding a polypeptide or polypeptide fragment having dihydroxy-acid dehydratase activity contained in a vector is considered isolated for the purposes of the present invention. Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in solution. Isolated polynucleotides or nucleic acids according to the present invention further include such molecules produced synthetically. An isolated polynucleotide fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

**[0056]** The term "gene" refers to a polynucleotide 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 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 coding sequences derived from the same source, but arranged in a manner different than that found in nature.

**[0057]** As used herein, a "coding region" is a portion of nucleic acid which consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it may be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, introns, and the like, are not part of a coding region. Two or more coding regions of the present invention can be present in a single polynucleotide construct, *e.g.*, on a single vector, or in separate polynucleotide constructs, *e.g.*, on separate (different) vectors. Furthermore, any vector may contain a single coding region, or may comprise two or more coding regions. In addition, a vector, polynucleotide, or nucleic acid of the invention may encode heterologous coding regions.

**[0058]** The term "endogenous," when used in reference to a polynucleotide, a gene, or a polypeptide refers to a native polynucleotide or gene in its natural location in the genome of an organism, or for a native polypeptide, is transcribed and translated from this location in the genome.

**[0059]** The term "heterologous" when used in reference to a polynucleotide, a gene, or a polypeptide refers to a polynucleotide, gene, or polypeptide not normally found in the host organism. "Heterologous" also 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, *e.g.*, not in its natural location in the organism's genome. The heterologous polynucleotide or gene may be introduced into the host organism by, *e.g.*, gene transfer. A heterologous gene may include a native coding region with non-native regulatory regions that is reintroduced into the native host. A "transgene" is a gene that has been introduced into the genome by a transformation procedure.

**[0060]** The term "recombinant genetic expression element" refers to a nucleic acid fragment that expresses one or more specific proteins, including regulatory sequences preceding (5' non-coding sequences) and following (3' termination sequences) coding sequences for the proteins. A chimeric gene is a recombinant genetic expression element. The coding regions of an operon may form a recombinant genetic expression element, along with an operably linked promoter and termination region.

**[0061]** "Regulatory sequences" refers 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 or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters, enhancers, operators, repressors, transcription termination signals, translation leader sequences, introns, polyadenylation recognition sequences, RNA processing site, effector binding site and stem-loop structure.

**[0062]** The term "promoter" refers to a nucleic acid sequence capable of 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 nucleic acid segments. It is understood by 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". "Inducible promoters," on the other hand, cause a gene to be expressed when the promoter is induced or turned on by a promoter-specific signal or molecule. 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.

**[0063]** 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 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.

**[0064]** The term "expression", as used herein, refers to the transcription and 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. The process includes any manifestation of the functional presence of the expressed polynucleotide, gene, or polypeptide within the cell including, without limitation, gene knockdown as well as both transient expression and stable expression.

**[0065]** The term "over-expression", as used herein, refers to expression that is higher than endogenous expression of the same or related polynucleotide or gene. A heterologous polynucleotide or gene is also over-expressed if its expression is higher than that of a comparable endogenous gene, or if its expression is higher than that of the same polynucleotide or gene introduced by a means that does not overexpress the polynucleotide or gene. For example, a polynucleotide can be expressed in a host cell from a low copy number plasmid, which is present in only limited or few copies, and the same polynucleotide can be over-expressed in a host cell from a high copy number plasmid or a plasmid with a copy number that can be regulated, which is present in multiple copies. Any means can be used to over-express a polynucleotide, so long as it increases the copies of the polynucleotide in the host cell. In addition to using a high copy number plasmid, or a plasmid with a copy number that can be regulated, a polynucleotide can be over-expressed by multiple chromosomal integrations.

**[0066]** Expression or over-expression of a polypeptide of the invention in a recombinant host cell can be quantified according to any number of methods known to the skilled artisan and can be represented, *e.g.*, by a percent of total cell protein. The percent of total protein can be an amount selected from greater than about 0.001% of total cell protein; greater than about 0.01% of total cell protein; greater than about 0.1% of total cell protein; greater than about 0.5% of total cell protein; greater than about 1.0% of total cell protein; greater than about 2.0% of total cell protein; greater than about 3% of total cell protein; greater than about 4.0% of total cell protein; greater than about 5% of total cell protein; greater than about 6.0% of total cell protein; greater than about 7.0% of total cell protein; greater than about 8.0% of total cell protein; greater than about 9.0% of total cell protein; greater than about 10% of total cell protein; or greater than about 20% of total cell protein. In one embodiment, the amount of polypeptide expressed is greater that about 0.5% of total cell protein. In another embodiment, the amount of polypeptide expressed is greater than about 1.0% of total cell protein or greater than about 2.0% of total cell protein.

**[0067]** As used herein the term "transformation" refers to the transfer of a nucleic acid fragment into a host organism, resulting in genetically stable inheritance with or without selections. Host organisms containing the transformed nucleic acid fragments are referred to as "transgenic" or "recombinant" or "transformed" organisms.

**[0068]** 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.

**[0069]** 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.

**[0070]** 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. Such optimization includes replacing at least one, or more than one, or a significant number, of codons with one or more codons that are more frequently used in the genes of that organism.

**[0071]** Deviations in the nucleotide sequence that comprise the codons encoding the amino acids of any polypeptide chain allow for variations in the sequence coding for the gene. Since each codon consists of three nucleotides, and the nucleotides comprising DNA are restricted to four specific bases, there are 64 possible combinations of nucleotides, 61 of which encode amino acids (the remaining three codons encode signals ending translation). The "genetic code" which shows which codons encode which amino acids is reproduced herein as Table 1. As a result, many amino acids are designated by more than one codon. For example, the amino acids alanine and proline are coded for by four triplets, serine and arginine by six, whereas tryptophan and methionine are coded by just one triplet. This degeneracy allows for DNA base composition to vary over a wide range without altering the amino acid sequence of the proteins encoded by the DNA.

**Table 1. The Standard Genetic Code**

| | **T** | **C** | **A** | **G** |
|---|---|---|---|---|
| **T** | TTT Phe (F)<br>TTC "<br>TTA Leu (L)<br>TTG " | TCT Ser (S)<br>TCC "<br>TCA "<br>TCG " | TAT Tyr (Y)<br>TAC "<br>TAA **Stop**<br>TAG **Stop** | TGT Cys (C)<br>TGC<br>TGA **Stop**<br>TGG Trp (W) |
| **C** | CTT Leu (L)<br>CTC "<br>CTA "<br>CTG " | CCT Pro (P)<br>CCC "<br>CCA "<br>CCG " | CAT His (H)<br>CAC "<br>CAA Gln (Q)<br>CAG " | CGT Arg (R)<br>CGC "<br>CGA "<br>CGG " |
| **A** | ATT Ile (I)<br>ATC "<br>ATA "<br>**ATG** Met (M) | ACT Thr (T)<br>ACC "<br>ACA "<br>ACG " | AAT Asn (N)<br>AAC "<br>AAA Lys (K)<br>AAG " | AGT Ser (S)<br>AGC "<br>AGA Arg (R)<br>AGG " |
| **G** | GTT Val (V)<br>GTC "<br>GTA "<br>GTG " | GCT Ala (A)<br>GCC "<br>GCA "<br>GCG " | GAT Asp (D)<br>GAC "<br>GAA Glu (E)<br>GAG " | GGT Gly (G)<br>GGC "<br>GGA "<br>GGG " |

**[0072]** Many organisms display a bias for use of particular codons to code for insertion of a particular amino acid in a growing peptide chain. Codon preference, or codon bias, differences in codon usage between organisms, is afforded by degeneracy of the genetic code, and is well documented among many organisms. Codon bias often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, *inter alia*, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization.

**[0073]** Given the large number of gene sequences available for a wide variety of animal, plant and microbial species, it is possible to calculate the relative frequencies of codon usage. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at http://www.kazusa.or.jp/codon/ (visited March 20, 2008), and these tables can be adapted in a number of ways. *See* Nakamura, Y., *et al. Nucl. Acids*

*Res*. *28*:292 (2000). Codon usage tables for yeast, calculated from GenBank Release 128.0 [15 February 2002], are reproduced below as Table 2. This table uses mRNA nomenclature, and so instead of thymine (T) which is found in DNA, the tables use uracil (U) which is found in RNA. Table 2 has been adapted so that frequencies are calculated for each amino acid, rather than for all 64 codons.

**Table 2. Codon Usage Table for *Saccharomyces cerevisiae* Genes**

| Amino Acid | Codon | Number | Frequency per thousand |
|---|---|---|---|
| Phe | UUU | 170666 | 26.1 |
| Phe | UUC | 120510 | 18.4 |
| | | | |
| Leu | UUA | 170884 | 26.2 |
| Leu | UUG | 177573 | 27.2 |
| Leu | CUU | 80076 | 12.3 |
| Leu | CUC | 35545 | 5.4 |
| Leu | CUA | 87619 | 13.4 |
| Leu | CUG | 68494 | 10.5 |
| | | | |
| Ile | AUU | 196893 | 30.1 |
| Ile | AUC | 112176 | 17.2 |
| Ile | AUA | 116254 | 17.8 |
| | | | |
| Met | AUG | 136805 | 20.9 |
| | | | |
| Val | GUU | 144243 | 22.1 |
| Val | GUC | 76947 | 11.8 |
| Val | GUA | 76927 | 11.8 |
| Val | GUG | 70337 | 10.8 |
| | | | |
| Ser | UCU | 153557 | 23.5 |
| Ser | UCC | 92923 | 14.2 |
| Ser | UCA | 122028 | 18.7 |
| Ser | UCG | 55951 | 8.6 |
| Ser | AGU | 92466 | 14.2 |
| Ser | AGC | 63726 | 9.8 |
| | | | |
| Pro | CCU | 88263 | 13.5 |
| Pro | CCC | 44309 | 6.8 |
| Pro | CCA | 119641 | 18.3 |
| Pro | CCG | 34597 | 5.3 |
| | | | |
| Thr | ACU | 132522 | 20.3 |

| Amino Acid | Codon | Number | Frequency per thousand |
|---|---|---|---|
| Thr | ACC | 83207 | 12.7 |
| Thr | ACA | 116084 | 17.8 |
| Thr | ACG | 52045 | 8.0 |
| | | | |
| Ala | GCU | 138358 | 21.2 |
| Ala | GCC | 82357 | 12.6 |
| Ala | GCA | 105910 | 16.2 |
| Ala | GCG | 40358 | 6.2 |
| | | | |
| Tyr | UAU | 122728 | 18.8 |
| Tyr | UAC | 96596 | 14.8 |
| | | | |
| His | CAU | 89007 | 13.6 |
| His | CAC | 50785 | 7.8 |
| | | | |
| Gln | CAA | 178251 | 27.3 |
| Gln | CAG | 79121 | 12.1 |
| | | | |
| Asn | AAU | 233124 | 35.7 |
| Asn | AAC | 162199 | 24.8 |
| | | | |
| Lys | AAA | 273618 | 41.9 |
| Lys | AAG | 201361 | 30.8 |
| | | | |
| Asp | GAU | 245641 | 37.6 |
| Asp | GAC | 132048 | 20.2 |
| | | | |
| Glu | GAA | 297944 | 45.6 |
| Glu | GAG | 125717 | 19.2 |
| | | | |
| Cys | UGU | 52903 | 8.1 |
| Cys | UGC | 31095 | 4.8 |
| | | | |
| Trp | UGG | 67789 | 10.4 |
| | | | |
| Arg | CGU | 41791 | 6.4 |
| Arg | CGC | 16993 | 2.6 |
| Arg | CGA | 19562 | 3.0 |
| Arg | CGG | 11351 | 1.7 |
| Arg | AGA | 139081 | 21.3 |
| Arg | AGG | 60289 | 9.2 |
| | | | |
| Gly | GGU | 156109 | 23.9 |
| Gly | GGC | 63903 | 9.8 |

| Amino Acid | Codon | Number | Frequency per thousand |
|---|---|---|---|
| Gly | GGA | 71216 | 10.9 |
| Gly | GGG | 39359 | 6.0 |
| | | | |
| Stop | UAA | 6913 | 1.1 |
| Stop | UAG | 3312 | 0.5 |
| Stop | UGA | 4447 | 0.7 |

**[0074]** By utilizing this or similar tables, one of ordinary skill in the art can apply the frequencies to any given polypeptide sequence, and produce a nucleic acid fragment of a codon-optimized coding region which encodes the polypeptide, but which uses codons optimal for a given species.

**[0075]** Randomly assigning codons at an optimized frequency to encode a given polypeptide sequence, can be done manually by calculating codon frequencies for each amino acid, and then assigning the codons to the polypeptide sequence randomly. Additionally, various algorithms and computer software programs are readily available to those of ordinary skill in the art. For example, the "EditSeq" function in the Lasergene Package, available from DNAstar, Inc., Madison, WI, the backtranslation function in the VectorNTI Suite, available from InforMax, Inc., Bethesda, MD, and the "backtranslate" function in the GCG-Wisconsin Package, available from Accelrys, Inc., San Diego, CA. In addition, various resources are publicly available to codon-optimize coding region sequences, *e.g.*, the "backtranslation" function at http://www.entelechon.com/bioinformatics/backtranslation.php?lang=eng (visited April 15, 2008) and the "backtranseq" function available at http://bioinfo.pbi.nrc.ca:8090/EMBOSS/index.html (visited July 9, 2002). Constructing a rudimentary algorithm to assign codons based on a given frequency can also easily be accomplished with basic mathematical functions by one of ordinary skill in the art.

**[0076]** Codon-optimized coding regions can be designed by various methods known to those skilled in the art including software packages such as "synthetic gene designer" (http://phenotype.biosci.umbc.edu/codon/sgd/index.php).

**[0077]** As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term "polypeptide" refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, "protein, " "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included within the definition of "polypeptide," and the term "polypeptide" may be used instead of, or interchangeably with any of these terms. A polypeptide may be derived from a natural biological source or produced by recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. It may be generated in any manner, including by chemical synthesis.

**[0078]** By an "isolated" polypeptide or a fragment, variant, or derivative thereof is intended a polypeptide that is not in its natural milieu. No particular level of purification is required. For example, an isolated polypeptide can be removed from its native or natural environment. Recombinantly produced polypeptides and proteins expressed in host cells are considered isolated for purposed of the invention, as are native or recombinant polypeptides which have been separated, fractionated, or partially or substantially purified by any suitable technique.

**[0079]** As used herein, the term "variant" refers to a polypeptide differing from a specifically recited polypeptide of the invention, such as DHAD, by amino acid insertions, deletions, mutations, and substitutions, created using, *e.g.*, recombinant DNA techniques, such as mutagenesis. Guidance in determining which amino acid residues may be replaced, added, or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous polypeptides, *e.g.*, yeast or bacterial, and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequences.

**[0080]** Alternatively, recombinant polynucleotide variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector for expression. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide.

**[0081]** Amino acid "substitutions" may be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements, or they may be the result of replacing one amino acid with an amino acid having different structural and/or chemical properties, *i.e.*, non-conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Alternatively, "non-conservative" amino acid substitutions may be made by selecting the differences in polarity, charge, solubility, hydrophobicity, hydrophilicity, or the amphipathic nature of any of these amino acids. "Insertions" or "deletions" may be within the range of variation as structurally or functionally tolerated by the recombinant proteins. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

**[0082]** 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.

**[0083]** 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, adenine is complementary to thymine and cytosine is complementary to guanine, and with respect to RNA, adenine is complementary to uracil and cytosine is complementary to guanine.

**[0084]** 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.) Humania: 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).

**[0085]** Preferred methods to determine identity are designed to give the 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 alignments of the 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 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, 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 "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 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.

**[0086]** 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, or in describing the corresponding polynucleotides. 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 polynucleotide fragments not only have the above homologies but typically comprise a polynucleotide having at least 50 nucleotides, at least 100 nucleotides, at least 150 nucleotides, at least 200 nucleotides, or at least 250 nucleotides. Further, suitable polynucleotide fragments having the above homologies encode a polypeptide having at least 50 amino acids, at least 100 amino acids, at least 150 amino acids, at least 200 amino acids, or at least 250 amino acids.

**[0087]** 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.

**[0088]** Standard recombinant DNA and molecular cloning techniques used herein 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., Bennan, 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).

**[0089]** The Functions of Fe-S Cluster-Requiring Proteins

**[0090]** The functions of proteins that contain Fe-S clusters are diverse. One of the more complete efforts to classify these functions is given in the following table which is adapted from Johnson, D.C., et al., *Structure, function, and formation of biological iron-sulfur clusters*. Annu. Rev. Biochem., 2005. **74**: p. 247-281.

**Table 3 Functions of Biological [Fe-S] clusters[a]**

| Function | Examples | Cluster type |
|---|---|---|

| | | |
|---|---|---|
| Electron transfer | Ferredoxins; redox enzymes | [2Fe-2S]; [3Fe-4S]; [4Fe-4S] |
| Coupled electron/proton transfer | Rieske protein | [2Fe-2S] |
| | Nitrogenase | [8Fe-7S] |
| Substrate binding and activation | (de)Hydratases | [4Fe-4S], [2Fe-2S] |
| | Radical SAM enzymes | [4Fe-4S] |
| | Acetyl-CoA synthase | Ni-Ni-[4Fe-4S], [Ni-4Fe-5S] |
| | Sulfite reductase | [4Fe-4S]-siroheme |
| Fe or cluster storage | Ferredoxins | [4Fe-4S] |
| | Polyferredoxins | [4Fe-4S] |
| Structural | Endonuclease III | [4Fe-4S] |
| | MutY | [4Fe-4S] |
| Regulation of gene expression | SoxR | [2Fe-2S] |
| | FNR | [4Fe-4S]/[2Fe-2S] |
| | IRP | [4Fe-4S] |
| | IscR | [2Fe-2S] |
| Regulation of enzyme activity | Glutamine PRPP amidotransferase | [4Fe-4S] |
| | Ferrochelatase | [2Fe-2S] |
| Disulfide reduction | Ferredoxin:thioredoxin reductase | [4Fe-4S] |
| | Heterodisulfide reductase | [4Fe-4S] |
| Sulfur donor | Biotin synthase | [2Fe-2S] |

aAbbreviations used are SAM, S-adenosylmethionine; acetyl-CoA, acetyl coenzymeA; FNR, fumarate and nitrate reduction; IRP, iron-regulatory protein; IscR, iron-sulfur cluster assembly regulatory protein; PRPP, phosphoribosylpyrophosphate.

**[0091]** It is believed that an increase in the supply and the efficiency of loading Fe-S clusters into one or more of the members of the above classes will have commercial and/or medical benefits. Of the many possibilities that will be appreciated by the skilled artisan, three examples are given. 1) When an Fe-S cluster containing enzyme is used in a pathway to a fermentation product and needs to be expressed at high levels to maintain a high flux in the pathway to the product (e.g., dihydroxy-acid dehydratase in the pathway to isobutanol). 2) When an Fe-S cluster containing enzyme is used in a pathway to a fermentation product and the Fe-S cluster undergoes turnover during the catalysis (e.g., biotin synthase in the commercial fermentation of glucose to biotin). 3) In a diseased state such that the normal concentration of an Fe-S cluster containing protein important for good health is low (e.g., in cases of Friedreich’s ataxia).

**[0092]** DHAD and DHAD Assays

**[0093]** DHAD is an Fe-S cluster requiring protein of the dehydratase (more properly hydro-lyase) class. A gene encoding a DHAD enzyme can be used to provide expression of DHAD activity in a recombinant host cell. DHAD catalyzes the conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate and of 2,3-dihydroxymethylvalerate to α-ketomethylvalerate and is classified as E.C. 4.2.1.9. Coding sequences for DHADs that are suitable for use in a recombinant host cell can be derived from bacterial, fungal, or plant sources. DHADs that may be used may have a [4Fe-4S] cluster or a [2Fe-2S]. Tables 4a, 4b, 5, and 6 list SEQ ID NOs for coding regions and proteins of representative DHADs that may be used in the present invention. Proteins with at least about 95% identity to certain listed sequences have been omitted for simplification, but it is understood that proteins, including those omitted for simplification, with at least about 95% sequence identity to any of the proteins listed in Tables 4a, 4b, 5, and 6 and having DHAD activity may be used as disclosed herein. Additional DHAD proteins and their encoding sequences may be identified by BLAST searching of public databases, as well known to one skilled in the art. Typically BLAST (described above) searching of publicly available databases with known DHAD sequences, such as those provided herein, is used to identify DHADs and their encoding sequences that may be expressed in the present cells. For example, DHAD proteins having amino acid sequence identities of at least about 80-85%, at least about 85-90%, at least about 90-95%, or at least about 98% sequence identity to any of the DHAD proteins of Table 3 may be expressed in the present cells. 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.

Table 4a. SEQ ID NOs of Representative Bacterial [2Fe-2S] DHAD Proteins and Encoding Sequences

| Organism of derivation | SEQ ID NO: Nucleic acid | SEQ ID NO: Peptide |
|---|---|---|
| *Mycobacterium* sp. MCS | 1 | 2 |
| *Mycobacterium gilvum* PYR-GCK | 3 | 4 |
| *Mycobacterium smegmatis* str. MC2 155 | 5 | 6 |
| *Mycobacterium vanbaalenii* PYR-1 | 7 | 8 |
| *Nocardia farcinica* IFM 10152 | 9 | 10 |

| | | |
|---|---|---|
| *Rhodococcus* sp. RHA1 | 11 | 12 |
| *Mycobacterium ulcerans* Agy99 | 13 | 14 |
| *Mycobacterium avium* subsp. paratuberculosis K-10 | 15 | 16 |
| *Mycobacterium tuberculosis* H37Ra | 17 | 18 |
| *Mycobacterium leprae* TN * | 19 | 20 |
| *Kineococcus radiotolerans* SRS30216 | 21 | 22 |
| *Janibacter* sp. HTCC2649 | 23 | 24 |
| *Nocardioides* sp. JS614 | 25 | 26 |
| *Renibacterium salmoninarum* ATCC 33209 | 27 | 28 |
| *Arthrobacter aurescens* TC1 | 29 | 30 |
| *Leifsonia xyli subsp. xyli* str. CTCB07 | 31 | 32 |
| marine actinobacterium PHSC20C1 | 33 | 34 |
| *Clavibacter michiganensis* subsp. michiganensis NCPPB 382 | 35 | 36 |
| *Saccharopolyspora erythraea* NRRL 2338 | 37 | 38 |
| *Acidothermus cellulolyticus* 11B | 39 | 40 |
| *Corynebacterium efficiens* YS-314 | 41 | 42 |
| *Brevibacterium linens* BL2 | 43 | 44 |
| *Tropheryma whipplei* TW08/27 | 45 | 46 |
| *Methylobacterium extorquens* PA1 | 47 | 48 |
| *Methylobacterium nodulans* ORS 2060 | 49 | 50 |
| *Rhodopseudomonas palustris* BisB5 | 51 | 52 |
| *Rhodopseudomonas palustris* BisB18 | 53 | 54 |
| *Bradyrhizobium* sp. ORS278 | 55 | 56 |
| *Bradyrhizobium japonicum* USDA 110 | 57 | 58 |
| *Fulvimarina pelagi* HTCC2506 | 59 | 60 |
| *Aurantimonas* sp. SI85-9A1 | 61 | 62 |
| *Hoeflea phototrophica* DFL-43 | 63 | 64 |
| *Mesorhizobium loti* MAFF303099 | 65 | 66 |
| *Mesorhizobium* sp. BNC1 | 67 | 68 |
| *Parvibaculum lavamentivorans* DS-1 | 69 | 70 |
| *Loktanella vestfoldensis* SKA53 | 71 | 72 |
| *Roseobacter* sp. CCS2 | 73 | 74 |
| *Dinoroseobacter shibae* DFL 12 | 75 | 76 |
| *Roseovarius nubinhibens* ISM | 77 | 78 |
| *Sagittula stellata* E-37 | 79 | 80 |
| *Roseobacter* sp. AzwK-3b | 81 | 82 |
| *Roseovarius* sp. TM1035 | 83 | 84 |

| | | |
|---|---|---|
| *Oceanicola batsensis* HTCC2597 | 85 | 86 |
| *Oceanicola granulosus* HTCC2516 | 87 | 88 |
| *Rhodobacterales bacterium* HTCC2150 | 89 | 90 |
| *Paracoccus denitrificans* PD1222 | 91 | 92 |
| *Oceanibulbus indolifex* HEL-45 | 93 | 94 |
| *Sulfitobacter* sp. EE-36 | 95 | 96 |
| *Roseobacter denitrificans* OCh 114 | 97 | 98 |
| *Jannaschia* sp. CCS1 | 99 | 100 |
| *Caulobacter* sp. K31 | 101 | 102 |
| *Candidatus Pelagibacter ubique* HTCC1062 | 103 | 104 |
| *Erythrobacter litoralis* HTCC2594 | 105 | 106 |
| *Erythrobacter* sp. NAP1 | 107 | 108 |
| *Comamonas testosterone* KF-1 | 109 | 110 |
| *Sphingomonas wittichii* RW1 | 111 | 112 |
| *Burkholderia xenovorans* LB400 | 113 | 114 |
| *Burkholderia phytofirmans* PsJN | 115 | 116 |
| *Bordetella petrii* DSM 12804 | 117 | 118 |
| *Bordetella bronchiseptica* RB50 | 119 | 120 |
| *Bradyrhizobium* sp. ORS278 | 121 | 122 |
| *Bradyrhizobium* sp. BTAi1 | 123 | 124 |
| *Bradhyrhizobium japonicum* | 125 | 126 |
| *Sphingomonas wittichii* RW1 | 127 | 128 |
| *Rhodobacterales bacterium* HTCC2654 | 129 | 130 |
| *Solibacter usitatus* Ellin6076 | 131 | 132 |
| *Roseiflexus* sp. RS-1 | 133 | 134 |
| *Rubrobacter xylanophilus* DSM 9941 | 135 | 136 |
| *Salinispora tropica* CNB-440 | 137 | 138 |
| *Acidobacteria bacterium* Ellin345 | 139 | 140 |
| *Thermus thermophilus* HB27 | 141 | 142 |
| *Maricaulis maris* MCS10 | 143 | 144 |
| *Parvularcula bermudensis* HTCC2503 | 145 | 146 |
| *Oceanicaulis alexandrii* HTCC2633 | 147 | 148 |
| *Plesiocystis pacifica* SIR-1 | 149 | 150 |
| *Bacillus* sp. NRRL B-14911 | 151 | 152 |
| *Oceanobacillus iheyensis* HTE831 | 153 | 154 |
| *Staphylococcus saprophyticus* subsp. saprophyticus ATCC 15305 | 155 | 156 |
| *Bacillus selenitireducens* MLS10 | 157 | 158 |

| | | |
|---|---|---|
| *Streptococcus pneumoniae* SP6-BS73 | 159 | 160 |
| *Streptococcus sanguinis* SK36 | 161 | 162 |
| *Streptococcus thermophilus* LMG 18311 | 163 | 164 |
| *Streptococcus suis* 89/1591 | 165 | 166 |
| *Streptococcus mutans* UA159 | 167 | 168 |
| *Leptospira borgpetersenii serovar Hardjo-bovis* L550 | 169 | 170 |
| *Candidatus Vesicomyosocius okutanii* HA | 171 | 172 |
| *Candidatus Ruthia magnifica* str. Cm (*Calyptogena magnifica*) | 173 | 174 |
| *Methylococcus capsulatus* str. Bath | 175 | 176 |
| uncultured marine bacterium EB80_02D08 | 177 | 178 |
| uncultured marine gamma proteobacterium EBAC31A08 | 179 | 180 |
| uncultured marine gamma proteobacterium EBAC20E09 | 181 | 182 |
| uncultured gamma proteobacterium eBACHOT4E07 | 183 | 184 |
| *Alcanivorax borkumensis* SK2 | 185 | 186 |
| *Chromohalobacter salexigens* DSM 3043 | 187 | 188 |
| *Marinobacter algicola* DG893 | 189 | 190 |
| *Marinobacter aquaeolei* VT8 | 191 | 192 |
| *Marinobacter* sp. ELB17 | 193 | 194 |
| *Pseudoalteromonas haloplanktis* TAC125 | 195 | 196 |
| *Acinetobacter* sp. ADP1 | 197 | 198 |
| *Opitutaceae* bacterium TAV2 | 199 | 200 |
| *Flavobacterium* sp. MED217 | 201 | 202 |
| *Cellulophaga* sp. MED134 | 203 | 204 |
| *Kordia algicida* OT-1 | 205 | 206 |
| *Flavobacteriales bacterium* ALC-1 | 207 | 208 |
| *Psychroflexus torquis* ATCC 700755 | 209 | 210 |
| *Flavobacteriales bacterium* HTCC2170 | 211 | 212 |
| unidentified eubacterium SCB49 | 213 | 214 |
| *Gramella forsetii* KT0803 | 215 | 216 |
| *Robiginitalea biformata* HTCC2501 | 217 | 218 |
| *Tenacibaculum* sp. MED152 | 219 | 220 |
| *Polaribacter irgensii* 23-P | 221 | 222 |
| *Pedobacter* sp. BAL39 | 223 | 224 |
| *Flavobacteria bacterium* BAL38 | 225 | 226 |
| *Flavobacterium psychrophilum* JIP02/86 | 227 | 228 |

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|---|---|---|
| *Flavobacterium johnsoniae* UW101 | 229 | 230 |
| *Lactococcus lactis* subsp. cremoris SK11 | 231 | 232 |
| *Psychromonas ingrahamii* 37 | 233 | 234 |
| *Microscilla marina* ATCC 23134 | 235 | 236 |
| *Cytophaga hutchinsonii* ATCC 33406 | 237 | 238 |
| *Rhodopirellula baltica* SH 1 | 239 | 240 |
| *Blastopirellula marina* DSM 3645 | 241 | 242 |
| *Planctomyces maris* DSM 8797 | 243 | 244 |
| *Algoriphagus* sp. PR1 | 245 | 246 |
| *Candidatus Sulcia muelleri* str. Hc (*Homalodisca coagulata*) | 247 | 248 |
| *Candidatus Carsonella ruddii* PV | 249 | 250 |
| *Synechococcus* sp. RS9916 | 251 | 252 |
| *Synechococcus* sp. WH 7803 | 253 | 254 |
| *Synechococcus* sp. CC9311 | 255 | 256 |
| *Synechococcus* sp. CC9605 | 257 | 258 |
| *Synechococcus* sp. WH 8102 | 259 | 260 |
| *Synechococcus* sp. BL107 | 261 | 262 |
| *Synechococcus* sp. RCC307 | 263 | 264 |
| *Synechococcus* sp. RS9917 | 265 | 266 |
| *Synechococcus* sp. WH 5701 | 267 | 268 |
| *Prochlorococcus marinus* str. MIT 9313 | 269 | 270 |
| *Prochlorococcus marinus* str. NATL2A | 271 | 272 |
| *Prochlorococcus marinus* str. MIT 9215 | 273 | 274 |
| *Prochlorococcus marinus* str. AS9601 | 275 | 276 |
| *Prochlorococcus marinus* str. MIT 9515 | 277 | 278 |
| *Prochlorococcus marinus* subsp. pastoris str. CCMP1986 | 279 | 280 |
| *Prochlorococcus marinus* str. MIT 9211 | 281 | 282 |
| *Prochlorococcus marinus* subsp. marinus str. CCMP1375 | 283 | 284 |
| *Nodularia spumigena* CCY9414 | 285 | 286 |
| *Nostoc punctiforme* PCC 73102 | 287 | 288 |
| *Nostoc* sp. PCC 7120 | 289 | 290 |
| *Trichodesmium erythraeum* IMS101 | 291 | 292 |
| *Acaryochloris marina* MBIC11017 | 293 | 294 |
| *Lyngbya* sp. PCC 8106 | 295 | 296 |

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|---|---|---|
| *Synechocystis* sp. PCC 6803 | 297 | 298 |
| *Cyanothece* sp. CCY0110 | 299 | 300 |
| *Thermosynechococcus elongatus* BP-1 | 301 | 302 |
| *Synechococcus* sp. JA-2-3B'a(2-13) | 303 | 304 |
| *Gloeobacter violaceus* PCC 7421 | 305 | 306 |
| *Nitrosomonas eutropha* C91 | 307 | 308 |
| *Nitrosomonas europaea* ATCC 19718 | 309 | 310 |
| *Nitrosospira multiformis* ATCC 25196 | 311 | 312 |
| *Chloroflexus aggregans* DSM 9485 | 313 | 314 |
| *Leptospirillum* sp. Group II UBA | 315 | 316 |
| *Leptospirillum* sp. Group II UBA | 317 | 318 |
| *Halorhodospira halophila* SL1 | 319 | 320 |
| *Nitrococcus mobilis* Nb-231 | 321 | 322 |
| *Alkalilimnicola ehrlichei* MLHE-1 | 323 | 324 |
| *Deinococcus geothermalis* DSM 11300 | 325 | 326 |
| *Polynucleobacter* sp. QLW-P1DMWA-1 | 327 | 328 |
| *Polynucleobacter necessarius* STIR1 | 329 | 330 |
| *Azoarcus* sp. EbN1 | 331 | 332 |
| *Burkholderia phymatum* STM815 | 333 | 334 |
| *Burkholderia xenovorans* LB400 | 335 | 336 |
| *Burkholderia multivorans* ATCC 17616 | 337 | 338 |
| *Burkholderia cenocepacia* PC184 | 339 | 340 |
| *Burkholderia mallei* GB8 horse 4 | 341 | 342 |
| *Ralstonia eutropha* JMP134 | 343 | 344 |
| *Ralstonia metallidurans* CH34 | 345 | 346 |
| *Ralstonia solanacearum* UW551 | 347 | 348 |
| *Ralstonia pickettii* 12J | 349 | 350 |
| *Limnobacter* sp. MED105 | 351 | 352 |
| *Herminiimonas arsenicoxydans* | 353 | 354 |
| *Bordetella parapertussis* | 355 | 356 |
| *Bordetella petrii* DSM 12804 | 357 | 358 |
| *Polaromonas* sp. JS666 | 359 | 360 |
| *Polaromonas naphthalenivorans* CJ2 | 361 | 362 |
| *Rhodoferax ferrireducens* T118 | 363 | 364 |
| *Verminephrobacter eiseniae* EF01-2 | 365 | 366 |
| *Acidovorax* sp. JS42 | 367 | 368 |
| *Delftia acidovorans* SPH-1 | 369 | 370 |
| *Methylibium petroleiphilum* PM1 | 371 | 372 |

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|---|---|---|
| *gamma proteobacterium* KT 71 | 373 | 374 |
| *Tremblaya princeps* | 375 | 376 |
| *Blastopirellula marina* DSM 3645 | 377 | 378 |
| *Planctomyces maris* DSM 8797 | 379 | 380 |
| *Microcystis aeruginosa* PCC 7806 | 381 | 382 |
| *Salinibacter ruber* DSM 13855 | 383 | 384 |
| *Methylobacterium chloromethanicum* | 385 | 386 |

Table 4b. Additional representative bacterial [2Fe-2S] DHAD proteins and encoding sequences

| Organism of derivation | Nucleic acid SEQ ID NO: | Amino acid SEQ ID NO: |
|---|---|---|
| *Burkholderia ambifaria* AMMD | 387 | 388 |
| *Bradyrhizobium sp.* BTAi1 | 389 | 390 |
| *Delftia acidovorans* SPH-1 | 391 | 392 |
| *Microcystis aeruginosa* NIES-843 | 393 | 394 |
| uncultured marine microorganism HF4000_APKG8C21 | 395 | 396 |
| *Burkholderia ubonensis* Bu | 397 | 398 |
| *Gemmata obscuriglobus* UQM 2246 | 399 | 400 |
| *Mycobacterium abscessus* | 401 | 402 |
| *Synechococcus sp.* PCC 7002 | 403 | 404 |
| *Burkholderia graminis* C4D1M | 405 | 406 |
| *Methylobacterium radiotolerans* JCM 2831 | 407 | 408 |
| *Leptothrix cholodnii* SP-6 | 409 | 410 |
| *Verrucomicrobium spinosum* DSM 4136 | 411 | 412 |
| *Cyanothece sp.* ATCC 51142 | 413 | 414 |
| *Opitutus terrae* PB90-1 | 415 | 416 |
| *Leptospira biflexa* serovar Patoc strain 'Patoc 1 (Paris)' | 417 | 418 |
| *Methylacidiphilum infernorum* V4 | 419 | 420 |
| *Cupriavidus taiwanensis* | 421 | 422 |
| *Chthoniobacter flavus* Ellin428 | 423 | 424 |
| *Cyanothece sp.* PCC 7822 | 425 | 426 |
| *Phenylobacterium zucineum* HLK1 | 427 | 428 |
| *Leptospirillum sp.* Group II '5-way CG' | 429 | 430 |
| *Arthrospira maxima* CS-328 | 431 | 432 |
| *Oligotropha carboxidovorans* OM5 | 433 | 434 |
| *Rhodospirillum centenum* SW | 435 | 436 |
| *Cyanothece sp.* PCC 8801 | 437 | 438 |

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|---|---|---|
| *Thermus aquaticus* Y51MC23 | 439 | 440 |
| *Cyanothece sp.* PCC 7424 | 441 | 442 |
| *Acidithiobacillus ferrooxidans* ATCC 23270 | 443 | 444 |
| *Cyanothece sp.* PCC 7425 | 445 | 446 |
| *Arthrobacter chlorophenolicus* A6 | 447 | 448 |
| *Burkholderia multivorans* CGD2M | 449 | 450 |
| *Thermomicrobium roseum* DSM 5159 | 451 | 452 |
| bacterium Ellin514 | 453 | 454 |
| *Desulfobacterium autotrophicum* HRM2 | 455 | 456 |
| *Thioalkalivibrio sp.* K90mix | 457 | 458 |
| Flavobacteria bacterium MS024-3C | 459 | 460 |
| Flavobacteria bacterium MS024-2A | 461 | 462 |
| *'Nostoc azollae'* 0708 | 463 | 464 |
| *Acidobacterium capsulatum* ATCC 51196 | 465 | 466 |
| *Gemmatimonas aurantiaca* T-27 | 467 | 468 |
| *Gemmatimonas aurantiaca* T-27 | 469 | 470 |
| *Rhodococcus erythropolis* PR4 | 471 | 472 |
| *Deinococcus deserti* VCD115 | 473 | 474 |
| *Rhodococcus opacus* B4 | 475 | 476 |
| *Chryseobacterium gleum* ATCC 35910 | 477 | 478 |
| *Thermobaculum terrenum* ATCC BAA-798 | 479 | 480 |
| *Kribbella flavida* DSM 17836 | 481 | 482 |
| *Gordonia bronchialis* DSM 43247 | 483 | 484 |
| *Geodermatophilus obscurus* DSM 43160 | 485 | 486 |
| *Xylanimonas cellulosilytica* DSM 15894 | 487 | 488 |
| *Sphingobacterium spiritivorum* ATCC 33300 | 489 | 490 |
| *Meiothermus silvanus* DSM 9946 | 491 | 492 |
| *Meiothermus ruber* DSM 1279 | 493 | 494 |
| *Nakamurella multipartita* DSM 44233 | 495 | 496 |
| *Cellulomonas flavigena* DSM 20109 | 497 | 498 |
| *Rhodothermus marinus* DSM 4252 | 499 | 500 |
| *Planctomyces limnophilus* DSM 3776 | 501 | 502 |
| *Beutenbergia cavernae* DSM 12333 | 503 | 504 |
| *Spirosoma linguale* DSM 74 | 505 | 506 |
| *Sphaerobacter thermophilus* DSM 20745 | 507 | 508 |
| *Lactococcus lactis* | 509 | 510 |
| *Thermus thermophilus* HB8 | 511 | 512 |
| *Anabaena variabilis* ATCC 29413 | 513 | 514 |

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|---|---|---|
| *Roseovarius sp.* 217 | 515 | 516 |
| uncultured *Prochlorococcus marinus* clone HF10-88D1 | 517 | 518 |
| *Burkholderia xenovorans* LB400 | 519 | 520 |
| *Saccharomonospora viridis* DSM 43017 | 521 | 522 |
| *Pedobacter heparinus* DSM 2366 | 523 | 524 |
| *Microcoleus chthonoplastes* PCC 7420 | 525 | 526 |
| *Acidimicrobium ferrooxidans* DSM 10331 | 527 | 528 |
| *Rhodobacterales bacterium* HTCC2083 | 529 | 530 |
| *Candidatus Pelagibacter* sp. HTCC7211 | 531 | 532 |
| *Chitinophaga pinensis* DSM 2588 | 533 | 534 |
| *Alcanivorax sp*. DG881 | 535 | 536 |
| *Micrococcus luteus* NCTC 2665 | 537 | 538 |
| *Verrucomicrobiae bacterium* DG1235 | 539 | 540 |
| *Synechococcus sp*. PCC 7335 | 541 | 542 |
| *Brevundimonas sp.* BAL3 | 543 | 544 |
| *Dyadobacter fermentans* DSM 18053 | 545 | 546 |
| *gamma proteobacterium* NOR5-3 | 547 | 548 |
| *gamma proteobacterium* NOR51-B | 549 | 550 |
| *Cyanobium sp.* PCC 7001 | 551 | 552 |
| *Jonesia denitrificans* DSM 20603 | 553 | 554 |
| *Brachybacterium faecium* DSM 4810 | 555 | 556 |
| *Paenibacillus sp.* JDR-2 | 557 | 558 |
| *Octadecabacter antarcticus* 307 | 559 | 560 |
| *Variovorax paradoxus* S110 | 561 | 562 |

Table 5. SEQ ID NOs of Representative Fungal and Plant [2Fe-2S] DHAD Proteins and Encoding Sequences

| Description | SEQ ID NO: Nucleic acid | SEQ ID NO: Peptide |
|---|---|---|
| *Schizosaccharomyces pombe* ILV3 | 563 | 564 |
| *Saccharomyces cerevisiae* ILV3 | 565 | 566 |
| *Kluyveromyces lactis* ILV3 | 567 | 568 |
| *Candida albicans* SC5314 ILV3 | 569 | 570 |
| *Pichia stipitis* CBS 6054 ILV3 | 571 | 572 |
| *Yarrowia lipolytica* ILV3 | 573 | 574 |
| *Candida galbrata CBS 138* ILV3 | 575 | 576 |
| *Chlamydomonas reinhardtii* | 577 | 578 |

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|---|---|---|
| *Ostreococcus lucimarinus* CCE9901 | 579 | 580 |
| *Vitis vinifera*<br>(Unnamed protein product: CAO71581.1) | 581 | 582 |
| *Vitis vinifera*<br>(Hypothetical protein: CAN67446.1) | 583 | 584 |
| *Arabidopsis thaliana* | 585 | 586 |
| *Oryza sativa (*indica cultivar-group) | 587 | 588 |
| *Physcomitrella patens* subsp. Patens | 589 | 590 |
| *Chaetomium globosum* CBS 148.51 | 591 | 592 |
| *Neurospora crassa* OR74A | 593 | 594 |
| *Magnaporthe grisea* 70-15 | 595 | 596 |
| *Gibberella zeae* PH-1 | 597 | 598 |
| *Aspergillus niger* | 599 | 600 |
| *Neosartorya fischeri* NRRL 181<br>(XP_001266525.1) | 601 | 602 |
| *Neosartorya fischeri* NRRL 181<br>(XP_001262996.1) | 603 | 604 |
| *Aspergillus niger*<br>(hypothetical protein An03g04520) | 605 | 606 |
| *Aspergillus niger*<br>(Hypothetical protein An14g03280) | 607 | 608 |
| *Aspergillus terreus* NIH2624 | 609 | 610 |
| *Aspergillus clavatus* NRRL 1 | 611 | 612 |
| *Aspergillus nidulans* FGSC A4 | 613 | 614 |
| *Aspergillus oryzae* | 615 | 616 |
| *Ajellomyces capsulatus* NAm1 | 617 | 618 |
| *Coccidioides immitis* RS | 619 | 620 |
| *Botryotinia fuckeliana* B05.10 | 621 | 622 |
| *Phaeosphaeria nodorum* SN15 | 623 | 624 |
| *Pichia guilliermondii* ATCC 6260 | 625 | 626 |
| *Debaryomyces hansenii* CBS767 | 627 | 628 |
| *Lodderomyces elongisporus* NRRL YB-4239 | 629 | 630 |
| *Vanderwaltozyma polyspora* DSM 70294 | 631 | 632 |
| *Ashbya gossypii* ATCC 10895 | 633 | 634 |
| *Laccaria bicolor* S238N-H82 | 635 | 636 |
| *Coprinopsis cinerea okayama*7#130 | 637 | 638 |
| *Cryptococcus neoformans var. neoformans* JEC21 | 639 | 640 |
| *Ustilago maydis* 521 | 641 | 642 |

| | | |
|---|---|---|
| *Malassezia globosa* CBS 7966 | 643 | 644 |
| *Aspergillus clavatus* NRRL 1 | 645 | 646 |
| *Neosartorya fischeri* NRRL 181 (Putative) | 647 | 648 |
| *Aspergillus oryzae* | 649 | 650 |
| *Aspergillus niger* (hypothetical protein An18g04160) | 651 | 652 |
| *Aspergillus terreus* NIH2624 | 653 | 654 |
| *Coccidioides immitis RS* (hypothetical protein CIMG_04591) | 655 | 656 |
| *Paracoccidioides brasiliensis* | 657 | 658 |
| *Phaeosphaeria nodorum* SN15 | 659 | 660 |
| *Gibberella zeae* PH-1 | 661 | 662 |
| *Neurospora crassa* OR74A | 663 | 664 |
| *Coprinopsis cinerea okayama* 7#130 | 665 | 666 |
| *Laccaria bicolor* S238N-H82 | 667 | 668 |
| *Ustilago maydis* 521 | 669 | 670 |

Table 6. SEQ ID NOs of Representative [4Fe-4S] DHAD Proteins and Encoding Sequences

| Organism | SEQ ID NO: Nucleic acid | SEQ ID NO: Peptide |
|---|---|---|
| *Escherichia coli* str. K-12 substr. MG1655 | 671 | 672 |
| *Bacillus subtilis subsp. subtilis* str. 168 | 673 | 674 |
| *Agrobacterium tumefaciens* str. C58 | 675 | 676 |
| *Burkholderia cenocepacia* MC0-3 | 677 | 678 |
| *Psychrobacter cryohalolentis* K5 | 679 | 680 |
| *Psychromonas* sp. CNPT3 | 681 | 682 |
| *Deinococcus radiodurans* R1 | 683 | 684 |
| *Wolinella succinogenes* DSM 1740 | 685 | 686 |
| *Zymomonas mobilis* subsp. mobilis ZM4 | 687 | 688 |
| *Clostridium acetobutylicum* ATCC 824 | 689 | 690 |
| *Clostridium beijerinckii* NCIMB 8052 | 691 | 692 |
| *Pseudomonas fluorescens* Pf-5 | 693 | 694 |
| *Methanococcus maripaludis* C7 | 695 | 696 |
| *Methanococcus aeolicus* Nankai-3 | 697 | 698 |
| *Vibrio fischeri ATCC 700601 (ES114)* | 699 | 700 |
| *Shewanella oneidensis MR-1 ATCC 700550* | 701 | 702 |

**[0094]** Additional [2Fe-2S] DHADs may be identified using the analysis described in U.S. Patent Appl. No. 12/569,636, filed Sept. 29, 2009, which is herein incorporated by reference. The analysis is as follows: 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:309; protein SEQ ID NO:310), Synechocystis sp. PCC6803 (DNA SEQ ID:297; protein SEQ ID NO:298), Streptococcus mutans (DNA SEQ ID NO:167; protein SEQ ID NO:168), Streptococcus thermophilus (DNA SEQ ID NO:163; SEQ ID No:164), Ralstonia metallidurans (DNA SEQ ID NO:345; protein SEQ ID NO:346), Ralstonia eutropha (DNA SEQ ID NO:343; protein SEQ ID NO:344), and Lactococcus lactis (DNA SEQ ID NO:231; protein SEQ ID NO:232). In addition the DHAD from Flavobacterium johnsoniae (DNA SEQ ID NO:229; protein SEQ ID NO:230) 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. The Profile HMM prepared for the eight DHAD proteins is given in U.S. Appl. No. 12/569,636, filed Sept. 29, 2009 and in Table 12.

**[0095]** 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. In embodiments, 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] 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% occurance): 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.

**[0096]** Additionally, the sequences of DHAD coding regions provided herein may be used to identify other homologs in nature. Such methods are well-known in the art, and various methods that may be used to isolate genes encoding homologous proteins are described in U.S. Appl. No. 12/569,636, filed Sept. 29, 2009, which such methods are incorporated by reference herein.

**[0097]** The presence of DHAD activity in a cell engineered to express a heterologous DHAD can be confirmed using methods known in the art. As one example, and as demonstrated in the Examples herein, crude extracts from cells engineered to express a bacterial DHAD may be used in a DHAD assay as described by Flint and Emptage (J. Biol. Chem. (1988) 263(8): 3558-64) using dinitrophenylhydrazine. In another example, DHAD activity may be assayed by expressing a heterologous DHAD identifiable by the methods disclosed herein in a yeast strain that lacks endogenous DHAD activity. If DHAD activity is present, the yeast strain will grow in the absence of branched-chain amino acids. DHAD activity may also be confirmed by more indirect methods, such as by assaying for a downstream product in a pathway requiring DHAD activity. Any product that has α-ketoisovalerate or α-ketomethylvalerate as a pathway intermediate may be measured in an assay for DHAD activity. A list of such products includes, but is not limited to, valine, isoleucine, leucine, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, and isobutanol.

**[0098]** Over-Expression of DHAD Activity

**[0099]** Applicants have found that expression of a heterologous DHAD can provide DHAD activity when expressed in a host cell. Expression of a DHAD which may be identified as described herein can provide DHAD activity for a biosynthetic pathway that includes conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate or 2,3-dihydroxymethylvalerate to α-ketomethylvalerate. In addition, the *S. mutans* [2Fe-2S] DHAD was shown in related U.S. Appl. No. 12/569,636, filed Sept. 29, 2009, incorporated by reference herein, to have higher stability in air as compared to the sensitivity in air of the E. coli [4Fe-4S] DHAD, which is desirable for obtaining better activity in a heterologous host cell.

**[00100]** Furthermore, as described herein, it has been found that expressing a heterologous DHAD protein at higher levels can provide increased DHAD activity when expressed in a host cell. High expression of a recombinant polynucleotide can be accomplished in at least two ways: 1) by increasing the copy number of a plasmid comprising the recombinant polynucleotide; or 2) by integrating multiple copies of the gene of interest into the host cell's chromosome. As exemplified herein, expression of multiple copies of the heterologous DHAD, provides an increase in specific activity of heterologous DHAD

**[00101]** Recombinant polynucleotides are typically cloned for expression using the coding sequence as part of a chimeric gene used for transformation, which includes a promoter operably linked to the coding sequence as well as a ribosome binding site and a termination control region. The coding region may be from the host cell for transformation and combined with regulatory sequences that are not native to the natural gene encoding DHAD. Alternatively, the coding region may be from another host cell.

**[00102]** Vectors useful for the transformation of a variety of host cells are common and described in the literature. Typically the vector contains a selectable marker and sequences allowing autonomous replication or chromosomal integration in the desired host. In addition, suitable vectors may comprise a promoter region which harbors transcriptional initiation controls and a transcriptional termination control region, between which a coding region DNA fragment may be inserted, to provide expression of the inserted coding region. Both control regions may be derived from genes homologous to the transformed host cell, although it is to be understood that such control regions may also be derived from genes that are not native to the specific species chosen as a production host.

**[00103]** Yeast cells that can be hosts for expression or over-expression of a heterologous bacterial DHAD are any yeast cells that are amenable to genetic manipulation and include, but are not limited to, *Saccharomyces, Schizosaccharomyces, Hansenula, Candida, Kluyveromyces, Yarrowia, Issatchenkia*, 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*. In one embodiment, the host is *Saccharomyces cerevisiae*.

**[00104]** Expression is achieved by transforming a host cell with a gene comprising a sequence encoding DHAD, for example, a DHAD listed in Tables 4a, 4b, 5 or 6, or identified using the screening methods in related U.S. Appl. No. 12/569,636, filed Sept. 29, 2009, incorporated by reference herein. The coding region for the DHAD 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, e.g., 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, FBAt, GPDt, GPMt, ERG10t, GAL1t, CYC1, and ADH1.

**[00105]** Suitable promoters, transcriptional terminators, and DHAD 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. In one embodiment, the vector used contains a selectable marker and sequences allowing autonomous replication or chromosomal integration in the desired host. Examples of plasmids used 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-micron 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 DHADs can be performed by either standard molecular cloning techniques in *E. coli* or by the gap repair recombination method in yeast.

**[00106]** The gap repair cloning approach takes advantage of the highly efficient homologous recombination in yeast. For example, 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.

**[00107]** Like the gap repair technique, integration into the yeast genome also takes advantage of the homologous recombination system in yeast. For example, 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 verified either by colony PCR or by direct sequencing of chromosomal DNA.

**[00108]** In addition to the above materials and methods that may be used to express a heterologous DHAD, these same, or similar, materials and methods may be used to over-express a heterologous DHAD using modifications known to one of skill in the art. For example, when using a plasmid-based system to over-express the recombinant polynucleotide, a high-copy number vector, or a vector with a copy number that can be regulated, may be constructed. Such a regulatable or inducible system is described herein in Example 1; however, other systems are known to one of skill in the art and may be used to construct other high-copy number or copy number regulatable vectors. Alternatively, when using an integration-based system to over-express the recombinant polypeptide, an integration vector is required for targeting at multiple integration sites. A multiple integration-based system is described herein in Example 2; however, other multiple integration-based systems are known to one of skill in the art and may be used to target multiple integrations of a recombinant polypeptide, for example integration into rDNA regions.

**[00109]** Expression of the heterologous DHAD in the recombinant host cell can be quantified, *e.g.*, by a percent of total cell protein. Such over-expression can be quantified in an amount selected from the group consisting of: (a) greater than about 0.001% of total cell protein; (b) greater than about 0.01% of total cell protein; (c) greater than about 0.1% of total cell protein; (d) greater than about 0.5% of total cell protein; (e) greater than about 1.0% of total cell protein; (f) greater than about 2.0% of total cell protein; (g) greater than about 5% of total cell protein; (h) greater than about 10% of total cell protein; and (i) greater than about 20% of total cell protein.

**[00110]** The specific activity of the heterologous DHAD produced in a recombinant host cell can be quantified, *e.g.*, as U/mg. The heterologous DHAD specific activity can be selected from the group consisting of: (a) greater than about 0.25 U/mg; (b) greater than about 0.3 U/mg; (c) greater than about 0.5 U/mg; (d) greater than about 1.0 U/mg; (e) greater than about 1.5 U/mg; (f) greater than about 2.0 U/mg; (g) greater than about 3.0 U/mg; (h) greater than about 4.0 U/mg; (i) greater than about 5.0 U/mg; (j) greater than about 6.0 U/mg; (k) greater than about 7.0 U/mg; (l) greater than about 8.0 U/mg; (m) greater than about 9.0 U/mg; (n) greater than about 10.0 U/mg; (o) greater than about 20.0 U/mg; and (p) greater than about 50.0 U/mg.

**[00111]** The heterologous DHAD specific activity can also be quantified, e.g., as a percent comparison to an endogenous DHAD specific activity or to some other control DHAD specific activity. An example of a "control" DHAD specific activity is that from a heterologous DHAD expressed in a recombinant host cell using a low copy number plasmid or a plasmid that is not other wise inducible or regulatable. Such a control establishes a baseline from which to compare the specific activity of the same heterologous DHAD expressed in a recombinant host cell using a high copy number plasmid or a plasmid with copy number that can be regulated, or co-expressed with polynucleotides encoding polypeptides affecting Fe-S cluster biosynthesis or Fe uptake and utilization, as described below. Thus, the increase in specific activity of the heterologous DHAD when compared to the control DHAD specific activity can be in an amount selected from the group consisting of: greater than an about 10% increase; greater than an about 20% increase; greater than an about 30% increase; greater than an about 40% increase; greater than an about 50% increase; greater than an about 60% increase; greater than an about 70% increase; greater than an about 80% increase; greater than an about 90% increase; greater than an about 95% increase; greater than an about 98% increase; and greater than an about 99% increase. The heterologous DHAD specific activity can also be expressed by "fold increase" over control. Thus, the increase in specific activity can be selected from the group consisting of: (a) greater than about 2-fold higher, (b) greater than about 5-fold higher, (c) greater than about 8-fold higher, or (d) greater than about 10-fold higher than control.

**[00112]** Fe-S Cluster Forming Proteins and Fe Regulation, Utilization, and Homeostasis

**[00113]** As described above, DHAD enzymes require Fe-S clusters for functioning, therefore, they must be expressed in a host having the genetic machinery to produce and load Fe-S clusters into the apo-protein if they are going to be expressed in functional form. As described elsewhere herein, in normal yeast, the mitochondria play an important role in Fe-S cluster biosynthesis. The flux in the formation and movement of Fe-S cluster precursors from mitochondria to Fe-S cluster requiring proteins in the cytosol of normal yeast is believed to be limited. For example, after a point a further increase in the expression of the protein of heterologous DHADs in the cytosol does not result in a corresponding increase in DHAD activity. While not wishing to be bound by theory, it is believed that this is because the increased amounts of the heterologous DHAD are not getting loaded with the Fe-S cluster requisite for activity because the cell is not able to supply the increased demand for Fe-S clusters that arises in the conditions described above. Demonstrated herein is that yeast cells can be genetically modified in 2 ways (separately or contemporaneously) that will result in an increased fraction of the heterologous DHAD expressed in the cytosol being loaded with its requisite Fe-S cluster. One way is to to modify the expression of yeast genes involved in the Fe-S cluster formation, such as Fe-S cluster biosynthesis pathway genes or Fe uptake and utilization genes, The other way is to express heterologous genes involved in Fe-S cluster biosynthesis or Fe uptake and utilization in the cytoplasm of yeast.

**[00114]** Yeast genes that encode polypeptides that are involved in Fe uptake and utilization and Fe-S cluster biosynthesis are candidates for modification of expression. In embodiments, the modification results in increased function of a selected Fe-S cluster requiring protein.

**[00115]** As an example, Aft1 has been found to act as a transcriptional activator for genes into the iron regulon (Kumanovics, et al. J. Biol. Chem., 2008. 283, p. 10276-10286; Li, H., et al., *The Yeast Iron Regulatory Proteins Grx3/4 and Fra2 form Heterodimeric Complexes Containing a [2Fe-2S] Cluster with Cysteinyl and Histidyl Ligation.* Biochemistry, 2009. **48**(40): p. 9569-9581. As exemplified herein, the deletion of known inhibitors of Aft1 translocation, results in an increase in specific activity of an Fe-S cluster requiring protein because it leads to an increase Fe-S cluster loading of the protien. While not wishing to be bound by theory, it is thus believed that altering expression of certain genes of the Fe regulon, whether directly or through deletion or upregulation of inhibitors, will likewise increase the loading and function of Fe-S cluster requiring proteins. For example, genes that play a role in, or are part of, Fe utilization and homeostasis in yeast, such as Fe Regulon genes, may be targeted for altered expression. Such genes are known in the art, and examples of these genes are listed in Table 7. (The list in Table 7 is taken from [1] Rutherford, J.C., et al., *Activation of the Iron Regulon by the Yeast Aft1/Aft2 Transcription Factors Depends on Mitochondrial but Not Cytosolic Iron-Sulfur Protein Biogenesis.* J. Biol. Chem., 2005. **280**(11): p. 10135-10140; [2], i.e., Foury, F. and D. Talibi, *Mitochondrial control of iron homeostasis. A* *genome wide analysis of gene expression in a yeast frataxin-deficient strain.* J. Biol. Chem., 2001. **276**(11): p. 7762-7768.; and [3] Shakoury-Elizeh, M., et al., *Transcriptional remodeling in response to iron deprivation in Saccharomyces cerevisiae.* Mol. Biol. Cell, 2004. **15**(3): p. 1233-1243.)

Table 7. Example Fe Uptake and Utilization Genes

| **Gene Name** | **Putative Function** | **Nucleic Acid** | **Amino Acid** |
|---|---|---|---|
| | | SEQ ID NO: | SEQ ID NO: |
| *ARN1* | Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to ferrirubin, ferrirhodin, and related siderophores | 805 | 738 |
| *ARN2* | Transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; responsible for uptake of iron bound to the siderophore triacetylfusarinine C | 806 | 739 |
| *ATX1* | Cytosolic copper metallochaperone that transports copper to the secretory vesicle copper transporter Ccc2p for eventual insertion into Fet3p, which is a multicopper oxidase required for high-affinity iron uptake | 802 | 735 |
| *CCC2* | Cu(+2)-transporting P-type ATPase, required for export of copper from the cytosol into an extracytosolic compartment; has similarity to human proteins involved in Menkes and Wilsons diseases | 803 | 736 |
| *COT1* | Vacuolar transporter that mediates zinc transport into the vacuole; overexpression confers resistance to cobalt and rhodium | 816 | 749 |
| *ENB1 (ARN4)* | Endosomal ferric enterobactin transporter, expressed under conditions of iron deprivation; member of the major facilitator superfamily; expression is regulated by Rcs1p and affected by chloroquine treatment | 808 | 741 |
| *FET3* | Ferro-O2-oxidoreductase required for high-affinity iron uptake and involved in mediating resistance to copper ion toxicity, belongs to class of integral membrane multicopper oxidases | 800 | 733 |
| *FET5* | Multicopper oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport | 814 | 747 |
| *FIT1* | Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall | 792 | 725 |
| *FIT2* | Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall | 793 | 726 |
| *FIT3* | Mannoprotein that is incorporated into the cell wall via a glycosylphosphatidylinositol (GPI) anchor, involved in the retention of siderophore-iron in the cell wall | 794 | 727 |
| *FRE1* | Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; expression induced by low copper and iron levels | 795 | 728 |
| *FRE2* | Ferric reductase and cupric reductase, reduces siderophore-bound iron and oxidized copper prior to uptake by transporters; | 796 | 729 |

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| | expression induced by low copper and iron levels | | |
| *FRE3* | Ferric reductase, reduces siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels | 797 | 730 |
| *FRE4* | Ferric reductase, reduces a specific subset of siderophore-bound iron prior to uptake by transporters; expression induced by low iron levels | 798 | 731 |
| *FRE5* | Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies | 799 | 732 |
| *FRE6* | Putative ferric reductase with similarity to Fre2p; expression induced by low iron levels | 817 | 750 |
| *FTH1* | Putative high affinity iron transporter involved in transport of intravacuolar stores of iron; forms complex with Fet5p; expression is regulated by iron; proposed to play indirect role in endocytosis | 813 | 746 |
| *FTR1* | High affinity iron permease involved in the transport of iron across the plasma membrane; forms complex with Fet3p; expression is regulated by iron | 801 | 734 |
| *HMX1* | ER localized, heme-binding peroxidase involved in the degradation of heme; does not exhibit heme oxygenase activity despite similarity to heme oxygenases; expression regulated by AFT1 | 823 | 756 |
| *SIT1* (*ARN3*) | Ferrioxamine B transporter, member of the ARN family of transporters that specifically recognize siderophore-iron chelates; transcription is induced during iron deprivation and diauxic shift; potentially phosphorylated by Cdc28p | 807 | 740 |
| *SMF3* | Putative divalent metal ion transporter involved in iron homeostasis; transcriptionally regulated by metal ions; member of the Nramp family of metal transport proteins | 815 | 741 |
| *TIS11* (*CTH2*) | mRNA-binding protein expressed during iron starvation; binds to a sequence element in the 3'-untranslated regions of specific mRNAs to mediate their degradation; involved in iron homeostasis | 824 | 757 |
| *VHT1* | High-affinity plasma membrane H+-biotin (vitamin H) symporter; mutation results in fatty acid auxotrophy; 12 transmembrane domain containing major facilitator subfamily member; mRNA levels negatively regulated by iron deprivation and biotin | 822 | 755 |

**[00116]** Based on their functions and association with Fe uptake and utilization, the proteins encoded by the genes disclosed in Table 7 are candidates for affecting Fe-S cluster biosynthesis. Additional yeast genes associated with Fe uptake and utilization or Fe-S cluster biosynthesis include those listed in Table 8.

Table 8. Genes Associated With Yeast Fe Uptake and Utilization or Fe-S Cluster Biosynthesis

| **Gene Name** | **Nucleic Acid SEQ ID NO:** | **Amino Acid SEQ ID NO:** | **Putative Function** |
|---|---|---|---|
| *AFT1* | 770 | 703 | Transcription factor involved in iron utilization and homeostasis; binds the consensus site PyPuCACCCPu and activates the expression of target genes in |

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|---|---|---|---|
| | | | response to changes in iron availability |
| *AFT2* | 771 | 704 | Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required for iron homeostasis and resistance to oxidative stress; similar to Aft1p |
| *AIM1* | 779 | 712 | Interacts with Grx3/4 |
| *ARH1* | 855 | 837 | Oxidoreductase of the mitochondrial inner membrane, involved in cytoplasmic and mitochondrial iron homeostasis and required for activity of Fe-S cluster-containing enzymes; one of the few mitochondrial proteins essential for viability (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *ATM1* | 830 | 763 | Mitochondrial inner membrane ATP-binding cassette (ABC) transporter, exports mitochondrially synthesized precursors of iron-sulfur (Fe/S) clusters to the cytosol (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *BUD32* | 778 | 711 | Interacts with Grx3/4 and Aft1p |
| *CAD1 (YAP2)* | 791 | 724 | Stress responses including Fe deprivation; also regulates CTI6 and MRS4 genes |
| *CCC1* | 811 | 744 | Putative vacuolar Fe2+/Mn2+ transporter; suppresses respiratory deficit of yfh1 mutants, which lack the ortholog of mammalian frataxin, by preventing mitochondrial iron accumulation |
| *CFD1* | 834 | 767 | Highly conserved, iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with Nbp35p that is involved in iron-sulfur protein assembly in the cytosol (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *CIA1* | 836 | 769 | WD40 repeat protein involved in assembly of cytosolic and nuclear iron-sulfur proteins; similar to the human Ciao1 protein; YDR267C is an essential gene (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *CMK1* | 784 | 717 | Interacts with Grx4p |
| *CTH1* | 825 | 758 | mRNA binding and degradation under Fe depletion conditions |
| *CTI6* | 786 | 719 | Growth in low iron conditions |
| *CYC8* (*SSN6*) | 787 | 720 | General transcriptional co-repressor, acts together with Tup1p; also acts as part of a transcriptional co-activator complex that recruits the SWI/SNF and SAGA complexes to promoters; can form the prion [OCT+] |
| *DAP1* | 820 | 753 | |
| *DRE2* | 781 | 714 | Interacts with Grx3p |
| *ERV1* | 856 | 838 | Flavin-linked sulfhydryl oxidase of the mitochondrial intermembrane space (IMS), oxidizes Mia40p as part of a disulfide relay system that promotes IMS retention of imported proteins; ortholog of human hepatopoietin (ALR) (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008))<br>Central players of the export pathway are the ABC transporter Atm1p of the mitochondrial inner membrane, the sulfhydryl oxidase Erv1p of the intermembrane space, and the tripeptide glutathione (23, 27, 50) (*see* Gerber, J., *et al.*, *Mol. Cell. Biol. 24*(11):4848-57 (2004)) |
| *ESA1* | 782 | 715 | Interacts with Grx4p/Aft1p |
| *FET4* | 809 | 742 | Low-affinity Fe(II) transporter of the plasma membrane |
| *FRA1* | 772 | 705 | Protein involved in negative regulation of transcription of iron regulon; forms |

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| | | | an iron independent complex with Fra2p, Grx3p, and Grx4p; cytosolic; mutant fails to repress transcription of iron regulon and is defective in spore formation |
| *FRA2* | 773 | 706 | Protein involved in negative regulation of transcription of iron regulon; forms an iron independent complex with Fra2p, Grx3p, and Grx4p; null mutant fails to repress iron regulon and is sensitive to nickel |
| *GEF1* | 804 | 737 | Copper transporter/loading for Fet3p |
| *GGC1* (*YHM1*) | 857 | 839 | Mitochondrial GTP/GDP transporter, essential for mitochondrial genome maintenance; has a role in mitochondrial iron transport; member of the mitochondrial carrier family |
| *GRX1* | 858 | 840 | Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase with active site cysteine pair; protects cells from oxidative damage |
| *GRX2* | 832 | 765 | Cytoplasmic glutaredoxin, thioltransferase, glutathione-dependent disulfide oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity, expression induced in response to stress |
| *GRX3* | 774 | 707 | Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx4p and Grx5p; protects cells from oxidative damage |
| *GRX4* | 775 | 708 | Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx3p and Grx5p; protects cells from oxidative damage. |
| *GRX5* | 831 | 764 | Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; mitochondrial matrix protein involved in the synthesis/assembly of iron-sulfur centers; monothiol glutaredoxin subfamily member along with Grx3p and Grx4p (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *HDA1* | 790 | 723 | Interacts with Tup1p, Ssn6p for Aft1/2p regulation in the absence of heme |
| *IBA57* | 859 | 841 | Mitochondrial matrix protein involved in the incorporation of iron-sulfur clusters into mitochondrial aconitase-type proteins; activates the radical-SAM family members Bio2p and Lip5p; interacts with Ccr4p in the two-hybrid system (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *ISA1* | 860 | 842 | Mitochondrial matrix protein involved in biogenesis of the iron-sulfur (Fe/S) cluster of Fe/S proteins, isa1 deletion causes loss of mitochondrial DNA and respiratory deficiency; depletion reduces growth on nonfermentable carbon sources (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *ISA2* | 861 | 843 | Protein required for maturation of mitochondrial and cytosolic Fe/S proteins, localizes to the mitochondrial intermembrane space, overexpression of ISA2 suppresses grx5 mutations (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *ISU1* | 828 | 761 | Conserved protein of the mitochondrial matrix, performs a scaffolding function during assembly of iron-sulfur clusters, interacts physically and functionally with yeast frataxin (Yfh1p); isu1 isu2 double mutant is inviable (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 |

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| | | | (2008)) |
| *ISU2* | 829 | 762 | Conserved protein of the mitochondrial matrix, required for synthesis of mitochondrial and cytosolic iron-sulfur proteins, performs a scaffolding function in mitochondria during Fe/S cluster assembly; isu1 isu2 double mutant is inviable (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *JAC1* | 862 | 844 | Specialized J-protein that functions with Hsp70 in Fe-S cluster biogenesis in mitochondria, involved in iron utilization; contains a J domain typical to J-type chaperones; localizes to the mitochondrial matrix (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *MGE1* | 863 | 845 | Mitochondrial matrix cochaperone, acts as a nucleotide release factor for Ssc1p in protein translocation and folding; also acts as cochaperone for Ssq1p in folding of Fe-S cluster proteins; homolog of E. coli GrpE (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *MRS3* | 819 | 752 | Iron transporter that mediates Fe2+ transport across the inner mitochondrial membrane; mitochondrial carrier family member, similar to and functionally redundant with Mrs4p; active under low-iron conditions; may transport other cations (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *MRS4* | 818 | 751 | Iron transporter that mediates Fe2+ transport across the inner mitochondrial membrane; mitochondrial carrier family member, similar to and functionally redundant with Mrs3p; active under low-iron conditions; may transport other cations (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *MSN5* | 776 | 709 | Exporting Aft1p and other proteins from the nucleus |
| *NAR1* | 833 | 766 | Component of the cytosolic iron-sulfur (FeS) protein assembly machinery, required for maturation of cytosolic and nuclear FeS proteins and for normal resistance to oxidative stress; homologous to human Narf (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *NBP35* | 835 | 768 | Essential iron-sulfur cluster binding protein localized in the cytoplasm; forms a complex with Cfd1p that is involved in iron-sulfur protein assembly in the cytosol; similar to P-loop NTPases (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *NFS1* | 864 | 846 | Cysteine desulfurase involved in iron-sulfur cluster (Fe/S) biogenesis; required for the post-transcriptional thio-modification of mitochondrial and cytoplasmic tRNAs; essential protein located predominantly in mitochondria (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *NFU1* | 865 | 847 | Protein involved in iron utilization in mitochondria; similar to NifU, which is a protein required for the maturation of the Fe/S clusters of nitrogenase in nitrogen-fixing bacteria (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *NHP6a and b* | 788,789 | 721, 722 | Both are high-mobility group non-histone chromatin protein, functionally redundant with Nhp6Bp; homologous to mammalian high mobility group proteins 1 and 2; acts to recruit transcription factor Rcs1p to certain promoters |
| *PSE1* | 777 | 710 | Importing Aft1p and other proteins to the nucleus |

| | | | |
|---|---|---|---|
| *SMF1* | 810 | 743 | Low affinity Fe(II) transporter of the plasma membrane |
| *SNF1* | 866 | 848 | AMP-activated serine/threonine protein kinase found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis |
| *SNF2* | 867 | 849 | Catalytic subunit of the SWI/SNF chromatin remodeling complex involved in transcriptional regulation; contains DNA-stimulated ATPase activity; functions interdependently in transcriptional activation with Snf5p and Snf6p |
| *SNF3* | 868 | 850 | Plasma membrane glucose sensor that regulates glucose transport; has 12 predicted transmembrane segments; long cytoplasmic C-terminal tail is required for low glucose induction of hexose transporter genes HXT2 and HXT4 |
| *SNF4* | 869 | 851 | Activating gamma subunit of the AMP-activated Snf1p kinase complex (contains Snf1p and a Sip1p/Sip2p/Gal83p family member); activates glucose-repressed genes, represses glucose-induced genes; role in sporulation, and peroxisome biogenesis |
| *SSQ1*<br>. | 827 | 760 | Mitochondrial hsp70-type molecular chaperone, required for assembly of iron/sulfur clusters into proteins at a step after cluster synthesis, and for maturation of Yfh1p, which is a homolog of human frataxin implicated in Friedreich's ataxia (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008))<br>. |
| *TIM12*<br>(*MRS5*) | 871 | 853 | Essential protein of the inner mitochondrial membrane, peripherally localized; component of the TIM22 complex, which is a twin-pore translocase that mediates insertion of numerous multispanning inner membrane protein. |
| *TUP1* | 785 | 718 | General repressor of transcription |
| *NP_011911.1* | 821 | 754 | |
| *VPS41*<br>(*FET2*) | 872 | 854 | Vacuolar membrane protein that is a subunit of the homotypic vacuole fusion and vacuole protein sorting (HOPS) complex; essential for membrane docking and fusion at the Golgi-to-endosome and endosome-to-vacuole stages of protein transport |
| *YAH1* | 870 | 852 | Ferredoxin of the mitochondrial matrix required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis; homologous to human adrenodoxin (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *YAP5* | 812 | 745 | Regulation (CCC1) |
| *YFH1*<br>(Frataxin) | 826 | 759 | Mitochondrial matrix iron chaperone; oxidizes and stores iron; interacts with Isu1p to promote Fe-S cluster assembly; mutation results in multiple Fe/S-dependent enzyme deficiencies; human frataxin homolog is mutated in Friedreich's ataxia (*see, e.g.*, Lill, R. and U. Muehlenhoff, Ann. Rev. Biochem. 77:669-700 (2008)) |
| *YRA1* | 783 | 716 | Interacts with Grx4p |
| *ZPR1* | 780 | 713 | Interacts with Aft1p |

**[00117]** Additional genes encoding polypeptides affecting Fe-S cluster biosynthesis from other host cells have been identified and include, but are not limited to, those genes listed in Table 9.

Table 9. Genes Directly Involved in Fe-S Cluster Biosynthesis from Various Cells

| *Gene Name SEQ ID NOs(Amino Acid, Nucleic Acid)* | **Function (Accession; CDS)** |
|---|---|
| ***Azotobacter vinelandii nif* genes**<br>(Figures 6A and 6B; *see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)) | |
| *iscA*$^{nif}$<br>*(873, 894)* | [Fe-S] cluster scaffold protein (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002797399.1; nucleotides 153037 to 153360 of NC_012560.1) |
| *nifU*<br>(875, 896) | NifU is a scaffold protein for assembly and transfer of iron-sulfur clusters (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)).<br>(YP_002797400.1; nucleotides 153425 to 154363 of NC_012560.1) |
| *nifS*<br>(874, 895) | Cysteine desulfurase involved in the mobilization of S for nitrogenase maturation (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)).<br>(YP_002797401.1; nucleotides 154365 to 155573 of NC_012560.1) |
| *cysE1*<br>*(876, 897)* | Involved in cysteine biosynthesis (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002797403.1; nucleotides 156797 to 157594 of NC_012560.1) |
| *cysE2*<br>*(929, 947)* | Involved in cysteine biosynthesis (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801153.1; reverse complement of nucleotides 4092159 to 4092938 of NC_012560.1) |
| *iscS*<br>*(930, 948)* | Cysteine desulfurase involved in the mobilization of S (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801151.1; reverse complement of nucleotides of 4090290 to 4091504 of NC_012560.1) |
| *iscU*<br>*(931, 949)* | [Fe-S] cluster scaffold protein (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801150.1; reverse complement of nucleotides 4089860 to 4090246 of NC_012560.1) |
| *iscA*<br>*(932, 950)* | [Fe-S] cluster scaffold protein (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801149.1; reverse complement of nucleotides 4089511 to 4089834 of NC_012560.1) |
| *hscB*<br>*(933, 951)* | HscB heat shock cognate protein associated with Isc-directed [Fe-S] protein maturation (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem.* |

| | |
|---|---|
| | *74*:247-81 (2005))<br>(YP_002801148.1; reverse complement of nucleotides 4088980 to 4089501 of NC_012560.1) |
| *hscA*<br>*(934, 952)* | HscA heat shock cognate protein associated with Isc-directed [Fe-S] protein maturation (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem.* *74*:247-81 (2005))<br>(YP_002801147.1; reverse complement of nucleotides 4087072 to 4088937 of NC_012560.1) |
| *Fdx*<br>*(935, 953)* | Ferredoxin<br>(YP_002801146.1; reverse complement of nucleotides 4086730 to 4087071 of NC_012560.1) |
| *sufS*<br>*(936, 954)* | Cysteine desulfurase involved in the mobilization of S (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801025.1; nucleotides 3961166 to 3962515 of NC_012560.1) |
| *sufE*<br>*(937, 955)* | (YP_002801026.1; nucleotides 3962512 to 3962916 of NC_012560.1) |
| *cysE3*<br>*(938, 956)* | Involved in cysteine biosynthesis (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002799274.1; nucleotides 2093069 to 2094052 of NC_012560.1) |
| *sufS2*<br>*(939, 957)* | Cysteine desulfurase involved in the mobilization of S (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002799276.1; nucleotides 2095267 to 2097081 of NC_012560.1) |
| *iscA2* also known as *eprA*<br>*(877, 898)* | [Fe-S] cluster scaffold protein (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005))<br>(YP_002801687.1; reverse complement of nucleotides 4681573 to 4681923 of NC_012560.1) |
| *Nfu* also known as *NfuA*<br>*(878, 899)* | Human nfu appears to be a persulfide reductase according to the equation shown in Figure 6C. (*see* Liu, Y., W. Qi, and J.A. Cowan, *Biochem. 48*(5):973-80 (2009))<br>(YP_002800022.1; reverse complement of nucleotides 2961161 to 2961745 of NC_012560.1) |
| *nfuA* also known as *AnfU*<br>*(879, 900)* | Spectroscopic and analytical studies indicate that one [4Fe-4S] cluster can be assembled *in vitro* within a dimeric form of NfuA. The resultant [4Fe-4S] cluster-loaded form of NfuA is competent for rapid in vitro activation of apo-aconitase. Based on these results a model is proposed where NfuA could represent a class of intermediate [Fe-S] cluster carriers involved in [Fe-S] protein maturation. (*see* Bandyopadhyay, S., *et al.*, *J Biol. Chem. 283*(20):14092-99 (2008))<br>(YP_002801977.1; nucleotides 4963727 to 4964017 of NC_012560.1) |
| *nfuV* also known as *VnfU*<br>*(880, 901)* | Could have specialized functions related to the maturation, protection, or repair of specific [Fe-S] proteins (*see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)).<br>(YP_002797514.1; reverse complement of nucleotides 263828 to 264118 of NC_012560.1) |
| ***Helicobacter pylori nif* genes** | |

| | |
|---|---|
| (Figure 7; *see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)) | |
| *nifS*<br>*(881, 902)* | NifS is a cysteine desulfurase.<br>(YP_003057033.1; nucleotides 218891 to 220054 of NC_012973.1) |
| *nifU*<br>*(882, 903)* | NifU is a scaffold protein for assembly and transfer of iron-sulfur clusters.<br>(YP_003057034.1; nucleotides 220076 to 221056 of NC_012973.1) |
| *nfu*<br>*(927, 945)* | (YP_003058109.1; nucleotides 1448886 to 1449155 of NC_012973.1) |
| *iscS*<br>*(928, 946)* | (YP_003057709.1; reverse complement of nucleotides 1012615 to 1013937 of NC_012973.1) |
| ***E. coli isc* genes**<br>(Figure 8; *see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)) | |
| *iscS*<br>*(883, 904)* | **EcoCyc:** IscS is a cysteine desulfurase that catalyzes the conversion of cysteine into alanine and sulfur via intermediate formation of a cysteine persulfide.<br>(YP_026169.1; reverse complement of nucleotides 2658339 to 2659553 of NC_000913.2) |
| *iscU*<br>*(884, 905)* | **EcoCyc:** IscU is a scaffold protein for assembly and transfer of iron-sulfur clusters. IscU is able to form 2Fe-2S clusters and transfer them to apo-ferredoxin, acting catalytically. The chaperones HscA and HscB and ATP hydrolysis by HscA accelerate cluster transfer.<br>(NP_417024.1; reverse complement of nucleotides 2657925 to 2658311 of NC_000913.2) |
| *iscA*<br>*(885, 906)* | **EcoCyc:** IscA is an iron-sulfur cluster assembly protein that forms the [2Fe-2S] cluster of ferredoxin. It has been shown to bind iron with an apparent association constant of 3x10-19 M$^{-1}$. *In vitro* in the presence of IscS and cysteine, IscA can provide iron to iscU.<br>Native [2Fe-2S] SufA can transfer its Fe-S cluster to both [2Fe-2S] and [4Fe-4S] apoproteins. (*see* Gupta, V., *et al.*, *J. Am. Chem. Soc. 131*(17):6149-53 (2009))<br>The results suggest that the biogenesis of the [4Fe-4S] clusters and the [2Fe-2S] clusters may have distinct pathways and that IscA/SufA paralogues are essential for the [4Fe-4S] cluster assembly, but are dispensable for the [2Fe-2S] cluster assembly in E. coli under aerobic conditions. (Tan, G., *et al.*, *Biochem. J.*, 420(3):463-72 (2009))<br>(NP_417023.1; reverse complement of nucleotides 2657585 to 2657908 of NC_000913.2) |
| *hscB*<br>*(886, 907)* | **EcoCyc:** HscB is a co-chaperone that stimulates HscA (Hsc66) ATPase activity. HscB does not exhibit its own chaperone activity. HscB is required for wild-type stimulation of HscA ATPase activity by the substrate, IscU, and for wild-type interaction between HscA and IscU. This system is involved in iron-sulfur cluster assembly.<br>(NP_417022.1; reverse complement of nucleotides 2656974 to 2657489 of NC_000913.2) |

| | |
|---|---|
| *hscA*<br>*(887, 908)* | **EcoCyc:** Hsc66 together with Hsc20 may comprise a chaperone system similar to DnaK/DnaJ. Hsc66 is required for the assembly of iron-sulfur clusters. IscU may be a substrate for Hsc66. In the presence of Hsc20, IscU stimulates the ATPase activity of Hsc66 up to 480-fold; the *in vivo* turnover rate of the chaperone cycle may be determined by the availability of the IscU-Hsc20 complex. Hsc66 directly interacts with IscU, IscA, and Fdx.<br>(NP_417021.1; reverse complement of nucleotides 2655107 to 2656957 of NC_000913.2) |
| *Fdx*<br>*(888, 909)* | **EcoCyc:** [2Fe-2S] ferridoxin<br>(NP_417020.1; reverse complement of nucleotides 2654770 to 2655105 of NC_000913.2) |
| ***E. coli suf* genes**<br>(Figure 9; *see* Johnson, D.C., *et al.*, *Ann. Rev. Biochem. 74*:247-81 (2005)) | |
| *sufA*<br>*(889, 910)* | **EcoCyc:** SufA is part of the protein machinery that is involved in the biosynthesis of iron-sulfur clusters. *In vitro*, purified apoSufA can chelate iron-sulfur clusters by treatment with iron and sulfide under anaerobic conditions. HoloSufA then can form a fast and tight association with the target apoprotein biotin synthase (BioB) and transfers a [4Fe-4S] cluster to BioB in a slow reaction.<br>(NP_416199.1; reverse complement of nucleotides 1762042 to 1762410 of NC_000913.2) |
| *sufB*<br>*(890, 911)* | **EcoCyc:** The SufB-SufC-SufD complex activates the cysteine desulfurase activity SufS in conjunction with the SufE sulfur acceptor protein.<br>(NP_416198.2; reverse complement of nucleotides 1760546 to 1762033 of NC_000913.2) |
| *sufC*<br>*(891, 912)* | **EcoCyc:** SufC is part of the protein machinery that is involved in the biosynthesis of iron-sulfur clusters. The SufB-SufC-SufD complex activates the cysteine desulfurase activity of SufS in conjunction with the SufE sulfur acceptor protein.<br>(NP_416197.1; reverse complement of nucleotides 1759790 to 1760536 of NC_000913.2) |
| *sufD*<br>*(892, 913)* | **EcoCyc:** The SufB-SufC-SufD complex activates the cysteine desulfurase activity SufS in conjunction with the SufE sulfur acceptor protein<br>(NP_416196.1; reverse complement of nucleotides 1758544 to 1759815 of NC_000913.2) |
| *sufS*<br>*(893, 914)* | **EcoCyc:** SufS is a member of the NifS protein family. SufS exhibits activity with respect to assembly of the ferredoxin iron-sulfur cluster in an *in vitro* assay.<br>(NP_416195.1; reverse complement of nucleotides 1757327 to 1758547 of NC_000913.2) |
| *sufE1 also known as suf E*<br>*(925, 943)* | (NP_416194.1; reverse complement of nucleotides 1756898 to 1757314 of NC_000913.2) |
| *sufS2 also* | (NP_417290.1; NC_000913.2 nucleotides 2941359 to 2942564) |

| | |
|---|---|
| *known as csdA (924, 942)* | |
| *sufE2 also known as csdE (926, 944)* | (NP_417291.1; nucleotides 2942564 to 2943007 of NC_000913.2) |
| *iscA2 also known as erpA (922, 940)* | (NP_414698.1; nucleotides 176610 to 176954 of NC_000913.2) |
| *nfu also known as nfuA (923, 941)* | (NP_417873.1; nucleotides 3543646 to 3544221 of NC_000913.2) |

**[0100]** Provided herein are recombinant host cells that comprise an alteration in the expression of any polypeptide encoded by an Fe uptake and utilization or an Fe-S cluster biosynthesis gene. Encompassed are recombinant host cells that comprise at least one heterologous polynucleotide of any one of the above-referenced Fe-S cluster biosynthesis genes. Also encompassed are recombinant host cells, wherein the host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene of any one of the above-referenced Fe uptake and utilization or Fe-S cluster biosynthesis genes. Also provided are recombinant host cells that comprise at least one heterologous polynucleotide of any one of the above-referenced Fe uptake and utilization or Fe-S cluster biosynthesis genes, wherein the host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene of any one of the above-referenced Fe uptake and utilization or Fe-S cluster biosynthesis genes.

**[0101]** These recombinant host cells can also comprise at least one heterologous Fe-S cluster requiring protein. For example, provided herein is a recombinant host cell comprising at least one heterologous DHAD and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis. Also provided is a recombinant host cell comprising at least one heterologous DHAD, wherein the host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis. Also provided is a recombinant host cell comprising at least one heterologous DHAD and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis, wherein the host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis.

**[0102]** Host cells that can be used in the present invention include yeast host cells including, but not limited to, *Saccharomyces*, *Schizosaccharomyces, Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia, Issatchenkia,* and *Pichia*. Bacterial host cells can also be used to create recombinant host cells that comprise at least one heterologous polynucleotide encoding a polypeptide having DHAD activity and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis. For example, lactic acid bacteria comprising recombinant DHAD and at least one recombinant genetic expression element encoding Fe-S cluster forming proteins are the subject of U.S. Appl. No. 12/569,103, filed Sept. 29, 2009, which is incorporated by reference herein. The present recombinant host cells comprising at least one heterologous polynucleotide encoding a polypeptide having DHAD activity and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis do not include those lactic acid bacteria described in U.S. Appl. No. 12/569,103, filed Sept. 29, 2009, which is incorporated by reference herein.

**[0103]** The polypeptide affecting Fe-S cluster biosynthesis can be selected from the group consisting of the Fe uptake and utilization or Fe-S cluster biosynthesis pathway genes in Tables 7, 8 and 9. In one embodiment, the polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, FRA2, GRX3, MSN5, and combinations thereof. In another embodiment, the polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, FRA2, GRX3, MSN5, and combinations thereof, and the polypeptide affecting Fe-S cluster biosynthesis is encoded by a polynucleotide comprising a plasmid. In some embodiments, DHAD is co-expressed with AFT1, AFT2, PSE1, and combinations thereof. The polypeptide affecting Fe-S cluster biosynthesis may be a constitutive mutant, such as, but not limited to, AFT1 L99A, AFT1 L102A, AFT1 C291F, AFT1 C293F, and combinations thereof. The deletion, mutation, and/or substitution in the endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis can be selected from the group consisting of FRA2, GRX3, MSN5, and combinations thereof.

**[0104]** The present invention also provides a method for increasing the activity of an Fe-S cluster requiring protein in a recombinant host cell comprising providing a recombinant host cell comprising an Fe-S cluster requiring protein, changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis in the host cell, and growing the recombinant host cell with the changed expression or activity under conditions whereby the activity of the Fe-S cluster requiring protein is increased. Such a method can be used to increase the activity of an endogenous Fe-S cluster requiring protein, or a heterologous Fe-S cluster requiring protein. Such a method can be used to increase the specific activity of a DHAD described herein, or identified by the methods described herein. The increase in the activity of the Fe-S cluster requiring protein can be in an amount selected from greater than about 10%; greater than about 15%; greater than about 20%; greater than about 25%; greater than about 30%; greater than about 35%; greater than about 40%; greater than about 45%; greater than about 50%; greater than about 55%; greater than about 60%; greater than about 65%; greater than about 70%; greater than about 75%; greater than about 80%; greater than about 85%; greater than about 90%; and greater than about 95%. The increase in activity may be greater than about 3 fold, greater than about 5 fold, greater than about 8 fold, or greater than about 10 fold. In embodiments, the activity of the Fe-S cluster requiring protein can be in an amount that is at least about 60% of theoretical, at least about 70% of theoretical, at least about 80% theoretical, or at least about 90% theoretical.

**[0105]** The present invention can also be used to increase the flux in the Fe-S cluster biosynthesis pathway in a host cell and to identify polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell. In one embodiment a method is provided for increasing the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising providing a recombinant host cell comprising an Fe-S cluster requiring protein and either at least one polypeptide affecting Fe-S cluster biosynthesis, at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis, or a combination of both, and growing the recombinant host cell under conditions whereby the flux in the Fe-S cluster biosynthesis pathway in the host cell is increased. In another embodiment, a method is provided for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising: (a) changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis; (b) measuring the activity of a Fe-S cluster requiring protein; and (c) comparing the activity of the Fe-S cluster requiring protein measured in the presence of the change in expression or activity polypeptide of step (a) to the activity of the Fe-S cluster requiring protein measured in the absence of the change in expression or activity polypeptide of step (a), wherein an increase in the activity of the heterologous Fe-S cluster requiring protein indicates an increase in the flux in said Fe-S cluster biosynthesis pathway. In such methods, the Fe-S cluster requiring protein may be endogenous or heterologous to the host cell.

**[0106]** The expression or activity of the polypeptide affecting Fe-S cluster biosynthesis can be changed by methods well known in the art, including, but not limited to, deleting, mutating, substituting, expressing, up-regulating, down-regulating, altering the cellular location, altering the state of the protein, and/or adding a cofactor, and combinations thereof. Altering the state of the protein can include, but are not limited to, such alterations as phosphorylation or ubiquitination. Any number of methods described herein or known in the art can be used to measure the activity of the Fe-S cluster requiring protein, depending upon the Fe-S cluster requiring protein chosen. For example, if DHAD is the Fe-S cluster requiring protein, the assay described in the Example 6 can be used to measure the activity of the DHAD to determine if there is an increase in the flux in the Fe-S cluster biosynthesis pathyway of the host cell.

**[0107]** Isobutanol and Other Products

**[0108]** Expression of a DHAD in a recombinant host cell, as described herein, provides the transformed, recombinant host cell with dihydroxy-acid dehydratase activity for conversion of 2,3-dihydroxyisovalerate to α-ketoisovalerate or 2,3-dihydroxymethylvalerate to α-ketomethylvalerate. A product that has α-ketoisovalerate or α-ketomethylvalerate as a pathway intermediate may be produced with greater effectiveness in a host cell disclosed herein having the described heterologous DHAD. A list of such products includes, but is not limited to, valine, isoleucine, leucine, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, and isobutanol.

**[0109]** For example, biosynthesis of valine in yeast includes steps of acetolactate conversion to 2,3-dihydroxy-isovalerate by acetohydroxyacid reductoisomerase (ILV5), conversion of 2,3-dihydroxy-isovalerate to α-ketoisovalerate (also called 2-keto-isovalerate) by dihydroxy-acid dehydratase, and conversion of α-ketoisovalerate to valine by branched-chain amino acid transaminase (BAT2) and branched-chain animo acid aminotransferase (BAT1). Biosynthesis of leucine includes the same steps to α-ketoisovalerate, followed by conversion of α-ketoisovalerate to alpha-isopropylmalate by alpha-isopropylmalate synthase (LEU9, LEU4), conversion of alpha-isopropylmalate to beta-isopropylmalate by isopropylmalate isomerase (LEU1), conversion of beta-isopropylmalate to alpha-ketoisocaproate by beta-IPM dehydrogenase (LEU2), and finally conversion of alpha-ketoisocaproate to leucine by branched-chain amino acid transaminase (BAT2) and branched-chain amino acid aminotransferase (BAT1). The bacterial pathway is similar, involving differently named proteins and genes. Increased conversion of 2,3-dihydroxy-isovalerate to α-ketoisovalerate will increase flow in these pathways, particularly if one or more additional enzymes of a pathway is overexpressed. Thus, it is desired for production of valine or leucine to use a strain disclosed herein.

**[0110]** Biosynthesis of pantothenic acid includes a step performed by DHAD, as well as steps performed by ketopantoate hydroxymethyltransferase and pantothenate synthase. Engineering of expression of these enzymes for enhanced production of pantothenic acid biosynthesis in microorganisms is described in U.S. Patent No. 6,177,264.

**[0111]** The α-ketoisovalerate product of DHAD is an intermediate in isobutanol biosynthetic pathways disclosed in U.S. Patent Appl. Pub. No. 20070092957 A1, which is incorporated by reference herein. A diagram of the disclosed isobutanol biosynthetic pathways is provided in Figure 5. Production of isobutanol in a strain disclosed herein benefits from increased DHAD activity. As disclosed herein, increased DHAD activity is provided by expression of a DHAD in a host cell, for example, by over-expressing the DHAD, by modulating the expression or activity of a polypeptide having Fe-S cluster regulatory activity, or a combination of both expression of a DHAD and modulation of the expression or activity of a polypeptide having Fe-S cluster regulatory activity. As described in U.S. Patent Appl. Pub. No. 20070092957 A1, which is incorporated by reference herein, steps in an example isobutanol biosynthetic pathway include conversion of:

**[0112]** - pyruvate to acetolactate (*see* Fig. 5, pathway step a therein), as catalyzed for example by acetolactate synthase,

**[0113]** - acetolactate to 2,3-dihydroxyisovalerate (*see* Fig. 5, pathway step b therein) as catalyzed for example by acetohydroxy acid isomeroreductase;

**[0114]** - 2,3-dihydroxyisovalerate to α-ketoisovalerate (*see* Fig. 5, pathway step c therein) as catalyzed for example by acetohydroxy acid dehydratase, also called dihydroxy-acid dehydratase (DHAD);

**[0115]** - α-ketoisovalerate to isobutyraldehyde (*see* Fig. 5, pathway step d therein) as catalyzed for example by branched-chain α-keto acid decarboxylase; and

**[0116]** - isobutyraldehyde to isobutanol (*see* Fig. 5, pathway step e therein) as catalyzed for example by branched-chain alcohol dehydrogenase.

**[0117]** 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 U.S. Patent Appl. Pub. No. 20070092957 A1, which is incorporated by reference herein.

**[0118]** Genes that can be used for expression of the pathway step enzymes named above other than the DHADs disclosed herein, as well as those for two additional isobutanol pathways, are described in U.S. Patent Appl. Pub. No. 20070092957 A1, which is incorporated by reference herein. Additional genes that may be used can be identified by one skilled in the art through bioinformatics or using methods well-known in the art, such as the various methods described in U.S. Appl. No. 12/569,636, filed Sept. 29, 2009, which is incorporated by reference herein, to isolate homologs. The use in all three pathways of ketol-acid reductoisomerase (KARI) enzymes with particularly high activities is disclosed in U.S. Patent Appl. Pub. No. 20080261230 A1, which is incorporated by reference herein. Examples of high activity KARIs disclosed therein are those from *Vibrio cholerae*, *Pseudomonas aeruginosa* PAO1, and *Pseudomonas fluorescens* PF5. U.S. Patent Appl. Publ No. 2009/0163376 and U.S. Patent Application 12/637,905, filed December 15, 2009, incorporated herein by reference, describes acetohydroxy acid isomeroreductases; U.S. Patent Appl. Publ. No. 2009/0269823, incorporated by reference herein, describes a suitable alcohol dehydrogenase.

**[0119]** Additionally described in U.S. Patent Appl. Pub. No. 20070092957 A1, which is incorporated by reference herein, are construction of chimeric genes and genetic engineering of bacteria and yeast for isobutanol production using the disclosed biosynthetic pathways.

**[0120]** <u>Growth for production</u>

**[0121]** Recombinant host cells disclosed herein are grown in fermentation media which contains suitable carbon substrates. Suitable carbon substrates may include, but are not limited to, monosaccharides such as glucose, fructose, oligosaccharides such as lactose maltose, galactose, 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. Other carbon substrates may include ethanol, lactate, succinate, or glycerol.

**[0122]** 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. Two-carbon substrates such as ethanol may also suitable. In addition to one and two carbon substrates, methylotrophic organisms are also known to utilize a number of other carbon containing compounds such as methylamine, glucosamine and a variety of amino acids for metabolic activity. For example, methylotrophic yeasts 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 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 organism.

**[0123]** Although it is contemplated that all of the above mentioned carbon substrates and mixtures thereof are suitable in the present invention, in some embodiments, the carbon substrates are glucose, fructose, and sucrose, or mixtures of these with C5 sugars such as xylose and/or arabinose for yeasts cells modified to use C5 sugars. Sucrose may be derived from renewable sugar sources such as sugar cane, sugar beets, cassava, sweet sorghum, and mixtures thereof. Glucose and dextrose may be derived from renewable grain sources through saccharification of starch based feedstocks including grains such as corn, wheat, rye, barley, oats, and mixtures thereof. In addition, fermentable sugars may be derived from renewable cellulosic or lignocellulosic biomass through processes of pretreatment and saccharification, as described, for example, in co-owned and co-pending U.S. Patent Appl. Pub. No. 20070031918 A1, which is herein incorporated by reference. Biomass refers to any cellulosic or lignocellulosic material and includes materials comprising cellulose, and optionally further comprising hemicellulose, lignin, starch, oligosaccharides and/or monosaccharides. Biomass may also comprise additional components, such as protein and/or lipid. Biomass may be derived from a single source, or biomass can comprise a mixture derived from more than one source; for example, biomass may comprise a mixture of corn cobs and corn stover, or a mixture of grass and leaves. Biomass includes, but is not limited to, bioenergy crops, agricultural residues, municipal solid waste, industrial solid waste, sludge from paper manufacture, yard waste, wood and forestry waste. Examples of biomass include, but are not limited to, corn grain, corn cobs, crop residues such as corn husks, corn stover, grasses, wheat, wheat straw, barley, barley straw, hay, rice straw, switchgrass, waste paper, sugar cane bagasse, sorghum, soy, components obtained from milling of grains, trees, branches, roots, leaves, wood chips, sawdust, shrubs and bushes, vegetables, fruits, flowers, animal manure, and mixtures thereof.

**[0124]** In addition to an appropriate carbon source, growth media 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 an enzymatic pathway comprising a Fe-S cluster requiring protein such as, for example, DHAD.

**[0125]** Culture Conditions

**[0126]** Typically cells are grown at a temperature in the range of about 20 °C to about 40 °C in an appropriate medium. Suitable growth media in the present invention are common commercially prepared media such as Luria Bertani (LB) broth, Sabouraud Dextrose (SD) broth, Yeast Medium (YM) broth, or 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. The use of agents known to modulate catabolite repression directly or indirectly, *e.g.*, cyclic adenosine 2':3'-monophosphate, may also be incorporated into the growth medium.

**[0127]** Suitable pH ranges for the growth are between about pH 5.0 to about pH 9.0. In one embodiment, about pH 6.0 to about pH 8.0 is used for the initial condition. Suitable pH ranges for the fermentation of yeast are typically between about pH 3.0 to about pH 9.0. In one embodiment, about pH 5.0 to about pH 8.0 is used for the initial condition. Suitable pH ranges for the fermentation of other microorganisms are between about pH 3.0 to about pH 7.5. In one embodiment, about pH 4.5 to about pH 6.5 is used for the initial condition.

[0128] Growth may be performed under aerobic or anaerobic conditions. In one embodiment, anaerobic or microaerobic conditions are used for growth.

[0129] Industrial Batch and Continuous Fermentations

[0130] Isobutanol, or other products, may be produced using 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. 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 amounts of substrate in the media. Batch and fed-batch fermentations are common and well known in the art and 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.

[0131] Isobutanol, or other products, may also be produced using 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 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. 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*.

[0132] It is contemplated that the production of isobutanol, or other products, may be practiced using batch, fed-batch or continuous processes and that any known mode of fermentation would be suitable. Additionally, it is contemplated that cells may be immobilized on a substrate as whole cell catalysts and subjected to fermentation conditions for isobutanol production.

[0133] Methods for Isobutanol Isolation from the Fermentation Medium

**[0134]** Bioproduced isobutanol may be isolated from the fermentation medium using methods known in the art for ABE fermentations (*see, e.g.*, Durre, *Appl. Microbiol. Biotechnol. 49*:639-648 (1998), Groot *et al.*, *Process. Biochem. 27*:61-75 (1992), and references therein). For example, solids may be removed from the fermentation medium by centrifugation, filtration, decantation, or the like. Then, the isobutanol may be isolated from the fermentation medium using methods such as distillation, azeotropic distillation, liquid-liquid extraction, adsorption, gas stripping, membrane evaporation, or pervaporation.

**[0135]** Because isobutanol forms a low boiling point, azeotropic mixture with water, distillation can 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, e.g.*, Doherty and Malone, *Conceptual Design of Distillation Systems*, McGraw Hill, New York, 2001).

**[0136]** The butanol-water mixture forms a heterogeneous azeotrope so that distillation may be used in combination with decantation to isolate and purify the isobutanol. In this method, the isobutanol containing fermentation broth is distilled to near the azeotropic composition. Then, the azeotropic mixture is condensed, and the isobutanol is separated from the fermentation medium by decantation. The decanted aqueous phase may be returned to the first distillation column as reflux. The isobutanol-rich decanted organic phase may be further purified by distillation in a second distillation column.

**[0137]** The isobutanol may also be isolated from the fermentation medium using liquid-liquid extraction in combination with distillation. In this method, the isobutanol is extracted from the fermentation broth using liquid-liquid extraction with a suitable solvent. The isobutanol-containing organic phase is then distilled to separate the butanol from the solvent.

**[0138]** Distillation in combination with adsorption may also be used to isolate isobutanol from the fermentation medium. In this method, the fermentation broth containing the isobutanol 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).

**[0139]** Additionally, distillation in combination with pervaporation may be used to isolate and purify the isobutanol from the fermentation medium. In this method, the fermentation broth containing the isobutanol 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

**[0140]** The meaning of abbreviations used is as follows: "min" means minute(s), "h" means hour(s), "sec" means second(s), "µl" means microliter(s), "ml" means milliliter(s), "L" means liter(s), "nm" means nanometer(s), "mm" means millimeter(s), "cm" means centimeter(s), "µm" means micrometer(s), "mM" means millimolar, "M" means molar, "mmol" means millimole(s), "µmole" means micromole(s), "g" means gram(s), "µg" means microgram(s), "mg" means milligram(s), "rpm" means revolutions per minute, "w/v" means weight/volume, "OD" means optical density, and "$OD_{600}$" means optical density measured at a wavelength of 600 nm.

**[0141]** GENERAL METHODS:

**[0142]** 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, N.Y., 1989, by T. J. Silhavy, M. L. Bennan, and L. W. Enquist, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1984, and by Ausubel, F. M. *et al.*, *Current Protocols in Molecular Biology*, Greene Publishing Assoc. and Wiley-Interscience, N.Y., 1987.

**[0143]** Materials and methods suitable for the maintenance and growth of bacterial cultures are also well known in the art. Techniques suitable for use in the following Examples may be found in *Manual of Methods for 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, 1989. All reagents, restriction enzymes and materials used for the growth and maintenance of bacterial 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.

**[0144]** **Example 1. Over-expression of DHAD protein encoded by the *ilvD* gene from *S. mutans* using a plasmid-based system.**

**[0145]** Over-expression of a recombinant polynucleotide can be accomplished by increasing the copy number of a plasmid comprising the recombinant polynucleotide. To over-express the DHAD protein in yeast, an inducible vector was constructed. The pHR81 vector contains a *Ura3* marker as well as a *LEU* marker with a defective promoter (*see* U.S. Patent Appl. Pub. No. 2007/0092957, which is incorporated by reference herein). When the yeast synthetic dropout (SD; also known as complete minimal media; Teknova) growth medium is switched from SD minus uracil to SD minus leucine, the copy number of the pHR81 plasmid increases, resulting in much higher level of expression of the recombinant polynucleotide. The pHR81 vector backbone was derived from pLH472 JEG4y (SEQ ID NO: 921) and was prepared by digesting the pLH472 JEG4y vector with SpeI and SacII.

**[0146]** For over-expression of a DHAD protein, the DHAD gene *ilvD* from *S. mutans* was used (*see* U.S. Published Patent Appl. No. US2009-0305363A1, which is incorporated by reference herein). This gene has been cloned under the control of the FBA promoter in vector pRS423 FBA ilvD Strep-lumio (*see* U.S. Published Patent Appl. No. US2009-0305363A1, which is incorporated by reference herein). The region containing the FBA promoter, the *ilvD* gene, and FBA terminator cassette was amplified with primer set FBAp-F(NheI) and FBAt-R(SacII) (SEQ ID NOS: 915 and 916) and cloned into the pHR81 vector. The resulting expression vector was designated as pHR81 FBA-IlvD(Sm)-lumio-FBAt (SEQ ID NO: 917; Figure 1A).

**[0147]** To over express the *S. mutans* DHAD protein, the expression vector pHR81 FBA-IlvD(Sm)-lumio-FBAt was transformed into wild-type yeast strain BY4741.

Transformants were selected on agar plates with SD minus uracil. For over-expression, yeast strains containing the plasmid were initially grown at 30° C in SD liquid medium minus uracil. A fresh overnight culture (5 ml) was then transferred to a 125 ml flask containing 75 ml of SD medium minus leucine. As a control, another 5 ml of fresh overnight culture was transferred into a flask containing 75 ml of SD minus uracil. The cultures were incubated overnight before harvesting by centrifugation. The DHAD activity was measured in crude extracts of these samples using the assay described in Example 6.

**[0148]** The DHAD specific activity obtained in the crude extract in the control samples grown in SD minus uracil was in the range of 0.2 U mg $^{-1}$. The average specific activity obtained from strains grown in the SD medium minus leucine, however, was 1.6 U mg $^{-1}$, much higher (~8-fold higher) than the activity from the control samples. DHAD requires Fe-S cluster for its function, and it was not previously known if the native yeast Fe-S cluster regulatory pathway could accommodate an over-expressed Fe-S cluster requiring protein. In a previous screening experiment using a non-inducible, low-copy number vector, the DHAD from *S. mutans* could be recombinantly expressed in yeast cytosol with a specific activity in the range of 0.1 to 0.2 U mg$^{-1}$ in the crude extract (*see* U.S. Patent Appl. No. 12/569,636, filed on Sept. 29, 2009, which is incorporated by reference herein). Thus, in one embodiment, over-expression of a Fe-S cluster requiring protein, such as DHAD, in yeast using a high-copy number vector provides increased specific activity, wherein the specific activity is increased by at least about 8 fold.

## **[0149]** **Example 2. Over-expression of DHAD protein encoded by the *ilvD* gene from *S. mutans* through chromosomal integration.**

**[0150]** An alternate way to increase the expression of a gene in yeast is to integrate multiple copies of the gene of interest into the host cell's chromosome. To integrate the *ilvD* gene from *S. mutans* (SEQ ID NO:167) into a yeast chromosome, integration vector pZK-Delta(s)-Leu2-FBA-ilvD(Sm)-FBAt (SEQ ID NO: 918; Figure 1B) was constructed. The integration vector backbone was derived from pSuperscript (Stratagene, La Jolla, CA). The *S. mutans ilvD* gene (nucleotides 1306-3018 of the complement strand) was cloned into the integration vector under the control of the FBA promoter (nucleotides

3026-4023 of the complement strand) so that the *ilvD* gene would be flanked by a yeast delta sequence (nucleotides 118-267 and 5061-5760 of the complement strand). *S. cerevisiae* contains more than 200 yeast delta sequences (Kim J M *et al.* Genome Res. 1998;8:464-478). These delta sequences are targets for multiple integrations. The integration vector was also engineered to contain the defective *LEU2* marker (nucleotides 4100-5191 of the complement strand) for selection of transformed strains with multiple integration events.

**[0151]** For integration, the vector DNA was linearized with AscI and AatII digestion to generate delta sequence flanked strands of vector DNA comprising the *ilvD* gene, which were then transformed into the yeast strain BY4741. Transformants were selected on SD agar medium minus leucine. These transformants were then grown on SD liquid medium minus leucine at 30° C, and the cultures were harvested and analyzed for DHAD activity. The specific activity of DHAD obtained in the crude extract ranged from 0.7 to 1.2 U $mg^{-1}$. This specific activity was about 3- to 6-fold higher than that found in BY4741 strains transformed with an *ilvD* gene-containing plasmid without over-expression or chromosomal integration.

**[0152]** **Example 3. Improvement of specific activity of DHAD in yeast deletion strains**

**[0153]** Although the over-expression strains described in Examples 1 and 2 had a high level of activity, not all of the DHAD protein expressed was active. For example, the over-expressed DHAD protein accounted for approximately 5 to 10% of the total cell protein, while yielding a specific activity of from about 0.7 to 1.6 U $mg^{-1}$. Expression of DHAD at 10% of total cell protein would be expected to yield a specific activity upwards of 6 to 10 U $mg^{-1}$. Thus, the over-expression strains can be further manipulated to lower the over-expressed DHAD protein levels while maximizing the specific activity of DHAD.

**[0154]** In order to improve the specific activity, yeast strains with deletions in genes involved in iron metabolism and Fe-S cluster sensing were chosen to investigate their effects on DHAD specific activity. These strains were purchased from Open Biosystem (Huntsville, AL) and included deletions of the following genes: *ISU1*, *FRA2*, *SIN4*, *MTM1*, *FRA1*, or *GRX3*. As described in Example 1, the high copy number plasmid pHR81 FBA-IlvD(sm)-lumio-FBAt was transformed into these strains, and DHAD over-expression was induced by changing the growth medium to SD minus leucine. Crude extracts from cultures were isolated and assayed for DHAD activity. The results, as shown in Table 11, indicate that deletions in certain genes had either a negative or a positive effect on the DHAD specific activity. Surprisingly, DHAD specific activity in the crude extract in strains with a deletion in either the *FRA2* or the *GRX3* gene increased by 2- to 3-fold as shown in Table 10. The DHAD activity obtained in other deletion strains is shown in Table 10.

Table 10. Effects of Deletions in Genes Involved in Iron Metabolism on DHAD Activity

| Strain Background | Clone ID | Accession No. | Gene | Average SA ($U\ mg^{-1}$) | SD |
|---|---|---|---|---|---|
| BY4741 | | Wildtype | | 1.69 | 0.20 |
| BY4741 | 2117 | YPL123W | *ISU1* | 1.31 | 0.56 |
| BY4741 | 4566 | YGL220W | *FRA2* | 3.41 | 0.24 |
| BY4741 | 1976 | YNL236W | *SIN4* | 1.65 | 0.20 |
| BY4741 | 7288 | YGR257C | *MTM1* | 0.54 | 0.12 |
| BY4741 | 1517 | YLL029W | *FRA1* | 0.97 | 0.05 |
| BY4741 | 4033 | YDR098C | *GRX3* | 5.45 | 0.14 |

**[0155]** These results demonstrate that modulating genes involved in iron metabolism can increase the activity of an Fe-S cluster requiring protein such as DHAD. The effect of deletions of the *FRA2* and *GRX3* genes on DHAD specific activity could result from, *e.g.*, activation of transcription of one or more of the genes in the iron regulon. Although not wishing to be bound by any one theory, activation of such genes could lead to an increase in iron uptake and an increase cytoplasmic Fe-S cluster biosynthesis. However, other factors in addition to affecting the iron regulon could also contribute to an increase in the iron content of the yeast cells. One protein that is involved in iron regulation is Aft1p, which controls many genes involved in iron uptake and metabolism.

**[0156]** **Example 4. Constitutive expression of genes involved in iron uptake and metabolism (PROPHETIC)**

**[0157]** It has been shown that Fra1, Fra2, Gxr3, and Grx4 are repressors that regulate the function of Aft1p (Kumánovics, *et al.*, *J. Biol. Chem. 283*:10276-10286 (2008)). Aft1p is a global regulator of iron. Activation of genes involved in iron uptake and metabolism requires the nuclear localization of Aft1p. Expression of the Aft1 constitutive mutants, *e.g.*, Aft1-$1^{up}$, or an increase in the expression of wild-type Aft1p, could lead to the activation of the Fe regulon in a wild-type strain or in an *AFT1* deletion strain (Yamaguchi-Iwai, *et al*, *EMBO J. 14*:1231-1239 (1995); Yamaguchi-Iwai, *et al*, *J. Biol. Chem. 277*:18914-18918 (2002); Kaplan, *et al*, *Chem. Rev.109*:4536-4552(2009)). This in turn may improve the active fraction of the DHAD enzyme which requires Fe-S clusters for its activity.

**[0158]** To further examine the effect of up-regulating Aft1, the wild-type *AFT1* gene and its constitutive mutants will be expressed using a centromere vector pRS411 (ATCC® Number: 87538; SEQ ID NO: 919). This vector has an ampicillin selection marker for growth in *E. coli* and a methionine nutritional marker for selection in yeast. The wild type *AFT1* gene, including its promoter and terminator, can be cloned between the KpnI and SacI sites, resulting in the construct pRS411-Aft1+flanking (SEQ ID NO: 920; Figure 2). A similar strategy can be used to clone genes that encode Aft1 constitutive mutants. The Aft1 constitutive mutants include, but are not limited to, mutants with substitutions at the following amino acids: L99 to A, L102 to A, C291 to F, or C293 to F (with respect to SEQ ID NO: 703). The pRS411 constructs with genes encoding the wild type *AFT1* gene or constitutive mutants will be transformed, along with the expression vector pHR81 FBA IlvD(Sm)-lumio-FBAt, into the wild-type yeast strain BY4741 or a yeast strain with a deletion in *AFT1*, *GRX3*, or *FRA2*. Transformants will be selected on agar plates with SD medium minus methionine and uracil. Transformed strains will be grown in SD medium minus methionine and leucine to over-express the DHAD protein in the presence of these genes or mutants. The DHAD activity in the crude extract of these cultures will be measured.

**[0159]** Aft2p protein (SEQ ID NO: 704) is a paralog of Aft1p (SEQ ID NO: 703). Aft2p is also a global regulator of iron metabolism in yeast. Similar experiments as with Aft1p can be designed and carried out to explore the possible improvement of DHAD activity by over-expression of Aft2p or its mutants.

**[0160]** Alternatively, a constitutive expression of genes involved in iron uptake and metabolism can be achieved with mutants defective in the export of Aft1p to the cytoplasm from the nucleus. It has been shown that Msn5 protein is the nuclear export receptor (Ueta, *et al, Mol. Biol. 18*:2980-2990(2007)). Deletion of the MSN5 gene (SEQ ID NO: 776) has been shown to prevent the export of the Aft1p protein from the nucleus. To determine the effect of the *MSN5* deletion, the deletion strain (commercially available from Open Biosystems) will be transformed with the DHAD expression vector pHR81 FBA IlvD(Sm)-lumio-FBAt as described in Example 1. The DHAD activity in the crude extract in these cultures will be measured.

**[0161]** Another alternative is to alter the expression of the *PSE1* ( NUCLEIC ACID SEQ ID NO: 777) gene, which encodes a protein involved in the import of Aft1p into the nucleus (Fukunaka, et al, 2003, J. of Biological Chem., vol. 278, p. 50120-50127). Expression of this gene can be accomplished by cloning it in vector pRS411 as described in this example.

**[0162]**

### Example 5. Modulation of other genes involved in Fe uptake and metabolism or Fe-S cluster biosynthesis to increase flux in an Fe-S cluster biosynthesis pathway and improve DHAD specific activity. (Prophetic)

**[0163]** Fe uptake and metabolism and/or Fe-S cluster biosynthesis genes, including, but not limited to, those listed in Tables 7, 8 and 9 can potentially be deleted, mutated, expressed, up-regulated, or down-regulated to increase the flux in an Fe-S cluster biosynthesis pathway and improve specific activity of Fe-S cluster requiring proteins such as DHAD. In addition, co-factors can be added to change the activity of polypeptides having Fe-S cluster regulatory activity to increase the flux in an Fe-S cluster biosynthesis pathway and improve DHAD specific activity.

**[0164]** For example, the genes that increase the flux in an Fe-S cluster biosynthesis pathway can be expressed to improve the activity of DHAD by providing an adequate amount of Fe-S clusters for the apo-enzyme. Any gene, or a combination of them, can be cloned and expressed in a pRS411 plasmid as described in Example 4. The resulting constructs, along with the DHAD expression vector pHR81 FBA ilvD(Sm)-lumio-FBAt, will then be transformed into wild-type BY4741. As a control, pRS411 without any gene of interest and vector pHR81 FBA ilvD(Sm)-lumio-FBAt are transformed into a wild-type strain. The transformants are selected on agar plates with SD medium without uracil and methionine to maintain both plasmids as described in Example 4. Enzymatic activity for DHAD in the crude extract of different strains from the transformation will be measured. The results will be compared with the specific activity obtained from the control pRS411 without any gene of interest and vector pHR81 FBA ilvD(Sm)-lumio-FBAt transformed into a wild-type strain. An increase in specific activity indicates a gene that can be used to increase the flux in an Fe-S cluster biosynthesis pathway. Similar screening experiments can be done with the beneficial yeast deletion strains, such as, but not limited to, those strains with deletions in FRA2 and GRX3, or those identified below.

**[0165]** As shown in Example 3, deletion or a reduction in expression of genes involved in Fe utilization and metabolism or Fe-S cluster biosynthesis, can improve the DHAD specific activity. Thus, in another example, potentially beneficial mutations for DHAD specific activity can be expanded to strains with a deletion in one or more genes listed in Tables 7, 8, or 9. In this example, the over-expression vector pHR81 FBA-IlvD(sm)-lumio-FBAt will be transformed into this collection of deletion strains, and the DHAD specific activity will be measured in the crude extract. The results will be compared with the specific activity obtained from the vector pHR81 FBA ilvD(Sm)-lumio-FBAt transformed into a wild-type strain. An increase in specific activity indicates a beneficial deletion to increase the flux in an Fe-S cluster biosynthesis pathway.

**[0166]** In addition, strains with deletions in more than one of the genes involved in Fe-S cluster regulatory activity can be created to provide additive effects in improving the enzymes or proteins containing Fe-S cluster. For example, double mutants with deletions in both *FRA2* and *GXR3* genes can be used to transform vector pHR81 FBA-IlvD(sm)-lumio-FBAt, and the DHAD activity in the crude extract from the transformants can be measured.

## **[0167]** Example 6. Determining the Specific Activity of DHAD. (Assay Method)

**[0168]** Quantitation of the activity of proteins requiring Fe-S clusters can be done in an assay format. If the protein is an enzyme, such as DHAD, the activity is typically expressed in terms of units of activity. A unit of enzyme activity has been defined by the

Enzyme Commission of the International Union of Biochemistry as the amount of enzyme that will catalyze the transformation of 1 micromole of the substrate per minute under standard conditions (International Union of Biochemistry, Report of the Commission on Enzymes, Oxford: Pergamon Press, 1961). Further, the term specific activity is defined as the units of activity in a given amount of enzyme. Thus, the specific activity is not directly measured but is calculated by dividing 1) the activity in units/ml of the enzyme sample by 2) the concentration of protein in that sample, so the specific activity is expressed as units/mg. The specific activity of a sample of pure, fully active enzyme is a characteristic of that enzyme. The specific activity of a sample of a mixture of proteins is a measure of the relative fraction of protein in that sample that is composed of the active enzyme of interest. DHAD activity can be measured spectrophotometrically in an end point assay using the 2,4-dinitrophenylhydrazine (2,4-DNPH) method as described in Flint, D.H. and M.H. Emptage, *J. Biol. Chem. 263*:3558-64 (1988). In this assay, the 2,4-DNPH reacts with the keto group of the 2-ketoisovaleric acid product to form a hydrazone, which is detected by its absorbance at 550 nm. The assay buffer contains 50 mM Tris-HC1, 10 mM $MgCl_2$, pH 8.0 (TM8 buffer). Sufficient 2,3-dihydroxyisovaleric acid is added to the assay buffer so that its final concentration in the assay mix is 10 mM. In each assay, an enzyme containing solution and sufficient substrate containing buffer are mixed so that the final volume is 1 ml. The assay mixture is normally incubated at 37°C for 30 minutes.

**[0169]** The assay is stopped by adding 250 μl of 10% (W/V) trichloroacetic acid. A few minutes later, 500 μl of a saturated solution of 2,4-DNPH in 1 N HCl is added. The mixture is incubated at room temperature for at least 10 min to allow formation of the hydrazone. Next, 1.75 ml of NaOH is added to solubilize the hydrazone and to precipitate unreacted 2,4-DNPH. A few minutes after the NaOH is added, the assay tubes are placed in a sonicator bath for 10 min to degas. The tubes are then centrifuged in a desk top centrifuge at top speed for 2 min to sediment the precipitate.

**[0170]** The absorbance of the supernatant is then read at 550 nm within 1 hour. The absorbance of the sample assays minus the control assays are divided by 2600 (determined from an α-ketoisovaleric acid standard curve) to find the units of enzyme activity in the assay. This assay was used in the Examples described herein in which DHAD specific activity was determined.

[0171] **Example 7. Purification and Characterization of DHAD from *S. mutans* expressed in *E. coli.***

[0172] DHAD from *S. mutans* was purified and characterized as follows. Six liters of culture of the *E. coli* Turner strain harboring the pET28a plasmid containing the *S. mutans ilvD* gene were grown and induced with IPTG. The *S. mutans* DHAD was purified by breaking the cells with a sonicator in TM8 buffer (*see* Example 6), centrifuging the crude extract to remove cell debris, then loading the supernatant of the crude extract on a Q Sepharose (GE Healthcare) column and eluting the DHAD with an increasing concentration of NaCl in TM8 buffer. The fractions containing DHAD were pooled, brought to 1 M $(NH_4)_2SO_4$, and loaded onto a Phenyl-Sepharose column (GE Healthcare) equilibrated with 1 M $(NH_4)_2SO_4$. The DHAD was eluted with a decreasing concentration of $(NH_4)_2SO_4$. The fractions containing DHAD were pooled, concentrated to ≤ 10 ml, loaded onto a 35 x 600 cm Superdex-200 column (577 ml bed volume) (GE Healthcare) column, and eluted with TM8 buffer. As judged by SDS gels, the purity of the *S. mutans* DHAD eluted from the Superdex column was estimated to be ≥ 90%.

[0173] The UV-visible spectrum of the purified *S. mutans* DHAD is shown in Figure 3. The number of peaks above 300 nm is typical of proteins with [2Fe-2S] clusters. The *S. mutans* DHAD was reduced with sodium dithionite, and its EPR spectra was measured at various temperatures. Figure 4 shows the EPR spectra measured at temperatures between 20°K and 70°K. The EPR spectrum of the *S. mutans* DHAD is measureable up to 70°K, which indicates that it contains a [2Fe-2S] cluster and not a [4Fe-4S] cluster because the EPR spectra of proteins containing [4Fe-4S] clusters are not observable at temperatures much above 10°K.

[0174] The exact protein content of the batch of purified *S. mutans* DHAD with the highest specific activity using the Bradford protein assay was determined by quantitative amino acid analysis. Combining the activity with the protein content gave a specific activity of 100 units/mg for this batch. The iron content of this batch determined by ICP-MS using methodology known in the art was 2 molecules of iron per molecule of DHAD. This is consistent with this batch of *S. mutans* DHAD containing a full complement of [2Fe-2S] clusters.

[0175] **Example 8. Determining the DHAD protein content in yeast crude extract and purified samples.**

[0176] A scheme to measure the concentration of the DHAD protein in the supernatant of yeast crude extracts was developed using a Mono Q column (GE Healthcare) and a C-4 column (4.6 X 250 mm Waters XBridge DEH300 C-4 3.5 μm, Waters, Milford, MA) in tandem as follows.

[0177] Frozen yeast cells were thawed, suspended in 50 mM Tris-HC1, 10 mM $MgCl_2$, pH 8.0, then broken by bead beating. The broken cells are centrifuged to remove the cell debris and generate the yeast crude extract. A 1 ml Mono Q column equilibrated with TM8 buffer containing 0.22 M NaCl and developed with a 30 ml linear gradient starting at TM8 buffer containing 0.22 M NaCl and ending at TM8 buffer containing 0.35 M NaCl was found to be ideal for separating *S. mutans* DHAD from other proteins in the yeast crude extract. 1 ml fractions were collected from this column and assayed for DHAD activity. The peak of DHAD activity was typically found in fraction 24. The sum of the activity of the DHAD in the fractions was close to that in the crude extract. Good separations using this column were obtained with as much as 1-2 mls of crude extract representing up to 200 mg of yeast cell paste.

[0178] A C-4 column equilibrated at a 7:3 mixture of 5% formic acid in water (solvent A) and 5% formic acid in acetonitrile (solvent B), was determined to bind *S. mutans* DHAD. After the sample injection, a step change in the eluting solvent to 40% solvent B, followed by a linear increase to 50% B over the next 11.5 mls, eluted DHAD and separated it from most of the proteins that co-eluted with DHAD on the Mono Q column. A UV monitor set at 210 nm was used to detect and quantify (see below) proteins eluting from this column. The elution volume of the DHAD protein from this column could not be determined by measuring the activity since the enzyme was inactivated by these solvents. However, fractions from this column run on SDS gels verified which fractions contained the *S. mutans* DHAD and the level of contamination with other yeast proteins.

[0179] Pure *S. mutans* DHAD was used to generate a standard curve of the relationship between the amount of protein injected onto the column and the area counts of the *S.*

*mutans* DHAD peak eluted from the column. The standard curve was found to be linear over the range of 0-20 μg DHAD.

[0180] For the yeast crude extracts examined, 100 μl of the DHAD activity-containing fractions from the Mono Q column was injected onto the C-4 column. Using the standard curve for the C-4 column, the amount of DHAD protein in each of the samples was determined. The DHAD specific activity in each of the fractions from the Mono Q column and in the original yeast crude extract were then calculated based on the activity in the samples and the amount of DHAD protein in the samples.

## [0181] Example 9. Determining the fraction of DHAD in the yeast crude extract loaded with Fe-S clusters

[0182] When a purified Fe-S cluster requiring protein contains a full complement of clusters, it will have a characteristic specific activity. As previously mentioned, for *S. mutans* DHAD this specific activity is 100 units/mg. If an Fe-S cluster requiring protein is only half-loaded with clusters, its specific activity will typically be half of a sample that is fully loaded with clusters. In the case of *S. mutans* DHAD, if the enzyme is half loaded with Fe-S clusters, the specific activity would be expected to be 50 units/mg. Knowing that 100 units/mg is the specific activity of fully active pure *S. mutans* DHAD enables us to determine the fraction of DHAD in a sample that is fully loaded with Fe-S clusters. If the activity and the amount of DHAD in a sample is known we can use these numbers to calculate the specific activity and then divide the specific activity by 100.

[0183] To make such a calculation, the specific activity must be based on the concentration of the DHAD protein (not the total protein concentration) in the sample. Determining the concentration of *S. mutans* DHAD in the presence of other proteins can be accomplished using methods described in Example 8.

[0184] Using this methodology, we have determined the specific activity of DHAD in the crude extract of different yeast strains grown under different conditions, using the methods described in Example 3. The following four are of particular interest:

[0185] 1) *S. mutans* DHAD expressed on a low copy number plasmid in yeast;

[0186] 2) *S. mutans* DHAD expressed on plasmid pHR81 FBA-IlvD(Sm)-lumio-FBAt, under the control of the $LEU2^{-}$ system;

**[0187]** 3) *S. mutans* DHAD expressed in a GRX3 deletion strain on plasmid pHR81 FBA-IlvD(Sm)-lumio-FBAt under the control of the LEU2$^-$ system; and

**[0188]** 4) *S. mutans* DHAD expressed in a FRA2 deletion strain on plasmid pHR81 FBA-IlvD(Sm)-lumio-FBAt under the control of the LEU2$^-$ system.

**[0189]** The specific activities and inferred fraction of the DHAD present in these strains that has an Fe-S cluster are shown in Table 11.

**[0190]**

Table 11. Specific Activities and Inferred Fraction of the DHAD Loaded Proteins

| Gene Deleted | Plasmid and Growth Conditions | DHAD SA in Crude Extracts (U/mg) | Fraction DHAD Active | Inferred Fraction of DHAD w/ Fe-S Clusters |
|---|---|---|---|---|
| | + leucine | 0.2 | | |
| | - leucine | 1.69 | 0.1 -0.2 | 0.1 -0.2 |
| FRA2 | - leucine | 3.41 | > 0.5 | > 0.5 |
| FRA1 | - leucine | 0.97 | 0.1 -0.2 | 0.1 -0.2 |
| GRX3 | - leucine | 5.45 | > 0.5 | > 0.5 |

**[0191]** These results indicate the level of Fe-S cluster loading in the DHAD strains lacking FRA2 and GRX3 is much higher than in cells containing functional copies of these genes.

**[0192]** The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance.

WHAT IS CLAIMED IS:

1. A recombinant host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity wherein said at least one heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated.

2. A recombinant host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity wherein said at least one heterologous polynucleotide is integrated at least once in the recombinant host cell DNA.

3. A recombinant host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity, wherein said host cell comprises at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis.

4. A recombinant host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity and at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis.

5. The recombinant host cell of any one of claims 3-4, wherein said heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of the genes in Tables 8 and 9.

6. The recombinant host cell of any one of claims 3-4, wherein said heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of the genes in Table 7.

7. The recombinant host cell of claim 5 or 6, wherein said heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, FRA2, GRX3, MSN5, and combinations thereof.

8. The recombinant host cell of claim 7, wherein said polypeptide is encoded by a polynucleotide that is constitutive mutant.

9. The recombinant host cell of claim 8, wherein said constitutive mutant is selected from the group consisting of AFT1 L99A, AFT1 L102A, AFT1 C291F, AFT1 C293F, and combinations thereof.

10. The recombinant host cell of claim 7, wherein said polypeptide affecting Fe-S cluster biosynthesis is encoded by a polynucleotide comprising a high copy number plasmid or a plasmid with a copy number that can be regulated.

11. The recombinant host cell of claim 7, wherein said polypeptide affecting Fe-S cluster biosynthesis is encoded by a polynucleotide integrated at least once in the recombinant host cell DNA.

12. The recombinant host cell of claim 3, wherein the at least one deletion, mutation, and/or substitution in an endogenous gene encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of FRA2, GRX3, MSN5, and combinations thereof.

13. The recombinant host cell of claim 4, wherein the at least one heterologous polynucleotide encoding a polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of AFT1, AFT2, PSE1, and combinations thereof.

14. The recombinant host cell of any one of claims 3-13, wherein said at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity is expressed in multiple copies.

15. The recombinant host cell of claim 14, wherein said at least one heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated.

16. The recombinant host cell of claim 14, wherein said at least one heterologous polynucleotide is integrated at least once in the recombinant host cell DNA.

17. The recombinant host cell of any one of claims 3-16, wherein said Fe-S cluster biosynthesis is increased compared to a recombinant host cell having endogenous Fe-S cluster biosynthesis.

18. The recombinant host cell of any one of claims 1-17, wherein said host cell is a yeast host cell.

19. The recombinant host cell of claim 18, wherein said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia* and *Pichia*.

20. The recombinant host cell of any one of claims 1-19, wherein said heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in the cytosol of the host cell.

21. The recombinant host cell of any one of claims 1-20, wherein said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168.

22. The recombinant host cell of any one of claims 1-21 wherein said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence with at least about 90% identity to SEQ ID NO: 168 or SEQ ID NO: 232.

23. The recombinant host cell of any one of claims 1-22 wherein said polypeptide having dihydroxy-acid dehydratase activity has a specific activity selected from the group consisting of:
    (a) greater than about 5-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity
    (b) greater than about 8-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity
    (c) greater than about 10-fold with respect to the control host cell comprising at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity.

24. The recombinant host cell of any one of claims 1-22, wherein said polypeptide having dihydroxy-acid dehydratase activity has a specific activity selected from the group consisting of:
    (a) greater than about 0.25 U/mg;
    (b) greater than about 0.3 U/mg;
    (c) greater than about 0.5 U/mg;
    (d) greater than about 1.0 U/mg;
    (e) greater than about 1.5 U/mg;
    (f) greater than about 2.0 U/mg;
    (g) greater than about 3.0 U/mg;
    (h) greater than about 4.0 U/mg;
    (i) greater than about 5.0 U/mg;
    (j) greater than about 6.0 U/mg;
    (k) greater than about 7.0 U/mg;
    (l) greater than about 8.0 U/mg;
    (m) greater than about 9.0 U/mg;
    (n) greater than about 10.0 U/mg;
    (o) greater than about 20.0 U/mg; and
    (p) greater than about 50.0 U/mg.

25. The recombinant host cell of any one of claims 1-24, wherein said recombinant host cell produces isobutanol.

26. The recombinant host cell of claim 25, wherein said recombinant host cell comprises an isobutanol biosynthetic pathway.

27. A method of making a product comprising:

    (a) providing the recombinant host cell of any one of claims 1-24; and

    (b) contacting the recombinant host cell of (a) with a fermentable carbon substrate in a fermentation medium under conditions wherein said product is produced; and

    (c) recovering said product,

    wherein the product is selected from the group consisting of branched chain amino acids, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, isobutanol, and combinations thereof.

28. A method of making isobutanol comprising:

    (a) providing the recombinant host cell of any one of claims 1-24;

    (b) contacting the recombinant host cell of (a) with a fermentable carbon substrate in a fermentation medium under conditions wherein isobutanol is produced; and

    (c) recovering said isobutanol.

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

    (a) providing the recombinant host of any one of claims 1-24;

    (b) growing the recombinant host cell of (a) under conditions where the 2,3-dihydroxyisovalerate is converted to α-ketoisovalerate,

    wherein 2,3-dihydroxyisovalerate is converted to α-ketoisovalerate.

30. A method for increasing the specific activity of a heterologous polypeptide having dihydroxy-acid dehydratase activity in a recombinant host cell comprising:

    (a) providing a recombinant host cell of any one of claims 1-24; and

    (b) growing the recombinant host cell of (a) under conditions whereby the heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in functional form having a specific activity greater than the same host cell lacking said heterologous polypeptide.

31. A method for increasing the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising:

(a) providing a recombinant host cell of any one of claims 3-24; and

(b) growing the recombinant host cell of (a) under conditions whereby the flux in the Fe-S cluster biosynthesis pathway in the host cell is increased.

32. A method of increasing the activity of an Fe-S cluster requiring protein in a recombinant host cell comprising:

(a) providing a recombinant host cell comprising an Fe-S cluster requiring protein;

(b) changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis in said host cell; and

(c) growing the recombinant host cell of (b) under conditions whereby the activity of the Fe-S cluster requiring protein is increased.

33. The method of claim 32, wherein said increase in activity is an amount selected from the group consisting of:

(a) greater than about 10%;

(b) greater than about 20%;

(c) greater than about 30%;

(d) greater than about 40%;

(e) greater than about 50%;

(f) greater than about 60%;

(g) greater than about 70%;

(h) greater than about 80%;

(i) greater than about 90%; and

(j) greater than about 95%.

34. The method of claim 32, wherein said increase in activity is an amount selected from the group consisting of:

(a) greater than about 5 fold;

(b) greater than about 8 fold;

(c) greater than about 10 fold.

35. A method for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising:

(a) changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis;

(b) measuring the activity of a heterologous Fe-S cluster requiring protein; and

(c) comparing the activity of the heterologous Fe-S cluster requiring protein measured in the presence of the changed expression or activity of a polypeptide of step (a) to the activity of the heterologous Fe-S cluster requiring protein measured in the absence of the changed expression or activity of a polypeptide of step (a),

wherein an increase in the activity of the heterologous Fe-S cluster requiring protein indicates an increase in the flux in said Fe-S cluster biosynthesis pathway.

36. A method for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell comprising:

(a) changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis;

(b) measuring the activity of a polypeptide having dihydroxy-acid dehydratase activity; and

(c) comparing the activity of the polypeptide having dihydroxy-acid dehydratase activity measured in the presence of the change in expression or activity of a polypeptide of step (a) to the activity of the polypeptide having dihydroxy-acid dehydratase activity measured in the absence of the change in expression or activity of a polypeptide of step (a),

wherein an increase in the activity of the polypeptide having dihydroxy-acid dehydratase activity indicates an increase in the flux in said Fe-S cluster biosynthesis pathway.

37. The method of any one of claims 30-36, wherein said changing the expression or activity of a polypeptide affecting Fe-S cluster biosynthesis comprises deleting, mutating, substituting, expressing, up-regulating, down-regulating, altering the cellular location, altering the state of the protein, and/or adding a cofactor.

38. The method of any one of claims 32-37, wherein the Fe-S cluster requiring protein has dihydroxy-acid dehydratase activity and wherein said Fe-S cluster requiring protein having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168.

39. The method of any one of claims 32-38, wherein said polypeptide affecting Fe-S cluster biosynthesis is selected from the group consisting of the genes in Tables 7, 8 and 9.

40. A recombinant host cell comprising at least one polynucleotide encoding a polypeptide identified by the methods of any one of claims 35-37.

41. The recombinant host cell of claim 40, wherein said host cell further comprises at least one heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity.

42. The recombinant host cell of claim 41, wherein said heterologous polynucleotide encoding a polypeptide having dihydroxy-acid dehydratase activity is expressed in multiple copies.

43. The recombinant host cell of claim 41, wherein said heterologous polynucleotide comprises a high copy number plasmid or a plasmid with a copy number that can be regulated.

44. The recombinant host cell of claim 41, wherein said heterologous polynucleotide is integrated at least once in the recombinant host cell DNA.

45. The method of claim 35 or 36, wherein said host cell is a yeast host cell.

46. The method of claim 45, wherein said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia,* and *Pichia*.

47. The method of any one of claims 28-39, wherein said host cell is a yeast host cell.

48. The method of claim 47, wherein said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia,* and *Pichia*.

49. The recombinant host cell of any one of claims 40-44, wherein said recombinant host cell is a yeast host cell.

50. The recombinant host cell of claim 49, wherein said yeast host cell is selected from the group consisting of *Saccharomyces*, *Schizosaccharomyces*, *Hansenula*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Issatchenkia,* and *Pichia*.

51. The recombinant host cell of any one of claims 40-44 or 49-50, wherein said heterologous polypeptide having dihydroxy-acid dehydratase activity is expressed in the cytosol of the host cell.

52. The recombinant host cell of any one of claims 40-44 or 49-50 wherein said heterologous polypeptide having dihydroxy-acid dehydratase activity has an amino acid sequence that matches the Profile HMM of Table 12 with an E value of $< 10^{-5}$ wherein the polypeptide

further comprises all three conserved cysteines, corresponding to positions 56, 129, and 201 in the amino acids sequences of the *Streptococcus mutans* DHAD enzyme corresponding to SEQ ID NO:168.

53. The recombinant host cell of any one of claims 40-44 or 49-50, wherein said recombinant host cell produces a product selected from the group consisting of branched chain amino acids, pantothenic acid, 2-methyl-1-butanol, 3-methyl-1-butanol, isobutanol, and combinations thereof.

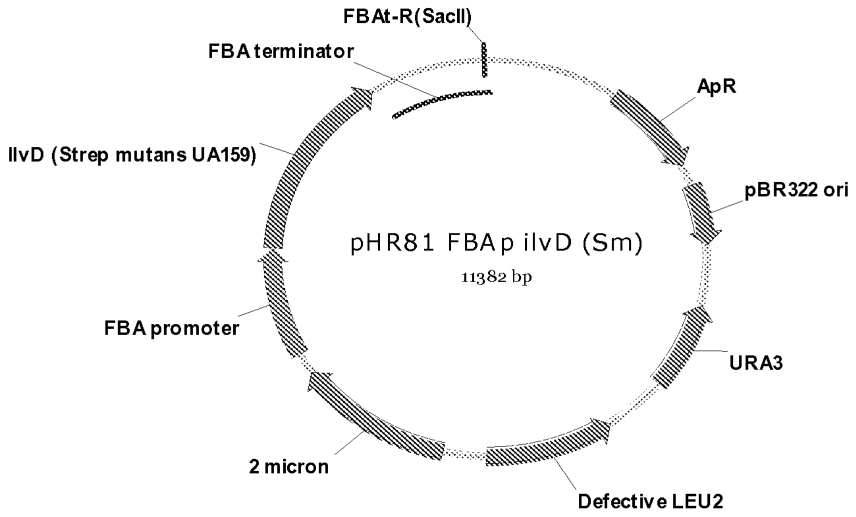
54. The recombinant host cell of claim 53, wherein said recombinant host cell produces isobutanol.

55. The recombinant host cell of claim 54, wherein said recombinant host cell comprises an isobutanol biosynthetic pathway.

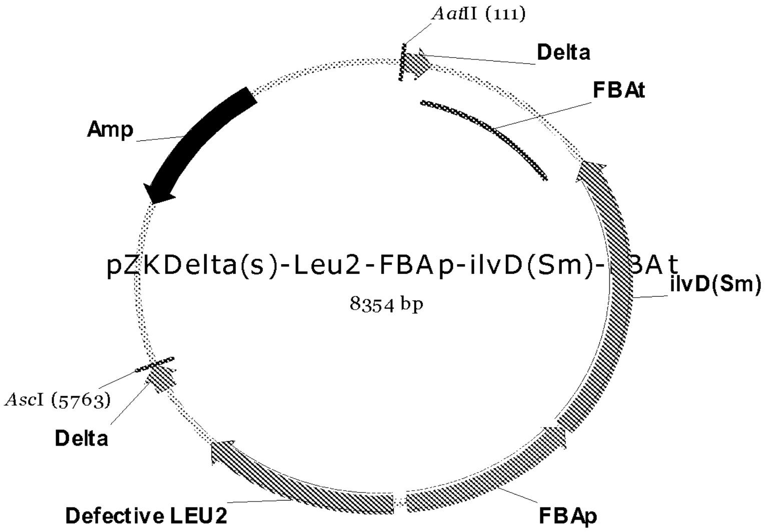
# ABSTRACT

The present invention is related to a recombinant host cell, in particular a yeast cell, comprising a dihydroxy-acid dehydratase polypeptide. The invention is also related to a recombinant host cell having increased specific activity of the dihydroxy-acid dehydratase polypeptide as a result of increased expression of the polypeptide, modulation of the Fe-S cluster biosynthesis of the cell, or a combination thereof. The present invention also includes methods of using the host cells, as well as, methods for identifying polypeptides that increase the flux in an Fe-S cluster biosynthesis pathway in a host cell.

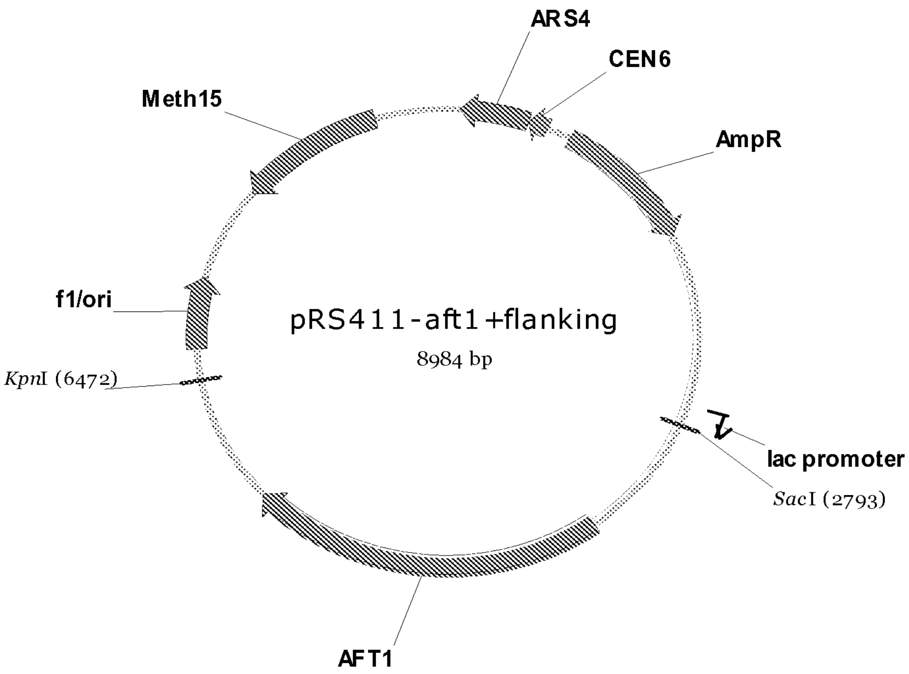
## Figure 1A



## Figure 1B



# Figure 2


ARS4
CEN6
Meth15
AmpR
f1/ori
pRS411-aft1+flanking
8984 bp
*Kpn*I (6472)
lac promoter
*Sac*I (2793)
AFT1

## Figure 3

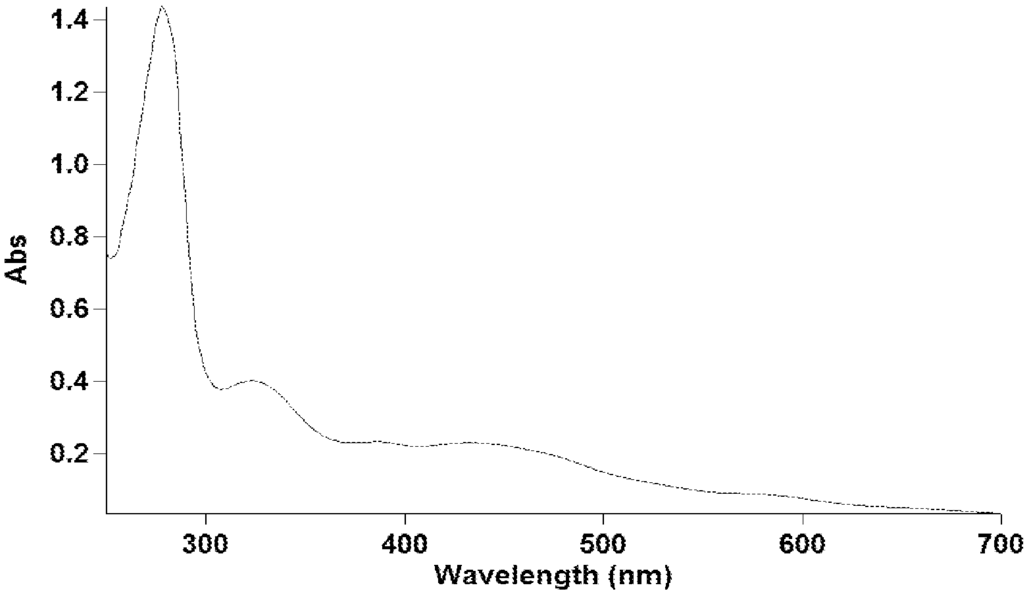
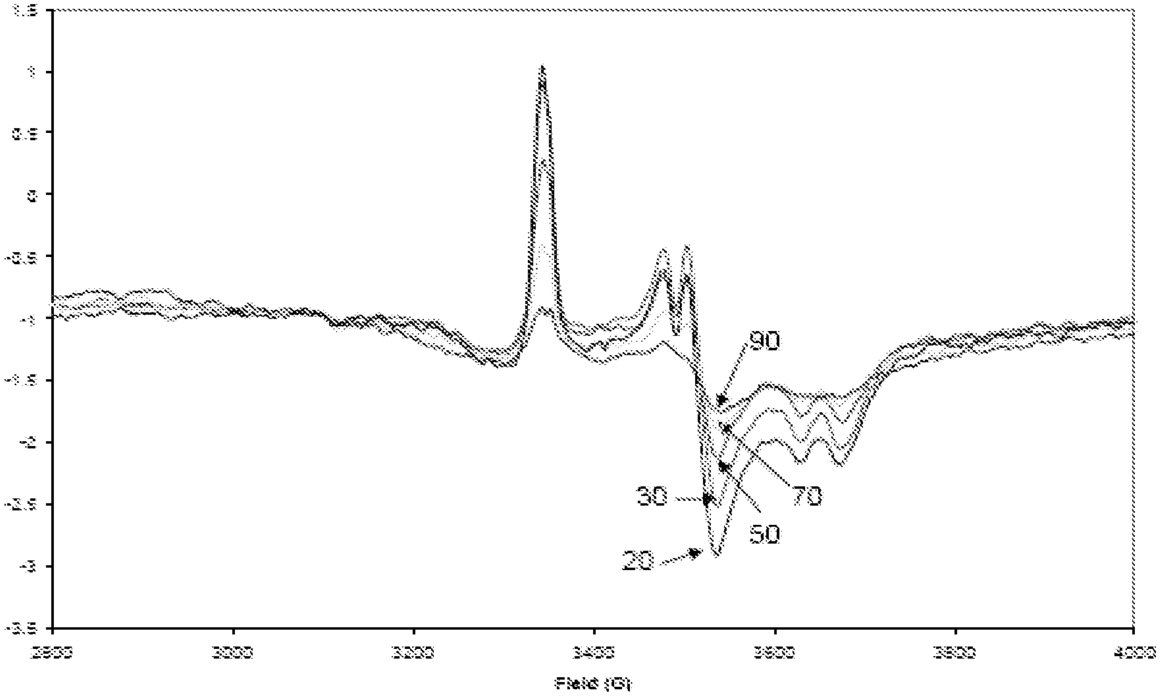
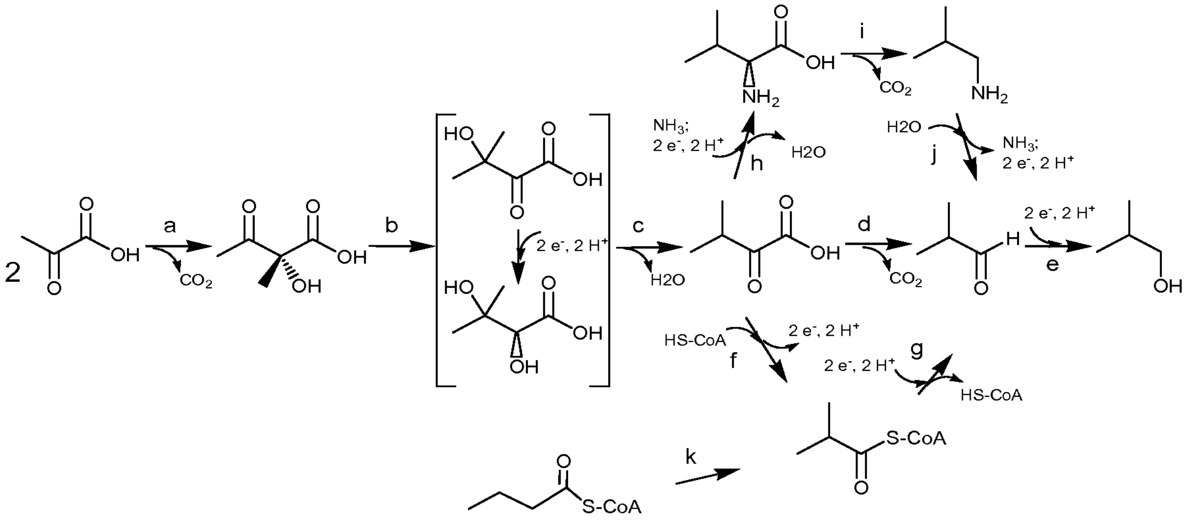


**Figure 4**



[Would it be possible to provide a less blurry version of this Figure?]

**Figure 5**



2
a
CO2
b
2 e-, 2 H+
c
H2O
d
CO2
e
2 e-, 2 H+
NH3;
2 e-, 2 H+
h
H2O
i
CO2
H2O
j
NH3;
2 e-, 2 H+
HS-CoA
f
2 e-, 2 H+
2 e-, 2 H+
g
HS-CoA
k
OH
NH2
S-CoA

**Figure 6A**

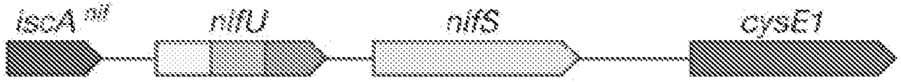


**Figure 6B**

**Figure 6C**

$$\text{apo-ISU} + 2\ \text{IscS-Cys-S-S}^{-} + 2\ \text{Fe}^{2+} + 2\ \mathbf{NFU}^{\mathbf{red}}$$

$$\rightarrow \quad \text{[2Fe-2S]-ISU} + 2\ \text{IscS-Cys-S}^{-} + 2\ \mathbf{NFU}^{\mathbf{ox}}$$

**Figure 7**

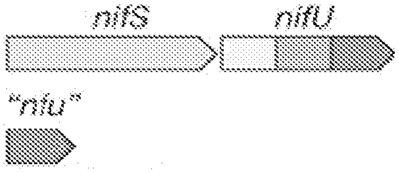


**Figure 8**

**Figure 9**

| | |
|---|---|
| HMMER2.0 [2.2g] | Program name and version |
| NAME dhad_for_hmm | Name of the input sequence alignment file |
| LENG 564 | Length of the alignment: include indels |
| ALPH Amino | Type of residues |
| MAP yes | Map of the match states to the columns of the alignment |
| COM /app/public/hmmer/current/bin/hmmbuild -F dhad-exp_hmm dhad_for_hmm.aln | Commands used to generate the file:  this one means that hmmbuild (default patrameters) was applied to the alignment file |
| COM /app/public/hmmer/current/bin/hmmcalibrate dhad-exp_hmm | Commands used to generate the file:  this one means that hmmcalibrate (default parametrs) was applied to the hmm profile |
| NSEQ 8 | Number of sequences in the alignment file |
| DATE Tue Jun 3 10:48:24 2008 | When was the file generated |
| XT -8455 -4 -1000 -1000 -8455 -4 -8455 -4 | |
| NULT -4 -8455 | The transition probability distribution for the null model (single G state). |
| NULE 595 -1558 85 338 -294 453 -1158 197 249 902 -1085 -142 -21 -313 45 531 201 384 -1998 | The symbol emission probability distribution for the null model (G state); consists of K (e.g. 4 or 20) integers. The null probability used to convert these back to model probabilities is 1/K. |
| EVD -499.650970 0.086142 | The extreme value distribution parameters μ and lambda respectively; both floating point values.   Lambda is positive and nonzero. These 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 20(M) | 445 | -796 | -1082 | -521 | -841 | -1643 | -412 | -403 | -370 | -692 | 2213 | -646 | 536 | 1166 | -698 | -630 | 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 | * | * | | | | | | | | | | | | |
| 21(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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 34(F) | -1511 | -1236 | -3511 | -3017 | 2747 | -2982 | -1069 | -260 | -2651 | 992 | 2737 | -2407 | -2904 | -2088 | -2418 | -2099 | -1434 | -489 | -537 | 2056 | **39** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 35(Q) | -576 | -1869 | -401 | 92 | -2232 | 831 | -173 | -1930 | 1505 | -1913 | -1042 | -186 | -1620 | 1653 | -51 | -482 | 1346 | -1534 | -2098 | -1490 | **40** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 36(D) | -1352 | -3066 | 3028 | 1349 | -3303 | -1566 | -724 | -3141 | 1155 | -3043 | -2267 | -165 | -1991 | -354 | -1350 | -1086 | -1368 | -2659 | -3221 | -2356 | **41** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 37(E) | -1507 | -3288 | 2042 | 2762 | -3520 | 515 | -853 | -3401 | -981 | -3296 | -2566 | -182 | -2064 | -503 | -1753 | -1209 | -1553 | -2895 | -3486 | -2547 | **42** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 38(D) | -1445 | -2778 | 3529 | -53 | -3524 | -1590 | -1129 | -3476 | -1367 | -3459 | -2774 | -396 | -2156 | -825 | -2122 | 554 | -1609 | -2880 | -3582 | -2717 | **43** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 39(F) | -2658 | -2176 | -4213 | -4000 | 3815 | -3933 | -1352 | -531 | -3638 | 1121 | -19 | -3184 | -3709 | -2820 | -3296 | -3219 | -2579 | -1037 | -601 | 403 | **44** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 40(D) | -684 | -2193 | 1738 | 1460 | -2494 | -1437 | -249 | -2257 | 1694 | -2199 | -1308 | -62 | -1637 | 185 | -450 | -531 | 633 | -1808 | -2374 | -1657 | **45** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 41(K) | -2620 | -2961 | -2461 | -2046 | -3743 | -2791 | -1570 | -3603 | 3784 | -3387 | -2839 | -2048 | -3039 | -1260 | -465 | -2604 | -2536 | -3331 | -3001 | -2988 | **46** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 42(P) | 1882 | -1119 | -2231 | -2302 | -3062 | -1360 | -2209 | -2710 | -2339 | -3013 | -2243 | -1676 | 3304 | -2117 | -2409 | -742 | -918 | -1916 | -3263 | -3022 | **47** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 43(I) | -1006 | -992 | -2347 | -1784 | -650 | -2452 | -1256 | 2372 | -1386 | 77 | 2213 | -1720 | -2455 | 2030 | -1490 | -1528 | -946 | 106 | -1441 | -1111 | **48** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 44(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **49** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 45(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **50** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 46(I) | -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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 59(H) | -1525 | -2164 | -1235 | -1346 | -2509 | 2296 | 4235 | -3172 | -1516 | -3178 | -2523 | -1448 | -2541 | -1520 | -1760 | -1591 | -1741 | -2656 | -2681 | -2065 | **64** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 60(L) | -2478 | -2009 | -4717 | -4196 | -568 | -4424 | -3262 | 1334 | -3887 | 2824 | 604 | -4085 | -3872 | -3088 | -3590 | -3717 | -2380 | -199 | -2217 | -2207 | **65** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 61(H) | -682 | -2191 | 1015 | 275 | -2485 | 396 | 2379 | -2251 | 62 | -2197 | -1307 | 1826 | -1636 | 1527 | -480 | -529 | -641 | -1803 | -2375 | -1654 | **66** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 62(D) | -575 | -1920 | 1979 | 184 | -2299 | 94 | -242 | -2029 | 114 | -2023 | -1144 | -120 | -1608 | 186 | 1063 | -469 | 1413 | -1605 | -2229 | -1561 | **67** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 63(L) | -2618 | -2139 | -4597 | -4163 | 2144 | -4285 | -2334 | -83 | -3854 | 2690 | 538 | -3771 | -3806 | -2950 | -3488 | -3563 | -2505 | -751 | -1442 | -808 | **68** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 64(A) | 2657 | -1033 | -2408 | -2532 | -3233 | 2193 | -2364 | -2950 | -2626 | -3237 | -2386 | -1719 | -2027 | -2301 | -2635 | -655 | -850 | -1988 | -3420 | -3231 | **69** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 65(K) | -443 | -1857 | 958 | 270 | -2158 | -1393 | -66 | -1890 | 1839 | -442 | -957 | -36 | -1499 | 1204 | -132 | 616 | -382 | -1469 | -2048 | -1383 | **70** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 66(C) | 605 | 1553 | 739 | -17 | -1374 | -1488 | -182 | 260 | 969 | -203 | -397 | -263 | -1573 | 159 | 691 | -426 | -331 | -761 | -1567 | -1032 | **71** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 67(A) | 2327 | -956 | -3193 | -2728 | -1289 | -2677 | -2114 | 1664 | -2485 | -601 | -288 | -2403 | -2839 | -2263 | -2523 | -1871 | -1126 | 1617 | -2143 | -1765 | **72** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 68(K) | -532 | -1656 | -490 | 1321 | -1891 | -1527 | -172 | -124 | 2206 | -1591 | -782 | -223 | -1619 | 237 | -106 | -482 | -464 | -98 | -1904 | -1326 | **73** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 69(H) | 384 | -1854 | 936 | 889 | -2165 | -1363 | 1498 | -1909 | 1111 | -1866 | -948 | 1091 | -1464 | 421 | -131 | -284 | -342 | -69 | -2043 | -1364 | **74** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 70(G) | 1823 | -932 | -2330 | -2313 | -3120 | 2511 | -2158 | -2865 | -2331 | -3098 | -2209 | -1563 | -1912 | -2032 | -2419 | 1138 | -706 | -1883 | -3328 | -3077 | **75** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 84(I) | -1286 | -1279 | -2907 | -2683 | -1446 | -2549 | -2198 | 3290 | -2407 | -726 | -534 | -2386 | 1172 | -2299 | -2437 | -1895 | -1392 | 283 | -2302 | -1913 | **90** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 85(T) | -493 | -1105 | -2189 | -2267 | -3101 | 1880 | -2196 | -2791 | -2334 | -3081 | -2269 | -1649 | -2058 | -2099 | -2410 | -719 | 3135 | -1948 | -3282 | -3046 | **91** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 86(V) | -1750 | -1296 | -4319 | -3957 | -1765 | -4038 | -3733 | 2364 | -3826 | -619 | -543 | -3716 | -3869 | -3685 | -3902 | -3354 | -1743 | 3012 | -3265 | -2817 | **92** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 87(S) | 923 | -962 | -2348 | -2422 | -3132 | -1207 | -2248 | -2850 | -2440 | -3140 | -2285 | -1624 | -1954 | -2158 | -2477 | 3171 | -758 | -1896 | -3362 | -3103 | **93** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 88(D) | -2784 | -3432 | 4016 | -1200 | -4140 | -2466 | -2197 | -4505 | -2621 | -4365 | -3956 | -1551 | -3014 | -2039 | -3232 | -2593 | -2938 | -4046 | -3710 | -3552 | **94** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 89(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **95** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 90(I) | -1880 | -1493 | -4193 | -3724 | -953 | -3837 | -2980 | 3251 | -3420 | 257 | 2372 | -3485 | -3608 | -3005 | -3310 | -3087 | -1840 | 617 | -2373 | -2155 | **96** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 91(S) | 2150 | -939 | -2407 | -2415 | -3075 | -1197 | -2205 | -2781 | -2384 | -3065 | -2205 | -1613 | -1936 | -2105 | -2436 | 2652 | -729 | -1850 | -3306 | -3049 | **97** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 92(M) | -979 | -1455 | -1242 | -1122 | -1434 | -1860 | -1131 | -1171 | -974 | -1285 | 4091 | 2176 | -2226 | -1017 | -1187 | -1166 | -1086 | -1063 | -1929 | -1345 | **98** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 93(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **99** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 94(T) | -959 | -1691 | -1249 | -949 | -2563 | -1747 | -929 | -2093 | 1282 | -2263 | -1554 | -995 | -2115 | -600 | -354 | -1037 | 3152 | -1726 | -2494 | -2098 | **100** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 95(E) | -572 | -1860 | -208 | 2213 | -2107 | -1461 | -191 | -1808 | 199 | -116 | -983 | -127 | 318 | 1199 | -269 | -475 | -517 | -1448 | -2078 | -1441 | **101** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 109(D) | -2784 | -3432 | 4016 | -1200 | -4140 | -2466 | -2197 | -4505 | -2621 | -4365 | -3956 | -1551 | -3014 | -2039 | -3232 | -2593 | -2938 | -4046 | -3710 | -3552 | **115** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 110(S) | -352 | 2942 | -2955 | -2957 | -2876 | -1254 | -2382 | -2573 | -2692 | -2927 | -2128 | -1827 | -2001 | -2405 | -2607 | 3103 | -778 | -1757 | -3171 | -2911 | **116** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 111(I) | -2091 | -1746 | -3971 | -3840 | -1676 | -3532 | -3289 | 3684 | -3581 | -659 | -693 | -3562 | -3674 | -3445 | -3521 | -3194 | -2146 | 449 | -2877 | -2493 | **117** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 112(E) | -2641 | -3308 | -896 | 3732 | -3966 | -2458 | -2043 | -4105 | -2128 | -4016 | -3555 | -1531 | -2959 | -1842 | -2560 | -2479 | -2750 | -3722 | -3563 | -3385 | **118** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 113(T) | 1556 | -936 | -2493 | -2457 | -2805 | -1256 | -2159 | -2210 | -2319 | -2681 | -1932 | -1656 | -1974 | -2089 | -2352 | -598 | 3235 | -1547 | -3111 | -2847 | **119** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 114(C) | 1784 | 2119 | -2013 | -1532 | -1093 | -1580 | -1089 | -436 | -1322 | -937 | -273 | 1093 | -1932 | -1127 | -1472 | -748 | -515 | 1585 | -1536 | -1163 | **120** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 115(M) | 1831 | 2019 | -2596 | -2038 | -605 | -1979 | -1126 | 244 | -1727 | -359 | 2501 | -1655 | -2145 | -1435 | -1683 | -1106 | -557 | 1087 | -1153 | -804 | **121** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 116(Q) | -987 | -2211 | -43 | -62 | -2833 | 2229 | -691 | -2616 | -407 | -2604 | -1797 | 1197 | -1917 | 2260 | -858 | -880 | -1045 | -2139 | -2772 | -2099 | **122** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 117(G) | 2313 | -1042 | -2391 | -2526 | -3250 | 2601 | -2372 | -2972 | -2637 | -3257 | -2407 | -1721 | -2032 | -2310 | -2646 | -662 | -859 | -2003 | -3434 | -3247 | **123** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 118(Q) | -914 | -2350 | -48 | 1661 | -2621 | -1571 | 2504 | -2400 | 68 | -2331 | -1486 | -201 | -1796 | 2646 | -351 | -754 | -865 | -1984 | -2463 | -1787 | **124** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 119(W) | -517 | -1294 | -733 | -183 | -1062 | -1605 | -234 | -1037 | 19 | -1207 | -456 | 1435 | -1690 | 33 | 756 | 411 | -454 | -819 | 3340 | 1286 | **125** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 120(M) | 410 | -469 | -2417 | -1828 | -341 | -2041 | -897 | 195 | -1513 | -156 | 3130 | -1534 | -2102 | -1230 | -1484 | -1117 | -507 | 954 | -894 | 2253 | **126** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | [illegible] | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 134(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **140** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 135(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **141** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 136(A) | 2180 | -935 | -2286 | -2196 | -3057 | 1098 | -2058 | -2796 | -2174 | -3021 | -2134 | -1516 | -1898 | -1906 | -2302 | 2146 | -689 | -1849 | -3256 | -2983 | **142** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 137(M) | -1799 | -1433 | -4142 | -3579 | -669 | -3668 | -2608 | 1558 | -3293 | 1235 | 3799 | -3296 | -3401 | -2717 | -3088 | -2843 | -1726 | 1156 | -2002 | -1868 | **143** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 138(I) | -2091 | -1746 | -3971 | -3840 | -1676 | -3532 | -3289 | 3684 | -3581 | -659 | -693 | -3562 | -3674 | -3445 | -3521 | -3194 | -2146 | 449 | -2877 | -2493 | **144** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 139(A) | 3103 | -1036 | -2445 | -2572 | -3222 | 1051 | -2380 | -2930 | -2650 | -3226 | -2381 | -1739 | -2034 | -2327 | -2648 | -664 | -857 | -1981 | -3412 | -3228 | **145** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 140(M) | -2325 | -1891 | -4598 | -4012 | -498 | -4222 | -3013 | 1242 | -3722 | 1864 | 3929 | -3855 | -3711 | -2910 | -3414 | -3439 | -2215 | -299 | -2076 | -2098 | **146** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 141(A) | 3103 | -1036 | -2445 | -2572 | -3222 | 1051 | -2380 | -2930 | -2650 | -3226 | -2381 | -1739 | -2034 | -2327 | -2648 | -664 | -857 | -1981 | -3412 | -3228 | **147** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 142(R) | -1588 | -2442 | -1399 | -953 | -3069 | -2171 | -708 | -2795 | 373 | -2625 | -1916 | 1858 | -2357 | -324 | 3294 | -1520 | -1505 | -2453 | -2523 | -2186 | **148** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 143(M) | -1448 | -1256 | -3396 | -2819 | -474 | -3024 | -1923 | 175 | -2473 | 2225 | 2756 | -2574 | -2922 | -2063 | -2375 | -2153 | 952 | -151 | -1599 | -1410 | **149** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 144(N) | -1662 | -3306 | 2055 | 78 | -3621 | -1643 | -1040 | -3622 | -1272 | -3531 | -2870 | 3477 | -2182 | -724 | -2071 | -1371 | -1757 | -3092 | -3633 | -2700 | **150** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 145(I) | -1066 | -921 | -2828 | -2239 | -1041 | -2675 | -1601 | 2235 | -1668 | -455 | -92 | -2067 | -2692 | -1688 | 1701 | -1795 | -1024 | 1960 | -1771 | -1396 | **151** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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(Y) | -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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | * | * | | | | | | | | | | | | |
| 159(H) | -744 | -2193 | -114 | 1118 | -2513 | -1512 | 2486 | -2252 | 1178 | -2183 | -1308 | 2230 | -1689 | 180 | -233 | -598 | -687 | -1823 | -2335 | -1670 | **165** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 160(W) | -2672 | -2139 | -3850 | -3748 | 941 | -3611 | -469 | -1691 | -3306 | 1047 | -1217 | -2551 | -3534 | -2514 | -2960 | -2788 | -2577 | -1799 | 4205 | 3466 | **166** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 161(K) | 386 | -1981 | 779 | 279 | -2295 | -1403 | -114 | -2043 | 2059 | -1991 | -1082 | 941 | -1536 | 1263 | -211 | -384 | -457 | -1602 | -2161 | -1476 | **167** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 162(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **168** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 163(K) | -1144 | -2365 | -912 | 2048 | -2856 | -1912 | -326 | -2459 | 2267 | -2295 | -1482 | -556 | -1989 | 108 | 1334 | -1013 | -1014 | -2093 | -2324 | -1881 | **169** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 164(D) | -1091 | -2610 | 2941 | 174 | -2957 | -1527 | -595 | -2750 | 1084 | -2696 | -1877 | -176 | -1885 | -206 | -1006 | 740 | -1098 | -2288 | -2880 | -2105 | **170** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 165(L) | -2387 | -1922 | -4674 | -4155 | -617 | -4366 | -3250 | 1889 | -3865 | 2650 | 558 | -4023 | -3847 | -3098 | -3586 | -3647 | -2296 | -38 | -2247 | -2224 | **171** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 166(N) | -1021 | -2427 | 1806 | 133 | -2870 | -1499 | -635 | -2647 | -521 | -2640 | -1825 | 2171 | -1874 | -255 | -1124 | -860 | 2122 | -2184 | -2853 | -2090 | **172** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 167(I) | -1830 | -1390 | -4327 | -3873 | -1210 | -3994 | -3274 | 2967 | -3678 | 1259 | -30 | -3633 | -3730 | -3283 | -3604 | -3249 | -1791 | 1570 | -2661 | -2417 | **173** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 168(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **174** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 169(S) | -897 | -1462 | -2333 | -2543 | -3185 | -1640 | -2474 | -3294 | -2686 | -3497 | -2780 | -1973 | -2360 | -2483 | -2703 | 3465 | -1316 | -2413 | -3310 | -3025 | **175** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 170(A) | 2440 | -824 | -2371 | -2082 | -1993 | -1344 | -1704 | -1264 | -1899 | -1832 | -1137 | -1517 | -1946 | -1674 | -2005 | 1075 | -641 | 1474 | -2390 | -2055 | **176** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 184(E) | 345 | -2074 | 925 | 1994 | -2378 | -1408 | -177 | -2135 | 922 | -2084 | -1183 | -38 | 641 | 264 | -356 | -444 | -536 | -1690 | -2261 | -1556 | **190** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 185(E) | -1493 | -2900 | 93 | 3174 | -2903 | -1743 | 1987 | -3042 | -646 | -2957 | -2238 | -411 | -2146 | -506 | -1121 | -1272 | -1503 | -2629 | -2905 | -2134 | **191** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 186(D) | -1293 | -2959 | 2673 | 2121 | -3219 | -1546 | -713 | -3043 | -707 | -2974 | -2191 | -158 | -1967 | -342 | -1394 | -1043 | 701 | -2567 | -3172 | -2311 | **192** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 187(F) | -1137 | -905 | -3250 | -2707 | 2365 | -2647 | -1016 | -34 | -2336 | 1239 | 267 | -2150 | -2626 | -1861 | -2133 | -1752 | -1069 | 1461 | -599 | 1844 | **193** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 188(K) | -479 | -1713 | -409 | 1031 | -1925 | -1467 | 1755 | -1650 | 1844 | -349 | -827 | -140 | -1556 | 319 | -75 | -403 | -411 | -1301 | -1900 | 843 | **194** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 189(G) | 433 | -2144 | 52 | 1047 | -2717 | 2303 | -615 | -2467 | -442 | -2482 | -1655 | 1123 | -1828 | -233 | -995 | -763 | -923 | -2000 | -2710 | -2005 | **195** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 190(V) | -1752 | -1320 | -4254 | -3806 | -1311 | -3916 | -3232 | 1701 | -3614 | 1188 | -140 | -3551 | -3693 | -3280 | -3568 | -3166 | -1718 | 2833 | -2703 | -2409 | **196** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 191(E) | -1199 | -1750 | -734 | 2668 | -1820 | -2038 | -1068 | 1892 | -867 | -1273 | -897 | -922 | -2295 | -797 | -1238 | -1340 | -1197 | -426 | -2325 | -1789 | **197** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 192(C) | -1182 | 3528 | -1398 | -620 | -2541 | -2038 | -358 | -2093 | 1181 | -2037 | -1272 | -747 | -2070 | 1553 | 2213 | -1123 | -1038 | -1817 | -2142 | -1774 | **198** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 193(N) | -1478 | -2527 | -261 | -403 | -2011 | -1837 | 2032 | -2925 | -735 | -2845 | -2195 | 3635 | -2259 | -721 | -1085 | -1352 | -1546 | -2522 | -2307 | -1431 | **199** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 194(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **200** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 195(C) | -1220 | 4911 | -3609 | -3314 | -1440 | -2525 | -2482 | 1565 | -2922 | -706 | -544 | -2678 | -2896 | -2710 | -2836 | -1869 | -1375 | 379 | -2371 | -1957 | **201** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | [illegible] | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 209(T) | -1213 | -1674 | -2755 | -2906 | -3163 | -1922 | -2659 | -2698 | -2788 | -3105 | -2612 | -2311 | -2600 | -2708 | -2753 | -1463 | 3819 | -2197 | -3286 | -3156 | **215** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 210(M) | -2355 | -1988 | -4343 | -3834 | -504 | -4051 | -2868 | 105 | -3385 | 1451 | 4460 | -3680 | -3671 | -2806 | -3171 | -3327 | -2274 | -474 | -2039 | -1925 | **216** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 211(S) | 2150 | -939 | -2407 | -2415 | -3075 | -1197 | -2205 | -2781 | -2384 | -3065 | -2205 | -1613 | -1936 | -2105 | -2436 | 2652 | -729 | -1850 | -3306 | -3049 | **217** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 212(S) | -344 | -979 | -2190 | -2162 | -2959 | -1227 | -2042 | -2651 | -2116 | -2934 | -2100 | -1526 | -1941 | -1909 | -2222 | 2940 | 1775 | -1804 | -3187 | -2882 | **218** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 213(A) | 3048 | -932 | -2480 | -2533 | -3075 | -1200 | -2274 | -2765 | -2501 | -3071 | -2221 | -1658 | -1948 | -2205 | -2512 | 1225 | -739 | -1842 | -3322 | -3078 | **219** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 214(I) | -1924 | -1546 | -4067 | -3658 | 2312 | -3663 | -2081 | 3030 | -3367 | 150 | 99 | -3197 | -3492 | -2821 | -3179 | -2894 | -1877 | 293 | -1445 | -692 | **220** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 215(E) | -2641 | -3308 | -896 | 3732 | -3966 | -2458 | -2043 | -4105 | -2128 | -4016 | -3555 | -1531 | -2959 | -1842 | -2560 | -2479 | -2750 | -3722 | -3563 | -3385 | **221** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 216(A) | 2389 | -814 | -2506 | -2162 | -1696 | -1545 | -1698 | -499 | -1942 | -1398 | -813 | -1640 | -2076 | -1723 | -2027 | -806 | 1148 | 1559 | -2200 | -1856 | **222** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 217(M) | -2576 | -2118 | -4725 | -4165 | -461 | -4430 | -3165 | 99 | -3811 | 2513 | 3454 | -4075 | -3839 | -2978 | -3488 | -3704 | -2457 | -591 | -2111 | -2145 | **223** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 218(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **224** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 219(M) | -2313 | -1968 | -4258 | -3765 | -518 | -3966 | -2806 | 98 | -3289 | 1292 | 4523 | -3599 | -3636 | -2769 | -3097 | -3249 | -2243 | -457 | -2026 | -1874 | **225** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 220(S) | -897 | -1462 | -2333 | -2543 | -3185 | -1640 | -2474 | -3294 | -2686 | -3497 | -2780 | -1973 | -2360 | -2483 | -2703 | 3465 | -1316 | -2413 | -3310 | -3025 | **226** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | -749 | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 234(K) | -2620 | -2961 | -2461 | -2046 | -3743 | -2791 | -1570 | -3603 | 3784 | -3387 | -2839 | -2048 | -3039 | -1260 | -465 | -2604 | -2536 | -3331 | -3001 | -2988 | **240** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 235(R) | 377 | -1802 | -415 | 988 | -2095 | -1474 | -95 | -1786 | 1452 | -1785 | -911 | -135 | -1560 | 343 | 1555 | -409 | -431 | 376 | -1986 | -1375 | **241** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 236(D) | 1083 | -1565 | 2662 | -244 | -1941 | -1573 | -679 | 612 | -527 | -1651 | -980 | -490 | -1869 | -358 | -1003 | -771 | -766 | -903 | -2208 | -1633 | **242** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 237(E) | -1225 | -2868 | 1894 | 1948 | -3149 | -1532 | -671 | -2975 | -630 | -2902 | -2101 | -150 | -1935 | -293 | -1299 | 1884 | -1241 | -2496 | -3093 | -2248 | **243** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 238(C) | 1375 | 3262 | -2620 | -2108 | -827 | -1866 | -1267 | 1631 | -1811 | -599 | -10 | -1674 | -2137 | -1531 | -1786 | -1034 | 790 | 249 | -1361 | -1010 | **244** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 239(E) | 635 | -1796 | 1055 | 1761 | -2018 | -1464 | -263 | 1191 | 28 | -1767 | -946 | -148 | -1637 | 135 | -481 | -520 | -553 | -1300 | -2077 | -1441 | **245** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 240(E) | 593 | -2044 | -252 | 2548 | -2437 | -1542 | -329 | -2133 | 151 | -2120 | -1274 | -244 | -1738 | 89 | 946 | -646 | -717 | -1734 | -2305 | -1686 | **246** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 241(S) | 1884 | -835 | -1962 | -1576 | -1634 | -1436 | -1320 | 1041 | -1409 | -1453 | -781 | -1293 | -1922 | -1241 | -1606 | 1973 | -597 | -669 | -2036 | -1656 | **247** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 242(G) | 2267 | -1043 | -2388 | -2526 | -3253 | 2642 | -2373 | -2975 | -2639 | -3260 | -2410 | -1722 | -2033 | -2311 | -2648 | -663 | -860 | -2005 | -3436 | -3250 | **248** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 243(R) | -876 | -2087 | -829 | 1490 | -2474 | -1766 | -229 | -2106 | 1269 | -44 | -1198 | -424 | -1829 | 205 | 2225 | -775 | -768 | -1753 | -2143 | -1647 | **249** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 244(V) | 2339 | -967 | -2970 | -2766 | -1878 | -1847 | -2252 | 32 | -2541 | -1299 | -918 | -2087 | -2399 | -2316 | -2545 | -1157 | -971 | 2345 | -2605 | -2251 | **250** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 245(I) | -1827 | -1398 | -4307 | -3831 | -1099 | -3939 | -3142 | 2286 | -3619 | 1835 | 69 | -3579 | -3671 | -3177 | -3511 | -3178 | -1781 | 1918 | -2524 | -2310 | **251** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 259(M) | -2252 | -1821 | -4572 | -3991 | -530 | -4164 | -2990 | 2068 | -3709 | 1993 | 3197 | -3808 | -3685 | -2916 | -3406 | -3378 | -2149 | -172 | -2084 | -2091 | **265** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 260(T) | -1213 | -1674 | -2755 | -2906 | -3163 | -1922 | -2659 | -2698 | -2788 | -3105 | -2612 | -2311 | -2600 | -2708 | -2753 | -1463 | 3819 | -2197 | -3286 | -3156 | **266** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 261(R) | -2131 | -2786 | -2704 | -1460 | -3618 | -2638 | -587 | -2976 | 1735 | -2645 | -1985 | -1353 | -2603 | -173 | 3492 | -2020 | -1828 | -2748 | -2484 | -2384 | **267** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 262(K) | -1349 | -2635 | -381 | 2083 | -3083 | -1857 | -565 | -2750 | 2690 | -2612 | -1837 | -514 | -2090 | -161 | -61 | -1178 | -1271 | -2369 | -2655 | -2138 | **268** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 263(A) | 2821 | -932 | -2451 | -2472 | -3065 | -1198 | -2233 | -2763 | -2434 | -3056 | -2201 | -1633 | -1940 | -2147 | -2468 | 1831 | -730 | -1840 | -3305 | -3055 | **269** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 264(F) | -2063 | -1686 | -4037 | -3677 | 3437 | -3644 | -1706 | 2063 | -3359 | 135 | 67 | -3095 | -3486 | -2739 | -3127 | -2876 | -2012 | -83 | -1038 | -158 | **270** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 265(E) | -2641 | -3308 | -896 | 3732 | -3966 | -2458 | -2043 | -4105 | -2128 | -4016 | -3555 | -1531 | -2959 | -1842 | -2560 | -2479 | -2750 | -3722 | -3563 | -3385 | **271** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 266(N) | -1662 | -3306 | 2055 | 78 | -3621 | -1643 | -1040 | -3622 | -1272 | -3531 | -2870 | 3477 | -2182 | -724 | -2071 | -1371 | -1757 | -3092 | -3633 | -2700 | **272** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 267(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **273** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 268(I) | -1760 | -1307 | -4325 | -3962 | -1735 | -4042 | -3726 | 3135 | -3828 | -579 | -515 | -3722 | -3869 | -3673 | -3896 | -3359 | -1752 | 2276 | -3240 | -2806 | **274** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 269(T) | 1428 | -904 | -2334 | -2158 | -2747 | -1206 | -1940 | -2392 | -2037 | -2678 | -1846 | -1504 | -1896 | -1809 | -2163 | 902 | 3001 | -1635 | -2999 | -2705 | **275** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 270(V) | -1745 | -1300 | -4286 | -3858 | -1446 | -3967 | -3370 | 2358 | -3688 | 852 | -261 | -3606 | -3749 | -3403 | -3673 | -3232 | -1717 | 2643 | -2856 | -2524 | **276** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 271(V) | -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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 272(M) | 866 | -1113 | -2656 | -2412 | -1322 | -1920 | -1883 | -487 | -2061 | -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 | -2686 | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 284(L) | -1623 | -1338 | -3726 | -3164 | -251 | -3255 | -1820 | 1373 | -2808 | 2371 | 514 | -2785 | -3086 | -2281 | -2613 | -2389 | -1543 | -161 | -1311 | 1782 | **290** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 285(L) | -2333 | -1873 | -4640 | -4127 | -650 | -4326 | -3241 | 2176 | -3843 | 2519 | 523 | -3982 | -3833 | -3105 | -3579 | -3604 | -2247 | 56 | -2268 | -2230 | **291** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 286(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **292** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 287(M) | -1886 | -1507 | -4178 | -3693 | -877 | -3806 | -2901 | 3008 | -3380 | 335 | 3109 | -3451 | -3570 | -2934 | -3251 | -3044 | -1840 | 524 | -2288 | -2089 | **293** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 288(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **294** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 289(H) | -1490 | -2484 | -362 | -476 | -1816 | -1880 | 4320 | -2854 | -684 | -2770 | -2133 | 2185 | -2285 | -728 | -1000 | -1377 | -1550 | -2475 | -2146 | -1255 | **295** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 290(A) | 2439 | -911 | -2326 | -2131 | -2811 | -1197 | -1934 | -2480 | -2011 | -2745 | -1898 | -1490 | -1888 | -1785 | -2153 | 1898 | 1073 | -1682 | -3044 | -2749 | **296** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 291(I) | 2038 | -985 | -3388 | -2919 | -1320 | -2893 | -2277 | 2155 | -2677 | -587 | -297 | -2593 | -2992 | -2450 | -2697 | -2087 | -1208 | 1681 | -2229 | -1846 | **297** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 292(G) | -1243 | -2769 | 311 | 1902 | -3172 | 1980 | -744 | -2992 | -697 | -2936 | -2152 | 1923 | -1974 | -377 | -1331 | -1030 | -1284 | -2506 | -3125 | -2308 | **298** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 293(V) | -1738 | -1298 | -4281 | -3921 | -1737 | -3979 | -3665 | 1917 | -3774 | -601 | -528 | -3671 | -3834 | -3628 | -3843 | -3293 | -1735 | 3205 | -3215 | -2770 | **299** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 294(E) | -833 | -2344 | 1092 | 2412 | -2643 | -1464 | -386 | -2413 | -146 | -2369 | -1505 | -96 | 562 | 29 | -717 | -666 | 862 | -1966 | -2562 | -1818 | **300** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 295(W) | -1380 | -1116 | -3614 | -3026 | 1322 | -2981 | -1582 | 1966 | -2661 | 1775 | 556 | -2562 | -2865 | -2117 | -2424 | -2098 | -1302 | -187 | 2908 | -629 | **301** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 308(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **314** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 309(V) | -1090 | -1215 | -2097 | -1824 | -819 | -2221 | 2699 | -287 | -1392 | -1027 | -591 | -1674 | -2482 | -1446 | -1482 | -1482 | -1143 | 2879 | -1420 | -707 | **315** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 310(L) | -2439 | -1972 | -4702 | -4181 | -588 | -4401 | -3258 | 1582 | -3881 | 2757 | 587 | -4061 | -3862 | -3093 | -3590 | -3689 | -2344 | -130 | -2230 | -2217 | **316** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 311(C) | 2157 | 4166 | -3012 | -2973 | -2780 | 1022 | -2337 | -2398 | -2724 | -2744 | -1930 | -1786 | -1943 | -2372 | -2623 | -540 | -692 | -1624 | -3091 | -2881 | **317** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 312(D) | -1732 | -3453 | 3468 | 99 | -3733 | -1645 | -1066 | -3747 | -1356 | -3641 | -3008 | 1690 | -2201 | -755 | -2209 | -1416 | -1833 | -3208 | -3752 | -2776 | **318** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 313(L) | -2477 | -2023 | -4713 | -4122 | 1592 | -4329 | -2920 | 72 | -3835 | 2593 | 2472 | -3948 | -3754 | -2914 | -3466 | -3550 | -2350 | -634 | -1927 | -1830 | **319** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 314(K) | -2620 | -2961 | -2461 | -2046 | -3743 | -2791 | -1570 | -3603 | 3784 | -3387 | -2839 | -2048 | -3039 | -1260 | -465 | -2604 | -2536 | -3331 | -3001 | -2988 | **320** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 315(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **321** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 316(S) | -897 | -1462 | -2333 | -2543 | -3185 | -1640 | -2474 | -3294 | -2686 | -3497 | -2780 | -1973 | -2360 | -2483 | -2703 | 3465 | -1316 | -2413 | -3310 | -3025 | **322** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 317(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **323** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 318(K) | 2 | -2257 | -1073 | -374 | -2740 | -1908 | -278 | -2339 | 2328 | -2192 | -1373 | -562 | -1953 | 2273 | 1344 | -952 | -933 | -1980 | -2234 | -1799 | **324** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 319(Y) | -3482 | -2868 | -3701 | -3919 | 238 | -3552 | -1112 | -3000 | -3638 | -2516 | -2526 | -3027 | -3772 | -3101 | -3341 | -3418 | -3527 | -3071 | -441 | 4711 | **325** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 320(M) | -1559 | -1267 | -3829 | -3380 | -1103 | -3357 | -2655 | 805 | -3067 | -64 | 3046 | -3065 | -3326 | -2779 | -3011 | -2591 | -1556 | 2855 | -2312 | -1998 | **326** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 334(M) | -2355 | -1988 | -4343 | -3834 | -504 | -4051 | -2868 | 105 | -3385 | 1451 | 4460 | -3680 | -3671 | -2806 | -3171 | -3327 | -2274 | -474 | -2039 | -1925 | **340** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 335(K) | -2620 | -2961 | -2461 | -2046 | -3743 | -2791 | -1570 | -3603 | 3784 | -3387 | -2839 | -2048 | -3039 | -1260 | -465 | -2604 | -2536 | -3331 | -3001 | -2988 | **341** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 336(Y) | -1187 | -974 | -3186 | -2638 | -117 | -2732 | -1255 | 1905 | -2270 | 73 | 1977 | -2217 | -2699 | -1882 | -2144 | -1841 | -1124 | 71 | -907 | 3254 | **342** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 337(L) | -2871 | -2457 | -4231 | -4103 | -1033 | -3803 | -3165 | -541 | -3734 | 3130 | -31 | -3935 | -3797 | -3286 | -3484 | -3713 | -2869 | -1136 | -2394 | -2220 | **343** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 338(L) | -2871 | -2457 | -4231 | -4103 | -1033 | -3803 | -3165 | -541 | -3734 | 3130 | -31 | -3935 | -3797 | -3286 | -3484 | -3713 | -2869 | -1136 | -2394 | -2220 | **344** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 339(K) | -864 | -1785 | -860 | -366 | -2128 | -1763 | -407 | -1612 | 2624 | -1800 | -1045 | 629 | -1900 | -28 | 62 | -851 | -805 | 1127 | -2064 | -1581 | **345** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 340(N) | 602 | -1686 | -275 | 1008 | -1926 | -1415 | 1528 | -1618 | 244 | -1673 | -815 | 1897 | -1530 | 299 | -244 | -371 | -391 | 322 | -1934 | -1306 | **346** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 341(G) | -1709 | -2639 | 1362 | -690 | -3785 | 3257 | -1671 | -3805 | -1946 | -3792 | -3137 | -980 | -2480 | -1424 | -2576 | -1630 | -1936 | -3150 | -3628 | -3155 | **347** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 342(F) | -942 | -799 | -2828 | -2226 | 1797 | -2476 | -1269 | 1109 | 581 | 1793 | 516 | -1952 | -2453 | -1557 | -1815 | -1558 | -875 | 52 | -1138 | -794 | **348** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 343(L) | -2451 | -1983 | -4707 | -4186 | -582 | -4409 | -3259 | 1510 | -3884 | 2778 | 592 | -4069 | -3865 | -3091 | -3590 | -3698 | -2355 | -150 | -2226 | -2214 | **349** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 344(H) | -3205 | -3079 | -2723 | -2890 | -2110 | -3046 | 5295 | -4135 | -2617 | -3813 | -3561 | -2886 | -3482 | -2833 | -2620 | -3291 | -3356 | -3895 | -2397 | -1681 | **350** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 345(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **351** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | -3563 | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 359(L) | -2153 | -1779 | -4360 | -3884 | -675 | -3965 | -3012 | 392 | -3561 | 2726 | 467 | -3673 | -3662 | -2955 | -3355 | -3239 | -2102 | 1281 | -2207 | -2099 | **365** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 360(E) | 1136 | -2084 | -175 | 2027 | -2436 | -1510 | -274 | -2147 | 1525 | -2118 | -1254 | -175 | -1692 | 152 | -251 | -593 | -670 | -1736 | -2296 | -1650 | **366** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 361(H) | 893 | -1761 | 1357 | 214 | -2092 | -1387 | 1862 | -1810 | 229 | -1825 | -942 | -83 | -1527 | 293 | -273 | 640 | 793 | -1409 | -2050 | -1397 | **367** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 362(I) | 608 | -458 | -2776 | -2176 | 1666 | -2202 | -1113 | 1712 | -1836 | -222 | 338 | -1782 | -2245 | -1512 | -1731 | -1292 | 867 | 1366 | -1036 | -684 | **368** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 363(P) | -922 | -1912 | 1681 | -141 | -2123 | -1604 | -687 | -1787 | -550 | 187 | -1245 | -427 | 2677 | -363 | -1049 | -882 | -947 | -1524 | -2338 | -1711 | **369** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 364(D) | -1692 | -3605 | 3364 | 1256 | -3770 | -1599 | -957 | -3700 | -1216 | -3569 | -2909 | 1025 | -2138 | -628 | -2083 | -1346 | -1761 | -3174 | -3765 | -2738 | **370** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 365(Q) | -877 | -1646 | -633 | 499 | -1610 | -1781 | -505 | -1210 | -63 | 1648 | -649 | -558 | -1931 | 2241 | -360 | -907 | -814 | -1097 | -1882 | -1385 | **371** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 366(P) | -648 | -2019 | 1139 | 203 | -2354 | -1436 | -285 | -2089 | 29 | -2086 | -1217 | -114 | 1965 | 1445 | -492 | -529 | 1244 | -1672 | -2300 | -1616 | **372** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -571 | -7108 | -1646 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 367(R) | -422 | -1009 | -851 | -304 | 1406 | -1496 | -183 | -740 | 147 | -894 | -230 | -440 | 775 | 21 | 2009 | -539 | -381 | -568 | -1136 | -521 | **373** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -23 | -6560 | -7602 | -894 | -1115 | -341 | -2249 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 368(D) | 1472 | -1668 | 1835 | -70 | -2356 | -1385 | -511 | -2062 | -246 | -2128 | -1275 | -318 | 1353 | -118 | -746 | -526 | 425 | -1602 | -2380 | -1752 | **374** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 369(G) | -1044 | -2230 | 2141 | -100 | -3222 | 2291 | -982 | -3045 | -1033 | -3050 | -2258 | -395 | -1985 | -644 | -1669 | 858 | -1207 | -2428 | -3250 | -2493 | **375** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 370(Q) | -2562 | -2904 | -1886 | -1971 | -3251 | -2661 | -2079 | -3690 | -1565 | -3469 | -3081 | -2107 | -3091 | 4371 | -1665 | -2585 | -2674 | -3411 | -3077 | -2821 | **376** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 384(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **390** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 385(H) | -964 | -2089 | -200 | -136 | -2264 | -1600 | 3833 | -2320 | -296 | -2338 | -1558 | 1362 | 1479 | -276 | -699 | -881 | -992 | -1924 | -2364 | -1652 | **391** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 386(L) | -2451 | -1983 | -4707 | -4186 | -582 | -4409 | -3259 | 1510 | -3884 | 2778 | 592 | -4069 | -3865 | -3091 | -3590 | -3698 | -2355 | -150 | -2226 | -2214 | **392** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 387(Q) | 1643 | -1017 | -1196 | -721 | -1189 | -1714 | -668 | 1336 | -497 | -907 | -297 | -823 | -1893 | 2044 | -794 | -784 | -569 | -339 | -1579 | -1135 | **393** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 388(I) | -1760 | -1308 | -4323 | -3961 | -1730 | -4039 | -3721 | 3156 | -3825 | -575 | -512 | -3720 | -3867 | -3669 | -3893 | -3356 | -1753 | 2241 | -3236 | -2802 | **394** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 389(L) | -2871 | -2457 | -4231 | -4103 | -1033 | -3803 | -3165 | -541 | -3734 | 3130 | -31 | -3935 | -3797 | -3286 | -3484 | -3713 | -2869 | -1136 | -2394 | -2220 | **395** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 390(K) | -1259 | -2115 | -1267 | -676 | -970 | -2105 | 1794 | -2040 | 2549 | -1955 | -1282 | -808 | -2165 | -167 | 114 | -1192 | -1140 | -1801 | -1301 | 2517 | **396** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 391(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **397** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 392(N) | -2171 | -2655 | -1458 | -1748 | -3334 | -2364 | -2267 | -3943 | -2365 | -3936 | -3437 | 4205 | -2932 | -2205 | -2608 | -2224 | -2439 | -3392 | -3253 | -2909 | **398** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 393(L) | -2871 | -2457 | -4231 | -4103 | -1033 | -3803 | -3165 | -541 | -3734 | 3130 | -31 | -3935 | -3797 | -3286 | -3484 | -3713 | -2869 | -1136 | -2394 | -2220 | **399** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 394(A) | 3121 | -934 | -2489 | -2561 | -3081 | -1203 | -2295 | -2766 | -2533 | -3080 | -2234 | -1669 | -1953 | -2234 | -2533 | 936 | -746 | -1844 | -3331 | -3090 | **400** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 395(E) | -522 | -1773 | -240 | 1676 | -2248 | -1396 | -289 | -1968 | 50 | -1989 | -1115 | -174 | 1198 | 131 | -448 | 1226 | 677 | -1538 | -2214 | -1565 | **401** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 409(V) | -419 | -634 | -1376 | -807 | 1053 | -1737 | -499 | -198 | -623 | -505 | 178 | 600 | -1807 | -475 | 475 | 313 | -360 | 1389 | -1016 | 1303 | **415** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 410(I) | -1282 | -1082 | -3022 | -2555 | 2426 | -2683 | 1767 | 2555 | -2191 | -443 | -88 | -2038 | -2692 | -1794 | -2075 | -1793 | -1220 | -317 | -361 | 552 | **416** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 411(T) | -499 | -1595 | -431 | 966 | -1830 | -1487 | -185 | -1449 | 1092 | -1574 | -754 | -207 | -1601 | 213 | -206 | -458 | 2067 | 159 | -1877 | -1296 | **417** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 412(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **418** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 413(P) | -632 | -1230 | -2074 | -2144 | -2996 | -1453 | -2116 | -2631 | -2128 | -2928 | -2213 | -1658 | 3610 | -2006 | -2221 | -852 | 1302 | -1931 | -3185 | -2917 | **419** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 414(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **420** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 415(R) | -1454 | -2316 | -1780 | -878 | -2834 | -2232 | -428 | -2292 | 2281 | -2200 | -1473 | -940 | -2240 | -17 | 2627 | -1386 | -1270 | 588 | -2249 | -1960 | **421** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 416(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **422** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 417(F) | -3342 | -2776 | -4026 | -4232 | 4354 | -3545 | -1431 | -2315 | -4038 | -1801 | -1900 | -3299 | -3780 | -3350 | -3645 | -3490 | -3420 | -2566 | -739 | 349 | **423** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 418(D) | -1572 | -3426 | 2573 | 2447 | -3613 | -1583 | -879 | -3513 | -1050 | -3393 | -2684 | 1292 | -2085 | -535 | -1855 | -1253 | -1623 | -3000 | -3585 | -2609 | **424** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 419(S) | -879 | -1989 | 1498 | -177 | -3045 | 1600 | -939 | -2843 | -904 | -2867 | -2046 | -438 | -1922 | -591 | -1483 | 2171 | -1044 | -2226 | -3072 | -2372 | **425** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 420(E) | -2641 | -3308 | -896 | 3732 | -3966 | -2458 | -2043 | -4105 | -2128 | -4016 | -3555 | -1531 | -2959 | -1842 | -2560 | -2479 | -2750 | -3722 | -3563 | -3385 | **426** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 434(A) | 1954 | -1836 | 1733 | -180 | -2714 | -1429 | -806 | -2438 | -679 | -2518 | -1698 | -430 | 1775 | -448 | -1211 | -736 | -894 | -1923 | -2765 | -2117 | **440** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 435(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **441** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 436(D) | -1736 | -3455 | 3490 | 97 | -3737 | -1646 | -1070 | -3753 | -1363 | -3647 | -3016 | 1602 | -2204 | -760 | -2218 | -1420 | -1838 | -3213 | -3756 | -2780 | **442** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 437(V) | -1721 | -1302 | -4229 | -3874 | -1705 | -3894 | -3582 | 1607 | -3706 | -582 | -513 | -3610 | -3786 | -3559 | -3767 | -3209 | -1725 | 3294 | -3158 | -2712 | **443** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 438(V) | 594 | -988 | -3391 | -2911 | -1164 | -2888 | -2187 | 845 | -2637 | 765 | -154 | -2576 | -2962 | -2387 | -2622 | -2074 | -1205 | 2800 | -2084 | -1724 | **444** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 439(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **445** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 440(I) | -1754 | -1308 | -4295 | -3867 | -1434 | -3978 | -3377 | 2661 | -3697 | 862 | -247 | -3617 | -3754 | -3406 | -3679 | -3243 | -1725 | 2373 | -2852 | -2526 | **446** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 441(R) | -2957 | -3022 | -3318 | -2735 | -3796 | -2998 | -1968 | -3912 | -846 | -3631 | -3157 | -2611 | -3280 | -1724 | 4056 | -3026 | -2913 | -3650 | -3096 | -3185 | **447** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 442(Y) | -1321 | -1438 | -1994 | -1608 | 2186 | 527 | -450 | -1117 | -1481 | -1211 | -693 | 1178 | -2522 | -1217 | -1665 | -1518 | -1275 | -1021 | -198 | 3178 | **448** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 443(C) | -675 | 2205 | -2544 | 972 | -572 | -2236 | -1121 | 1373 | -1671 | 679 | 261 | -1700 | -2270 | -1403 | -1668 | -1311 | -621 | 1601 | -1150 | -790 | **449** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 444(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **450** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 445(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **451** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 459(S) | -897 | -1462 | -2333 | -2543 | -3185 | -1640 | -2474 | -3294 | -2686 | -3497 | -2780 | -1973 | -2360 | -2483 | -2703 | 3465 | -1316 | -2413 | -3310 | -3025 | **465** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 460(M) | 2706 | -986 | -2433 | -2144 | -1502 | -1684 | -1706 | -700 | -1858 | -968 | 2744 | -1705 | -2188 | -1713 | -1932 | -963 | -862 | -592 | -2145 | -1794 | **466** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 461(I) | -2103 | -1659 | -4461 | -3992 | -869 | -4152 | -3233 | 3082 | -3723 | 1619 | 290 | -3801 | -3788 | -3171 | -3557 | -3432 | -2046 | 487 | -2418 | -2265 | **467** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 462(I) | -1761 | -1312 | -4317 | -3954 | -1713 | -4027 | -3703 | 3225 | -3814 | -556 | -498 | -3712 | -3859 | -3653 | -3877 | -3344 | -1754 | 2110 | -3216 | -2787 | **468** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 463(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **469** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 464(K) | 1641 | -2033 | -323 | 914 | -2415 | -1565 | -296 | -2097 | 2052 | -2080 | -1233 | -257 | -1736 | 125 | -133 | -646 | -702 | -1707 | -2258 | -1657 | **470** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 465(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **471** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 466(L) | -1699 | -1807 | -2268 | -1925 | -830 | -2795 | -1551 | -455 | -1225 | 2510 | 90 | -1958 | -2845 | 1927 | -1308 | -2067 | -1651 | -846 | -1841 | -1454 | **472** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 467(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **473** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 468(D) | -853 | -2415 | 2115 | 1717 | -2702 | -1468 | -378 | -2484 | 1085 | -2417 | -1546 | -84 | -1732 | 41 | -699 | 696 | -824 | -2025 | -2594 | -1839 | **474** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 469(S) | -892 | -1780 | -931 | -688 | -2757 | -1643 | -830 | -2472 | 1671 | -2492 | -1708 | -799 | -2018 | -468 | -365 | 2676 | -1004 | -1981 | -2598 | -2130 | **475** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 470(C) | -1135 | 3503 | -3700 | -3406 | -1670 | -2549 | -2675 | 653 | -3101 | -916 | -667 | -2727 | -2925 | -2870 | -3030 | -1868 | -1288 | 2927 | -2619 | -2222 | **476** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | -1996 | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 484(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **490** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 485(M) | -2322 | -1904 | -4536 | -3951 | 2387 | -4112 | -2676 | 67 | -3649 | 2034 | 3156 | -3710 | -3633 | -2803 | -3311 | -3309 | -2204 | -588 | -1794 | -1586 | **491** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 486(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **492** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 487(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **493** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 488(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **494** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 489(H) | -3205 | -3079 | -2723 | -2890 | -2110 | -3046 | 5295 | -4135 | -2617 | -3813 | -3561 | -2886 | -3482 | -2833 | -2620 | -3291 | -3356 | -3895 | -2397 | -1681 | **495** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 490(V) | -1754 | -1297 | -4329 | -3968 | -1770 | -4053 | -3752 | 2604 | -3840 | -621 | -545 | -3728 | -3878 | -3699 | -3917 | -3370 | -1746 | 2859 | -3276 | -2829 | **496** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 491(A) | 2587 | -828 | -2477 | -2155 | -1837 | -1468 | -1728 | -743 | -1941 | -1564 | -954 | -1607 | -2033 | -1725 | -2034 | -738 | 1178 | 1108 | -2310 | -1972 | **497** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 492(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **498** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 493(E) | -2641 | -3308 | -896 | 3732 | -3966 | -2458 | -2043 | -4105 | -2128 | -4016 | -3555 | -1531 | -2959 | -1842 | -2560 | -2479 | -2750 | -3722 | -3563 | -3385 | **499** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 494(A) | 3438 | -1472 | -2846 | -3040 | -3287 | -1726 | -2735 | -2840 | -3028 | -3257 | -2662 | -2236 | -2447 | -2798 | -2944 | -1216 | -1387 | -2183 | -3405 | -3320 | **500** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 495(Y) | -866 | -976 | -1863 | -1331 | 1353 | -2145 | 1318 | -556 | -1116 | -777 | -173 | -1242 | -2197 | 1714 | -1301 | -1173 | -802 | 888 | -445 | 2749 | **501** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 496(D) | 417 | -1831 | 1647 | 1094 | -2065 | -1488 | -353 | -1618 | -107 | -1820 | -1019 | -189 | -1698 | 30 | -623 | -603 | -643 | 1629 | -2154 | -1520 | **502** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **503** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **504** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -835 | -1680 | -1161 | **505** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 500(I) | -2091 | -1746 | -3971 | -3840 | -1676 | -3532 | -3289 | 3684 | -3581 | -659 | -693 | -3562 | -3674 | -3445 | -3521 | -3194 | -2146 | 449 | -2877 | -2493 | **506** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -1981 | -3412 | -3228 | **507** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -945 | -573 | 2562 | **508** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | 3014 | -2536 | -2219 | **509** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -1958 | -2245 | -1765 | **510** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -2385 | -2990 | -2169 | **511** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -3150 | -3636 | -3124 | **512** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | -4046 | -3710 | -3552 | **513** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 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 | 102 | -957 | -585 | **514** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 509(I) | -1761 | -1312 | -4317 | -3954 | -1713 | -4027 | -3703 | 3225 | -3814 | -556 | -498 | -3712 | -3859 | -3653 | -3877 | -3344 | -1754 | 2110 | -3216 | -2787 | **515** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 510(T) | 782 | -1467 | -550 | 1029 | -2202 | -1425 | -709 | -1791 | -472 | -1993 | -1203 | -528 | -1787 | -368 | -902 | -617 | 2685 | -1400 | -2333 | -1783 | **516** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 511(I) | -1766 | -1333 | -4283 | -3923 | -1635 | -3967 | -3619 | 3388 | -3759 | -473 | -437 | -3672 | -3822 | -3576 | -3804 | -3285 | -1764 | 1695 | -3126 | -2717 | **517** |
| - | -149 | -500 | 233 | 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 1

| | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 512(D) | -2784 | -3432 | 4016 | -1200 | -4140 | -2466 | -2197 | -4505 | -2621 | -4365 | -3956 | -1551 | -3014 | -2039 | -3232 | -2593 | -2938 | -4046 | -3710 | -3552 | **518** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 513(A) | 2705 | -1451 | -1036 | -913 | -2506 | -1504 | -1143 | -2174 | -794 | -2337 | -1613 | -946 | -1993 | 2040 | -1061 | -809 | -910 | -1703 | -2633 | -2156 | **519** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 514(H) | -615 | -1680 | 1444 | 66 | -1883 | 168 | 2650 | -1558 | -86 | -1691 | -891 | -223 | -1680 | 31 | -577 | -571 | -585 | 1267 | -2007 | -1397 | **520** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 515(K) | -654 | -2006 | -546 | 42 | -2376 | -1581 | -133 | -2066 | 1935 | -1987 | -1107 | 1132 | -1658 | 1043 | 1058 | -540 | 1180 | -1660 | -2113 | -1532 | **521** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 516(N) | -933 | -2085 | -946 | -284 | -2472 | -1822 | -253 | -2090 | 1711 | 76 | -1204 | 1918 | -1876 | 175 | 1799 | -841 | -817 | -1755 | -2132 | -1663 | **522** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 517(E) | -416 | -987 | -843 | 1107 | -1070 | -1583 | -338 | -623 | -183 | 879 | -172 | -489 | -1679 | -94 | -565 | 544 | 813 | 265 | -1379 | -905 | **523** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 518(I) | -2258 | -1804 | -4588 | -4084 | -706 | -4269 | -3231 | 2527 | -3807 | 2292 | 465 | -3923 | -3814 | -3118 | -3570 | -3544 | -2181 | 190 | -2303 | -2237 | **524** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 519(Q) | -477 | -1909 | 958 | 282 | -2211 | -1389 | 1484 | -1953 | 285 | -1921 | -1018 | -32 | -1517 | 2318 | -225 | 630 | 559 | -1525 | -2110 | -1430 | **525** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 520(L) | -2127 | -1743 | -4402 | -3796 | 1257 | -3918 | -2674 | 149 | -3492 | 2527 | 2164 | -3553 | -3509 | -2714 | -3181 | -3095 | -2019 | 570 | -1870 | -1818 | **526** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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 | -2599 | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 534(W) | -805 | -687 | -2581 | -2028 | 138 | -2236 | -697 | 897 | -1681 | -421 | 141 | -1645 | -2282 | -1369 | -1627 | -1315 | 636 | -90 | 4479 | 1809 | **540** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 535(H) | -408 | -1801 | -274 | 1284 | -2096 | -1385 | 1500 | -1822 | 1168 | -1802 | -899 | -33 | -1479 | 1381 | -102 | -303 | 595 | 221 | -1996 | -1339 | **541** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 536(Q) | -650 | -1737 | -627 | -72 | -1981 | -1615 | -209 | -1625 | 1223 | 392 | -866 | -318 | 1222 | 2120 | 50 | -598 | -572 | -1326 | -1932 | -1394 | **542** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 537(P) | -2931 | -2878 | -3420 | -3706 | -4181 | -2925 | -3468 | -4621 | -3859 | -4490 | -4165 | -3491 | 4225 | -3781 | -3695 | -3182 | -3279 | -4087 | -3594 | -4064 | **543** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -324 | -7108 | -2368 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 538(A) | 2195 | -924 | -968 | -546 | -1397 | -1356 | -583 | -812 | -365 | -1167 | -487 | -618 | -1660 | 1324 | -684 | -483 | -404 | 462 | -1703 | -1242 | **544** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -19 | -6804 | -7846 | -894 | -1115 | -428 | -1961 | * | * | | | | | | | | | | | | |
| 539(P) | 411 | -1017 | -1886 | -1616 | -1600 | -1588 | -1411 | -962 | -1408 | 495 | -755 | -1384 | 3156 | -1323 | -1577 | -847 | -785 | -783 | -2111 | -1716 | **545** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 540(R) | -1612 | -2397 | -2037 | -1033 | -2897 | -2352 | -458 | -2365 | 2184 | 665 | -1520 | -1051 | -2334 | -51 | 2602 | -1545 | -1395 | -2143 | -2262 | -2014 | **546** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 541(Y) | 712 | -796 | -2334 | -1883 | -370 | -2028 | -986 | -143 | -1607 | -663 | -131 | -1587 | -2243 | -1383 | -1656 | -1178 | -771 | 1114 | -965 | 3479 | **547** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 542(T) | -527 | -1669 | 1091 | -27 | -2315 | -1379 | -443 | -2033 | -151 | -2081 | -1218 | -282 | 557 | -41 | -650 | 1128 | 2077 | -1576 | -2321 | -1690 | **548** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 543(R) | -2957 | -3022 | -3318 | -2735 | -3796 | -2998 | -1968 | -3912 | -846 | -3631 | -3157 | -2611 | -3280 | -1724 | 4056 | -3026 | -2913 | -3650 | -3096 | -3185 | **549** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 544(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **550** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 545(V) | -1747 | -1296 | -4310 | -3948 | -1758 | -4023 | -3716 | 2215 | -3813 | -615 | -540 | -3705 | -3860 | -3670 | -3887 | -3339 | -1741 | 3087 | -3252 | -2806 | **551** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 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 | * | * | | | | | | | | | | | | |

Table 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 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(Y) | -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 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| 559(G) | -2594 | -2690 | -3304 | -3623 | -4328 | 3747 | -3462 | -4761 | -3953 | -4671 | -4212 | -3320 | -3352 | -3748 | -3779 | -2839 | -2981 | -4004 | -3668 | -4222 | **565** |
| - | -149 | -500 | 233 | 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 1

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | | | | | | | | | | | | |
| 560(C) | 2804 | 3772 | -3185 | -3198 | -2739 | -1303 | -2462 | -2065 | -2882 | -2628 | -1924 | -1927 | -2044 | -2547 | -2727 | -661 | -799 | -1463 | -3099 | -2886 | **566** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 561(V) | -1771 | -1603 | -3750 | -3689 | -2037 | -3050 | -3231 | 403 | -3479 | -1154 | -1076 | -3246 | -3399 | -3383 | -3437 | -2628 | -1917 | 3536 | -3074 | -2677 | **567** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 562(T) | -1213 | -1674 | -2755 | -2906 | -3163 | -1922 | -2659 | -2698 | -2788 | -3105 | -2612 | -2311 | -2600 | -2708 | -2753 | -1463 | 3819 | -2197 | -3286 | -3156 | **568** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -16 | -7108 | -8150 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 563(D) | -2784 | -3432 | 4016 | -1200 | -4140 | -2466 | -2197 | -4505 | -2621 | -4365 | -3956 | -1551 | -3014 | -2039 | -3232 | -2593 | -2938 | -4046 | -3710 | -3552 | **569** |
| - | -149 | -500 | 233 | 43 | -381 | 399 | 106 | -626 | 210 | -466 | -720 | 275 | 394 | 45 | 96 | 359 | 117 | -369 | -294 | -249 | |
| - | -21 | -6715 | -7757 | -894 | -1115 | -701 | -1378 | * | * | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | |
| 564(F) | -525 | -445 | -2202 | -1627 | 1946 | -2001 | -744 | 1247 | -1346 | 952 | 561 | 1079 | -2030 | -1067 | -1362 | -1067 | -465 | 338 | -714 | -230 | **570** |
| - | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | * | |
| - | * | * | * | * | * | * | * | * | 0 | | | | | | | | | | | | |