



(12) **DEMANDE DE BREVET CANADIEN**
CANADIAN PATENT APPLICATION

(13) **A1**

(86) **Date de dépôt PCT/PCT Filing Date:** 2022/02/17
(87) **Date publication PCT/PCT Publication Date:** 2022/08/25
(85) **Entrée phase nationale/National Entry:** 2023/08/16
(86) **N° demande PCT/PCT Application No.:** US 2022/016820
(87) **N° publication PCT/PCT Publication No.:** 2022/178145
(30) **Priorité/Priority:** 2021/02/17 (US63/150,515)

(51) **Cl.Int./Int.Cl.** **C12P 19/56** (2006.01),
C12P 19/18 (2006.01)
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(54) **Titre : COMPOSITIONS ET PROCEDES DE PRODUCTION DE REBAUDIOSIDE D**
(54) **Title: COMPOSITIONS AND METHODS FOR PRODUCING REBAUDIOSIDE D**

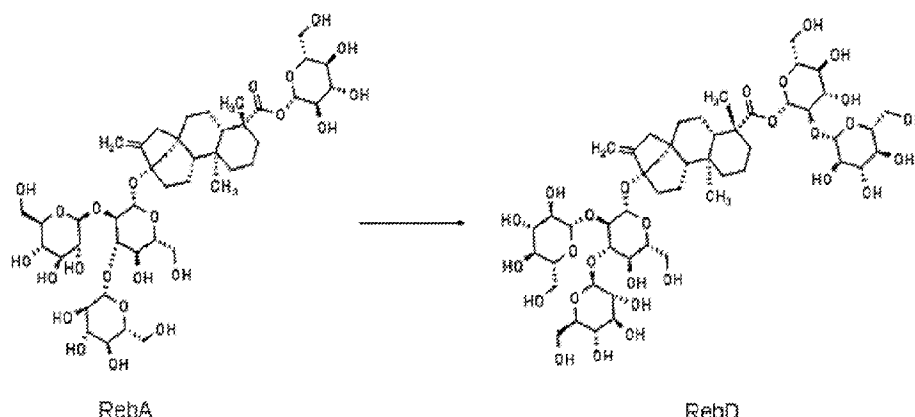


FIG. 1

(57) **Abrégé/Abstract:**

The present disclosure provides enzymes and a method to use those enzymes to transfer a sugar moiety to a substrate steviol glycoside. Specifically, designed beta-1,2-glycosyltransferases and sucrose synthases are used in a one-pot reaction to convert stevioside and Reb A into Reb E and Reb D.



Date Submitted: 2023/08/16

CA App. No.: 3208720

Abstract:

The present disclosure provides enzymes and a method to use those enzymes to transfer a sugar moiety to a substrate steviol glycoside. Specifically, designed beta-1,2-glycosyltransferases and sucrose synthases are used in a one-pot reaction to convert stevioside and Reb A into Reb E and Reb D.

COMPOSITIONS AND METHODS FOR PRODUCING REBAUDIOSIDE D**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/150,515, filed February 17, 2021, the content of which is herein incorporated by reference in its entirety.

INCORPORATION OF THE SEQUENCE LISTING

[0002] The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (file-name: ARZE_034_01WO_SeqList_ST25.txt, date recorded: February 17, 2022, file size ~6.84 megabytes).

FIELD OF THE DISCLOSURE

[0003] The present disclosure relates to enzymes and biocatalytic processes for producing steviol glycosides. The present disclosure particularly relates to use of glycosyltransferases that can transfer a glucose moiety from an ADP-glucose sugar donor to steviol glycosides.

BACKGROUND

[0004] Excess sugar consumption has been linked to worldwide health epidemics including diabetes and heart disease. Healthcare systems incur exorbitant costs associated with treating these diseases. Replacing added sugar in food with a low calorie, high-intensity sweetener would have significant health and economic impact.

[0005] The species *Stevia rebaudiana* is commonly grown for its sweet leaves, which have traditionally been used as a sweetener. Stevia extract is 200-300 times sweeter than sugar and is used commercially as a high intensity sweetener. The main glycoside components of stevia leaf are steviosides and rebaudiosides. Over ten different steviol glycosides are present in appreciable quantities in the leaf. The principal sweetening compounds are stevioside and rebaudioside A. Rebaudioside A (Reb A) is considered a higher value compared to stevioside because of its increased sweetness and decreased bitterness.

[0006] The sweetness and bitterness profile of rebaudioside D (Reb D) is improved compared to Reb A, but Reb D is present at very low quantities in the stevia leaf. Reb D can be made by the addition of a single glucose molecule to Reb A. Native glycosyltransferases that make Reb D use UDP-glucose as the glucose source for transferring to Reb A.

BRIEF SUMMARY

[0007] The present disclosure provides enzymes, particularly non-natural enzymes, and methods to use those enzymes to transfer a sugar moiety to a substrate steviol glycoside (also referred to herein as a “SG”). Specifically, a beta-1,2-glycosyltransferase (also referred to herein as a “B12GT”) and sucrose synthase (also referred to herein as a “SuSy”) are used in a one-pot reaction to convert stevioside and Reb A into rebaudioside E (Reb E) and Reb D, respectively.

[0008] In contrast to native glycosyltransferases, the disclosure provides glycosyltransferase polypeptides that can utilize ADP-glucose as the sugar donor to convert Reb A to Reb D. The disclosure provides glycosyltransferase polypeptides that comprise an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 6-882 and 1333-1466. The glycosyltransferase polypeptide may comprise, or consist of, an amino acid sequence selected from the group consisting of SEQ ID NOs: 6-882 and 1333-1466. The polypeptides may comprise one or more peptide tags used for solubility, expression and/or purification; for example, a polyhistidine tag of between 4 and 10 histidine residues, and preferably 6 histidine residues. Other suitable tags include, but are not limited to, glutathione *S*-transferase (GST), FLAG, maltose binding protein (MBP), calmodulin binding peptide (CBP), and Myc tag. Suitable linkers include, but are not limited to, polypeptides composed of glycine and serine, such as GSGS, polyglycine linkers, EAAAK repeats, and sequences containing cleavage sites for enzymes such as factor Xa, enterokinase, and thrombin.

[0009] Nucleotide sugar donors, including both UDP-glucose and ADP-glucose, are expensive co-substrates and add significant costs to any process that utilizes the compounds. Sucrose synthases (SuSy; EC 2.4.1.13) catalyze the chemical reaction of nucleotide diphosphate (NDP) and sucrose to form NDP-glucose and fructose. Therefore, sucrose synthases can be used to convert an NDP into an NDP-glucose required by B12GTs (an exemplary glycosyltransferase). The disclosure provides SuSy polypeptides that comprise an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 890-1227 and 1231-1332. Specifically, the disclosed sucrose synthases can convert ADP into the ADP-glucose cofactor required by the disclosed B12GTs.

[0010] The disclosure additionally provides a method to utilize a SuSy ADP-glucose recycling system combined with a B12GT polypeptide in a one-pot reaction to convert Reb A and/or

stevioside into Reb D and Reb E, respectively. In some embodiments, the method comprises contacting a stevia leaf extract purified to contain greater than 50% Reb A (RA50), ADP, and sucrose with a B1,2 glycosyltransferase and sucrose synthase to make Reb D and/or Reb E.

5 BRIEF DESCRIPTION OF THE DRAWINGS

[0011] The accompanying drawings are included to provide a further understanding of the disclosure. The drawings illustrate embodiments of the disclosure and together with the description, serve to explain the principles of the embodiments of the disclosure.

10 [0012] **FIG. 1** shows the conversion (glycosylation) of rebaudioside A (Reb A) to rebaudioside D (Reb D).

[0013] **FIG. 2** shows the measured Reb A to Reb D activity of three native UDP-glucose B12GTs when using either ADP-glucose or GDP-glucose as the sugar donor.

[0014] **FIG. 3** shows the measured ability of native sucrose synthases to convert ADP to ADP-glucose (top), GDP to GDP-glucose (middle), and UDP to UDP-glucose (bottom).

15 [0015] **FIG. 4 (top)** shows the measured conversion of Reb A to Reb D to Reb M2 in a one-pot reaction of the B12GT pA10143 and one of seven native sucrose synthases. **FIG. 4 (bottom)** shows the measured conversion of Reb A to Reb D in a one-pot reaction of the B12GT pA12549 and one of seven native sucrose synthases.

20 [0016] **FIG. 5** shows the top designs of pA10143 from an active-site site saturation mutagenesis library. The parent enzyme, pA10143, is shown in gray.

[0017] **FIG. 6** shows the measured Reb A to Reb D conversion for all enzymes from the pA10143 active-site SSM library by mutated residue.

[0018] **FIG. 7** shows the LCMS chromatogram of the reaction product produced from a scaled-up one-pot reaction of pA21841 and pA29798.

25 [0019] **FIG. 8** shows the LCMS chromatogram of the reaction product produced from a scaled-up one-pot reaction of pA21841 and pA29646.

[0020] **FIG. 9** shows an SDS-PAGE gel of designed B12GTs purified from *Pichia pastoris* expression.

30 [0021] **FIG. 10A** shows an SDS-PAGE gel of two designed B12GTs purified from a 1L *Pichia pastoris* fermentation (order from left to right: pA29798 (B12GT-1), ladder, pA32946 (B12GT-2)). **FIG. 10B** shows SDS-PAGE gels of two designed SuSys purified from a 1L *Pichia pastoris* fermentation (order from left to right: ladder, pA34103 (SuSy-1), ladder, pA32691 (SuSy-2)).

DETAILED DESCRIPTION

[0022] The present disclosure provides enzymes and biocatalytic processes for preparing a composition comprising a target steviol glycoside by contacting a starting composition comprising a substrate steviol glycoside, sucrose, and NDP with an NDP-glucosyltransferase polypeptide and a sucrose synthase, thereby producing a composition comprising a target steviol glycoside comprising one or more additional glucose units than the substrate steviol glycoside.

[0023] As used herein, "biocatalysis" or "biocatalytic" refers to the use of natural catalysts, such as protein enzymes, to perform chemical transformations on organic compounds. Biocatalysis is alternatively known as biotransformation or biosynthesis. Both isolated and whole cell biocatalysis methods are known in the art. Biocatalyst protein enzymes can be naturally occurring or recombinant proteins.

[0024] As used herein, the term "steviol glycoside(s)" refers to a glycoside of steviol, including, but not limited to, naturally occurring steviol glycosides, e.g. steviol-13-O-glucoside, steviol-19-O-glucoside, rubusoside, steviol-1,2-bioside, steviol-1,3-bioside, rubusoside, dulcoside B, dulcoside A, rebaudioside B, rebaudioside G, stevioside, rebaudioside C, rebaudioside F, rebaudioside A, rebaudioside I, rebaudioside E, rebaudioside H, rebaudioside L, rebaudioside K, rebaudioside J, rebaudioside M, rebaudioside D, rebaudioside N, rebaudioside O, rebaudioside Q, synthetic steviol glycosides, e.g. enzymatically glucosylated steviol glycosides and combinations thereof.

[0025] As used herein, "starting composition" refers to any composition (generally an aqueous solution) containing one or more steviol glycosides, where the one or more steviol glycosides serve as the substrate for the biotransformation.

[0026] As used herein, the terms "polynucleotide" or "nucleic acid" are used interchangeably, unless indicated by context, and is used to refer to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides, typically DNA.

[0027] As used herein, "expression" refers to either or both steps, depending on context, of the two-step process by which polynucleotides are transcribed into mRNA and the transcribed mRNA is subsequently translated into polypeptides.

[0028] "Under transcriptional control" means that transcription of a polynucleotide, usually a DNA sequence, depends on its being operatively linked to an element that promotes transcription.

[0029] "Operatively linked" means that the polynucleotide elements are arranged in a manner that allows them to function in a cell; typically to produce polypeptides in the cell; for example,

the disclosure provides promoters operatively linked to the downstream sequences encoding polypeptides.

[0030] The term "encode" refers to the ability of a polynucleotide to produce an mRNA or a polypeptide if it can be transcribed to produce the mRNA and then translated to produce the polypeptide or a fragment thereof. In each case, the polynucleotide is referred to as encoding the mRNA and encoding the polypeptide. The antisense strand is the complement of such a nucleic acid, and the encoding sequence can be deduced therefrom. Similarly, a "coding sequence" refers to a region of a nucleic acid that encodes an mRNA or a polypeptide.

[0031] The term "promoter" as used herein refers to a control sequence that is a portion of a polynucleotide sequence that controls the initiation and rate of transcription of a coding sequence. An "enhancer" is a regulatory element that increases the expression of a target sequence. A "promoter/enhancer" is a polynucleotide with sequences that provide both promoter and enhancer functions.

[0032] The regulatory elements, e.g. enhancers and promoters, may be "homologous" or "heterologous." A "homologous" regulatory element is one which is naturally linked with a given polynucleotide in the genome; for example, it may be the promoter found natively in the organism upstream of the encoded polypeptide. A "heterologous" regulatory element is one which is placed in juxtaposition to a polynucleotide by means of recombinant molecular biological techniques but is not a combination found in nature. Often, promoters, enhancers and other regulatory elements are heterologous so as to facilitate expression of a polypeptide in a host cell other than one in which a polypeptide naturally occurs. Thus, "heterologous expression", as used herein, refers to producing an mRNA and/or a polypeptide in a host cell, such as a microorganism, where the polynucleotide is not found naturally or one or more regulatory elements are not naturally found operably linked to the polynucleotide in the host cell.

[0033] The term "polypeptide" is used here to refer to a molecule of two or more subunits of amino acids linked by peptide bonds. Typically, though not always, the polypeptides contain several hundred amino acids; for example, about 400 to about 800 amino acids.

[0034] A "plasmid" is a DNA molecule that is typically separate from and capable of replicating independently of the chromosomal DNA. In many cases, it is circular and double-stranded.

It is known in the art that while plasmid vectors often exist as extrachromosomal circular DNA molecules, plasmid vectors may also be designed to be stably integrated into a host chromosome either randomly or in a targeted manner. Many plasmids are commercially available for varied uses. The gene to be replicated is inserted into copies of a plasmid containing genes that make cells resistant to particular antibiotics, and a multiple cloning site (MCS, or polylinker),

which is a short region containing several commonly used restriction sites allowing the easy insertion of DNA fragments at this location. Typically, the polypeptides disclosed herein are expressed from plasmids.

[0035] The term “about” or “approximately” when immediately preceding a numerical value means a range (e.g., plus or minus 10% of that value). For example, “about 50” can mean 45 to 55, “about 25,000” can mean 22,500 to 27,500, etc., unless the context of the disclosure indicates otherwise, or is inconsistent with such an interpretation. For example, in a list of numerical values such as “about 49, about 50, about 55, ...”, “about 50” means a range extending to less than half the interval(s) between the preceding and subsequent values, e.g., more than 49.5 to less than 52.5. Furthermore, the phrases “less than about” a value or “greater than about” a value should be understood in view of the definition of the term “about” provided herein. Similarly, the term “about” when preceding a series of numerical values or a range of values (e.g., “about 10, 20, 30” or “about 10-30”) refers, respectively to all values in the series, or the endpoints of the range.

[0036] As used herein the terms “microorganism” or “microbe” should be taken broadly. These terms are used interchangeably and include, but are not limited to, the two prokaryotic domains, Bacteria and Archaea, as well as certain eukaryotic fungi and protists. In some embodiments, the disclosure refers to the “microorganisms” or “microbes” of lists and figures present in the disclosure. This characterization can refer to not only the identified taxonomic genera but also the identified taxonomic species, as well as the various novel and newly identified or designed strains of any organism in said tables or figures. The same characterization holds true for the recitation of these terms in other parts of the Specification, such as in the Examples.

[0037] When referring to a nucleic acid sequence or protein sequence, the term “identity” is used to denote similarity between two sequences. Sequence similarity or identity may be determined using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith & Waterman, *Adv. Appl. Math.* 2, 482 (1981), by the sequence identity alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48,443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85, 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., *Nucl. Acid Res.* 12, 387-395 (1984), or by inspection. Another suitable algorithm is the BLAST algorithm, described in Altschul et al., *J Mol. Biol.* 215, 403-410, (1990) and Karlin et al., *Proc. Natl. Acad. Sci. USA* 90, 5873-5787 (1993). An exemplary BLAST program is the WU-

BLAST-2 program which was obtained from Altschul et al., *Methods in Enzymology*, 266, 460-480 (1996); blast.wustl.edu/blast/README.html. WU-BLAST-2 uses several search parameters, which are optionally set to the default values. The parameters are dynamic values and are established by the program itself depending upon the composition of the sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. Another algorithm is gapped BLAST as reported by Altschul et al, (1997) *Nucleic Acids Res.* 25, 3389-3402. Other algorithms may be described herein.

[0038] The present disclosure provides non-natural, engineered β -1,2-ADP glycosyltransferases (B12GTs) that can use an ADP-glucose sugar donor to convert stevioside to Reb E and Reb A to Reb D. In a particular embodiment, the glucosyltransferase polypeptide is one of SEQ ID NOs: 6-882 and 1333-1466. In another embodiment, the glucosyltransferase polypeptide is a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to one of SEQ ID NOs: 6-882 and 1333-1466.

[0039] In bioinformatics, several methods have been developed to find and determine related polypeptide sequences. For example, percent sequence identity, position-specific scoring matrices (PSSMs) and hidden Markov models (HMMs) are all commonly employed to find sequences that are similar to a given query sequence. Percent sequence identity calculates the number of amino acids that are shared between two sequences. Percent sequence identity is calculated in the context of a given alignment between two sequences. Percentage identity may be calculated using the alignment program Clustal Omega (available at www.ebi.ac.uk/Tools/msa/clustalo/) with default settings. The default transition matrix is Gonnet, gap opening penalty is 6 bits, and gap extension is 1 bit. Clustal Omega uses the HAlign algorithm and its default settings as its core alignment engine. The algorithm is described in Söding, J. (2005) 'Protein homology detection by HMM-HMM comparison'. *Bioinformatics* 21, 951-960.

[0040] Position-specific scoring matrices (PSSMs) are a concise way to represent many related sequences. PSSMs are often generated using multiple sequence alignments. The sequence search tool PSI-BLAST generates PSSMs and uses them to search for related polypeptide sequences. A PSSM used to score polypeptide sequences is a matrix (i.e. table) composed of 21 columns by N rows, where N is the length of the related sequences. Each row corresponds to a position within the polypeptide sequence and each column represents a different amino acid (or gap) that the residue position can take on. Each entry in the PSSM represents a score for

the specific amino acid at the specific position within the polypeptide sequence. A sequence can be scored with a PSSM by first aligning the sequence to a reference sequence, and then calculating the following sum: $S_{PSSM} = \sum_{i=1}^N PSSM(i, aa_i)$, where i is the sequence position and aa_i is the amino acid at position i . Related polypeptide sequences will all have high PSSM scores, while unrelated sequences will yield low scores.

[0041] The present disclosure also provides non-natural, engineered sucrose synthases (SuSys) that can use a sucrose sugar donor to convert ADP to ADP-glucose. In a particular embodiment, the SuSy polypeptide is one of SEQ ID NOs: 890-1227 and 1231-1332. In another embodiment, the SuSy polypeptide is a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to one of SEQ ID NOs: 890-1227 and 1231-1332.

[0042] In some embodiments, the glucosyltransferase and/or sucrose synthase polypeptides are prepared by expression in a host microorganism. Suitable host microorganisms include, but are not limited to, *E. coli*, *Saccharomyces* sp., *Aspergillus* sp., *Pichia* sp., *Bacillus* sp. In a particular embodiment, the glucosyltransferase and sucrose synthase are expressed in *E. coli*. In another embodiment, the glucosyltransferase and sucrose synthase are expressed in *Pichia pastoris*.

[0043] The B12GT and/or SuSy polypeptide can be provided in any suitable form, including free, immobilized, or as a whole cell system. The degree of purity of the glucosyltransferase polypeptide may vary, e.g., it may be provided as a crude, semi-purified, or purified enzyme preparation(s). In one embodiment, the glucosyltransferase polypeptide is free. In another embodiment, the glucosyltransferase polypeptide is immobilized to a solid support, for example on an inorganic or organic support. In some embodiments, the solid support is derivatized cellulose, glass, ceramic, methacrylate, styrene, acrylic, a metal oxide, or a membrane. In some embodiments, the glucosyltransferase polypeptide is immobilized to the solid support by covalent attachment, adsorption, cross-linking, entrapment, or encapsulation.

[0044] In yet another embodiment, the B12GT and/or SuSy polypeptide is provided in the form of a whole cell system, for example as a living fermentative microbial cell, or as dead and stabilized microbial cell, or in the form of a cell lysate.

[0045] The present disclosure provides a biocatalytic process for the preparation of a composition comprising a target steviol glycoside from a starting composition comprising a substrate steviol glycoside, wherein the target steviol glycoside comprises one or more additional glucose units than the substrate steviol glycoside. The biocatalytic process comprises contacting a

B12GT and a SuSy with a starting composition comprising one or more steviol glycosides, a non-UDP nucleotide diphosphate, and sucrose. In another embodiment, the biocatalytic process comprises contacting an engineered B12GT and a SuSy with a starting composition comprising one or more steviol glycosides, a non-UDP nucleotide diphosphate, and sucrose. In another embodiment, the biocatalytic process comprises contacting an engineered B12GT and an engineered SuSy with a starting composition comprising one or more steviol glycosides, a non-UDP nucleotide diphosphate, and sucrose. In some embodiments, the method comprises contacting RA50, ADP, and sucrose with an engineered B1,2 glycosyltransferase and a sucrose synthase to make Reb D and Reb E.

[0046] In one embodiment, the B12GT polypeptide is one of SEQ ID NOs: 1-882 and 1333-1466. In another embodiment, the glucosyltransferase polypeptide is a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to one of SEQ ID NOs: 1-882. In another embodiment, the glucosyltransferase polypeptide is a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to one of SEQ ID NOs: 6-882 and 1333-1466. Preferably, the catalytic domain in the B12GT polypeptide contains residues corresponding to H at position 15, D at position 114, D at position 357, and Q at position 358, numbered according to SEQ ID NO: 5.

[0047] In one embodiment, the sucrose synthase is any polypeptide with sucrose synthase activity. In another embodiment, the sucrose synthase is derived from an organism from the Bacteria domain. In another embodiment, the sucrose synthase is derived from an organism from the Plantae kingdom. In another embodiment, the sucrose synthase is derived from an organism from the Plantae kingdom. In another embodiment, the sucrose synthase is derived from an organism from the proteobacteria, deferribacteres, or cyanobacteria phylum. In another embodiment, the sucrose synthase is derived from the species *Acidithiobacillus caldus*, *Nitrosomonas europaea*, *Denitrovibrio acetiphilus*, *Thermosynechococcus elongatus*, *Oryza sativa*, *Arabidopsis thaliana*, or *Coffea arabica*. In one embodiment, the sucrose synthase is one of SEQ ID NOs: 883-1227 and 1231-1332. In another embodiment, the sucrose synthase is an engineered sucrose synthase with a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to one of SEQ ID NOs: 883-1227. In another embodiment, the sucrose synthase is an engineered sucrose synthase with a polypeptide sequence that is at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, 99%, or more sequence identity to one of SEQ ID NOs: 890-1227 and 1231-1332. Preferably, the catalytic domain in the SuSy polypeptide contains residues corresponding to H at position 425, R at position 567, K at position 572, and E at position 663, numbered according to SEQ ID NO: 885 or residues corresponding to H at position 436, R at position 578, K at position 583, and E at position 674, numbered according to SEQ ID NO: 888.

[0048] In some embodiments, the glucosyltransferase and/or sucrose synthase polypeptides are prepared by expression in a host microorganism. Suitable host microorganisms include, but are not limited to, *E. coli*, *Saccharomyces* sp., *Aspergillus* sp., *Pichia* sp., *Bacillus* sp. In a particular embodiment, the glucosyltransferase and sucrose synthase are expressed in *E. coli*. In another embodiment, the glucosyltransferase and sucrose synthase are expressed in *Pichia pastoris*. In another embodiment, the glucosyltransferase and/or sucrose synthase polypeptides are prepared by cell-free expression.

[0049] The B12GT and sucrose synthase polypeptides can be provided in any suitable form, including free, immobilized, or as a whole cell system. The degree of purity of the polypeptides may vary, e.g., they may be provided as a crude, semi-purified, or purified enzyme preparation(s). In one embodiment, the B12GT and/or SuSy polypeptide is free. In another embodiment, the B12GT and/or SuSy polypeptide is immobilized to a solid support, for example on an inorganic or organic support. In some embodiments, the solid support is derivatized cellulose, glass, ceramic, methacrylate, styrene, acrylic, a metal oxide, or a membrane. In some embodiments, the B12GT and/or SuSy polypeptide is immobilized to the solid support by covalent attachment, adsorption, cross-linking, entrapment, or encapsulation.

[0050] In yet another embodiment, the B12GT and/or SuSy polypeptide is provided in the form of a whole cell system, for example as a living fermentative microbial cell, or as dead and stabilized microbial cell, or in the form of a cell lysate.

[0051] The steviol glycoside component(s) of the starting composition serves as a substrate(s) for the production of the target steviol glycoside(s), as described herein. The target steviol glycoside target(s) differs chemically from its corresponding substrate steviol glycoside(s) by the addition of one or more glucose units.

[0052] The starting steviol glycoside composition can contain at least one substrate steviol glycoside. In an embodiment, the substrate steviol glycoside is selected from the group consisting of steviol, steviol-13-O-glucoside, steviol-19-O-glucoside, rubusoside, steviol-1,2-bioside, steviol-1,3-bioside, rubusoside, dulcoside B, dulcoside A, rebaudioside B, rebaudioside G, stevioside, rebaudioside C, rebaudioside F, rebaudioside A, rebaudioside I, rebaudioside E, rebaudioside H, rebaudioside L, rebaudioside K, rebaudioside J, rebaudioside M, rebaudioside

D, rebaudioside N, rebaudioside O, rebaudioside Q, an isomer thereof, a synthetic steviol glycoside or combinations thereof. In another embodiment, the starting steviol glycoside composition is composed of stevioside and Reb A. In another embodiment, the starting steviol glycoside composition is composed of stevioside. In yet another embodiment, the starting steviol glycoside composition is composed of Reb A.

[0053] The starting steviol glycoside composition may be synthetic or purified (partially or entirely), commercially available or prepared. One example of a starting composition useful in the method of the present disclosure is an extract obtained from purification of *Stevia rebaudiana* plant material (e.g. leaves). Another example of a starting composition is a commercially available *stevia* extract brought into solution with a solvent. Yet another example of a starting composition is a commercially available mixture of steviol glycosides brought into solution with a solvent. Other suitable starting compositions include by-products of processes to isolate and purify steviol glycosides.

[0054] In one embodiment, the starting composition comprises a purified substrate steviol glycoside. For example, the starting composition may comprise greater than about 50%, greater than about 60%, greater than about 70%, greater than about 80%, greater than about 85%, greater than about 90%, greater than about 91%, greater than about 92%, greater than about 93%, greater than about 94%, greater than about 95%, greater than about 96%, greater than about 97%, greater than about 98%, greater than about 99%, or greater than about 99.6% of one or more substrate steviol glycosides by weight on an anhydrous basis.

[0055] In another embodiment, the starting composition comprises a partially purified substrate steviol glycoside composition. For example, the starting composition contains greater than about 0.5%, greater than about 1%, greater than about 2%, greater than about 3%, greater than about 4%, greater than about 5%, greater than about 10%, greater than about 20%, greater than about 30%, greater than about 40%, or greater than about 50%, of one or more substrate steviol glycosides by weight on an anhydrous basis.

[0056] In another embodiment, the substrate steviol glycoside is purified rebaudioside A, or isomers thereof. In a particular embodiment, the substrate steviol glycoside contains greater than 99% rebaudioside A, or isomers thereof, by weight on an anhydrous basis. In another embodiment, the substrate steviol glycoside comprises partially purified rebaudioside A. In a particular embodiment, the substrate steviol glycoside contains greater than about 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% rebaudioside A by weight on an anhydrous basis.

[0057] In yet another embodiment, the substrate steviol glycoside comprises purified stevioside, or isomers thereof. In a particular embodiment, the substrate steviol glycoside contains greater than 99% stevioside, or isomers thereof, by weight on an anhydrous basis. In another embodiment, the substrate steviol glycoside comprises partially purified stevioside. In a particular embodiment, the substrate steviol glycoside contains greater than about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% stevioside by weight on an anhydrous basis.

[0058] In yet another embodiment, the substrate steviol glycoside is a combination of stevioside and rebaudioside A. In a particular embodiment, the substrate steviol glycoside contains greater than about 5% stevioside and greater than about 5% Reb A, greater than about 10% stevioside and greater than about 10% Reb A, greater than about 20% stevioside and greater than about 20% Reb A, greater than about 30% stevioside and greater than about 30% Reb A, greater than about 40% stevioside and greater than about 40% Reb A, greater than about 45% stevioside and greater than about 45% Reb A, greater than about 40% stevioside and greater than about 50% Reb A, greater than about 30% stevioside and greater than about 60% Reb A, greater than about 20% stevioside and greater than about 70% Reb A, greater than about 10% stevioside and greater than about 80% Reb A, greater than about 5% stevioside and greater than about 90% Reb A, greater than about 50% stevioside and greater than about 40% Reb A, greater than about 60% stevioside and greater than about 30% Reb A, greater than about 70% stevioside and greater than about 20% Reb A, greater than about 80% stevioside and greater than about 10% Reb A, or greater than about 90% stevioside and greater than about 5% Reb A by weight on an anhydrous basis.

[0059] In still another embodiment, the substrate steviol glycoside is derived from stevia leaf extract. In one embodiment, RA50, stevia leaf extract purified to contain greater than 50% Reb A, is used as the steviol glycoside substrate. In one embodiment, RA50 is used at a concentration between about 1 and 800 mg/mL. In another embodiment, RA50 is used at a concentration of about 100 mg/mL.

[0060] The one pot reaction can be carried out with a nucleotide cofactor that can be converted to an NDP-glucose by sucrose synthase. In some embodiments, the nucleotide can be a non-UDP nucleotide (i.e. ADP-glucose, GDP-glucose, CDP-glucose, or TDP-glucose). In another embodiment, the nucleotide is ADP. In a particular embodiment, the one pot reaction can be carried out with ADP at a concentration between about 0.01 and 10 mM, such as, for example, between 0.01 mM and 0.05 mM, between 0.05 mM and 0.1 mM, between 0.1 mM and 0.5 mM, between 0.5 mM and 1 mM, between 1 mM and 5 mM, or between 5 mM and 10 mM. In a particular embodiment, ADP is used at a concentration of 0.5 mM.

[0061] The one pot reaction can be carried out with a sucrose concentration between about 10 mM and 2M, such as, for example, greater than 10 mM, greater than 50 mM, greater than 100 mM, greater than 250 mM, greater than 500 mM, greater than 1 M, greater than 1.5 M and greater than 2 M. In a particular embodiment, sucrose is used at a concentration of 250 mM.

5 [0062] In one embodiment, the reaction is run at any temperature. In another embodiment, the one-pot reaction is run at a temperature between about 10 °C and 80 °C. Such as, for example, between 10° C to 20° C, between 20° C to 30° C, between 30° C to 40° C, between 40° C to 50° C, between 50° C to 60° C, between 60° C to 70° C, between 70° C to 80° C or 80° C. In a particular embodiment, the one-pot reaction is carried out at 60 °C.

10 [0063] The reaction medium for conversion is generally aqueous, e.g., purified water, buffer, or a combination thereof. In a particular embodiment, the reaction medium is a buffer. Suitable buffers include, but are not limited to, acetate buffer, citrate buffer, HEPES, and phosphate buffer. In a particular embodiment, the reaction medium is phosphate buffer. The reaction medium can have a pH between about 4 and 10. In a particular embodiment, the reaction medium
15 has a pH of 6. The reaction medium can also be, alternatively, an organic solvent.

[0064] The step of contacting the starting composition with the glycosyltransferase and sucrose synthase polypeptides can be carried out in a duration of time between about 1 hour and 1 week, such as, for example, between 30 minutes and 1 hours, between 1 hour and 4 hours, between 4 hours and 6 hours, between 6 hours and 12 hours, between 12 hours and 24 hours,
20 between 1 day and 2 days, between 2 days and 3 days, 3 days and 4 days, between 4 days and 5 days, between 6 days and 7 days. In a particular embodiment, the reaction is carried out for 24 hours.

[0065] The reaction can be monitored by suitable method including, but not limited to, HPLC, LCMS, TLC, IR or NMR.

25 [0066] The target steviol glycoside can be any steviol glycoside. In one embodiment, the target steviol glycoside is steviol-13-O-glucoside, steviol-19-O-glucoside, rubusoside, steviol-1,2-bioside, steviol-1,3-bioside, rubusoside, dulcoside B, dulcoside A, rebaudioside B, rebaudioside G, stevioside, rebaudioside C, rebaudioside F, rebaudioside A, rebaudioside I, rebaudioside E, rebaudioside H, rebaudioside L, rebaudioside K, rebaudioside J, rebaudioside M, rebaudioside
30 D, rebaudioside N, rebaudioside O, rebaudioside Q, a rebaudioside with 7 covalently attached glucose units (e.g. rebaudioside M plus 1 glucose unit), a synthetic steviol glycoside, an isomer thereof, and/or a steviol glycoside composition. In another embodiment, the target steviol gly-

coside is rebaudioside E, or isomers thereof. In another embodiment, the target steviol glycoside is rebaudioside D, or isomers thereof. In still another embodiment, the target steviol glycosides are Reb D and Reb E.

[0067] In one embodiment, the conversion of Reb A to Reb D and/or Reb D isomer(s) is at least about 2% complete, as determined by any of the methods mentioned above. In a particular embodiment, the conversion of Reb A to Reb D and/or Reb D isomer(s) is at least about 10% complete, at least about 20% complete, at least about 30% complete, at least about 40% complete, at least about 50% complete, at least about 60% complete, at least about 70% complete, at least about 80% complete, or at least about 90% complete. In a particular embodiment, the conversion of reb A to reb D and/or rebD isomer(s) is at least about 95% complete. In some embodiments, at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the Reb A in the starting composition is converted to Reb D and/or Reb D isomer(s).

[0068] In one embodiment, the conversion of stevioside to Reb E and/or Reb E isomer(s) is at least about 2% complete, as determined by any of the methods mentioned above. In a particular embodiment, the conversion of stevioside to Reb E and/or Reb E isomer(s) is at least about 10% complete, at least about 20% complete, at least about 30% complete, at least about 40% complete, at least about 50% complete, at least about 60% complete, at least about 70% complete, at least about 80% complete, or at least about 90% complete. In a particular embodiment, the conversion of stevioside to Reb E and/or Reb E isomer(s) is at least about 95% complete. In some embodiments, at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the stevioside in the starting composition is converted to Reb E and/or Reb E isomer(s).

[0069] The target steviol glycoside(s) can be in any polymorphic or amorphous form, including hydrates, solvates, anhydrous or combinations thereof.

[0070] Optionally, the method of the present disclosure further comprises separating the target steviol glycoside from the target composition. The target steviol glycoside(s) can be separated by any suitable method, such as, for example, crystallization, separation by membranes, centrifugation, extraction, chromatographic separation or a combination of such methods.

[0071] In one embodiment, the separation of target steviol glycosides produces a composition comprising greater than about 80% by weight of the target steviol glycoside(s) on an anhydrous basis, i.e., a highly purified steviol glycoside composition. In another embodiment, separation produces a composition comprising greater than about 0.5%, greater than about 1%, greater than about 2%, greater than about 3%, greater than about 4%, greater than about 5%, 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 85%, greater than about 90%, greater than about 91%, greater than about 92%, greater than about 93%, greater than about 94%, greater than about 95%, greater than about 96%, greater than about 97%, greater than about 98%, greater than about 99%, or greater than about 99.6% by weight of the target steviol glycosides. In particular embodiments,

the composition comprises greater than about 95% by weight of the target steviol glycoside(s).
[0072] Purified target steviol glycosides can be used in consumable products as a sweetener. Suitable consumer products include, but are not limited to, food, beverages, pharmaceutical compositions, tobacco products, nutraceutical compositions, oral hygiene compositions, and cosmetic compositions.

[0073] Plasmids containing nucleic acids encoding enzymes having SEQ ID NOS:1-1227 and 1231-1466 are described in the Table 1 below.

Table 1

SEQ ID NO	Plasmid ID	SEQ ID NO	Plasmid ID	SEQ ID NO	Plasmid ID
1	pA10132	489	pA33193	977	pA32698
2	pA10143	490	pA33194	978	pA32700
3	pA12549	491	pA33195	979	pA32701
4	pA12550	492	pA33196	980	pA32702
5	pA28422	493	pA33197	981	pA32704
6	pA30328	494	pA33198	982	pA32706
7	pA30329	495	pA33199	983	pA32708
8	pA30331	496	pA33200	984	pA32712
9	pA30332	497	pA33201	985	pA32715
10	pA30333	498	pA33202	986	pA32716
11	pA30334	499	pA33203	987	pA32717
12	pA30335	500	pA33204	988	pA32719
13	pA30337	501	pA33205	989	pA32721
14	pA30338	502	pA33206	990	pA32723
15	pA30339	503	pA33207	991	pA32731
16	pA30340	504	pA33208	992	pA32732
17	pA30341	505	pA33209	993	pA32734
18	pA30342	506	pA33210	994	pA32736
19	pA30343	507	pA33211	995	pA32737

20	pA30345	508	pA33212	996	pA32739
21	pA30347	509	pA33213	997	pA32748
22	pA30348	510	pA33214	998	pA32750
23	pA30350	511	pA33215	999	pA32754
24	pA30351	512	pA33216	1000	pA32758
25	pA30352	513	pA33217	1001	pA32767
26	pA30354	514	pA33218	1002	pA32770
27	pA30358	515	pA33219	1003	pA32779
28	pA30362	516	pA33220	1004	pA32781
29	pA30463	517	pA33221	1005	pA32787
30	pA30468	518	pA33222	1006	pA32790
31	pA30471	519	pA33223	1007	pA32793
32	pA30472	520	pA33224	1008	pA32796
33	pA30473	521	pA33225	1009	pA32797
34	pA30557	522	pA33226	1010	pA32799
35	pA30565	523	pA33227	1011	pA32800
36	pA30568	524	pA33228	1012	pA32801
37	pA30569	525	pA33229	1013	pA32802
38	pA30570	526	pA33230	1014	pA32804
39	pA30571	527	pA33231	1015	pA32806
40	pA30785	528	pA33232	1016	pA32808
41	pA30787	529	pA33233	1017	pA32816
42	pA30790	530	pA33234	1018	pA32819
43	pA30791	531	pA33235	1019	pA32820
44	pA30793	532	pA33236	1020	pA32821
45	pA30796	533	pA33237	1021	pA32824
46	pA30797	534	pA33238	1022	pA32825
47	pA30798	535	pA29767	1023	pA32826
48	pA30799	536	pA29768	1024	pA32828
49	pA30802	537	pA29769	1025	pA32831
50	pA30803	538	pA29770	1026	pA32834
51	pA30805	539	pA29771	1027	pA32835

52	pA30806	540	pA29772	1028	pA32837
53	pA30808	541	pA29773	1029	pA32842
54	pA30811	542	pA29774	1030	pA32844
55	pA30812	543	pA29775	1031	pA32845
56	pA30814	544	pA29776	1032	pA32847
57	pA30817	545	pA29777	1033	pA32848
58	pA30820	546	pA29778	1034	pA32854
59	pA30879	547	pA29779	1035	pA32855
60	pA30880	548	pA29780	1036	pA32858
61	pA30882	549	pA29781	1037	pA32863
62	pA30883	550	pA29782	1038	pA32864
63	pA30884	551	pA29783	1039	pA32865
64	pA30885	552	pA29784	1040	pA32866
65	pA30886	553	pA29785	1041	pA32868
66	pA30887	554	pA29786	1042	pA32876
67	pA30888	555	pA29787	1043	pA32880
68	pA30892	556	pA29788	1044	pA32916
69	pA30894	557	pA29789	1045	pA32919
70	pA30895	558	pA29790	1046	pA32924
71	pA30935	559	pA29791	1047	pA32926
72	pA30936	560	pA29792	1048	pA32934
73	pA30937	561	pA29793	1049	pA32632
74	pA30938	562	pA29794	1050	pA32634
75	pA30939	563	pA29795	1051	pA32638
76	pA30940	564	pA29796	1052	pA32646
77	pA30941	565	pA29797	1053	pA32653
78	pA30942	566	pA29798	1054	pA32722
79	pA30943	567	pA29799	1055	pA32724
80	pA30944	568	pA29800	1056	pA32727
81	pA30945	569	pA29801	1057	pA32729
82	pA30946	570	pA29802	1058	pA32735
83	pA30947	571	pA29803	1059	pA32738

84	pA30948	572	pA29804	1060	pA32742
85	pA30949	573	pA29805	1061	pA32743
86	pA30951	574	pA29806	1062	pA32746
87	pA30952	575	pA29807	1063	pA32747
88	pA30953	576	pA29808	1064	pA32749
89	pA30997	577	pA29809	1065	pA32751
90	pA30998	578	pA29810	1066	pA32752
91	pA31001	579	pA29811	1067	pA32757
92	pA31003	580	pA29812	1068	pA32760
93	pA31004	581	pA29813	1069	pA32761
94	pA31005	582	pA29814	1070	pA32763
95	pA31006	583	pA29815	1071	pA32765
96	pA31009	584	pA29816	1072	pA32769
97	pA31011	585	pA29817	1073	pA32775
98	pA31012	586	pA29818	1074	pA32780
99	pA31014	587	pA29615	1075	pA32782
100	pA31016	588	pA29616	1076	pA32785
101	pA31017	589	pA29617	1077	pA32791
102	pA31018	590	pA29618	1078	pA32869
103	pA31020	591	pA29619	1079	pA32871
104	pA31022	592	pA29620	1080	pA32875
105	pA31024	593	pA29621	1081	pA32879
106	pA31026	594	pA29622	1082	pA32881
107	pA31029	595	pA29623	1083	pA32882
108	pA31068	596	pA29624	1084	pA32884
109	pA31069	597	pA29625	1085	pA32885
110	pA31070	598	pA29626	1086	pA32886
111	pA31071	599	pA29627	1087	pA32888
112	pA31073	600	pA29628	1088	pA32892
113	pA31074	601	pA29629	1089	pA32894
114	pA31075	602	pA29630	1090	pA32895
115	pA31076	603	pA29631	1091	pA32902

116	pA31078	604	pA29632	1092	pA32903
117	pA31080	605	pA29633	1093	pA32904
118	pA31081	606	pA29634	1094	pA32906
119	pA31086	607	pA29635	1095	pA32908
120	pA31125	608	pA29636	1096	pA32912
121	pA31126	609	pA29637	1097	pA32913
122	pA31127	610	pA29638	1098	pA32914
123	pA31128	611	pA29639	1099	pA32917
124	pA31129	612	pA29640	1100	pA32918
125	pA31130	613	pA29641	1101	pA32922
126	pA31134	614	pA29642	1102	pA32923
127	pA31135	615	pA29643	1103	pA32930
128	pA31136	616	pA29645	1104	pA32932
129	pA31138	617	pA29646	1105	pA32579
130	pA31142	618	pA29647	1106	pA32581
131	pA31163	619	pA29648	1107	pA32583
132	pA31167	620	pA29649	1108	pA32585
133	pA31169	621	pA29650	1109	pA32587
134	pA31172	622	pA29651	1110	pA32597
135	pA31173	623	pA29652	1111	pA32599
136	pA31174	624	pA29653	1112	pA32610
137	pA31175	625	pA29654	1113	pA32613
138	pA31177	626	pA29655	1114	pA32617
139	pA31178	627	pA29656	1115	pA32619
140	pA31179	628	pA29657	1116	pA32621
141	pA31181	629	pA29658	1117	pA32627
142	pA31258	630	pA29659	1118	pA32631
143	pA31259	631	pA29660	1119	pA32633
144	pA31261	632	pA29661	1120	pA32637
145	pA31262	633	pA29662	1121	pA32641
146	pA31263	634	pA29664	1122	pA32647
147	pA31264	635	pA29665	1123	pA32656

148	pA31265	636	pA29666	1124	pA32658
149	pA31267	637	pA29667	1125	pA32673
150	pA31268	638	pA29668	1126	pA32677
151	pA31273	639	pA29669	1127	pA32679
152	pA31274	640	pA29671	1128	pA32681
153	pA31276	641	pA29672	1129	pA32683
154	pA31278	642	pA29673	1130	pA32685
155	pA31279	643	pA29675	1131	pA32689
156	pA31280	644	pA29676	1132	pA32691
157	pA31282	645	pA29677	1133	pA32693
158	pA31285	646	pA29678	1134	pA32695
159	pA31286	647	pA29679	1135	pA32711
160	pA31287	648	pA29680	1136	pA32725
161	pA31288	649	pA29681	1137	pA32740
162	pA31289	650	pA29682	1138	pA32744
163	pA31290	651	pA29683	1139	pA32764
164	pA31291	652	pA29684	1140	pA32768
165	pA31294	653	pA29685	1141	pA32772
166	pA31297	654	pA29686	1142	pA32773
167	pA31298	655	pA29687	1143	pA32774
168	pA31300	656	pA29688	1144	pA32776
169	pA31302	657	pA29689	1145	pA32777
170	pA31303	658	pA29690	1146	pA32778
171	pA31304	659	pA29692	1147	pA32795
172	pA31305	660	pA29693	1148	pA32803
173	pA31306	661	pA29694	1149	pA32805
174	pA31307	662	pA29695	1150	pA32807
175	pA31308	663	pA29696	1151	pA32809
176	pA31309	664	pA29697	1152	pA32813
177	pA31310	665	pA29698	1153	pA32815
178	pA31311	666	pA29699	1154	pA32817
179	pA31313	667	pA29700	1155	pA32827

180	pA31336	668	pA29701	1156	pA32832
181	pA31345	669	pA29702	1157	pA32833
182	pA31346	670	pA29703	1158	pA32839
183	pA31347	671	pA29704	1159	pA32841
184	pA31350	672	pA30015	1160	pA32843
185	pA31352	673	pA30016	1161	pA32849
186	pA31353	674	pA30017	1162	pA32851
187	pA31354	675	pA30018	1163	pA32853
188	pA31355	676	pA30019	1164	pA32857
189	pA31356	677	pA30020	1165	pA32859
190	pA31358	678	pA30021	1166	pA32867
191	pA31360	679	pA30022	1167	pA32872
192	pA31362	680	pA30023	1168	pA32873
193	pA31364	681	pA30024	1169	pA32887
194	pA31366	682	pA30025	1170	pA32889
195	pA31367	683	pA30026	1171	pA32891
196	pA31368	684	pA30027	1172	pA32897
197	pA31369	685	pA30028	1173	pA32901
198	pA31505	686	pA30029	1174	pA32907
199	pA31506	687	pA30030	1175	pA32911
200	pA31507	688	pA30031	1176	pA32915
201	pA31508	689	pA30032	1177	pA32920
202	pA31509	690	pA30033	1178	pA32927
203	pA31510	691	pA30034	1179	pA32929
204	pA31511	692	pA30035	1180	pA32931
205	pA31512	693	pA30036	1181	pA34086
206	pA31513	694	pA30037	1182	pA34087
207	pA31515	695	pA30038	1183	pA34088
208	pA31516	696	pA30039	1184	pA34089
209	pA31517	697	pA30040	1185	pA34090
210	pA31518	698	pA30041	1186	pA34091
211	pA31519	699	pA30042	1187	pA34092

212	pA31520	700	pA30044	1188	pA34094
213	pA31521	701	pA30045	1189	pA34095
214	pA31522	702	pA30046	1190	pA34096
215	pA31523	703	pA30047	1191	pA34097
216	pA31545	704	pA30048	1192	pA34098
217	pA31548	705	pA30049	1193	pA34099
218	pA31549	706	pA30050	1194	pA34100
219	pA31558	707	pA32939	1195	pA34101
220	pA31559	708	pA32940	1196	pA34102
221	pA31560	709	pA32941	1197	pA34103
222	pA31561	710	pA32942	1198	pA34104
223	pA29916	711	pA32943	1199	pA34105
224	pA29917	712	pA32944	1200	pA34106
225	pA29918	713	pA32945	1201	pA34107
226	pA29919	714	pA32946	1202	pA34109
227	pA29920	715	pA32947	1203	pA34110
228	pA29921	716	pA32948	1204	pA34111
229	pA29922	717	pA32949	1205	pA34112
230	pA29923	718	pA32950	1206	pA34113
231	pA29924	719	pA32951	1207	pA34115
232	pA29925	720	pA32952	1208	pA34116
233	pA29926	721	pA32953	1209	pA34117
234	pA29927	722	pA32954	1210	pA34118
235	pA29928	723	pA32955	1211	pA34119
236	pA29929	724	pA32956	1212	pA34120
237	pA29930	725	pA32957	1213	pA34121
238	pA29931	726	pA32958	1214	pA34122
239	pA29932	727	pA32959	1215	pA34123
240	pA29933	728	pA32960	1216	pA34124
241	pA29934	729	pA32962	1217	pA34125
242	pA29935	730	pA32963	1218	pA34126
243	pA29937	731	pA32965	1219	pA34127

244	pA29938	732	pA32966	1220	pA34128
245	pA29939	733	pA32967	1221	pA34129
246	pA29941	734	pA32968	1222	pA34130
247	pA29942	735	pA32969	1223	pA34131
248	pA29943	736	pA32970	1224	pA34132
249	pA29944	737	pA32971	1225	pA34133
250	pA29945	738	pA32972	1226	pA34134
251	pA29946	739	pA32973	1227	pA34135
252	pA29947	740	pA32977	1231	pA35407
253	pA29948	741	pA32978	1232	pA35408
254	pA29949	742	pA32979	1233	pA35409
255	pA29950	743	pA32980	1234	pA35410
256	pA29951	744	pA32981	1235	pA35411
257	pA29952	745	pA32982	1236	pA35412
258	pA29953	746	pA32983	1237	pA35413
259	pA29954	747	pA32984	1238	pA35414
260	pA29955	748	pA32985	1239	pA35415
261	pA29956	749	pA32987	1240	pA35416
262	pA29957	750	pA32988	1241	pA35417
263	pA29958	751	pA32989	1242	pA35418
264	pA29959	752	pA32990	1243	pA35419
265	pA29960	753	pA32991	1244	pA35420
266	pA29961	754	pA32992	1245	pA35421
267	pA29962	755	pA32993	1246	pA35422
268	pA29963	756	pA32994	1247	pA35423
269	pA29964	757	pA32995	1248	pA35424
270	pA29965	758	pA32996	1249	pA35425
271	pA29966	759	pA32997	1250	pA35426
272	pA29967	760	pA32998	1251	pA35427
273	pA29968	761	pA32999	1252	pA35428
274	pA29969	762	pA33000	1253	pA35429
275	pA29970	763	pA33001	1254	pA35430

276	pA29971	764	pA33002	1255	pA35431
277	pA29972	765	pA33004	1256	pA35432
278	pA29973	766	pA33005	1257	pA35434
279	pA29976	767	pA33006	1258	pA35435
280	pA29977	768	pA33007	1259	pA35436
281	pA29978	769	pA33008	1260	pA35437
282	pA29979	770	pA33009	1261	pA35438
283	pA29980	771	pA33010	1262	pA35439
284	pA29981	772	pA33011	1263	pA35440
285	pA29982	773	pA33012	1264	pA35441
286	pA29983	774	pA33014	1265	pA35442
287	pA29984	775	pA33015	1266	pA35443
288	pA29985	776	pA33016	1267	pA35444
289	pA29986	777	pA33017	1268	pA35872
290	pA29987	778	pA33018	1269	pA35873
291	pA29989	779	pA33019	1270	pA35874
292	pA29990	780	pA33020	1271	pA35875
293	pA29991	781	pA33021	1272	pA35876
294	pA29992	782	pA33023	1273	pA35877
295	pA29993	783	pA33024	1274	pA35878
296	pA29994	784	pA33025	1275	pA35879
297	pA29995	785	pA33027	1276	pA35880
298	pA29996	786	pA33028	1277	pA35881
299	pA29997	787	pA33029	1278	pA35882
300	pA29998	788	pA33030	1279	pA35884
301	pA30000	789	pA33031	1280	pA35886
302	pA30001	790	pA33032	1281	pA35887
303	pA30002	791	pA33033	1282	pA35888
304	pA30003	792	pA33035	1283	pA35889
305	pA30004	793	pA33036	1284	pA35890
306	pA30005	794	pA33037	1285	pA35891
307	pA30006	795	pA33038	1286	pA35892

308	pA30007	796	pA33040	1287	pA35893
309	pA30008	797	pA33041	1288	pA35895
310	pA30009	798	pA33042	1289	pA35896
311	pA30010	799	pA33043	1290	pA35897
312	pA30011	800	pA33044	1291	pA35898
313	pA30012	801	pA33046	1292	pA35899
314	pA30013	802	pA33047	1293	pA35901
315	pA30014	803	pA33048	1294	pA35902
316	pA29705	804	pA33051	1295	pA35903
317	pA29706	805	pA33053	1296	pA35904
318	pA29707	806	pA33054	1297	pA35905
319	pA29708	807	pA33056	1298	pA35906
320	pA29709	808	pA33057	1299	pA35907
321	pA29710	809	pA33058	1300	pA35908
322	pA29711	810	pA33059	1301	pA35909
323	pA29712	811	pA33060	1302	pA35910
324	pA29713	812	pA33061	1303	pA35911
325	pA29714	813	pA33063	1304	pA35912
326	pA29715	814	pA33065	1305	pA35913
327	pA29716	815	pA33066	1306	pA35914
328	pA29717	816	pA33067	1307	pA35915
329	pA29718	817	pA33068	1308	pA35916
330	pA29719	818	pA33069	1309	pA35917
331	pA29720	819	pA33070	1310	pA35919
332	pA29721	820	pA33071	1311	pA35921
333	pA29722	821	pA33074	1312	pA35922
334	pA29723	822	pA33075	1313	pA35923
335	pA29724	823	pA33076	1314	pA35924
336	pA29725	824	pA33077	1315	pA35925
337	pA29726	825	pA33078	1316	pA35926
338	pA29727	826	pA33079	1317	pA35927
339	pA29728	827	pA33080	1318	pA35928

340	pA29729	828	pA33081	1319	pA35929
341	pA29730	829	pA33082	1320	pA35930
342	pA29731	830	pA29819	1321	pA35931
343	pA29732	831	pA29820	1322	pA35932
344	pA29733	832	pA29821	1323	pA35933
345	pA29734	833	pA29822	1324	pA35935
346	pA29735	834	pA29823	1325	pA35936
347	pA29736	835	pA29824	1326	pA35937
348	pA29737	836	pA29825	1327	pA35938
349	pA29738	837	pA29826	1328	pA35939
350	pA29740	838	pA29827	1329	pA35940
351	pA29741	839	pA29828	1330	pA35941
352	pA29742	840	pA29829	1331	pA35942
353	pA29743	841	pA29830	1332	pA35943
354	pA29744	842	pA29831	1333	pA35481
355	pA29745	843	pA29832	1334	pA35482
356	pA29746	844	pA29833	1335	pA35483
357	pA29747	845	pA29834	1336	pA35484
358	pA29748	846	pA29835	1337	pA35485
359	pA29749	847	pA29836	1338	pA35486
360	pA29750	848	pA29837	1339	pA35487
361	pA29751	849	pA29838	1340	pA35488
362	pA29752	850	pA29839	1341	pA35489
363	pA29753	851	pA29840	1342	pA35490
364	pA29754	852	pA29841	1343	pA35491
365	pA29755	853	pA29842	1344	pA35492
366	pA29756	854	pA29843	1345	pA35493
367	pA29757	855	pA29844	1346	pA35494
368	pA29758	856	pA29845	1347	pA35495
369	pA29759	857	pA29846	1348	pA35496
370	pA29760	858	pA29847	1349	pA35497
371	pA29761	859	pA29848	1350	pA35498

372	pA29762	860	pA29849	1351	pA35499
373	pA29763	861	pA29850	1352	pA35500
374	pA29764	862	pA29851	1353	pA35501
375	pA29765	863	pA29852	1354	pA35502
376	pA32567	864	pA29853	1355	pA35503
377	pA32568	865	pA29854	1356	pA35504
378	pA32569	866	pA29855	1357	pA35505
379	pA32570	867	pA29856	1358	pA35506
380	pA32571	868	pA29857	1359	pA35507
381	pA32572	869	pA29858	1360	pA35508
382	pA32573	870	pA29859	1361	pA35509
383	pA32574	871	pA29860	1362	pA35510
384	pA32576	872	pA29861	1363	pA35511
385	pA33083	873	pA29862	1364	pA35512
386	pA33084	874	pA29863	1365	pA35513
387	pA33085	875	pA29864	1366	pA35514
388	pA33086	876	pA29865	1367	pA35515
389	pA33087	877	pA29866	1368	pA35516
390	pA33088	878	pA29867	1369	pA35517
391	pA33089	879	pA29868	1370	pA35518
392	pA33090	880	pA29869	1371	pA35519
393	pA33091	881	pA29870	1372	pA35520
394	pA33092	882	pA29871	1373	pA35521
395	pA33094	883	pA10142	1374	pA35522
396	pA33095	884	pA12546	1375	pA35523
397	pA33096	885	pA21838	1376	pA35524
398	pA33097	886	pA21839	1377	pA35525
399	pA33098	887	pA21840	1378	pA35526
400	pA33099	888	pA21841	1379	pA35527
401	pA33100	889	pA21842	1380	pA35528
402	pA33101	890	pA33240	1381	pA35529
403	pA33102	891	pA33241	1382	pA35530

404	pA33103	892	pA33242	1383	pA35531
405	pA33104	893	pA33244	1384	pA35532
406	pA33105	894	pA33246	1385	pA35533
407	pA33106	895	pA33247	1386	pA35534
408	pA33107	896	pA33248	1387	pA35535
409	pA33108	897	pA33249	1388	pA35536
410	pA33109	898	pA33250	1389	pA35537
411	pA33110	899	pA33252	1390	pA35538
412	pA33111	900	pA33253	1391	pA35539
413	pA33112	901	pA33254	1392	pA35540
414	pA33114	902	pA33255	1393	pA35541
415	pA33115	903	pA33258	1394	pA35542
416	pA33116	904	pA33259	1395	pA35543
417	pA33117	905	pA33260	1396	pA35544
418	pA33118	906	pA33261	1397	pA35545
419	pA33119	907	pA33262	1398	pA35546
420	pA33120	908	pA33263	1399	pA35547
421	pA33122	909	pA33264	1400	pA35548
422	pA33123	910	pA33267	1401	pA35549
423	pA33124	911	pA33269	1402	pA35550
424	pA33125	912	pA33270	1403	pA35551
425	pA33129	913	pA33271	1404	pA35552
426	pA33130	914	pA33272	1405	pA35553
427	pA33131	915	pA33273	1406	pA35554
428	pA33132	916	pA33274	1407	pA35555
429	pA33133	917	pA33276	1408	pA35556
430	pA33134	918	pA33278	1409	pA35557
431	pA33135	919	pA33279	1410	pA35558
432	pA33136	920	pA33280	1411	pA35559
433	pA33137	921	pA33281	1412	pA35560
434	pA33138	922	pA33282	1413	pA35561
435	pA33139	923	pA33285	1414	pA35562

436	pA33140	924	pA33286	1415	pA35563
437	pA33141	925	pA32582	1416	pA35564
438	pA33142	926	pA32586	1417	pA35565
439	pA33143	927	pA32589	1418	pA35566
440	pA33144	928	pA32591	1419	pA35567
441	pA33145	929	pA32594	1420	pA35568
442	pA33146	930	pA32595	1421	pA35569
443	pA33147	931	pA32596	1422	pA35570
444	pA33148	932	pA32600	1423	pA35571
445	pA33149	933	pA32601	1424	pA35572
446	pA33150	934	pA32602	1425	pA35573
447	pA33151	935	pA32603	1426	pA35574
448	pA33152	936	pA32605	1427	pA35575
449	pA33153	937	pA32606	1428	pA35576
450	pA33154	938	pA32608	1429	pA35577
451	pA33159	939	pA32609	1430	pA35578
452	pA33160	940	pA32614	1431	pA35579
453	pA33162	941	pA32616	1432	pA35580
454	pA33163	942	pA32620	1433	pA35581
455	pA33164	943	pA32622	1434	pA35582
456	pA33165	944	pA32623	1435	pA35583
457	pA33166	945	pA32625	1436	pA35584
458	pA33167	946	pA32629	1437	pA35585
459	pA33168	947	pA32639	1438	pA35586
460	pA32557	948	pA32650	1439	pA35587
461	pA32558	949	pA32651	1440	pA35588
462	pA32559	950	pA32652	1441	pA35589
463	pA32560	951	pA32655	1442	pA35590
464	pA32562	952	pA32657	1443	pA35591
465	pA32563	953	pA32659	1444	pA35592
466	pA32565	954	pA32661	1445	pA35593
467	pA32566	955	pA32662	1446	pA35594

468	pA33169	956	pA32663	1447	pA35595
469	pA33171	957	pA32664	1448	pA35596
470	pA33172	958	pA32665	1449	pA35597
471	pA33173	959	pA32666	1450	pA35598
472	pA33174	960	pA32667	1451	pA35599
473	pA33175	961	pA32668	1452	pA35600
474	pA33176	962	pA32669	1453	pA35601
475	pA33177	963	pA32670	1454	pA35602
476	pA33178	964	pA32671	1455	pA35603
477	pA33179	965	pA32672	1456	pA35604
478	pA33180	966	pA32675	1457	pA35605
479	pA33181	967	pA32678	1458	pA35606
480	pA33182	968	pA32680	1459	pA35607
481	pA33184	969	pA32682	1460	pA35608
482	pA33185	970	pA32684	1461	pA35609
483	pA33186	971	pA32686	1462	pA35610
484	pA33188	972	pA32688	1463	pA35611
485	pA33189	973	pA32690	1464	pA35612
486	pA33190	974	pA32692	1465	pA35613
487	pA33191	975	pA32696	1466	pA35614
488	pA33192	976	pA32697		

EXAMPLES

Example 1: *In vivo* Production of Native Beta-1,2-Glycosyltransferases (B12GTs)

[0074] Polynucleotides encoding the amino acid sequences for known beta-1,2-UDP-glycosyl-transferases from five different organisms (Table 1.1) were synthesized (Twist Bioscience) and inserted into the pARZ4 expression vector. Polynucleotides were either ordered as full-length genes or ordered as gene fragments and then assembled using Gibson assembly. The recombinant vectors were used in a heat shock method to transform *E. coli* HMS174(DE3) (Novagen), thereby preparing recombinant microorganisms.

[0075] Each transformed recombinant microorganism was inoculated to 1ml LB- kanamycin medium, cultured by shaking at 37°C overnight. The culture was inoculated to 5ml TB-kanamycin medium and grown for 2 hours at 37°C, followed by 25°C for 1 hour. The culture was

induced with 50 uL 50 mM IPTG and grown overnight. Finally, the culture was centrifuged at top-speed for 5 minutes and stored at -80°C.

Table 1.1. Native Beta-1,2-UDP-Glycosyltransferases

PlasmidID	Organism
pA10132	<i>Oryza sativa subsp. japonica (Rice)</i>
pA10143	<i>Solanum lycopersicum (Tomato)</i>
pA12549	<i>Lycium barbarum (Barbary matrimony-vine)</i>
pA12550	<i>Solanum lycopersicum (Tomato)</i>
pA28422	<i>Solanum tuberosum (Potato)</i>

Example 2: Purification of Beta-1,2-Glycosyltransferases (B12GTs)

[0076] The microorganisms created in *Example 1* were dissolved in a lysis buffer (lysozyme, DNaseI, Bugbuster, 300mL 20 mM HEPES pH 7.5, 500mM NaCl, and 20mM Imidazole). Two to three glass beads were added to each well and were disrupted by shaking at 25° C and 220rpm for 30 minutes. The disrupted liquid was centrifuged at 2200 x g for 6-10 minutes. The obtained supernatant was loaded onto a Ni-NTA plate and shaken for 10 minutes at room temperature. The plate was centrifuged for 4 minutes at 100 x g followed by two washes of 500 uL binding buffer (300mL 20mM HEPES pH 7.5, 500mM NaCl, 20mM Imidazole) and two-minute centrifugation (500 x g). The proteins were eluted with 150 uL elution buffer (15mL 20mM HEPES pH 7.5, 500mM NaCl, 500mM Imidazole) and shaken for 1 minute at 0.25 maximum shaking speed followed by centrifugation for 2 minutes at 500 x g. The recovered protein was desalted into a buffer solution for enzyme activity evaluation (50mM HEPES pH 7.5, 50mM NaCl).

Example 3: Measure Beta-1,2-Glycosyltransferase (B12GT) Activity with ADP-glucose and GDP-glucose

[0077] The wild-type beta-1,2-UDP-glycosyltransferases, pA10132, pA10143 and pA12549, were assayed for activity with ADP-glucose and GDP-glucose. Purified protein was reacted with 0.5 mM RA99 (99% Pure Reb A), 2 mM NDP-glucose (ADP-glucose or GDP-glucose) in 50 mM MOPS pH 7.8 buffer for 72 hours at 30 °C. Conversion of Reb A to Reb D, as schematized in **FIG. 1**, was monitored by liquid chromatography-mass spectrometry (LCMS) using an Agilent 6470 QQQ mass spectrometer (column: Waters ACQUITY UPLC HSS T3 Column, 100 mm x 2.1 mm). The QQQ was run with multi reaction monitoring (MS/MS) to

accurately quantitate steviol glycosides of interest. All three wild-type B12GTs had minimal Reb A to Reb D activity when using ADP-glucose or GDP-glucose as the reaction sugar donor (FIG. 2).

5 Example 4: *In vivo* Production of Native Sucrose Synthases

[0078] Polynucleotides encoding the amino acid sequences for sucrose synthases (SuSys) from seven different organisms (Table 2) were synthesized (Twist Bioscience) and inserted into the pARZ4 expression vector. Polynucleotides were either ordered as full-length genes or ordered as gene fragments and then assembled using Gibson assembly. The recombinant vectors were
10 used in a heat shock method to transform *E. coli* NEBT7EL (New England Biolabs), thereby preparing recombinant microorganisms.

[0079] Each transformed recombinant microorganism was inoculated to 1ml LB- kanamycin medium, cultured by shaking at 37°C overnight. The culture was inoculated to 5ml TB-kanamycin medium and grown for 2 hours at 37°C, followed by 25°C for 1 hour. The culture was
15 induced with 50 uL 50 mM IPTG and grown overnight. Finally, the culture was centrifuged at top-speed for 5 minutes and stored at -80°C.

Table 2. Wildtype Sucrose Synthase Sequences

PlasmidID	Organism
pA10142	<i>Arabidopsis thaliana</i>
pA12546	<i>Coffea arabica</i>
pA21838	<i>Acidithiobacillus caldus</i>
pA21839	<i>Nitrosomonas europaea</i>
pA21840	<i>Denitrovibrio acetiphilus</i>
pA21841	<i>Thermosynechococcus elongatus</i>
pA21842	<i>Oryza sativa</i> subsp. <i>japonica</i> (Rice)

Example 5: Purification of Native Sucrose Synthases

[0080] The microorganisms created in *Example 4* were dissolved in a lysis buffer (lysozyme, DNaseI, Bugbuster, 300mL 20 mM HEPES pH 7.5, 500mM NaCl, and 20mM Imidazole). Two to three glass beads were added to each well and were disrupted by shaking at 25° C and 220rpm for 30 minutes. The disrupted liquid was centrifuged at 2200 x g for 6-10 minutes. The obtained supernatant was loaded onto a Ni-NTA plate and shaken for 10 minutes at room tem-
25 perature. The plate was centrifuged for 4 minutes at 100 x g followed by two washes of 500 uL

binding buffer (300mL 20mM HEPES pH 7.5, 500mM NaCl, 20mM Imidazole) and two-minute centrifugation (500 x g). The proteins were eluted with 150 uL elution buffer (15mL 20mM HEPES pH 7.5, 500mM NaCl, 500mM Imidazole) and shaken for 1 minute at 0.25 maximum shaking speed followed by centrifugation for 2 minutes at 500 x g. The recovered protein was desalted into a buffer solution for enzyme activity evaluation (50mM MOPS pH 6.5, 50mM NaCl).

Example 6: Measure Sucrose Synthase Activity with UDP, GDP and ADP.

[0081] Purified enzyme from *Example 5* was reacted with 50 mM sucrose and 5 mM nucleotide (ADP, GDP or UDP) in 50 mM MOPS buffer (pH 6.5) and 50 mM NaCl for 24 hours at 60 °C. Conversion of NDP to NDP-glucose was monitored by liquid chromatography-mass spectrometry (LCMS) using an Agilent 6545 QTOF mass spectrometer (column: Agilent HILIC-OH 150x2.1mm). The wild-type sucrose synthases were active on all three nucleotides (**FIG. 3**).

Example 7: Conversion of Reb A to Reb D in a One-Pot Reaction

[0082] One-pot reactions containing a B12GT and a SuSy were conducted to demonstrate the ability to convert Reb A to Reb D using ADP-glucose generated by the SuSy. Purified B12GT (pA10143 (**FIG. 4 (top)**) or pA12549 (**FIG. 4 (bottom)**)) and purified SuSy (pA10142, pA12546, pA21838, pA21839, pA21840, pA21841, or pA21842) were reacted with 0.5 mg/mL RA99, 50 mM Sucrose, and 5 mM ADP in 50 mM pH 6.5 MOPS buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. All one-pot reactions were able to generate Reb D from Reb A (**FIG. 4**). The one-pot reactions containing pA10143 further converted the generated Reb D to Reb M2.

Example 8: Improved Activity of pA10143 by Site-Saturation Mutagenesis

[0083] Homology models of the B12GT encoded by pA10143 were generated and used to identify the active site residues of the protein. The following twenty active site residue positions were chosen for site-saturation mutagenesis: 81, 82, 88, 139, 178, 185, 260, 284, 317, 320, 324, 332, 336, 339, 341, 358, 359, 360, 362, 363. Gibson assembly using bridging oligos was used to create 217 single point mutant variants of pA10143 (SEQ ID NOs: 6-222). Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM

MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several variants showed improved activity compared to the parent pA10143 (**FIG. 5**). Active site positions 358, 341 and 317 had the greatest improvements in activity (**FIG. 6**).

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Example 9: Improved Activity of pA10143 by Computational Design

[0084] Homology models of the B12GT encoded by pA10143 were used as input to computational designs to improve pA10143. Computational designs were conducted to improve the stability and expression of the B12GT. Ninety-three computational designs were chosen for experimental validation (SEQ ID NOs: 223-315). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several variants showed improved expression and/or Reb D conversion compared to the parent pA10143 (18 % conversion, 39 uM purified protein; Table 3).

10
15

Table 3. Top Computational Designs of pA10143

ID	% Conversion	Purified Conc (uM)
pA29938	60.5	79.2
pA29923	44.5	24.6
pA29955	34.5	48
pA29979	34.4	56.4
pA29977	25.9	68
pA29983	25.7	65.3
pA29920	25.3	21.3
pA29932	25	74.1
pA29934	22	54.6
pA29939	21.8	38.5
pA29953	18.4	42.7
pA29918	16.1	119.5
pA29984	14	32.6
pA29967	13.3	38.2

pA30006	12.7	10
pA29957	11.2	22.5
pA29963	10.4	23.2
pA29944	9.5	64.5
pA29961	9.1	28
pA29916	8	35.5
pA29949	7.9	36.4
pA29966	7.9	22.8
pA29951	7.8	45.6
pA30008	7.7	7.6
pA29921	7.4	15.2
pA29981	7.1	39.8
pA29973	6.7	33.2
pA29995	5.2	61.9
pA29985	5	65.1
pA29969	4.8	22.6
pA29950	4.8	46.2
pA29931	4.7	22.5
pA29968	4.6	51.1
pA29933	4.6	8.6
pA30007	4.6	8
pA29917	4.5	26.6
pA29992	4.4	37.7
pA29978	4.4	44.6
pA29960	4.3	19
pA29986	4.3	17.5
pA29919	3.8	14.3
pA29942	3.7	43.3
pA29954	3.6	10.8
pA29970	3.5	13.4
pA29996	3.4	39.8
pA29922	2.9	13.2

pA29990	2.7	35.5
pA29926	2.5	81
pA29991	2.4	52.8
pA29964	2.3	14
pA29987	2.2	67.6
pA29937	2.1	10.4
pA29925	1.5	21.9
pA30003	1.5	30.4
pA29952	1.4	9.1
pA29941	1.4	9.8
pA29993	1.3	55.7
pA29971	1.3	11.1
pA29998	1.2	32.3
pA29935	1.2	14.6
pA30005	1.2	6.5
pA30001	1	37.6
pA29945	1	7.7
pA29962	1	6.3
pA29948	1	9.8
pA29980	0.9	14
pA29959	0.9	38.5
pA29976	0.8	17.8
pA29927	0.7	12
pA29989	0.7	35.3
pA29946	0.6	9.8
pA29928	0.6	39.5
pA29947	0.6	8.9
pA29924	0.4	130.4
pA29972	0.4	56.6
pA30009	0.3	6.4
pA29982	0.3	33

[0085] Computational designs of pA10143 were also conducted to improve the stability and expression of the B12GT using coevolutionary information. Sixty computational designs were chosen for experimental validation (SEQ ID NOs: 316-375). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Computational design variants showed improved expression and/or Reb D conversion compared to the parent pA10143 (4.7% conversion, 35 uM purified protein; Table 4).

Table 4. Top Computational Designs of pA10143

ID	% Conversion	Purified Conc (uM)
pA29711	6.7	45.4
pA29743	5.9	18.6
pA29733	5.6	27.8
pA29734	5.1	5.4
pA29713	3	20
pA29717	2.3	41.6
pA29729	2.1	12.4
pA29745	2.1	40.2
pA29741	1.6	27.7
pA29742	1.5	7.5
pA29723	1.3	30.4
pA29763	1.3	24.7
pA29719	1.1	29.3
pA29747	0.9	34.4
pA29735	0.9	21.1
pA29765	0.8	23.7
pA29740	0.8	12.5
pA29707	0.7	36.8
pA29751	0.7	28.3
pA29720	0.7	23.2
pA29705	0.7	38

pA29715	0.7	30
pA29760	0.7	18.2
pA29721	0.6	11.3
pA29757	0.5	27.6
pA29749	0.5	16.1
pA29709	0.5	45.5
pA29710	0.4	6.4
pA29759	0.4	24.5
pA29712	0.4	4.5
pA29764	0.4	0.6
pA29744	0.4	26
pA29736	0.4	24.8
pA29727	0.4	21.2
pA29737	0.4	31.1
pA29738	0.4	9.6
pA29725	0.4	19.8
pA29728	0.3	17.6
pA29731	0.3	3.2
pA29752	0.3	26.6
pA29718	0.3	3.4
pA29753	0.3	36.6
pA29746	0.2	3.6
pA29730	0.2	1.9
pA29750	0.2	1.6
pA29748	0.2	2.7
pA29722	0.2	ND
pA29756	0.1	1.7
pA29724	0.1	ND
pA29761	0.1	35.3
pA29708	0.1	1.7
pA29758	0.1	6.9
pA29732	0.1	ND

[0086] Computational designs of pA10143 were also conducted to combine active site mutations. Nine computational designs were chosen for experimental validation (SEQ ID NOs: 376-384). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. The top design, pA32576, showed activity comparable to the parent pA10143 (21% conversion; Table 5).

[0087] Table 5. Top Computational Designs of pA10143

ID	% Conversion	Purified Conc (uM)
pA32576	20.1	63.1
pA32568	0.9	20
pA32572	0.7	21.8
pA32569	0.7	25.2
pA32571	0.6	18.7
pA32570	0.6	24.5
pA32573	0.5	24.3
pA32567	0.5	21.7
pA32574	0.3	14.7

[0088] Computational designs of pA10143 were also conducted to combine additional mutations. Seventy-five computational designs were chosen for experimental validation (SEQ ID NOs: 385-459). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Computational design variants showed Reb A to Reb D conversion (Table 6).

Table 6. Top Computational Designs of pA10143

ID	% Conversion	Purified Conc (uM)
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pA33106	3.9	9.4
pA33091	2.7	11.8
pA33123	2.2	10.2
pA33137	1.1	57.5
pA33154	0.7	15.8
pA33149	0.6	14.7
pA33088	0.6	13.4
pA33086	0.5	17.3
pA33110	0.5	19.7
pA33083	0.2	21.9
pA33085	0.1	15.3
pA33165	0.1	17.2

Example 10: Improved Activity of pA12549 by Computational Design

- 5 [0089] Homology models of the B12GT encoded by pA12549 were used as input to computational designs to improve pA12549. Computational designs of pA12549 were conducted to combine active site mutations known to be beneficial in homologous B12GTs. Eight computational designs were chosen for experimental validation (SEQ ID NOs: 460-467). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 0.5 mg/mL RA99, 10 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer, 3.0 mM MgCl₂ and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several variants showed improved expression and/or Reb D conversion compared to the parent pA12549 (Table 7).

Table 7. Top pA12549 Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32563	12.7	9.2
pA32562	8	6.8
pA32565	6.5	38.9
pA32560	4.6	10.1

pA32566	4.5	11.2
pA32558	3.6	11.6
pA32559	1.7	12.1

[0090] Computational designs of pA12549 were also conducted to combine mutations known to be beneficial in homologous B12GTs. Sixty-seven computational designs were chosen for experimental validation (SEQ ID NOs: 468-534). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with the SuSy, pA10142. The purified B12GT and SuSy were reacted with 0.5 mg/mL RA99, 10 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. One computational design variant showed an improvement in Reb A to Reb D conversion (Table 8).

Table 8. Top pA12549 Computational Designs

ID	% Conversion	Purified Conc (uM)
pA33202	25.2	11.4
pA33194	6.6	16.7
pA33196	5.3	14.1
pA33236	4.8	14.1
pA33200	4.2	8.8
pA33223	3	6.1
pA33177	1.9	9.9
pA33217	1.8	22.7
pA33205	1.7	10.6
pA33229	1.3	11
pA33176	1	16.7
pA33235	0.9	14.4
pA33174	0.5	15.2
pA33185	0.5	15.3
pA33171	0.5	15.8
pA33173	0.5	9.5
pA33220	0.4	7.8
pA33204	0.4	11.3

pA33180	0.3	10.5
pA33186	0.3	5.9
pA33172	0.3	13.7
pA33179	0.3	11.7
pA33175	0.2	10.8
pA33182	0.2	15.1
pA33232	0.2	18

Example 11: Improved Activity and Expression of the SUS1 from *Arabidopsis thaliana* by Computational Design

- 5 [0091] The crystal structure of SUS1 from *Arabidopsis thaliana* was used as input to computational designs to improve pA10142. Computational designs were conducted to improve the stability and expression of the SuSy. Thirty-five computational designs were chosen for experimental validation (SEQ ID NOs: 890-924). Expression plasmids for the computational designs were built as in *Example 1*. Each SuSy variant was expressed and purified as in *Example 2*.
- 10 Each SuSy variant was assayed in a one-pot reaction with the B12GT, pA10143. The purified B12GT and SuSy were reacted with 4 mg/mL RA50, 40 mM Sucrose, and 1 mM ADP in 50 mM pH 7 phosphate buffer and 50 mM NaCl for 24 hours at 30 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several variants showed improved expression and/or Reb D conversion compared to the parent pA10142. The top designs showed up to a 2-
- 15 fold improvement in yield and 3-fold improvement in expression (43% conversion, 8 uM purified protein; Table 9).

Table 9. Top Computational Designs of pA10142

ID	% Conversion	Purified Conc (uM)
pA33271	79.8	23.2
pA33264	79.7	11.3
pA33276	79	17.5
pA33273	78.1	11.2
pA33272	77.9	8.8
pA33279	77.6	24.6
pA33281	76.6	18.8
pA33248	76.4	32.9

pA33263	76.3	19.8
pA33285	75.9	17.2
pA33247	75.4	26.6
pA33261	74.5	12.1
pA33240	74	20.5
pA33262	74	21
pA33260	72.7	8.8
pA33259	71	23.7
pA33280	70.2	26.1
pA33267	70	20
pA33282	70	21.7
pA33269	68.3	12.5
pA33242	65.5	17.6
pA33254	64.8	15.9
pA33241	62.8	22.8
pA33274	57.8	8.6
pA33270	57.1	12.2
pA33244	45.7	26
pA33278	44.8	9.4
pA33258	42.3	25.1
pA33286	38.1	13
pA33249	26.4	16
pA33246	20.8	24.5
pA33250	16.8	15.1
pA33253	10.6	2.8
pA33255	1.6	11.2
pA33252	0.3	4.5

Example 12: Computational Design of ADP-Glucose Dependent B12GTs

[0092] Structural models of a B12GT variant of pA28422 were generated and used as the starting point for computational designs. Computational designs were conducted to improve the

5 stability and expression of the B12GT. Fifty-two computational designs were chosen for ex-

perimental validation (SEQ ID NOs: 535-586). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, 3 mM MgCl₂ and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 10).

Table 10. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA29798	76.1	57.3
pA29781	67.1	51.9
pA29807	64.9	17.9
pA29795	61.7	64.8
pA29796	57.8	74.3
pA29771	54.3	49.3
pA29775	53.6	67
pA29770	45	61
pA29808	43.4	95.1
pA29774	42.8	86.8
pA29784	38.5	44.1
pA29767	33.8	37
pA29801	16.9	74.7
pA29779	13	39.6
pA29773	12	49.7
pA29800	9.4	95.8
pA29799	9.3	39.7
pA29789	8.7	75.8
pA29804	7.9	88.1
pA29797	7.4	69.3
pA29806	7	77.9
pA29769	6.4	37.9
pA29787	5.2	68.6
pA29805	4.8	38.4

pA29817	3.3	37.3
pA29790	3.2	77.5
pA29802	3.1	35.8
pA29792	3	71.7
pA29816	2.2	30.9
pA29782	2.1	58.1
pA29809	1.9	56.5
pA29780	1.6	57.3
pA29783	1.3	41.3
pA29811	1	77.4
pA29813	1	37.3
pA29794	0.7	32.8
pA29785	0.6	19.6
pA29814	0.4	21.4
pA29791	0.4	17.5
pA29788	0.4	7.7
pA29812	0.1	44.6
pA29776	0.1	37.8

[0093] Computational designs were also conducted to improve the stability and expression of the B12GT using coevolutionary information. Eighty-five computational designs were chosen for experimental validation (SEQ ID NOs: 587-671). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, 3 mM MgCl₂ and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 11).

Table 11. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA29620	92.6	93.7
pA29619	91.8	29.7

pA29665	90.5	142.7
pA29621	88.7	62
pA29661	87	29.4
pA29618	82.5	77.7
pA29660	56	7.6
pA29615	54.4	191.9
pA29616	53.8	123
pA29646	40.4	60.8
pA29617	34.7	150.1
pA29642	32.3	71.3
pA29636	24.9	28.1
pA29662	22.7	12.4
pA29639	21.9	49.3
pA29669	21.4	60.3
pA29625	21.2	11.4
pA29632	20.9	94.1
pA29676	18.7	74.5
pA29664	18.5	19.7
pA29640	16.7	37.6
pA29683	13.2	19.9
pA29672	12.9	19
pA29624	12.7	66.8
pA29638	12.2	29.4
pA29671	11.8	12.6
pA29675	10.9	23
pA29650	9.9	18.9
pA29677	9.2	48.8
pA29657	8.5	11.8
pA29668	8.5	74.8
pA29666	8.1	108
pA29630	7.7	20.7
pA29652	7.1	11.2

pA29623	7	25.3
pA29667	6.7	67.9
pA29684	6.5	105.2
pA29678	6.4	15
pA29654	6.1	22.2
pA29685	5.8	91.7
pA29634	5.2	47.7
pA29627	4.9	26.6
pA29682	4.9	82.9
pA29622	4.8	68.4
pA29659	3.9	31.1
pA29635	3.9	29.1
pA29648	3.5	10.1
pA29633	3.4	9.7
pA29673	3.3	50.6
pA29626	3.2	26.5
pA29680	3	18.6
pA29679	1.9	15.2
pA29681	1.9	106.5
pA29631	1.6	34.9
pA29637	1.6	77.7
pA29687	0.9	44
pA29695	0.7	56.4
pA29690	0.7	36.3
pA29686	0.4	24.8
pA29689	0.4	52.7
pA29628	0.4	5.2
pA29688	0.4	11
pA29629	0.3	102.1
pA29696	0.2	31
pA29703	0.2	29
pA29698	0.1	43.9

[0094] Computational designs were also conducted to improve the stability and expression of the B12GT by redesigning and repacking buried protein cores. Thirty-five computational designs were chosen for experimental validation (SEQ ID NOs: 672-706). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, 3 mM MgCl₂ and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 12).

[0095] Table 12. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA30048	86.4	96.8
pA30047	50.9	106.7
pA30027	48.7	168
pA30050	35.9	185.3
pA30037	26.7	95.9
pA30019	24.4	93.4
pA30034	23.5	69.8
pA30028	14.1	229.9
pA30031	13.8	9.6
pA30036	13.3	107.1
pA30017	12.9	68.2
pA30040	8.5	48.2
pA30049	8.3	209.7
pA30032	8.3	7.6
pA30039	7.3	92.1
pA30042	4.8	60.4
pA30029	4.5	141
pA30035	3.6	21.6
pA30026	3	158.6
pA30030	2.8	280.3

pA30041	2.2	69.1
pA30025	1.9	74.8
pA30045	1.9	70
pA30046	1.4	103.1
pA30018	1.2	38.5
pA30038	1.1	94.4
pA30015	0.8	13.3
pA30020	0.7	69.8
pA30023	0.7	128.2
pA30016	0.3	16.3
pA30033	0.2	16.8

[0096] Computational designs were also conducted to improve the B12GT by combining mutations known to be beneficial in homologous B12GTs. Fifty-nine computational designs were chosen for experimental validation (SEQ ID NOs: 707-765). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 13). To distinguish between the top designs, they were re-assayed at lower protein concentrations (Table 14).

[0097] Table 13. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32962	92.3	95.6
pA32940	91.9	122.6
pA32945	91.3	74.5
pA32947	91.2	80

pA32952	90.9	83.3
pA32941	90.8	114.3
pA32946	90.7	75.8
pA32943	90.3	113.7
pA32942	89.4	120.4
pA32939	85.7	115.5
pA32944	77.4	31.6
pA32970	33.4	56.9
pA32960	30.3	12.6
pA32956	30.1	44.1
pA32951	27.5	81.2
pA32966	26.2	31.6
pA32967	12.6	64.9
pA32954	8	111
pA32950	6.6	48.2
pA32949	6.5	16.7
pA32978	5.1	33.9
pA32971	4.1	19.6
pA32988	3.9	18.7
pA33004	3.4	15.1
pA32987	3.3	17.6
pA32981	3.1	32.8
pA32958	2.7	26.6
pA32959	2.2	20.2
pA32963	1.8	13.4
pA32953	1.7	97
pA32973	1.3	64
pA32948	1.2	10.9
pA32965	1.2	7.6
pA32957	0.8	14.7
pA32955	0.7	19.1
pA32998	0.7	30

pA33001	0.7	12.8
pA32982	0.3	16
pA32997	0.2	32.2
pA33002	0.2	14.2

Table 14. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32947	82	89
pA32941	81.4	154
pA32940	78.3	120
pA32946	77.8	85.5
pA32962	60	96.1
pA32945	59.4	65.7
pA32943	55.3	102.9
pA32939	42	150.1
pA32942	40.5	96
pA32952	39.6	120.2
pA32944	28.5	31.4
pA32960	17.3	9.4
pA32966	15.5	52.8
pA32951	13	104.5
pA32970	11.3	44.3
pA32956	10.1	33.5
pA32967	6.4	56.9
pA32949	5.8	9.5
pA32950	4.6	45.5
pA32954	3.3	115.2

Example 13: Computational Design of ADP-Glucose Dependent B12GTs

- 5 [0098] Structural models of a second B12GT variant of pA28422 were generated and used as the starting point for computational designs. Computational designs were conducted to improve the B12GT by combining mutations known to be beneficial in homologous B12GTs. Sixty-four computational designs were chosen for experimental validation (SEQ ID NOs: 766-829).

Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 15). To distinguish between the top designs, they were re-assayed at lower protein concentrations (Table 16).

Table 15. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA33014	91	55.4
pA33009	90.8	39.3
pA33008	90.1	74.5
pA33016	89	64
pA33020	57.3	72.7
pA33007	52.7	31.9
pA33012	44.3	51.6
pA33019	40.2	143.3
pA33011	24.9	93.2
pA33043	20.5	59.7
pA33018	16	79.5
pA33005	14.3	26.9
pA33056	13.3	14.4
pA33015	9.4	29.2
pA33030	5.2	48.4
pA33006	4.9	37.5
pA33038	4.3	40.1
pA33010	3.1	49.7
pA33029	1.9	95.4
pA33065	1.8	32.1
pA33017	1	64.8
pA33025	0.8	29.3
pA33057	0.8	25.5

pA33031	0.4	19
pA33077	0.4	38.2
pA33069	0.3	25
pA33070	0.2	32
pA33078	0.1	37.5
pA33035	0.1	18.8
pA33068	0.1	46.5

Table 16. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA33008	88.7	37.4
pA33009	85.4	28.3
pA33016	71.5	25.4
pA33007	49.5	10.2
pA33014	41.7	54.1
pA33020	28.3	77.3
pA33005	27.9	16.2
pA33012	21.7	55
pA33019	19.9	120.2
pA33056	16.9	3.7
pA33011	15	58.3
pA33043	14.7	19.3
pA33018	10.4	52
pA33015	6.2	11.5
pA33006	3.9	15.1
pA33030	3	33.8

Example 14: Representing Successful B12GTs Designs with a PSSM

- 5 [0099] The successful B12GT designs from *Example 12* and *Example 13* were used to generate a PSSM (Table 17). The PSSM is a concise way to represent the successful designs and related sequences. Sequences that have a PSSM score greater than 266.7 are considered related to the active computational designs described in *Example 12* and *Example 13*. To score a sequence with the PSSM, it must first be aligned with the representative sequence Seq ID No: 5.

For example, the following successful designs, pA29646, pA32946, pA29642, pA29798, have the following PSSM scores: 287.2, 288.0, 279.2, 276.8, while the wild-type B12GT pA28422, has a PSSM score of only 257.4.

[00100] Table 17. Position Specific Scoring Matrix (PSSM) of Successful B12GT Designs

Seq Pos	Amino Acid																			
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	0	1	0	1	0	0.6	0	0	0	0	0	0	0	0	1	1	1	0	0	0
2	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	0.6	0	0	0
3	0	0	0	0	0	1	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0
4	0	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6
6	1	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0.6	0	0	1
7	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0	0	0	0	0	1
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
11	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
12	0.6	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6
17	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
19	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	1	0
20	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
21	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	0	0	0	1
23	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0.6	0	0	0	0	0	1	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0.6	0	1	0	0	0	0	0	0	0

27	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0.6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
29	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	1	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	0	0	1	0.6
33	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1
34	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6	0
35	0	0	0	0	0	0	0	0	0	0	0.6	0	1	0	0	0	0	0	0	1
36	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.6
37	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0
39	0.6	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1
41	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
42	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
43	0	0	1	0	0	0	0.6	0	0	0	0	1	0	0	0	1	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0.6	0	0	0	0
45	1	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	1	0	0	0
46	0	1	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	1	1	0	0	0.6	0	0	0	0	0	0	0	0
48	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	1	0	0	0
51	0	0	1	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	1	0
52	1	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
54	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0.6	0	0	0	1
55	0	0	0.6	1	0	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	0
57	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
58	0	0	0	0	0	1	1	0	0.6	1	0	0	0	0	0	0	0	0	0	0

59	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
60	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6
61	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0
62	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	1	0	0	1	1
63	0.6	0.6	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0
64	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
66	0	0	0	0	0	1	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0
67	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
69	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
70	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0
73	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1	0
74	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.6	0
75	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	1	0	0
76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0
77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0
78	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
79	1	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
80	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
83	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
84	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
85	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
86	0	0	0	0	0	0	0	0.6	0	0	0	0.6	0	0	0	0	0	0	0	0
87	0	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0.6	0	0	1
88	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
89	0	1	0	0	0	1	0	0	0.6	1	0	1	0	0	0	0	0	0	0	0
90	0	1	0	0	0	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0

91	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
92	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	1
93	0	1	0	0	0	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0	0	0	0	0
95	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
96	0.6	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
98	0	0	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
99	0	0	0	0	0	0	0	0	0	1	1	0	0	0.6	0	0	0	0	0	1
100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
101	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
102	0	0	0	0	0	1	0	0	0	0.6	1	0	0	0	0	0	1	0	0	1
103	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	1
104	0	1	0	0	0	0.6	1	0	0	0	0	1	0	0	0	1	0	0	0	0
105	1	0	0.6	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
106	0	0	0	0	0	0	0	0	0	0.6	0.6	0	0	0	0	0	0	1	0	0
107	0	0	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
108	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	1
109	1	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
110	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
111	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.6
112	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	1
113	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0.6	1
114	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	0	0	0	0	0	0	0	0	0	1	1	0	1	0.6	0	0	0	0	0	0
116	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
117	1	0	0	0	0	0.6	0	0	0	1	1	0	0	0	0	0	0	0	0	0.6
118	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
120	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
121	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	1	0	0	0	0
122	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0

123	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0.6	0
124	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
125	0	0	1	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	0	0	0	0
126	0	0	0	1	0	0	0.6	0	0	0	0	0	0	0	0	1	0	0	0	0	0
127	0	1	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
128	0	0	1	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
129	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1	0
130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
131	0.6	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0
132	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6	0
133	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0
135	1	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	1	0	0	0
136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0	0	0
138	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
139	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
140	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0	0	0	1	0	0	0
143	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
145	0	0	0	0	0	0	0	0	0	1	1	0	0	0.6	0	0	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	1	0	1	0.6	0	0	0	1	0	1	0
147	0	0	0.6	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	1	0
150	0	1	0	1	0	0	0	0	0	0	0	0.6	0	0	0	0	1	0	0	0	0
151	0	0.6	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0.6	0	0	0	0	0	0
153	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	1	0	0	0	0.6	0	0.6	0	0	0	0	0	0	0	0	0	0	1	0

155	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	1	0	0	0	0	0	0
156	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
157	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0.6	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
160	0.6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
162	0	0.6	0	1	0	0	1	0	1	0	0	1	1	0	0	1	0	0	1	0	0
163	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
164	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
165	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
166	0	0.6	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	1	0	0
167	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
168	0	0	0	0	0	0.6	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
169	1	0	0	0.6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
170	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	1	0	0	0
171	0	0	0	0	0	0	0	0	1	0	1	0	0.6	0	0	0	0	0	0	0	0
172	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
173	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
174	1	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0	0	0	0	0	0
175	0	0	0	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0
176	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
177	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	0
178	1	0	0	0	0	1	0.6	1	0	0	0	0	0	0	0	0	0	0	0	1	0
179	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.6	0	0	0	0	0	0
180	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0.6	0	0.6	0	0	0	0
181	0	0	0	1	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
182	0	1	0	1	0	0	0.6	0	0	0	1	1	0	0	0	0	0	0	0	0	0
183	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
184	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
185	0	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0
186	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

187	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0.6	0	0	0	0	1	0
188	0.6	0	0	0	0	0	0	0.6	0	0	0	0	0	1	0	0	0	0	0	0	0
189	0	1	0.6	0	0	0.6	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
190	0.6	0	1	0	1	0	0	0	0	0	0	1	1	0	0	1	1	0	0	0	0
191	1	0	0	0	0	1	0	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0
192	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	1	0	0
193	0	0	0	0	0	0	0	0	0	1	1	0	0.6	0	0	0	1	0	0	1	0
194	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
195	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0	0	0	0	0	0	1	0
196	0	0	0	0	0.6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0
198	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
199	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0.6	0
201	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	0	0	0	0	0
202	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
205	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
206	0	0	0	0	0	0	0	0	0	1	0.6	0	1	0	0	0	0	0	0	0	0
207	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
209	0	0	0	0	0.6	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
210	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0	1	0.6	0	0	0	0
211	0	0	0	0	0	0	0.6	0	0	0	0	1	0	0	0	0	1	0	0	0	0
212	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	1	0	0	0
213	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0.6	0	0	0	0
214	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
215	0	1	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0.6	0
216	0	0	0	0	0	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
217	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6	0
218	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0

219	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
220	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
221	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
222	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
223	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	1	1	0	0	0	0
224	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	1	1	0
225	0	0	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
226	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0
227	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0.6	0	0	0	0	0	0
228	0	0	1	0	0	0	0	0	0	0	0.6	0	0	0	0	0	1	0	0	1	0
229	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0.6	0	1	0	0
230	0	0	1	1	0	0	0.6	0	0	0	1	0	0	0	0	1	0	0	0	0	0
231	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
232	1	0	1	1	0	0	1	0	0	0.6	1	0	0	0	0	0	0	0	0	0	0
233	0	1	0	0.6	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0
234	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0.6	1	0	0	0	1	0
236	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
237	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
238	0	0	0	0	0	0	0	0	0	0.6	0	0	0.6	0	0	0	0	0	0	0	0
239	0	1	0	0.6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
240	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0
241	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
242	0	0	0	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
243	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	0
244	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
245	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
246	0	0	0	0	0	0	0.6	0	0	0	1	0	0	0	1	0	1	0	0	0	0
247	0	0	0.6	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
248	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0
250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6

251	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0
252	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
253	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
254	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
255	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
257	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
258	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
259	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
260	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
261	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
262	0	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
263	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
264	0	0	0	0.6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
265	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0	0	0	0	0	0
266	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
267	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
268	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.6	0
269	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
270	0	0	0	0	0	0	0	0	1	0	0	0	0	0.6	0	0	0	1	0	0	0
271	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
272	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
273	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	1	0
274	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
275	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
276	0	0	0.6	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
277	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0.6	0
278	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
279	1	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
280	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
281	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.6	0	0	0
282	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0

283	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
284	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
285	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
286	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
287	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
288	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
289	1	1	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	1	0
290	0	1	0	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	0	0	0
291	1	1	0	0	0	0.6	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0
292	0	0.6	0.6	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0
293	1	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
294	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	0	0	0
295	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
296	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
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298	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
299	0	1	0	0	0	0	0	0	0	0	0	0.6	0	0	1	1	0	0	0	0	0
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301	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0
302	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0
303	0	0	0	1	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
304	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
305	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0.6	0
306	0	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
307	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
308	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
309	1	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
310	0	0.6	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0
312	0	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
313	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
314	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0

315	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
316	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6
317	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0
318	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
319	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
320	0	0	0	0	1	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
321	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
322	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
323	0	0	0.6	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
324	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
325	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6	1	0	0	0	0
326	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
327	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.6	0	0	1
328	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
329	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
330	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
331	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0	1
332	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
333	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
334	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
335	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
336	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0
337	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
338	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
339	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0.6
340	0	0	0	0	0	0	0	0	0	0	1	0	0.6	0	0	0	0	0	0	0
341	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
342	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
343	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	0	0	0	0
344	0	0	0	0.6	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
345	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
346	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0

347	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
348	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0
349	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
350	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
351	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
352	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
353	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
354	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
355	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
356	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0
357	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
358	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
359	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0
360	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0
361	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
362	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
363	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
364	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
365	0	0	0	0	0	0	0	0	0	1	0.6	0	1	0	0	0	0	0	0	1	0
366	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
367	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
368	0	0	0	0	0	0	0	0	0	0	0.6	0	1	0	0	0	0	1	0	0	0
369	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
370	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.6	0
371	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0
373	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
374	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	1	0
375	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0.6	0
376	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
377	0	1	0	0.6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
378	0	0	0	1	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0

379	0	0	1	0.6	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
380	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
381	0	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
382	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0.6
383	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	1	0	0	0	0	0
384	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
385	0.6	0	1	1	0	0	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0
386	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
387	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
388	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
389	0	0.6	0	0	0	0.6	1	0	0	0	0	1	0	0	0	0	0	0	0	0
390	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6
391	0	0	0	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	1
392	0	1	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
393	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
394	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6
395	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	0	0	1
396	0	0	1	0	1	0	0	1	0	0	0	0	0	1	0	0.6	1	0	0	1
397	0	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0
398	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0.6	0	0	0	0	0
399	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0.6	0	0	0
400	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0
401	0	0	0	0	0	1	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0
402	0	0	1	0	0	0	1	0	0	0.6	0	1	0	0	0	0	0	0	0	0
403	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0
404	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
405	0.6	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0
406	0	0	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
407	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.6
408	1	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
409	0	0	0	0.6	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
410	0	0	0	0	0	0	0	0	0	0.6	1	0	0	0	0	0	0	0	0	0

411	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.6	0	0	0	0	0
412	0.6	1	0	0	0	0	1	0	0	0	1	0.6	0	0	0	0	1	0	0	0	0
413	0	0.6	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
414	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	1	0	0	0
415	0	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
416	0.6	1	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0
417	1	0.6	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0
418	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
419	0	0	1	1	0	0	0.6	1	0	0	0	1	0	0	0	0	0	0	0	0	0
420	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	1	0	0	0	0	1	0
421	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
422	0	0	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0
423	0	0	0.6	1	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
424	0.6	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
425	0.6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
426	0.6	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
427	0	0	0	0	0	0	0.6	0	0	0	1	0	0	0	0	0	0	0	0	0	0
428	1	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
429	0	0	0	0	0	0	0	0	0	0	0.6	0	0	1	0	0	0	0	1	0	0
430	0	0	0	0	0	0	0	0	0	0.6	1	1	1	0	0	0	0	0	0	0	0
431	1	1	0	0	0	0.6	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0
432	0	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	0	0	0
433	0	0	0	0	0.6	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
434	0	0.6	0	0	0	1	0	0	1	0	0	1	0	1	1	0	1	0	1	1	0
435	0	0	0.6	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0
436	0	0.6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
437	1	1	0.6	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
438	0.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
439	1	0	0	0	0	0	0	0	0	0	1	1	0	1	0	1	1	0	0.6	0	0
440	0	0	1	0	0	0	0	0	0	0	0	0.6	0	0	0	0	0	0	0	1	0

Example 15: Computational Design of ADP-Glucose Dependent B12GTs

[00101] Improved B12GTs were designed by using the designed B12GTs from *Example 12* and *Example 13* as starting scaffolds for further design rounds. Computational design methods were used to improve the stability and expression of seven B12GTs from *Example 12* and *Example 13*. One hundred thirty-four computational designs were chosen for experimental validation (SEQ ID NOs: 1333-1466). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of pA21838. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 18).

Table 18. Computational Designs of Improved B12GTs

ID	% Conversion	Purified Conc (uM)
pA35535	42.8	38.1
pA35532	38.9	27.1
pA35534	37.9	44.6
pA35594	36	12.7
pA35536	35.5	65.5
pA35568	33.5	25
pA35531	33	20.7
pA35574	32.5	42.4
pA35526	31.8	13.6
pA35565	31.8	28.5
pA35576	30	13.5
pA35564	28.9	23.8
pA35575	25.6	22.3
pA35525	22.7	10.5
pA35511	22.4	42.9
pA35562	20.6	43.2
pA35508	19.2	92.7
pA35561	18.3	37.3
pA35503	18.1	86.4

pA35533	17.6	56.9
pA35522	17.1	13.2
pA35530	16.9	38.6
pA35613	16.5	11.8
pA35515	13.4	66.4
pA35507	12.1	76.3
pA35510	11.9	33.2
pA35516	11.8	57.7
pA35506	11.5	63.3
pA35513	11.1	48.3
pA35514	9.8	65.8
pA35592	8.5	18.4
pA35563	8.2	32.9
pA35593	8.1	6
pA35567	7.2	49.1
pA35614	6.5	9
pA35501	6.3	69.1
pA35496	6.1	36.6
pA35598	5.9	8.4
pA35502	5.9	69.7
pA35493	5.6	40.5
pA35570	5.6	25.5
pA35497	5.4	27.3
pA35509	5.4	53.2
pA35495	5.4	40.9
pA35499	5.2	67.2
pA35517	5.1	6.4
pA35569	5	47
pA35505	4.8	97.3
pA35528	4.7	14.1
pA35490	4.6	68.8
pA35603	4.5	10.1

pA35487	4.4	44.9
pA35498	4.4	31.1
pA35584	4.3	17.6
pA35566	4.3	47.6
pA35492	4.2	55
pA35527	4.1	11.8
pA35518	3.9	5.7
pA35520	3.8	2.6
pA35529	3.7	13.5
pA35504	3.6	50.1
pA35484	3.6	13.9
pA35489	3.6	36.2
pA35548	3.6	5.4
pA35571	3.5	27.6
pA35524	3.5	3.1
pA35488	3.5	36
pA35483	3.5	14.8
pA35543	3.5	2.9
pA35541	3.5	3.6
pA35482	3.5	16.2
pA35500	3.4	46.5
pA35546	3.4	2.2
pA35545	3.4	4.1
pA35494	3.4	44.3
pA35519	3.4	3.1
pA35491	3.3	44.5
pA35604	3.3	6.9
pA35521	3.3	4.4
pA35542	3.3	3.9
pA35486	3.2	31.2
pA35547	3.2	2.1
pA35544	3.1	4.2

pA35523	3.1	1.8
pA35481	3.1	18.4
pA35537	3	0.8
pA35485	3	31.3
pA35538	3	2.1
pA35540	2.8	3.2
pA35559	2.7	14.6
pA35539	2.7	3.9
pA35557	2.7	25
pA35581	1.5	24.3
pA35560	1.4	40.5
pA35512	1.1	24
pA35588	1.1	16.5
pA35580	1.1	6.8
pA35589	0.9	2.8
pA35591	0.8	16.6
pA35587	0.6	10
pA35556	0.5	16.5
pA35602	0.4	3.8
pA35586	0.4	13.2
pA35590	0.4	16.2
pA35553	0.4	9.9
pA35555	0.2	15.9
pA35558	0.2	30.4

Example 16: Computational Design of ADP-Glucose Dependent B12GTs

[00102] Structural models of a third B12GT variant of pA28422 were generated and used as the starting point for computational designs. Computational designs were conducted to improve the stability and expression of the B12GT. Fifty-three computational designs were chosen for experimental validation (SEQ ID NOs: 830-882). Expression plasmids for the computational designs were built as in *Example 1*. Each B12GT variant was expressed and purified as in *Example 2*. Each B12GT variant was assayed in a one-pot reaction with a SuSy variant of

pA21838. The purified B12GT and SuSy were reacted with 10 mg/mL RA50, 100 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, 3 mM MgCl₂ and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 19).

[00103] Table 19. Top B12GT Computational Designs

ID	% Conversion	Purified Conc (uM)
pA29846	21	11.3
pA29856	20	27.6
pA29850	19.6	28.9
pA29870	13.6	18.2
pA29845	13.5	20.1
pA29823	10.6	0.6
pA29847	9.7	12.1
pA29822	8.7	20.7
pA29837	8.4	-3.1
pA29848	7.6	54
pA29829	7	9.1
pA29821	6.4	5.7
pA29828	6.1	3.8
pA29859	5.3	12.6
pA29853	4.7	29.8
pA29824	4.3	10.5
pA29854	3.9	16.9
pA29852	3.7	
pA29836	3.4	0.5
pA29839	3.1	2
pA29864	2.9	75.3
pA29860	2.8	44.5
pA29831	0.7	20.3

Example 17: Computational Design of ADP Dependent Sucrose Synthases

[00104] Structural models of two SuSy variants of pA21838 were generated and used as the starting point for computational designs. The design strategies used to design ADPG-dependent B12GTs were used to design improved ADP dependent sucrose synthases. Two hundred and fifty-six computational designs were chosen for experimental validation (SEQ ID NOs: 925-1180). Expression plasmids for the computational designs were built as in *Example 4*. Each SuSy variant was expressed and purified as in *Example 5*. Each SuSy variant was assayed in a one-pot reaction with a B12GT variant of pA28422. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, 3 mM MgCl₂ and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. The relative expression and Reb A to Reb D conversion of the designed enzymes, SEQ ID: 925-1048, are shown in Table 20. The relative expression and Reb A to Reb D conversion of the designed enzymes, SEQ ID: 1049-1104, are shown in Table 21. The top hits from the previous two experiments were re-evaluated with more relevant protein concentrations (Table 22). Finally, the relative expression and Reb A to Reb D conversion of the designed enzymes, SEQ ID: 1105-1180 are shown in Table 23.

Table 20. Top SuSy Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32819	11.9	15.5
pA32719	11.7	22.2
pA32712	11	13.6
pA32667	10.5	22.7
pA32602	9.9	19
pA32854	9.9	26.9
pA32924	9.9	18
pA32858	9.6	30.2
pA32732	9.6	31.1
pA32652	9.6	23.5
pA32582	9.5	32.3
pA32692	9.5	35.4
pA32657	9.2	13.2
pA32734	9.2	26.3
pA32821	9.1	25.3
pA32704	9.1	20.9

pA32601	9	15
pA32706	8.8	28
pA32721	8.6	20.6
pA32614	8.5	23.8
pA32684	8.5	26.7
pA32736	8.3	33.2
pA32609	8.3	30.3
pA32926	8.3	19.5
pA32639	8.2	13.1
pA32655	8.1	64.4
pA32696	8.1	30.3
pA32855	8	30.2
pA32704	7.9	19.4
pA32820	7.9	20.1
pA32651	7.9	8.4
pA32819	7.7	10.6
pA32697	7.7	11.2
pA32602	7.6	19.4
pA32723	7.5	59
pA32625	7.5	27.1
pA32678	7.4	51.5
pA32622	7.3	15
pA32731	7	5.4
pA32629	6.9	11.8
pA32700	6.7	24.4
pA32608	6.6	26.4
pA32708	6.4	9.3
pA32686	6.2	15
pA32698	6	28.6
pA32589	5.9	35.5
pA32680	5.8	22.3
pA32586	5.7	22.8

pA32700	5.7	28.6
pA32606	5.6	24.6
pA32620	5.6	15.6
pA32596	5.5	54.2
pA32616	5.4	39
pA32696	5.4	66.8
pA32600	4.8	29.4
pA32669	4.7	56.5
pA32682	4.6	33.2
pA32845	4.2	17.1
pA32868	4.1	9.6
pA32715	4.1	27.5
pA32650	3.8	29.7
pA32620	3.6	16.4
pA32690	3.6	15
pA32716	3.5	37.9
pA32702	3.5	13.2
pA32863	3.4	10
pA32605	3.2	29.1
pA32595	2.9	41.2
pA32847	2.6	8.8
pA32594	2.5	23.5
pA32670	2.4	24.7
pA32675	2.2	28.8
pA32880	2.1	11.5
pA32837	2.1	19.6
pA32702	2.1	12.4
pA32688	2	22.8
pA32591	1.9	47.5
pA32662	1.9	23.6
pA32701	1.7	21.9
pA32758	1.5	19.7

pA32603	1.5	57.3
pA32671	1.2	15.6
pA32671	1.1	22.4
pA32842	0.9	5.5
pA32781	0.9	10
pA32934	0.9	15.3
pA32831	0.9	7.6
pA32793	0.8	7.4
pA32662	0.8	15.2
pA32701	0.8	23.3
pA32717	0.8	30.7
pA32748	0.8	28.3
pA32672	0.7	32.3
pA32826	0.7	2
pA32816	0.7	13.6
pA32664	0.7	9.7
pA32754	0.6	22.6
pA32666	0.6	46
pA32770	0.5	11.7
pA32779	0.5	8.3
pA32844	0.5	6.4
pA32665	0.4	21
pA32659	0.4	25.1
pA32799	0.3	33.5
pA32790	0.2	22.6
pA32787	0.2	14.3
pA32623	0.2	13.8
pA32866	0.2	29.3
pA32767	0.2	23
pA32828	0.2	9
pA32876	0.2	5.4
pA32797	0.1	9.6

Table 21. Top SuSy Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32930	89.9	2.7
pA32894	87.3	4.8
pA32892	86	9.6
pA32729	83.3	3.1
pA32732	80.2	3.3
pA32869	78.3	11.8
pA32734	77.3	3.4
pA32646	69.8	5.4
pA32735	53.9	4
pA32652	49.8	2.8
pA32923	47.8	5.5
pA32724	40.5	2.8
pA32722	36.8	1.3
pA32723	36.4	2.7
pA32727	30.5	1.8
pA32653	26.1	3.4
pA32888	25.3	3.9
pA32650	24.3	3.1
pA32868	21.7	2.6
pA32632	20.2	3
pA32634	19.2	2.7
pA32922	18	1.7
pA32765	12.3	2.8
pA32895	12.3	2.8
pA32884	10.9	4.3
pA32880	10.6	3
pA32638	10.2	3.3
pA32751	10.2	1.2
pA32903	9.5	3.3
pA32769	8.9	1.6

pA32871	8.5	2.8
pA32770	7.9	1.3
pA32780	7.9	1.9
pA32754	7.2	1.6
pA32752	6.6	3.8
pA32760	6.4	1.5
pA32775	6.3	2.5
pA32904	6.2	3.2
pA32761	6.2	2.2
pA32793	6	2.1
pA32881	5.7	1.4
pA32902	5.5	3.2
pA32779	5.5	1.7
pA32623	5.4	0.8
pA32918	5.2	4.8
pA32758	5.2	1.3
pA32746	5	3.8
pA32750	4.6	2.1
pA32882	4.6	1.9
pA32747	4.5	5.1
pA32876	4.2	1.2
pA32782	4.1	1.4
pA32767	4	2.2
pA32785	3.9	2.1
pA32749	3.9	3.1
pA32914	3.7	2.2
pA32875	3.7	2.1
pA32917	3.4	2
pA32763	3.2	2.1
pA32737	3.2	1.8
pA32886	3.2	2.4
pA32757	3.2	2.3

pA32743	2.8	3.6
pA32932	2.8	2.8
pA32885	2.8	2.6
pA32865	2.7	1.3
pA32791	2.7	2.4
pA32913	2.6	2.3
pA32742	2.5	1.4
pA32879	2.4	1
pA32738	2.1	3.7
pA32916	1.9	0.9
pA32912	1.7	0.8
pA32906	1.7	3.1

Table 22. Top SuSy Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32821	57.6	39.4
pA32888	54.8	40.1
pA32854	52.3	28.7
pA32858	51.8	55.2
pA32855	47.6	28.8
pA32868	46.4	35.4
pA32924	45.7	25.2
pA32930	45.7	44
pA32926	42.6	31.7
pA32692	41.7	28.5
pA32684	40.8	31.1
pA32819	40.7	19.5
pA32820	40	24.7
pA32731	37.9	67.2
pA32655	37.5	39.4
pA32894	37	48.2
pA32646	36.9	28.8

pA32892	35.9	50.8
pA32629	35.4	12.5
pA32625	34.5	11.4
pA32869	30.9	54.8
pA32732	30.7	83.5
pA32923	28.7	40.4
pA32706	28.7	41.3
pA32719	26.9	47.4
pA32729	26.6	87.8
pA32697	26.4	13.5
pA32652	26.3	37.2
pA32704	23.9	29.1
pA32696	23.3	56.5
pA32712	22.1	22.6
pA32650	21	34.9
pA32639	19.8	14.7
pA32722	18.5	44.1
pA32734	18.1	66
pA32724	17.7	25.7
pA32727	17.7	27
pA32922	17.3	25.2
pA32715	17.1	31.7
pA32845	16.9	7.4
pA32651	16.8	15.4
pA32620	16.1	19.3
pA32602	16	37.9
pA32735	15.5	76.1
pA32667	15	44.6
pA32736	14	59.7
pA32622	14	29.6
pA32708	13.7	9.7
pA32721	13.4	49.5

pA32723	12.8	53.7
pA32698	11.2	23.8
pA32680	10.5	18.6
pA32601	10.5	44.7
pA32586	8	45.5
pA32682	7.2	50.4
pA32582	7.1	55.4
pA32609	6.7	49.5
pA32600	6.6	23.1
pA32608	6.2	41.2
pA32700	6	47.4
pA32686	5.7	23.3
pA32669	5.5	52.3
pA32606	5.5	33.4
pA32589	4.9	74.3
pA32616	4.6	53.3
pA32678	4	70.8
pA32614	3.9	71
pA32657	3.6	18.5
pA32596	2.8	100.6

Table 23. Top SuSy Computational Designs

ID	% Conversion	Purified Conc (uM)
pA32929	86.6	7.5
pA32891	86.3	8.3
pA32853	86.2	13.7
pA32587	86	26.3
pA32887	85	17
pA32725	81.7	24.1
pA32889	79.2	7.2
pA32599	78.5	16.1
pA32633	78	10.8

pA32927	68.1	8.5
pA32691	58.5	17.9
pA32658	49.4	19.7
pA32683	48.3	18.4
pA32931	27.7	11.2
pA32597	24.8	33
pA32579	23.5	20.5
pA32679	21.7	13.3
pA32621	21.7	3.7
pA32581	21.3	19.5
pA32695	17.2	40.2
pA32647	15.8	5.9
pA32637	14.8	18.9
pA32873	11	10.9
pA32585	10.9	13.5
pA32631	10.4	5.4
pA32859	7.7	12.6
pA32619	6.6	5.9
pA32689	6.2	10.9
pA32617	4.9	3.8
pA32613	4.7	25.6
pA32641	4	24
pA32768	3.6	10.9
pA32774	2.9	5.9
pA32778	2.8	4.2
pA32773	2.5	5.4
pA32673	1.9	13.4
pA32843	1.7	3.8
pA32583	1.3	22.1
pA32897	1.1	3.1
pA32610	1	10.2
pA32776	0.7	5.3

pA32849	0.6	10.7
pA32685	0.5	37.1
pA32839	0.5	2.2

Example 18: Representing Successful SuSy Designs with a PSSM

[00105] The successful SuSy designs from *Example 17* were used to create a PSSM (Table 24). The PSSM is a concise way to represent the successful designs and related sequences.

- 5 Sequences that have a PSSM score greater than 556 are considered related to the active computational designs described in *Example 17*. To score a sequence with the generated PSSM, it must first be aligned with the representative sequence pA21838 (Seq ID No: 885). For example, the following successful designs, pA32853, pA32891, pA32892, pA32929, have the following PSSM scores: 557.2, 558.1, 558.1, 557.8, while the wild-type SuSy pA21838, has a PSSM
- 10 score of only 536.3.

Table 24. Position Specific Scoring Matrix (PSSM) of Successful SuSy Designs

Seq Pos	Amino Acid																			
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
4	1	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0.7
5	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
6	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
10	1	1	0	0	0	1	0	0	0	0	0.7	1	0	0	0	1	0	0	0	0
11	0	0	0	0.7	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0
12	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0
13	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
14	0	0.7	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
15	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0.7	1	0	0	0

16	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	1	0
17	0	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
18	0.7	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
21	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0
24	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
25	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0
27	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0.7	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0
30	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	0.7	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0
32	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
33	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0.7	0	0	0	0
35	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
38	0	0.7	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
39	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0.7	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
41	1	0	0	1	0	0	1	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
42	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
43	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
44	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
45	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
47	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0

48	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0
49	0	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0
52	1	0	0	0	0	0	1	1	0	0	1	0	0	0	0.7	0	0	0	0	0	0
53	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0
54	1	0	0	0.7	0	0	0	1	0	0	1	1	1	0	0	0	1	0	0	0	0
55	0	0	0	1	0	0	0	1	0	0.7	0	0	0	0	0	1	1	0	0	0	0
56	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0	0
57	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	1	0
58	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0
59	0.7	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
60	0	1	0	0.7	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
61	1	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	1
62	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0.7	0
63	0.7	1	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0
64	1	1	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0
65	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
66	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
67	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
68	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
69	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	1
70	0	0	0	0	0	0	0	0	0	1	1	0	0	0.7	0	0	0	0	0	0	1
71	0	0.7	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
72	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
75	1	0	0	0	0	0	0	0	0	1	0	0	0.7	1	0	0	0	0	0	0	1
76	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0
77	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0
78	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
79	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0.7	0	1	0

80	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	1	0	0	0	0.7	0	0	0	1	0	0	0	0	0
82	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
83	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1
84	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
85	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
87	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0
88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
89	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0.7
90	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
91	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0	0	0	0
92	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
93	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7
94	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
95	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	1	0	0	0
96	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
97	0.7	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1
98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
99	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
100	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
101	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	1
102	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
103	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1
104	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
105	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
106	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
107	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
108	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
109	0.7	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
110	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
111	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0

112	0	1	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
113	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
114	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
115	0	0	1	1	0	0	0	0.7	0	0	0	1	0	0	0	0	1	0	0	0
116	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0
117	1	0	1	1	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0
118	0.7	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1	0	0	0	0
119	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
120	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
121	0	0	1	1	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0	0
122	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
123	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
124	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	1	1	0	0
125	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0.7	0	0	0
126	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0.7
127	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	1	0	0
129	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0
132	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
133	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
134	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	1	1	0	0	0.7
135	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	1
136	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
137	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
140	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
141	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
142	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0

144	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
145	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
146	0	1	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
147	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1
149	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0
150	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
152	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
153	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
156	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
157	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
159	0	0	0	0	0	0	0	0	0	0.7	1	0	1	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
161	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0
162	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	1	0	0	0
164	0.7	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0
165	0.7	1	0	1	0	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0
166	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0.7	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
168	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0.7	0	0	1	0
169	0.7	1	0	0	0	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
171	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
172	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
173	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0
174	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
175	0	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0

176	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0
177	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
178	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
179	0	0	0	0	0	0	0	0	1	1	0.7	0	0	0	0	0	0	0	1	0
180	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
181	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
182	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
183	0	0	0.7	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
184	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
185	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0
186	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
187	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
188	0	0	0.7	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
189	0	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
190	0	0	0.7	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0
191	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0
192	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
193	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
194	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
195	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0.7	0	0	0	0
196	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
197	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
198	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
199	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1
200	0	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	0.7	0
201	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
203	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
204	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
205	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0.7	0	0	0
206	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
207	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0

208	1	0.7	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0
209	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
210	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
211	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
212	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0
213	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
214	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
215	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	1
216	1	0.7	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0
217	0	0	0	0	0	0	0.7	0	1	0	0	0	0	1	0	0	0	0	0
218	1	1	0	0.7	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0
219	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0
220	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
221	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
222	0	0.7	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0
223	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
224	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
225	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
226	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
227	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
228	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0
229	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
230	0	1	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
232	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
233	1	0	0	0	0	1	1	0.7	0	0	0	0	0	0	0	0	0	0	0
234	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0.7
236	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
237	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
238	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
239	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0

240	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
242	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
243	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	1	0
244	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
245	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
246	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
247	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
248	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
251	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
252	0.7	1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0
253	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
254	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
255	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
256	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0.7	1	0	0	0
257	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
258	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
259	1	0	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
260	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
261	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1
262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
263	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0
264	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
265	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0
266	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
267	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7
268	1	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	1	0	0	1
269	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
270	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7
271	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0

272	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	1	0
273	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
274	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
275	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0
276	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
277	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
278	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
279	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
280	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
281	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
282	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
283	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
284	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
285	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
286	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
287	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
288	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
289	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
290	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
291	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
292	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
293	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0
294	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
295	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
296	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
297	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
298	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
299	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
300	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
301	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
302	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
303	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

304	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
305	0	0	0	0	0	0	0	0	0	1	1	0	0.7	0	0	0	0	0	0	0
306	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
307	0	1	0.7	1	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0
308	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
309	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
310	1	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
311	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
312	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
313	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
314	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7	0
315	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
316	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
317	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
318	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
319	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
320	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
321	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
322	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
323	0.7	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0
324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
325	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
326	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
327	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
328	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
329	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
330	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
331	0	0	0	0.7	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0
332	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
333	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
334	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
335	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

336	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
337	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
338	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
339	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
340	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
341	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
342	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
343	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	1	0	0	0	1
344	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
345	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
346	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
347	0	0	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
348	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
349	0	1	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	1	0	0
350	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
351	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
352	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
353	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
355	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
356	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
357	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
358	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
359	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
360	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
361	0	0.7	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
362	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1
363	0	0	0	0	0	0	0	0	0.7	1	1	0	0	0	0	0	0	0	0	1
364	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
365	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
366	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
367	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0

368	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
369	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
370	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
371	0	1	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
372	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0
373	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
374	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
375	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
376	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
377	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
378	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
379	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0.7	0	0
380	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
381	0	0.7	0	0	0	1	1	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0
382	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
383	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
384	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
385	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
386	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
387	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7	0
388	0	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
389	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
390	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
391	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
392	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
393	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7	0	0	0	0	0
394	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
395	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
396	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
397	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
398	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
399	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0

400	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
401	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
402	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
403	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
404	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
405	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
406	0	0	0.7	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
407	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
408	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
409	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
410	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0
411	0	0	0	0	0	0	0	0	0	0.7	0.7	0	0	0	0	0	0	0	0	0
412	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0
413	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
414	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
415	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
416	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	1	0	0
417	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
418	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
419	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
420	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
421	0	0	0	0	0.7	0	0	0	0	1	0	0	1	0	0	0	1	0	0	1
422	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
423	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
424	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
425	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
426	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
427	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
428	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
429	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
430	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
431	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0

432	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
433	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0.7	0	0	0	0	0	0
434	0	0	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0.7	0	0
435	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
436	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
437	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
438	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0
439	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
440	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0
441	0	1	0	0.7	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
442	0	0	1	0	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0.7	0	0
443	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
444	1	0	0	1	0	0.7	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0
445	0	0	0	0.7	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
446	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0
447	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
448	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
449	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
450	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
451	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
452	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
453	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
454	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
455	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
456	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	1	0	0	0
457	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
458	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
459	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
460	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
461	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
462	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
463	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

464	1	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0	0	1	0
465	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
466	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
467	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
468	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
469	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
470	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
471	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
472	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
473	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
474	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
475	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
476	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
477	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
478	0	0.7	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
479	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0
480	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
481	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
482	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
483	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
484	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
485	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
486	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0
487	1	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	1	0	0	0	0
488	1	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
489	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
490	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
491	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0
492	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
493	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
494	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
495	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0

496	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
497	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
498	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	1	0
499	0	0	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
500	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
501	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
502	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
503	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
504	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
505	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0
507	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
508	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
509	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
510	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
511	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
512	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
513	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
514	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
515	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
516	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
517	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
518	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0
519	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	1
520	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
521	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
522	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0
523	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
524	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
525	0	0.7	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
526	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0.7	0	0	0
527	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0

528	0	1	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0
529	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
530	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0
531	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
532	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0
533	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
534	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7	0	0	0
535	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
536	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
537	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
538	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
539	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0.7	0	0	0	0
540	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0
541	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	1	0	1
542	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0
543	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0
544	0	0.7	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0
545	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
546	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0.7	0	0	0	0	0
547	0	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
548	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0
549	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
550	1	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0
551	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
552	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
553	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
554	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
555	1	0	0	0	0	0	0.7	0	0	0	0	1	0	0	0	1	0	0	0	0
556	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
557	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
558	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0
559	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0

560	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
561	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	1	0
562	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
563	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0
564	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
565	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0.7
566	0.7	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
567	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
568	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0
569	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
570	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
571	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
572	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
573	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
574	0	0	0	0	0	1	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0
575	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
576	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
577	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	1	0	0
578	0.7	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0
579	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
580	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	1	0	0
581	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	1
582	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
583	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
584	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
585	0.7	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0.7	0	0	0	0
586	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
587	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
588	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
589	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0
590	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
591	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

592	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
593	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
594	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0.7	0
595	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	1
596	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1
597	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
598	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
599	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
600	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7
601	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
602	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7
603	1	0	1	0	0	0.7	1	1	0	0	0	0	0	0	0	1	0	0	0	0
604	0.7	1	0.7	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0
605	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
606	1	1	1	1	0	0	0	1	0	0	0	0	0.7	0	0	1	1	0	0	0
607	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
608	0.7	1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0
609	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
610	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
611	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
612	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
613	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
614	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0	1
615	1	0.7	0	0	0	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0
616	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
617	0	0	0	0	0	0	0	0	0	1	1	0	0.7	0	0	0	0	0	0	0
618	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
619	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
620	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
621	0	0	0	0	0	0	0	0	0	1	1	0	0.7	0	0	0	0	0	0	0
622	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
623	0	0.7	0	0	0	0	1	0	0.7	0	0	1	0	0	0	0	0	0	0	0

624	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0
625	0	0	1	0	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
626	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
627	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
628	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
629	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
630	1	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	1	0
631	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
632	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0
633	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7	0
634	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
635	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	1	0
636	0	0	0	0	0	0.7	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
637	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
638	0	0	1	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
639	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
640	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0
641	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0.7	0
642	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
643	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
644	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
645	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0
646	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
647	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
648	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0.7	0
649	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7	0
650	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
651	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
652	0	1	0	0	0	1	0	0.7	1	0	0	1	0	0	0	0	1	0	0	0	0
653	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
654	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
655	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0

656	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	1	0
657	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0
658	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
659	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
660	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
661	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
662	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0	0
663	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
664	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
665	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
666	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
667	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
668	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
669	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
670	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
671	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
672	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
673	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
674	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
675	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
676	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
677	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
678	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
679	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0
680	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0
681	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
682	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
683	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
684	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0
685	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
686	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
687	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0

688	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
689	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
690	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
691	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
692	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
693	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
694	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
695	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
696	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
697	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
698	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
699	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
700	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
701	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
702	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
703	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
704	0	0	0	0.7	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
705	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0
706	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
707	0.7	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
708	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0.7
709	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
710	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
711	0	1	0	0	0	0	0	0	0	1	1	0.7	0	0	0	0	0	0	0	0
712	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0
713	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
714	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
715	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0
716	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0
717	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
718	0.7	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0
719	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

720	1	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
721	1	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
722	0	0.7	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
723	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
724	0	0	0	1	0	0	0	1	0	0	0	0.7	0	0	0	1	1	0	0	0
725	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
726	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
727	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
728	0	1	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0
729	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
730	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
731	0	1	0	0.7	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
732	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
733	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
734	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
735	0.7	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0
736	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
737	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
738	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	1	0
739	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0
740	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
741	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
742	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
743	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
744	0	0	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0
745	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
746	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0
747	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
748	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
749	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
750	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	1	0	0
751	1	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0

752	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
753	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0
754	0.7	0	0	0	0	0	0	0	0	1	1	0	1	0	0	1	0	0	0	0	0
755	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
756	1	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
757	1	0	0	0	0	0	0	0	0	1	0	0	1	0.7	0	0	0	0	1	0	0
758	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
759	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
760	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
761	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
762	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0	0
763	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
764	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	1	0	0	0	0
765	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0.7	0	0	0	0	0
766	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
767	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
768	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0
769	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
770	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
771	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0	0
772	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
773	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
774	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
775	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
776	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
777	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
778	0	0	0	0	0	0	0	0	0	1	0	0	0	0.7	0	0	0	0	0	0	0
779	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
780	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
781	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
782	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
783	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0.7	1	0	0

784	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
785	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
786	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
787	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
788	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
789	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
790	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
791	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
792	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0
793	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Example 19: Improved Activity and Expression of the SUSA from *Thermosynechococcus elongatus* by Computational Design

[00106] A homology model of the sucrose synthase SUSA from *Thermosynechococcus elongatus* was built and used as input to computational designs to improve pA21841. Computational designs were conducted to improve the stability and expression of the SuSy. Forty-seven computational designs were chosen for experimental validation (SEQ ID NOs: 1181-1227). Expression plasmids for the computational designs were built as in *Example 4*. Each SuSy variant was expressed and purified as in *Example 5*. Each SuSy variant was assayed in a one-pot reaction with the B12GT, pA29798. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several variants showed improved expression and/or Reb D conversion compared to the parent pA21841. The top designs showed up to a 2.2-fold improvement in yield or a 5.4-fold improvement in expression (34.6% conversion, 6.8 uM purified protein; Table 25.)

[00107] Table 25. Computational Designs of pA21841

ID	% Conversion	Purified Conc (uM)
pA34126	75.2	11.7
pA34103	73	9.5
pA34101	64.3	9.6
pA34127	59.9	9.2
pA34102	57.7	8.8

pA34112	57.2	4.5
pA34128	56.2	8.6
pA34116	53.4	13.2
pA34118	47.9	17.1
pA34115	47.5	3.6
pA34099	47	20.6
pA34117	46.2	7.2
pA34131	45.8	7.1
pA34125	45.4	18.3
pA34121	45.1	8.3
pA34134	43.7	13.3
pA34086	42.2	14
pA34111	42	2.2
pA34113	40.5	6
pA34135	40.3	13.7
pA34132	39.6	9.8
pA34087	38.2	5.8
pA34106	36.8	14.1
pA34094	34.4	14.6
pA34129	32.4	10.6
pA34119	32.1	23.7
pA34130	31.7	5.8
pA34092	30.7	10.9
pA34107	30.2	15.1
pA34096	29.7	2.6
pA34091	28.5	13.7
pA34110	26.6	25.6
pA34089	23.5	26
pA34088	22.4	28.6
pA34122	22.1	7.8
pA34109	21.9	28.4
pA34120	21.6	12.2

pA34097	15.7	4.2
pA34133	15.3	22.9
pA34095	13.5	17.9
pA34105	12.9	7.8
pA34090	12.1	30.7
pA34123	7.8	19
pA34104	7.7	36.3
pA34124	3.3	17.4

[00108] Computational designs were also conducted to improve the stability and expression of SUSA by redesigning and repacking buried protein cores. Thirty-eight computational designs were chosen for experimental validation (SEQ ID NOs: 1231-1267). Expression plasmids for the computational designs were built as in *Example 4*. Each SuSy variant was expressed and purified as in *Example 5*. Each SuSy variant was assayed in a one-pot reaction with the B12GT, pA29798. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM ADP in 50 mM pH 6 phosphate buffer, and 50 mM NaCl for 24 hours at 60 °C. Product rebaudiosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed well and were active for Reb A to Reb D conversion (Table 26).

[00109] Table 26. Computational Designs of pA21841

ID	% Conversion	Purified Conc (uM)
pA35407	78.3	10.3
pA35409	67.9	11.7
pA35431	55.3	10.2
pA35417	46.1	7.6
pA35437	37.5	12.3
pA35427	27	5
pA35432	24.8	8.9
pA35422	21.2	7.3
pA35423	17.4	4.6
pA35408	16.8	3.4
pA35426	15.3	4

pA35412	15.2	3
pA35425	15.1	5.6
pA35439	14.1	3.5
pA35416	12.9	8.7
pA35428	12.5	4.8
pA35429	10.2	5.2
pA35410	9.3	2.9
pA35424	8.6	5.8
pA35430	8.4	5.8
pA35434	7.5	8.2
pA35435	7.4	5.4
pA35436	5.8	4.3
pA35419	5.5	3
pA35440	5.4	3.1
pA35443	5.3	2.6
pA35444	5.3	2.4
pA35438	5.2	3.4
pA35441	5.1	3.7
pA35413	4.9	2.9
pA35418	4.8	2
pA35420	4.7	1.6
pA35442	4.5	2.4
pA35414	4.4	5
pA35411	4.3	2.4
pA35433	4.3	0
pA35421	0.2	10.8

[00110] Computational designs were also conducted to improve the stability and expression of the SuSy using coevolutionary information. Sixty-five computational designs were chosen for experimental validation (SEQ ID NOs: 1268-1332). Expression plasmids for the computational designs were built as in *Example 4*. Each SuSy variant was expressed and purified as in *Example 5*. Each SuSy variant was assayed in a one-pot reaction with the B12GT, pA29798. The purified B12GT and SuSy were reacted with 100 mg/mL RA50, 250 mM Sucrose, and 0.5 mM

ADP in 50 mM pH 6 phosphate buffer and 50 mM NaCl for 24 hours at 60 °C. Product rebau-
 diosides were monitored by LCMS similar to *Example 3*. Several designed enzymes expressed
 well and were active for Reb A to Reb D conversion (Table 27).

Table 27. Computational Designs of pA21841

ID	% Conversion	Purified Conc (uM)
pA35907	83.5	20.3
pA35928	82.9	8.5
pA35903	71.3	17.1
pA35933	71.2	8.9
pA35901	68.9	21.4
pA35932	68.1	11.3
pA35938	66.5	4.5
pA35882	65.3	11.2
pA35942	64.3	9.7
pA35897	60.2	15.8
pA35943	57	8.3
pA35896	56.8	21.2
pA35936	55.4	5.9
pA35927	55	16.1
pA35926	49.5	8.4
pA35929	49.4	10.1
pA35891	48.8	29.6
pA35898	47.3	6.6
pA35895	47.1	12.9
pA35937	46.3	8
pA35880	44.1	7.8
pA35910	41.1	13.5
pA35941	40.6	8.9
pA35904	40.5	11.9
pA35872	39.4	7.1
pA35930	39.1	6.2
pA35899	38.6	22.1

pA35873	38.5	11
pA35935	36.3	5.3
pA35905	34.4	16.5
pA35902	33.4	16.3
pA35911	32.8	18
pA35919	31.4	9.2
pA35912	29.7	6.4
pA35893	28.1	23.5
pA35889	27.7	6.8
pA35890	27.1	20.2
pA35874	26.5	8
pA35886	25.7	23.7
pA35888	24.6	9.2
pA35875	24.4	12.1
pA35908	24.1	13.6
pA35892	23.6	20.4
pA35887	23.4	13.9
pA35879	22.3	9.6
pA35931	19.5	5.9
pA35915	19.4	9.8
pA35940	18.7	8.8
pA35914	18.6	20.9
pA35876	18.4	23
pA35878	18	13.4
pA35921	17.9	11.7
pA35881	16.8	9.1
pA35877	13.9	22.6
pA35923	13	28.2
pA35925	12.1	13.2
pA35917	10.3	12.8
pA35906	9.1	7.2
pA35884	7.8	18.4

pA35922	7.6	6.2
pA35913	6.7	3.8
pA35939	6.4	5.9
pA35924	5.7	7.1
pA35909	2.1	10.5

Example 20: Representing Successful SuSy Designs with a PSSM

- 5 [00111] The successful SuSy designs from *Example 19* were used to create a PSSM (Table 28). The PSSM is a concise way to represent the successful designs and related sequences. Sequences that have a PSSM score greater than 569.5 are considered related to the active computational designs described in *Example 19*. To score a sequence with the generated PSSM, it must first be aligned with the representative sequence pA21841 (Seq ID No: 888). For example,
- 10 the following successful designs, pA34103, pA34119, pA34099 have the following PSSM scores: 576.7, 572.5, 577.0, while the wild-type SuSy pA21841, has a PSSM score of only 565.6.

Table 28. Position Specific Scoring Matrix (PSSM) of Successful SuSy Designs

Seq Pos	Amino Acids																			
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
3	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
4	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7
5	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0
8	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7
10	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0.7
11	0	0	1	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0

13	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0
15	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
16	0.7	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
17	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
19	0	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0.7	0	0	0	0
23	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	1	0	0	0	0.7	1	0	0	0	0	0	0	0	1	0
25	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
26	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	1	1	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	1	0	0	0
28	0	0	1	0	0	1	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0
29	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
31	0	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
33	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
35	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
40	0	0	1	0.7	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
41	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
43	0.7	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
46	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
47	0	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
48	1	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0.7	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
50	0	0	0	1	0	1	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
51	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
53	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0
55	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0
57	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0.7	0	0	0	0	0
58	0	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0
59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
60	0	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
61	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
62	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0
63	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
64	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
65	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0
66	0	1	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0	1	0	0
67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
69	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
70	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
71	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
72	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
73	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0.7	0
74	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
75	0	0	0.7	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
76	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0

77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0
78	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
79	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
81	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
82	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0
83	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
85	0	0.7	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
86	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
87	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
88	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
89	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
90	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
92	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0
93	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
95	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0
96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
97	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
98	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
99	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0
100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
101	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0	0	0	1	0
102	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
103	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
104	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0
105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
106	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
107	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
108	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0

109	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
110	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
111	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
112	1	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0
113	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
114	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
116	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
117	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
118	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
119	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
120	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
121	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
123	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
124	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
125	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7	0
128	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0
129	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
131	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0.7
133	0	1	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
137	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
139	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0
140	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0

141	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	1	0
142	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
143	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
144	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
145	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
146	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
147	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
148	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
149	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
150	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
151	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
153	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
154	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
155	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
156	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
158	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
159	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0
160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
162	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
163	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
164	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
165	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
166	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
168	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
169	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
170	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0
171	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
172	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0

173	1	1	0.7	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0	0
174	0	0	0	0	0	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0
175	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0
176	0	0	0.7	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
177	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
178	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0
179	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
180	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
181	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
182	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
183	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
184	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
185	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
186	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0
187	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
188	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
189	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0
190	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
191	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
192	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
193	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
194	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
195	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
196	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
197	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
198	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
199	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
200	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
201	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0
202	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0

205	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
206	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
209	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7
210	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	1	0.7
211	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
212	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
213	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
216	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
217	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
218	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
219	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
220	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
221	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0
222	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
223	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
224	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
226	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
227	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
228	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229	0	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
230	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
231	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
232	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
233	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
234	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
235	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
236	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0

237	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
238	0	1	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
239	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
240	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
241	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
242	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
243	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
244	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
245	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
247	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
248	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
249	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0
250	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0	0
251	1	0	0	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
252	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
253	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
254	1	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0	0
255	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
257	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
258	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
259	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
260	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
261	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
262	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
263	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
264	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
265	0	0	0	0	0	0	0	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0
266	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0.7	0
267	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
268	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

269	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
270	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
271	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
272	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
273	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
274	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
275	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
276	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
277	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
278	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
279	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
280	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
281	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
282	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
283	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
284	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
285	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
286	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
287	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
288	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
289	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
290	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
291	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
292	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
293	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
294	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
295	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
296	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
297	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
298	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
299	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
300	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0

301	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7	0	0
302	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
303	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
304	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
305	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
306	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
307	0	1	0	0	0	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
308	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
309	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
310	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
311	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
312	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
313	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0
314	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
315	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
316	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
317	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0
318	0	0	0	0	0	1	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0
319	0	0	0	0	0	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
320	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
321	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
322	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
323	0	0	0	1	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0
325	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
326	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
327	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
328	0	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
329	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
330	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
331	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
332	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0

333	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0
334	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
335	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
336	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
337	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
338	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
339	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
340	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
341	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
342	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
343	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
344	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
345	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	1	0	0	0
346	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
347	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
348	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
349	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
350	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
351	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
352	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
353	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
355	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
356	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
357	0	0	0.7	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
358	0	0	1	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
359	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
360	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
361	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
362	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
363	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
364	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0

365	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
366	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
367	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
368	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
369	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
370	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
371	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
372	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
373	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
374	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
375	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
376	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
377	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
378	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
379	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
380	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
381	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
382	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
383	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
384	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
385	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
386	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
387	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
388	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
389	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
390	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
391	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
392	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0
393	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
394	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
395	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
396	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0

397	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
398	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
399	0	0.7	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
400	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
401	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
402	0	0	0	0	0	0	0	0	0	0	1	0	1	0.7	0	0	0	0	0	0	0
403	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
404	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0
405	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0.7	0
406	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
407	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
408	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
409	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
410	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
411	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
412	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
413	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
414	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
415	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
416	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
417	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
418	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
419	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
420	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
421	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
422	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
423	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
424	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
425	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
426	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
427	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0
428	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0

429	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
430	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
431	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
432	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
433	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
434	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
435	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
436	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
437	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
438	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
439	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
440	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
441	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
442	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
443	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
444	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
445	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
446	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
447	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
448	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
449	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
450	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
451	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
452	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
453	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
454	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
455	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
456	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
457	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
458	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
459	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
460	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0

461	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0
462	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
463	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
464	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
465	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
466	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
467	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
468	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
469	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
470	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
471	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
472	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
473	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
474	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
475	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
476	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
477	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1
478	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
479	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
480	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
481	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
482	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
483	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
484	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
485	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
486	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
487	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
488	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
489	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
490	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
491	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
492	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0

493	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
494	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
495	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
496	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
497	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
498	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
499	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
500	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
501	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
502	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
503	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
504	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
505	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
506	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
507	0	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
508	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
509	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
510	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
511	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
512	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
513	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
514	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
515	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
516	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0	0
517	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
518	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
519	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
520	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
521	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7
522	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7
523	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
524	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0

525	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
526	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
527	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
528	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
529	0	0	1	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
530	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
531	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
532	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
533	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
534	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
535	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0
536	0	1	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
537	0	1	1	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0.7	0	0
538	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
539	0	1	1	1	0	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0
540	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
541	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	1	0
542	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
543	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0	0
544	0	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
545	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
546	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
547	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
548	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
549	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
550	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
551	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
552	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
553	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
554	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
555	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
556	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0

557	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
558	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
559	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	1	0	0	0	0	0
560	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
561	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
562	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
563	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
564	0	0	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0.7	0
565	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
566	0	0	0	1	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0	0
567	0.7	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
568	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0.7	0	0	0	0	0
569	0	0	1	0	0	1	0.7	0	1	0	0	1	0	0	0	1	0	0	0	0
570	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
571	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
572	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
573	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
574	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
575	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
576	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
577	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
578	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
579	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
580	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
581	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
582	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
583	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
584	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
585	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
586	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
587	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
588	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0

589	0.7	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
590	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
591	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
592	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0
593	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
594	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
595	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
596	0	0	0	0	0	1	0	0	0	0	0	0.7	0	0	1	0	0	0	0	0
597	0.7	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
598	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
599	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
600	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
601	0	0.7	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
602	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
603	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
604	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
605	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
606	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0
607	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
608	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
609	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
610	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	1	0
611	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0
612	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
613	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0
614	0.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
615	0	0	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
616	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
617	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0
618	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
619	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0
620	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0

621	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
622	0	1	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0	0
623	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
624	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
625	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
626	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
627	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
628	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0
629	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0
630	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
631	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0
632	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
633	0	0	0	1	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
634	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
635	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
636	0	0	0.7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
637	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
638	0	0	1	0	0	1	0	0	0.7	0	0	1	0	0	0	1	0	0	0	0	0
639	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
640	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
641	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
642	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
643	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.7	0	0	0
644	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
645	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
646	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
647	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
648	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
649	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
650	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
651	0.7	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
652	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

653	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
654	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
655	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
656	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
657	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
658	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
659	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
660	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
661	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
662	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
663	0	0.7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
664	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
665	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
666	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	1	0
667	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
668	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
669	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
670	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
671	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
672	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
673	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
674	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
675	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
676	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
677	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
678	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
679	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
680	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
681	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
682	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
683	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
684	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0

685	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
686	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
687	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
688	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
689	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
690	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
691	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
692	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
693	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
694	0	0.7	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
695	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
696	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
697	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
698	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
699	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
700	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
701	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
702	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
703	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
704	0	0	1	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
705	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
706	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.7
707	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
708	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0
709	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
710	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.7	0
711	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
712	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
713	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
714	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
715	0	0	0	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
716	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0

717	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
718	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
719	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	1	0	0	0
720	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
721	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
722	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0
723	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
724	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0.7
725	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
726	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0
727	0	0	0	0	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0
728	1	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
729	0.7	1	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0
730	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
731	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
732	0	0.7	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0
733	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
734	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
735	0	0	1	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	0	0
736	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0	0	0	1	0
737	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
738	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0	0	0	1	0
739	0	0.7	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
740	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0	0	0	0	0	0
741	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
742	0	0	0	0	0	1	1	0	0	0	0	0.7	0	0	0	0	0	0	0	0
743	0.7	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
744	1	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	1	0	0	0	0
745	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
746	0	0	0	0	0	1	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
747	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
748	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7

749	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
750	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
751	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0	0	0	0
752	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
753	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0
754	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0
755	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
756	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
757	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0	0	0	0	1	0	0
758	1	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
759	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0.7	0	0	0	0
760	0	0.7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
761	0	0	0	0	0	0	0	0	0	1	0.7	0	1	0	0	0	0	0	0	0	0
762	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0	0
763	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	1	0	0	0	0
764	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0
765	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
766	0	1	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
767	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
768	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0.7	0	0
769	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
770	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
771	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0
772	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
773	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0
774	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0.7	1	0	0	1	0
775	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
776	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
777	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
778	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
779	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
780	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0

781	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
782	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	0	0	0
783	0	0	0	0	0	0	0	0	0	0	1	0	0.7	0	0	0	0	1	0	0
784	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
785	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0
786	0	0	0	0	0	0	0	0	0	1	1	0	0.7	0	0	0	0	0	0	0
787	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
788	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
789	0	0	0	0	0	0	0	0	0	0	0.7	0	1	0	0	0	0	0	0	0
790	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	1	0
791	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
792	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
793	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
794	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0.7	0
795	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0
796	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0
797	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
798	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
799	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
800	0.7	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
801	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
802	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
803	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
804	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0
805	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0
806	0	0	0	0	0	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0
807	0	0	0	0	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
808	0	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Example 21: Scaled up one-pot reaction of pA21841 and pA29798

[00112] E. coli microorganisms containing either the SuSy, pA21841, or the B12GT, pA29798, were expressed in 1L and 10L fermenters. The cells were collected and lysed by

French press. The expressed protein was purified by immobilized metal affinity chromatography (IMAC) and dialyzed into desalt buffer (20mM KPO4 pH6, 50mM NaCl). A one-pot reaction to convert Reb A and stevioside to Reb D and Reb E, respectively, was carried out. pA21841 and pA29798 were reacted with 100 mg/ml RA50, 250mM Sucrose, and 0.5mM ADP in 50mM KPO4 pH6 and 50mM NaCl. In total, ten 20 mL 1pot reactions were conducted. The reactions were lyophilized and the combined reaction product was analyzed for rebaudioside content by liquid chromatography-mass spectrometry (LCMS) using an Agilent 6545 QTOF mass spectrometer (column: 150x2.1mm Phenomenex C18-PS). Full conversion of Reb A to Reb D and stevioside to Reb E was observed (FIG. 7 ; Table 29).

Table 29. Rebaudioside Content of pA21841 and pA29798 One-Pot Reaction Product

Rebaudioside	Retention Time (min)	Area	% (SG Only)
Unknown (mass: 1127)	4.6	28703	0.3
Reb E	5.2	3768926	37.5
Reb D	5.4	6011185	59.8
Reb A	8.1	164560	1.6
Stevioside	8.2	86265	0.9

Example 22: Scaled up one-pot reaction of pA21841 and pA29646

[00113] E. coli microorganisms containing either the SuSy, pA21841, or the B12GT, pA29646, were expressed in 10L fermenters. The cells were collected and lysed by French press. The expressed protein was purified by immobilized metal affinity chromatography (IMAC) and dialyzed into desalt buffer (20mM KPO4 pH6, 50mM NaCl). A one-pot reaction to convert Reb A and stevioside to Reb D and Reb E, respectively, was carried out. pA21841 and pA29646 were reacted with 100 mg/ml RA50, 250mM Sucrose, and 0.5mM ADP in 50mM KPO4 pH6 and 50mM NaCl. In total, ten 20 mL 1pot reactions were conducted. The reactions were lyophilized and the combined reaction product was analyzed for rebaudioside content by liquid chromatography-mass spectrometry (LCMS) using an Agilent 6545 QTOF mass spectrometer (column: 150x2.1mm phenomenex C18-PS). Full conversion of Reb A to Reb D and stevioside to Reb E was observed (FIG. 8; Table 30).

Table 30. Rebaudioside Content of pA21841 and pA29646 One-Pot Reaction Product

	Retention Time (min)	Area	% (SG Only)
Unknown (mass: 1127)	5	2075	0

Reb E	5.4	954516	32
Reb D	5.6	1658236	65
Reb A	8.7	49223	2
Stevioside	8.8	22057	1

Example 23: *Pichia pastoris* expression of designed B12GTs and SuSys

[00114] Polynucleotides optimized for *Pichia pastoris* expression of top designed B12GT (from *Examples 12, 13 and 15*) and SuSys (from *Examples 17 and 19*) were synthesized (Twist Bioscience) and inserted into a *Pichia* shuttle vector. The vectors were transformed into a commercially available *Pichia pastoris* strain (ATCC). The transformed microorganisms were grown in BMGY (buffered glycerol complex) media and protein expression was induced by feeding of methanol. The *Pichia* cells were lysed with Y-PER (Yeast Protein Extraction Reagent; Thermo Scientific) and the expressed proteins were purified by immobilized metal affinity chromatography (IMAC) and desalted into desalt buffer (20mM KPO4 pH6, 50mM NaCl). The designed B12GTs and SuSys solubly expressed and were catalytically active. **FIG. 9** shows an SDS-PAGE gel of designed B12GTs purified from *Pichia pastoris* expression.

[00115] Two designed B12GTs and two designed SuSys were also expressed in 1L fermentations. The *Pichia* microorganisms were grown with glycerol as the main carbon source for ~24 hours, and then were fed methanol for ~72 hours to express the desired B12GT or SUSY. The cells were collected and lysed by French press. The expressed protein was purified by immobilized metal affinity chromatography (IMAC) and dialyzed into desalt buffer (20mM KPO4 pH6, 50mM NaCl). **FIG. 10A** shows an SDS-PAGE gel of two designed B12GTs, pA29798 (left, B12GT-1) and pA32946 (right, B12GT-2), purified from 1L *Pichia pastoris* fermentations. **FIG. 10B** shows SDS-PAGE gels of two designed SuSys, pA34103 (left, SuSy-1) and pA32691 (right, SuSy-2), purified from 1L *Pichia pastoris* fermentations. All four enzymes successfully expressed in the fermentations and had the desired activity.

CLAIMS:

1. An engineered beta-1,2-glycosyltransferase polypeptide that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 6-882 and 1333-1466.
2. The engineered beta-1,2-glycosyltransferase polypeptide of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99% or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 6-459.
3. The engineered beta-1,2-glycosyltransferase polypeptide of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 460-534.
4. The engineered beta-1,2-glycosyltransferase polypeptide of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 535-765.
5. The engineered beta-1,2-glycosyltransferase of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 766-829.
6. The engineered beta-1,2-glycosyltransferase of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1333-1466.
7. An engineered beta-1,2-glycosyltransferase polypeptide that has a score greater than 266.7 when scored by the PSSM shown in Table 17.
8. A polypeptide having the sequence of:
 XXXXVXMXPWXLGHXNPXLRXAXXXAXRXXXXXXXXXXTXXXLXXXXXRIXX
 XYXXXIXLXXXXLPXLPELPXXXXTTNXLPPLNXXLXXXXXXXXXXPXXSKXXX

XXXXXLXXXDXLXXWXXXKXAXXXXXXPXXXXTXGXALXXYXXXXXXXXXXGX
 XFXFXIXLXXXXXXXXXXEXXXXXXXXXXXXXFXXXXXXXXXXXLXXXSRXXEAKYX
 DYXXXXXXXXXXVPVGXXXXXXXXXXDXDXELXXWLXXKXXXXXXVXVSFGSE
 XFLSXEXXEEXAXGLXLSXXNXIXVXRFPKGXXXXXXXXXXLPXGXXXRXXXRXX
 5 XXXHLVPQAXILXHXXXGGFXSHCGWNSXXEXXXFGVPIIAMPMQWDQPINAR
 LXXEXGXAVEXXRXXXGXXXRXXIAXXXXXVXXXXXGXXLRXXVXXXXXXXXX
 XXXRXXEMXXXXXXXXXXLXXXXXAXX

wherein residue 1 is R or D or Q or P or S or T

wherein residue 2 is N or L or S or T

10 wherein residue 3 is Q or L or F

wherein residue 4 is R or Q or T

wherein residue 6 is A or L or T or V

wherein residue 8 is L or F or V

wherein residue 12 is A or G

15 wherein residue 16 is I or V

wherein residue 19 is F or Y

wherein residue 22 is I or L or V

wherein residue 24 is R or K

wherein residue 25 is Q or K

20 wherein residue 26 is L or M

wherein residue 28 is D or K

wherein residue 30 is N or G

wherein residue 31 is M or F

wherein residue 32 is H or I or L or S or Y or V

25 wherein residue 33 is I or V

wherein residue 34 is H or Y

wherein residue 35 is L or M or V

wherein residue 36 is A or C or L or V

wherein residue 37 is N or S

30 wherein residue 39 is A or K or M or P

wherein residue 40 is I or V

wherein residue 41 is N or Q or V

wherein residue 43 is N or E or K or S

wherein residue 44 is L or M or S

wherein residue 45 is A or I or L or T

wherein residue 46 is R or K

wherein residue 47 is G or H or K

wherein residue 50 is P or T

5 wherein residue 51 is N or E or K or Y

wherein residue 52 is A or K

wherein residue 54 is A or Q or L or S or V

wherein residue 55 is N or D or Q or E or L or S

wherein residue 56 is L or S

10 wherein residue 58 is Q or E or H or I

wherein residue 60 is I or V

wherein residue 61 is E or T

wherein residue 62 is L or S or Y or V

wherein residue 63 is A or R or Q or H or S

15 wherein residue 66 is Q or E or L

wherein residue 72 is P or S

wherein residue 73 is H or Y

wherein residue 74 is L or Y

wherein residue 75 is H or W

20 wherein residue 79 is A or G

wherein residue 86 is G or K

wherein residue 87 is R or I or L or T or V

wherein residue 89 is R or Q or H or I or K

wherein residue 90 is R or Q or K

25 wherein residue 91 is A or L

wherein residue 92 is L or V

wherein residue 93 is R or Q or K

wherein residue 94 is L or M

wherein residue 95 is A or S

30 wherein residue 96 is A or R or Q

wherein residue 98 is N or E or T

wherein residue 99 is I or L or F or V

wherein residue 102 is Q or I or L or T or V

wherein residue 103 is I or L or V

wherein residue 104 is R or Q or E or K or S

wherein residue 105 is A or N or D or T

wherein residue 106 is I or L or W

wherein residue 107 is N or K

5 wherein residue 108 is A or P or S or V

wherein residue 109 is A or D or S or T

wherein residue 111 is I or L or V

wherein residue 112 is I or L or V

wherein residue 113 is L or F or Y or V

10 wherein residue 115 is I or L or M or F

wherein residue 117 is A or Q or I or L or V

wherein residue 118 is Q or P

wherein residue 120 is A or L

wherein residue 121 is E or S

15 wherein residue 123 is I or L or S or V

wherein residue 125 is N or L or K

wherein residue 126 is D or E or S

wherein residue 127 is R or Q or L

wherein residue 128 is N or G

20 wherein residue 129 is I or V

wherein residue 131 is A or G or S or V

wherein residue 132 is I or V

wherein residue 133 is R or K or P

wherein residue 134 is L or F

25 wherein residue 135 is A or I or L or W

wherein residue 137 is F or S

wherein residue 139 is A or L or V

wherein residue 142 is L or F or W

wherein residue 143 is A or S

30 wherein residue 145 is I or L or F

wherein residue 146 is L or M or F or W or V

wherein residue 147 is N or Q or E or H

wherein residue 148 is H or F

wherein residue 149 is L or V

wherein residue 150 is R or D or K or T

wherein residue 151 is R or N or K

wherein residue 152 is L or P

wherein residue 154 is N or E or H or V

5 wherein residue 155 is E or P

wherein residue 157 is L or P

wherein residue 159 is E or P

wherein residue 160 is A or E

wherein residue 162 is R or D or E or H or K or M or S or Y

10 wherein residue 164 is R or S

wherein residue 165 is E or K

wherein residue 166 is R or I or L or W or Y

wherein residue 167 is A or E

wherein residue 168 is Q or L or K

15 wherein residue 169 is A or D or Q or V

wherein residue 170 is K or W

wherein residue 171 is H or L or M

wherein residue 172 is R or Y

wherein residue 174 is A or L or M

20 wherein residue 175 is M or F

wherein residue 176 is E or G

wherein residue 177 is R or K or T

wherein residue 178 is A or Q or E or G or V

wherein residue 179 is G or P

25 wherein residue 180 is D or K or P or T

wherein residue 181 is D or E

wherein residue 182 is R or D or E or L or K

wherein residue 183 is D or F

wherein residue 185 is L or F

30 wherein residue 186 is A or V

wherein residue 187 is D or E or K or P or V

wherein residue 188 is A or G or F

wherein residue 189 is R or N or Q or P or S

wherein residue 190 is A or N or C or K or M or S or T

wherein residue 191 is A or Q or G or K

wherein residue 192 is A or I or Y

wherein residue 193 is I or L or M or T or V

wherein residue 195 is I or M or V

5 wherein residue 196 is C or M

wherein residue 197 is S or T

wherein residue 200 is A or E or I or V

wherein residue 201 is I or L

wherein residue 206 is I or L or M

10 wherein residue 209 is C or L

wherein residue 210 is A or Q or M or S or T

wherein residue 211 is E or K or T

wherein residue 212 is L or W

wherein residue 213 is M or S or T

15 wherein residue 214 is N or G

wherein residue 215 is R or I or L or K or W or V

wherein residue 216 is Q or K

wherein residue 217 is I or V

wherein residue 222 is A or P

20 wherein residue 223 is P or S or T

wherein residue 224 is F or Y or V

wherein residue 225 is Q or L

wherein residue 226 is D or T or V

wherein residue 227 is A or L or P

25 wherein residue 228 is N or L or T or V

wherein residue 229 is F or P or T or Y

wherein residue 230 is N or D or E or L or S

wherein residue 232 is A or N or D or E or I or L

wherein residue 233 is R or D or G or S or Y

30 wherein residue 235 is I or K or M or P or S or V

wherein residue 238 is I or M

wherein residue 239 is R or D or K

wherein residue 242 is D or G

wherein residue 243 is K or T

wherein residue 245 is D or P
wherein residue 246 is E or L or P or T
wherein residue 247 is N or H
wherein residue 248 is A or S
5 wherein residue 249 is T or V
wherein residue 251 is F or Y
wherein residue 258 is A or Y
wherein residue 262 is R or K
wherein residue 264 is D or Q
10 wherein residue 265 is L or M
wherein residue 268 is I or L or V
wherein residue 270 is H or F or W
wherein residue 273 is E or V
wherein residue 276 is N or G
15 wherein residue 277 is A or I or S or V
wherein residue 279 is A or F
wherein residue 281 is I or W
wherein residue 283 is A or V
wherein residue 289 is A or R or E or V
20 wherein residue 290 is R or E or K
wherein residue 291 is A or R or Q or I or L or V
wherein residue 292 is R or N or H or L or T
wherein residue 293 is A or L
wherein residue 294 is E or I
25 wherein residue 295 is D or E
wherein residue 296 is A or V
wherein residue 299 is R or K or P or S
wherein residue 301 is F or T
wherein residue 302 is L or S
30 wherein residue 303 is D or E
wherein residue 305 is G or I or V
wherein residue 306 is R or G
wherein residue 307 is D or E
wherein residue 309 is A or G

wherein residue 310 is R or M or Y
wherein residue 311 is W or V
wherein residue 312 is R or L
wherein residue 313 is D or P or T
5 wherein residue 320 is C or H
wherein residue 323 is N or K or S
wherein residue 325 is K or P or S
wherein residue 326 is A or S
wherein residue 327 is I or T or V
10 wherein residue 331 is I or M or V
wherein residue 339 is I or W or V
wherein residue 340 is L or M
wherein residue 342 is A or S
wherein residue 343 is I or L
15 wherein residue 344 is D or H or Y
wherein residue 365 is I or L or M or V
wherein residue 366 is R or N or V
wherein residue 368 is L or M or W
wherein residue 370 is I or V
20 wherein residue 374 is I or V
wherein residue 375 is R or P or S or V
wherein residue 377 is R or D or Q
wherein residue 378 is D or E
wherein residue 379 is N or D or E or L
25 wherein residue 381 is R or K or S
wherein residue 382 is I or V
wherein residue 383 is H or P
wherein residue 385 is A or N or D or E or G
wherein residue 386 is A or E
30 wherein residue 389 is R or Q or E or K
wherein residue 390 is C or T or V
wherein residue 391 is I or L or V
wherein residue 392 is R or K
wherein residue 393 is D or E or S

wherein residue 395 is I or M or V

wherein residue 396 is N or C or G or F or S or T or V

wherein residue 397 is E or G

wherein residue 398 is A or K or P

5 wherein residue 399 is I or L or T

wherein residue 401 is Q or E

wherein residue 402 is N or E or I or K

wherein residue 405 is A or R or H or K

wherein residue 406 is N or K

10 wherein residue 408 is A or R or K

wherein residue 409 is D or E

wherein residue 410 is I or L

wherein residue 411 is A or G or S

wherein residue 412 is A or R or E or L or K or T

15 wherein residue 413 is R or N or K

wherein residue 414 is L or W

wherein residue 415 is R or K

wherein residue 416 is A or R or E or L or S

wherein residue 417 is A or R or I or K or T

20 wherein residue 419 is N or D or E or G or K

wherein residue 420 is E or P or V

wherein residue 423 is N or D or Q or G or T

wherein residue 424 is A or I or K

wherein residue 425 is A or L

25 wherein residue 426 is A or M or V

wherein residue 427 is E or L

wherein residue 428 is A or E

wherein residue 429 is L or F or Y

wherein residue 430 is I or L or K or M

30 wherein residue 431 is A or R or Q or L or K or S

wherein residue 433 is C or G or H

wherein residue 434 is R or Q or H or K or F or P or T or Y or V

wherein residue 435 is N or H or K

wherein residue 436 is R or L

wherein residue 437 is A or R or N or L or S

wherein residue 439 is A or L or K or F or S or T or Y

wherein residue 440 is N or K or V (SEQ ID NO:1228)

9. The engineered beta-1,2-glycosyltransferase polypeptide of claim 1 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 830-882.

10. An engineered sucrose synthase polypeptide that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 886.

11. An engineered sucrose synthase polypeptide that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 888.

12. An engineered sucrose synthase polypeptide that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 890-1227 and 1231-1332.

13. The engineered sucrose synthase polypeptide of claim 12 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 890-924.

14. The engineered sucrose synthase polypeptide of claim 12 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 925-1180.

15. The engineered sucrose synthase polypeptide of claim 12 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1231-1267.

16. The engineered sucrose synthase polypeptide of claim 12 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1268-1332.

17. An engineered sucrose synthase polypeptide that has a score greater than 556 when scored by the PSSM shown in Table 24.

18. A polypeptide having the sequence of

MIEXLXXXLXXXXXXXXXXLRXXXXXXXXRXXXXXXXXDLXXXXXXFXXXXXXXXXX
 5 XXXXXXXXXXXXXXXXQEAXXXXPWXXXAXRXXRXXXWXYXRHXEXLXVEEX
 XXXEXLXXKEXLVXXXXEGXAVXXXDXXDXXXXXQXXKDESTIGXGXXHLNR
 HLXGRXWDXDXGXGXXXXXXXXLXXHXXXXXXXXLXLXXXXXXFDXLRXXXQYLG
 XXPXXXPXXXXXXXXXXXXXGFEFGXGXTXXRXXRXXRLLDXDLSPSPXXLEXF
 LXXRPXIXXXXIXSXHGXFQXXVLGXPDTGGQVVXILDQXRALEXEXRXRLXX
 10 QGDXDXEPXIXXXTRLIPXXXGTTCDQRLEPXXGXXXXXILRXPFREXGXXXPX
 WISRFXXWPYLERXXXDXEXEXXAELGXRPDXIIGNYSDGXLXAXXXXXKXGX
 TQXNXAHALEKXXYXXSDLXWXXXEXXXHFXCQFTADXIAMNAADXIXTSTY
 QEIAGXDXVVGQYESXXXXTXPGLYRXXXGXDVFDXXFNIXSPGADXXXYFXY
 XXXEXRXXXLXPEIEXXXXXXXXXXXXXXRGVLXDXXKPXXXXXXXXRXDRIKNXX
 15 GXXEXXGXXXRLRLANLXXXXGHXDXXXSXDXEEXXXXXRXHXXXDXXXL
 DGQXRXXGXXLXKXXVGEXYRXXADXRGXGXXQPALXEAFLTVIEXMXSGLP
 XXATXXGGPXEIIEXGVSGFHIDPNXXXXXXXXEXXADXXEXXXXXPXYWEXISXX
 ALXRVXXRYTWXXXAERXXTXXRXXGFWXXVXXREXQVXXRYLQMXRHLQ
 XRPLAHAVPXE

wherein residue 4 is A or R or E or S or V

wherein residue 6 is R or D or E

wherein residue 7 is Q or E

wherein residue 8 is Q or F

wherein residue 10 is A or R or Q or H or L or K or S

wherein residue 11 is D or Q or E or S

wherein residue 12 is N or H or S

wherein residue 13 is R or P

wherein residue 14 is R or N or D or E

wherein residue 15 is A or D or Q or E or S or T

wherein residue 16 is L or W or V

wherein residue 17 is R or H or Y

wherein residue 18 is A or R or L

wherein residue 19 is L or F

wherein residue 22 is R or H

wherein residue 23 is L or Y
wherein residue 24 is L or V
wherein residue 25 is A or G
wherein residue 26 is Q or L or S
5 wherein residue 27 is Q or G
wherein residue 29 is D or G or P or T
wherein residue 30 is I or L or M or F or S
wherein residue 31 is L or W
wherein residue 32 is Q or L
10 wherein residue 33 is R or H
wherein residue 34 is H or S or T
wherein residue 37 is Q or W
wherein residue 38 is R or D or H
wherein residue 39 is A or E
15 wherein residue 40 is C or L or F
wherein residue 41 is A or D or E or L or K
wherein residue 42 is A or R or N or D or E or T
wherein residue 44 is R or C or Y
wherein residue 45 is A or E
20 wherein residue 46 is Q or E or P
wherein residue 47 is D or Q or E or P
wherein residue 48 is D or G or P
wherein residue 49 is N or E
wherein residue 50 is E or G
25 wherein residue 51 is E or S or Y
wherein residue 52 is A or E or G or L or P
wherein residue 53 is E or L
wherein residue 54 is A or D or C or G or L or K or M or T
wherein residue 55 is D or G or I or S or T
30 wherein residue 56 is G or S
wherein residue 57 is A or P or W or V
wherein residue 58 is L or F
wherein residue 59 is A or E or G
wherein residue 60 is R or D or Q or E

wherein residue 61 is A or L or F or V
wherein residue 62 is I or V
wherein residue 63 is A or R or Q or E or K
wherein residue 64 is A or R or H or K
5 wherein residue 65 is A or C or T
wherein residue 69 is A or I or V
wherein residue 70 is I or L or F or V
wherein residue 71 is R or D or E or H or L
wherein residue 72 is A or D
10 wherein residue 75 is A or I or L or M or F or V
wherein residue 76 is C or Y or V
wherein residue 77 is L or F
wherein residue 79 is I or L or W or V
wherein residue 81 is E or L or P
15 wherein residue 83 is P or V
wherein residue 84 is A or G
wherein residue 85 is R or V
wherein residue 87 is R or E or Y
wherein residue 89 is L or Y or V
20 wherein residue 91 is I or F
wherein residue 93 is I or L or V
wherein residue 95 is D or Q or T
wherein residue 97 is A or D or E or T or V
wherein residue 101 is I or L or V
25 wherein residue 102 is D or S or T
wherein residue 103 is T or V
wherein residue 104 is D or E or S
wherein residue 106 is F or Y
wherein residue 108 is A or Q
30 wherein residue 109 is A or F
wherein residue 112 is R or Q or E
wherein residue 115 is N or D or G or K or T
wherein residue 116 is G or L
wherein residue 117 is A or N or D or E or G

wherein residue 118 is A or Q or G or H or P or S

wherein residue 121 is N or D or E or P

wherein residue 124 is L or T or W

wherein residue 125 is E or K or T

5 wherein residue 126 is I or W or V

wherein residue 128 is L or F or W

wherein residue 129 is E or G

wherein residue 131 is L or F

wherein residue 132 is R or N

10 wherein residue 133 is R or P

wherein residue 134 is N or E or G or H or S or T or V

wherein residue 135 is F or S or V

wherein residue 137 is R or K

wherein residue 138 is L or M

15 wherein residue 146 is R or N or D

wherein residue 148 is L or V

wherein residue 149 is Q or E or T

wherein residue 156 is A or S

wherein residue 159 is I or L or M

20 wherein residue 161 is Q or G or T

wherein residue 163 is L or T

wherein residue 164 is A or G or K

wherein residue 165 is A or R or D or Q or E or G or K

wherein residue 167 is R or D or L or M

25 wherein residue 168 is D or Q or E or S or Y

wherein residue 169 is A or R or Q or K

wherein residue 170 is I or L

wherein residue 171 is I or L

wherein residue 172 is D or E

30 wherein residue 173 is F or W

wherein residue 175 is R or G or S

wherein residue 176 is L or V

wherein residue 178 is R or Q

wherein residue 179 is H or I or L or Y

wherein residue 180 is R or D
wherein residue 181 is N or G
wherein residue 182 is R or Q
wherein residue 183 is N or Q or H
5 wherein residue 185 is G or M
wherein residue 187 is N or S
wherein residue 188 is N or D or E
wherein residue 189 is R or G
wherein residue 190 is N or I or M or F
10 wherein residue 191 is R or Q or K or T
wherein residue 192 is D or S
wherein residue 195 is A or E or G or S
wherein residue 198 is R or Q
wherein residue 199 is A or T or V
15 wherein residue 200 is E or I or L or M or V
wherein residue 205 is R or G or K or T
wherein residue 206 is Q or L
wherein residue 208 is A or R or D or E or P
wherein residue 209 is D or E
20 wherein residue 210 is A or T
wherein residue 212 is L or W
wherein residue 213 is A or E or S
wherein residue 214 is D or E
wherein residue 215 is L or F or V
25 wherein residue 216 is A or R or Q or E or G
wherein residue 217 is E or H or P
wherein residue 218 is A or R or D or E or K or T
wherein residue 219 is L or M
wherein residue 220 is R or Q
30 wherein residue 221 is R or E
wherein residue 222 is R or L or M or W
wherein residue 228 is L or W
wherein residue 230 is R or N or D
wherein residue 232 is A or V

wherein residue 233 is A or Q or E or G
wherein residue 235 is I or M or V
wherein residue 237 is D or E
wherein residue 239 is L or M
5 wherein residue 243 is M or V
wherein residue 245 is I or L
wherein residue 252 is A or R or E or G or S
wherein residue 253 is A or N or T
wherein residue 256 is R or E or K or S or T
10 wherein residue 259 is A or D or G
wherein residue 261 is I or V
wherein residue 263 is L or M
wherein residue 265 is F or S
wherein residue 266 is N or S
15 wherein residue 267 is I or L or V
wherein residue 268 is A or I or L or T or V
wherein residue 270 is I or L or V
wherein residue 272 is I or P or V
wherein residue 275 is W or Y
20 wherein residue 277 is A or G
wherein residue 279 is A or D or S
wherein residue 280 is N or K
wherein residue 284 is R or L or Y
wherein residue 293 is F or W or Y
25 wherein residue 298 is A or V
wherein residue 303 is R or K
wherein residue 305 is I or L or M
wherein residue 307 is R or N or D or Q or E or K
wherein residue 310 is A or R or H or Y
30 wherein residue 311 is Q or E
wherein residue 314 is L or V
wherein residue 316 is I or V
wherein residue 319 is R or Q
wherein residue 321 is I or L

wherein residue 322 is I or V

wherein residue 323 is A or I or L or V

wherein residue 329 is D or E

wherein residue 330 is A or S

5 wherein residue 331 is R or D or E or G or K

wherein residue 342 is I or V

wherein residue 343 is H or S or V

wherein residue 345 is A or T

wherein residue 346 is R or E

10 wherein residue 347 is N or H or Y

wherein residue 348 is A or V

wherein residue 349 is R or Q or H or W

wherein residue 353 is I or V

wherein residue 357 is N or Y

15 wherein residue 359 is D or S

wherein residue 361 is R or N or E or T

wherein residue 362 is I or V

wherein residue 363 is H or I or L or V

wherein residue 365 is Q or H

20 wherein residue 371 is R or E or K

wherein residue 372 is I or V

wherein residue 379 is F or W or Y

wherein residue 380 is A or V

wherein residue 381 is R or Q or E or L or S

25 wherein residue 383 is A or L or V

wherein residue 385 is R or K

wherein residue 387 is I or L or V

wherein residue 388 is L or K

wherein residue 393 is G or S

30 wherein residue 397 is A or L or V

wherein residue 406 is N or G

wherein residue 408 is I or V

wherein residue 410 is S or T

wherein residue 411 is I or L

wherein residue 412 is I or L or M

wherein residue 413 is A or S

wherein residue 414 is Q or E

wherein residue 416 is L or W

5 wherein residue 418 is I or V

wherein residue 421 is C or I or M or T or V

wherein residue 423 is I or F

wherein residue 430 is S or T

wherein residue 433 is L or P

10 wherein residue 434 is D or G or Y

wherein residue 438 is H or Y

wherein residue 440 is R or K or P

wherein residue 441 is R or D or L or K

wherein residue 442 is N or H or F or Y

15 wherein residue 444 is A or D or Q or E or P

wherein residue 445 is D or Q or K

wherein residue 446 is H or Y

wherein residue 449 is A or S

wherein residue 456 is L or W

20 wherein residue 464 is A or I or F or V

wherein residue 466 is I or V

wherein residue 476 is N or T

wherein residue 478 is R or N or D or H

wherein residue 479 is E or S

25 wherein residue 486 is H or Y

wherein residue 487 is A or Q or G or S or T

wherein residue 488 is A or D or H or S

wherein residue 489 is F or Y

wherein residue 491 is L or M

30 wherein residue 497 is I or V

wherein residue 498 is E or I or V

wherein residue 499 is N or H

wherein residue 501 is I or V

wherein residue 506 is P or S

wherein residue 507 is R or K
wherein residue 511 is I or V
wherein residue 517 is A or P
wherein residue 518 is R or D or E or S
5 wherein residue 519 is I or T or V
wherein residue 522 is P or S
wherein residue 524 is A or S or T
wherein residue 525 is R or D or E
wherein residue 526 is H or K or T
10 wherein residue 528 is R or E or K
wherein residue 530 is L or F
wherein residue 531 is S or T
wherein residue 532 is G or S
wherein residue 534 is H or W
15 wherein residue 539 is R or E or K or S
wherein residue 540 is I or L or M
wherein residue 541 is I or L or W or V
wherein residue 542 is F or Y
wherein residue 543 is G or S
20 wherein residue 544 is R or D or G or P
wherein residue 545 is D or E or P
wherein residue 546 is D or Q or E or P or T
wherein residue 547 is R or G
wherein residue 548 is A or G or P
25 wherein residue 549 is D or E or P
wherein residue 550 is A or H or I
wherein residue 555 is A or E or K or S
wherein residue 557 is R or P
wherein residue 558 is D or Q or S
30 wherein residue 561 is I or L or V
wherein residue 562 is I or L
wherein residue 563 is L or F
wherein residue 564 is S or T
wherein residue 565 is I or M or V

wherein residue 566 is A or M or S
wherein residue 568 is L or M
wherein residue 574 is Q or I or L or M
wherein residue 575 is S or T
5 wherein residue 577 is L or W
wherein residue 578 is A or L or M or V
wherein residue 580 is I or L or W
wherein residue 581 is F or Y or V
wherein residue 583 is A or R
10 wherein residue 584 is N or S
wherein residue 585 is A or N or E or P or S
wherein residue 589 is E or S
wherein residue 594 is I or L or V
wherein residue 595 is I or L or V
15 wherein residue 596 is I or V
wherein residue 597 is A or G
wherein residue 600 is I or V
wherein residue 602 is A or P or V
wherein residue 603 is A or N or Q or E or G or S
20 wherein residue 604 is A or R or N or Q or E or K
wherein residue 606 is A or R or N or D or G or M or S or T
wherein residue 608 is A or R or E or G or H or S
wherein residue 611 is R or Q
wherein residue 612 is A or E
25 wherein residue 613 is Q or E
wherein residue 614 is I or M or V
wherein residue 615 is A or R or Q or E or G or K
wherein residue 617 is I or L or M
wherein residue 619 is Q or E
30 wherein residue 620 is I or L
wherein residue 621 is I or L or M
wherein residue 623 is R or E or H or K
wherein residue 624 is H or Y
wherein residue 625 is N or Q or G

wherein residue 630 is A or M or F or V
wherein residue 632 is L or W
wherein residue 633 is I or L or V
wherein residue 635 is A or L or S or V
5 wherein residue 636 is Q or H
wherein residue 638 is N or D or E
wherein residue 640 is R or N or T or V
wherein residue 641 is R or L or W or V
wherein residue 645 is I or L
10 wherein residue 648 is W or Y or V
wherein residue 649 is I or L or V
wherein residue 652 is R or Q or G or H or K or T
wherein residue 655 is A or I or V
wherein residue 656 is F or W or V
15 wherein residue 657 is I or V
wherein residue 662 is F or Y
wherein residue 672 is A or V
wherein residue 674 is A or S or T
wherein residue 679 is T or V
20 wherein residue 680 is F or W
wherein residue 683 is R or C
wherein residue 684 is H or Y
wherein residue 688 is A or L
wherein residue 693 is D or H
25 wherein residue 704 is D or Q or H
wherein residue 705 is G or P
wherein residue 706 is D or E
wherein residue 707 is A or Q or E
wherein residue 708 is A or T or V
30 wherein residue 709 is A or L
wherein residue 711 is R or I or L or K
wherein residue 712 is I or L or M
wherein residue 715 is F or W
wherein residue 716 is L or F

wherein residue 718 is A or R or H or K

wherein residue 719 is A or C

wherein residue 720 is A or R or K

wherein residue 721 is A or N or E

5 wherein residue 722 is R or N or D or E

wherein residue 724 is D or G or K or S or T

wherein residue 728 is R or E or K

wherein residue 731 is R or D or Q

wherein residue 732 is A or G

10 wherein residue 735 is A or Q or E or K

wherein residue 738 is R or E or S or Y

wherein residue 739 is A or E or S

wherein residue 744 is E or K

wherein residue 745 is R or L

15 wherein residue 746 is W or Y

wherein residue 750 is L or M or W

wherein residue 751 is A or L or M

wherein residue 753 is I or L

wherein residue 754 is A or I or L or M or S or V

20 wherein residue 756 is A or C or I or V

wherein residue 757 is A or I or M or F or W or Y

wherein residue 761 is R or K

wherein residue 762 is F or Y

wherein residue 764 is L or S or T

25 wherein residue 765 is N or K or S

wherein residue 768 is R or H or S

wherein residue 771 is M or T

wherein residue 772 is R or E

wherein residue 778 is I or F

30 wherein residue 783 is F or W or Y

wherein residue 792 is L or M (SEQ ID NO:1229)

19. The engineered sucrose synthase polypeptide of claim 12 that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at

least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1181-1227.

20. An engineered sucrose synthase polypeptide that has a score greater than 569.5 when scored by the PSSM shown in Table 28.

5 21. A polypeptide having the sequence of

MTXXLLXXXXXSXXXXXLXQFXRXLXXXXKXYXLRNXILXAFXXYCXXXXXP
 XXXXXXSXLXKLXXYTQEIIIDXEXLXWIXRPXIAXQEVXRLXVXDXTXXPXTI
 XELLDXRDLVNXYHPNXGDXXEXDXXPYDYXPXIRDXXKNIGXGVEFLNRXX
 SSKXFQDPRQXQXXXXXXXXXXHXYNGXQLXXNXRIRXPXXLXEQXKQXLXXL
 10 SDXXXXXXXXXEXRFELQXLGXEPGXGXTXARVRXTLEXXXQXXDSPDHQVXE
 AXXSRIPMXFRXXXXSXHGWFQEXVLGRPDTGGQVVXILDQXXXLEXQXXED
 XXXAGLXXLEXPKIXXXTRLIPNXEGTXCNXRLEKXYGTXXAWILRXPREFN
 PKVTQNWIXRFEIWPYLETXXXDXEXEXXAEXXXPDXIIGNYSDGNLXAFL LX
 RRXKXTQXNXAHALEKXXKYLFSXLYWQDLEDKYHFSXQFTADLIXMNAAXXIX
 15 SSTYQEIVGTPDSIGQYESYQSFTMPXLYXXVNGXELFXPKFNVXPPGXNEXVYF
 PYXXXXXXRXEXXXXRLEELLFTLEDPPXXIXGXXXXXXXXKRXXFSMXXRXDRIKNX
 TGLXEXXGXXXXLQEXCNLXXVAGXXXXXXXXSXDXEEXXEIEKXXQXXXXXYL
 XGKXXRLGIRLPKXDSGEXYRXXADXXGXFXQPALFEAFGLTILEXMIXGLPTFX
 TXFGGPLEIIQXXXNGFXINPTXLEEXAXXXXXFXXXCXXDPXXWXXXSXXXIX
 20 RVXXXYTWKIXXXXXXXXXLXXIXGXWNXXSQENREDXXRYXEAXXHLLXKPRA
 QXLLAEHLQR

wherein residue 3 is A or C or S

wherein residue 4 is D or E or V

wherein residue 7 is E or K

25 wherein residue 8 is A or S

wherein residue 9 is M or V

wherein residue 10 is I or L or W or V

wherein residue 11 is N or D or E

wherein residue 13 is D or E

30 wherein residue 14 is E or H

wherein residue 15 is R or K

wherein residue 16 is A or N or E or T

wherein residue 17 is A or D or E

wherein residue 19 is R or H

wherein residue 22 is I or L or F or S
wherein residue 24 is Q or I or L or Y
wherein residue 26 is R or D or Q
wherein residue 27 is A or R or D or L or T
5 wherein residue 28 is N or Q or G or K or S
wherein residue 29 is E or G
wherein residue 31 is R or G
wherein residue 33 is L or F
wherein residue 37 is D or E
10 wherein residue 40 is N or D or Q or G
wherein residue 43 is A or D or E or H
wherein residue 44 is D or E
wherein residue 47 is R or H
wherein residue 48 is A or N or D
15 wherein residue 49 is Q or L or K
wherein residue 50 is D or Q or E or G
wherein residue 51 is R or K
wherein residue 53 is A or E or V
wherein residue 54 is P or Y
20 wherein residue 55 is F or P or T
wherein residue 56 is P or Y
wherein residue 57 is D or H or L or S
wherein residue 58 is N or E or S
wherein residue 60 is R or G or S
25 wherein residue 62 is A or S or W
wherein residue 65 is I or V
wherein residue 66 is R or H or F or Y
wherein residue 73 is I or F or V
wherein residue 75 is N or D or E
30 wherein residue 77 is S or W
wherein residue 79 is C or W
wherein residue 82 is I or V
wherein residue 85 is R or Q or K
wherein residue 88 is R or Q

wherein residue 92 is C or W or Y or V

wherein residue 95 is H or L

wherein residue 97 is D or E

wherein residue 99 is L or M

5 wherein residue 101 is I or F or V

wherein residue 102 is E or V

wherein residue 104 is I or M

wherein residue 107 is Q or P

wherein residue 112 is A or L or F

10 wherein residue 119 is R or H

wherein residue 124 is D or E

wherein residue 127 is L or V

wherein residue 128 is L or F or W

wherein residue 130 is I or L

15 wherein residue 132 is M or W or V

wherein residue 133 is R or Q or E

wherein residue 135 is L or F

wherein residue 139 is F or S

wherein residue 141 is H or I or K or V

20 wherein residue 145 is A or P

wherein residue 150 is R or K

wherein residue 158 is F or Y

wherein residue 159 is I or L or M

wherein residue 163 is A or L

25 wherein residue 170 is G or W

wherein residue 172 is Q or E

wherein residue 173 is A or R or N or L or K or T

wherein residue 174 is L or F

wherein residue 175 is I or L or F

30 wherein residue 176 is N or D or Q

wherein residue 177 is F or W

wherein residue 178 is L or M

wherein residue 179 is R or Q

wherein residue 180 is I or V

wherein residue 182 is R or Q
wherein residue 186 is Q or I or Y
wherein residue 189 is G or L
wherein residue 190 is I or W or V
5 wherein residue 192 is D or E
wherein residue 196 is N or S
wherein residue 198 is Q or P
wherein residue 199 is Q or H
wherein residue 201 is A or L or M or S
10 wherein residue 204 is I or V
wherein residue 207 is A or L
wherein residue 209 is K or V
wherein residue 210 is A or I or F or T or W or Y or V
wherein residue 214 is R or Q
15 wherein residue 215 is A or P
wherein residue 216 is P or S
wherein residue 217 is A or D or T
wherein residue 218 is A or E
wherein residue 219 is A or P
20 wherein residue 220 is F or W or Y
wherein residue 221 is Q or E or S
wherein residue 223 is I or F
wherein residue 229 is N or E
wherein residue 232 is F or W
25 wherein residue 236 is L or W
wherein residue 238 is R or N or K
wherein residue 240 is A or V
wherein residue 245 is D or E
wherein residue 249 is I or L
30 wherein residue 250 is I or L or M or W
wherein residue 251 is A or D or L
wherein residue 253 is A or L or V
wherein residue 254 is A or I or L or M
wherein residue 262 is L or W

wherein residue 265 is L or F or W

wherein residue 266 is L or F or V

wherein residue 272 is I or L

wherein residue 275 is I or V

5 wherein residue 276 is A or I or L or V

wherein residue 277 is I or L

wherein residue 278 is I or V

wherein residue 280 is A or I or M or P or V

wherein residue 288 is N or G

10 wherein residue 301 is I or L or W or Y

wherein residue 306 is A or V

wherein residue 307 is R or Q or K

wherein residue 308 is A or N or S

wherein residue 311 is R or K

15 wherein residue 313 is I or L or M

wherein residue 314 is R or Q

wherein residue 317 is I or L

wherein residue 318 is Q or E or K

wherein residue 319 is E or L

20 wherein residue 323 is D or E or G

wherein residue 324 is W or V

wherein residue 327 is A or I

wherein residue 328 is R or Q

wherein residue 332 is I or L or V

25 wherein residue 333 is I or V

wherein residue 334 is A or I or L

wherein residue 341 is A or C or S

wherein residue 345 is R or L or T

wherein residue 348 is Q or E

30 wherein residue 353 is I or V

wherein residue 357 is N or D or E

wherein residue 358 is N or D or H

wherein residue 364 is I or V

wherein residue 379 is S or T

wherein residue 390 is A or F or W
wherein residue 391 is A or T or V
wherein residue 392 is I or L
wherein residue 394 is A or I or L or V
5 wherein residue 396 is R or K or T
wherein residue 398 is A or I or L or V
wherein residue 399 is R or L
wherein residue 402 is L or M or F
wherein residue 403 is Q or G
10 wherein residue 404 is G or H
wherein residue 405 is R or H or V
wherein residue 408 is L or V
wherein residue 419 is I or V
wherein residue 424 is A or S
15 wherein residue 427 is L or M or W
wherein residue 429 is I or V
wherein residue 432 is C or I or L or V
wherein residue 434 is I or M
wherein residue 441 is S or T
20 wherein residue 447 is N or D
wherein residue 461 is L or M
wherein residue 469 is A or T
wherein residue 474 is N or D
wherein residue 475 is A or F
25 wherein residue 477 is I or V
wherein residue 504 is D or E
wherein residue 507 is R or H
wherein residue 508 is I or V
wherein residue 512 is I or L
30 wherein residue 516 is H or S
wherein residue 522 is I or V
wherein residue 526 is A or V
wherein residue 529 is N or Q or E
wherein residue 535 is T or Y

wherein residue 536 is R or E or H
wherein residue 537 is R or N or Q or K or T or Y
wherein residue 538 is Q or E or T
wherein residue 539 is R or N or D or E or K
5 wherein residue 541 is L or V
wherein residue 543 is N or G or S
wherein residue 544 is D or E
wherein residue 545 is A or R
wherein residue 546 is Q or E
10 wherein residue 559 is Q or E or S
wherein residue 560 is Q or E
wherein residue 562 is F or Y or V
wherein residue 564 is N or H or K or Y
wherein residue 565 is I or L
15 wherein residue 566 is D or E or S
wherein residue 567 is A or N or D or H
wherein residue 568 is Q or L or P
wherein residue 569 is N or Q or E or H or K or S
wherein residue 572 is M or P
20 wherein residue 573 is I or L
wherein residue 577 is A or S
wherein residue 579 is A or L
wherein residue 585 is Q or I or L
wherein residue 589 is A or L or M
25 wherein residue 591 is A or C or L
wherein residue 592 is F or Y or V
wherein residue 594 is R or K
wherein residue 595 is N or S
wherein residue 596 is Q or K or P
30 wherein residue 597 is A or E or K
wherein residue 601 is R or Q or H or K
wherein residue 605 is I or V
wherein residue 606 is I or L or V
wherein residue 610 is K or Y

wherein residue 611 is A or L or V
wherein residue 612 is R or D
wherein residue 613 is P or T or V
wherein residue 614 is A or E
5 wherein residue 615 is D or G
wherein residue 617 is S or T
wherein residue 619 is R or S or Y
wherein residue 622 is R or I or K
wherein residue 623 is A or D
10 wherein residue 628 is I or L or M
wherein residue 629 is H or Y
wherein residue 631 is I or L
wherein residue 632 is I or M or V
wherein residue 633 is D or E or H or K
15 wherein residue 634 is Q or E
wherein residue 636 is N or Q
wherein residue 638 is N or Q or H or K or S
wherein residue 641 is A or I or V
wherein residue 643 is L or F or W
20 wherein residue 651 is A or N or G or I
wherein residue 656 is I or V
wherein residue 659 is I or V
wherein residue 660 is I or V
wherein residue 663 is R or H
25 wherein residue 664 is Q or G
wherein residue 666 is A or I or V
wherein residue 668 is A or V
wherein residue 683 is A or S
wherein residue 686 is S or T
30 wherein residue 692 is A or G
wherein residue 694 is R or Q
wherein residue 704 is N or D or H
wherein residue 705 is Q or G
wherein residue 706 is K or V

wherein residue 710 is H or Y

wherein residue 715 is D or H

wherein residue 719 is M or T

wherein residue 721 is E or K

5 wherein residue 722 is A or K or T

wherein residue 723 is I or L

wherein residue 724 is L or M or F or V

wherein residue 725 is R or K

wherein residue 727 is I or L or F

10 wherein residue 728 is A or E

wherein residue 729 is A or R or Q or H or K

wherein residue 731 is N or D

wherein residue 732 is R or Q or H or K

wherein residue 735 is N or Q or E

15 wherein residue 736 is Q or E or H or Y

wherein residue 738 is Q or E or Y

wherein residue 739 is R or E

wherein residue 740 is I or L

wherein residue 742 is Q or E or K

20 wherein residue 743 is A or R or K

wherein residue 744 is A or G or S

wherein residue 746 is D or Q or E

wherein residue 749 is R or Y

wherein residue 750 is E or S

25 wherein residue 751 is N or K or T

wherein residue 757 is H or F or W or Y

wherein residue 758 is A or C or T

wherein residue 759 is E or K or S or T

wherein residue 760 is R or K

30 wherein residue 761 is I or L or M or W

wherein residue 762 is L or M

wherein residue 763 is S or T

wherein residue 765 is A or I or S or V

wherein residue 766 is R or K

wherein residue 768 is M or Y

wherein residue 770 is L or F

wherein residue 773 is F or Y

wherein residue 774 is I or M or S or T or V

5 wherein residue 782 is L or M

wherein residue 783 is L or M or W

wherein residue 786 is I or L or M

wherein residue 789 is I or L or M

wherein residue 790 is F or Y

10 wherein residue 794 is F or Y

wherein residue 800 is A or R or Q or K (SEQ ID NO: 1230)

22. A method for transferring a sugar moiety to a substrate steviol glycoside, the method comprising contacting a B12GT and a sucrose synthase with one or more steviol glycosides, a non-UDP nucleotide diphosphate, and sucrose.

15 **23.** The method of claim 22, wherein the B12GT polypeptide is an engineered B12GT that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-882 and 1333-1466.

20 **24.** The method of claim 22, wherein the SuSy polypeptide is an engineered sucrose synthase that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 883-1227 and 1231-1332.

25 **25.** The method of claim 22, wherein

(a) the B12GT polypeptide is an engineered B12GT that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-882 and 1333-1466, and

30

(b) the SuSy polypeptide is an engineered sucrose synthase that comprises an amino acid sequence that is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100%

identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 883-1227 and 1231-1332.

26. The method of claim 22, wherein the B12GT polypeptide is an engineered B12GT that has a score greater than 266.7 when scored by the PSSM shown in Table 17.

5 **27.** The method of claim 22, wherein the SuSy polypeptide is an engineered sucrose synthase that has a score greater than 556 when scored by the PSSM shown in Table 24.

28. The method of claim 22, wherein the SuSy polypeptide is an engineered sucrose synthase that has a score greater than 194.5 when scored by the PSSM shown in Table 28.

29. The method of claim 22, wherein

10 (a) the B12GT polypeptide is an engineered B12GT that has a score greater than 266.7 when scored by the PSSM shown in Table 17 and

(b) the SuSy polypeptide is an engineered sucrose synthase that has a score greater than 194.5 when scored by the PSSM shown in Table 28.

30. The method of claim 22, wherein

15 (a) the B12GT polypeptide is an engineered B12GT that has a score greater than 266.7 when scored by the PSSM shown in Table 17 and

(b) the SuSy polypeptide is an engineered sucrose synthase that has a score greater than 556 when scored by the PSSM shown in Table 24.

20 **31.** The method of any of claims 22 to 30, wherein the substrate steviol glycoside is steviol, steviol-13-O-glucoside, steviol-19-O-glucoside, rubusoside, steviol-1,2-bioside, steviol-1,3-bioside, rubusoside, dulcoside B, dulcoside A, rebaudioside B, rebaudioside G, stevioside, rebaudioside C, rebaudioside F, rebaudioside A, rebaudioside I, rebaudioside E, rebaudioside H, rebaudioside L, rebaudioside K, rebaudioside J, rebaudioside M, rebaudioside D, rebaudioside N, rebaudioside O, rebaudioside Q, an isomer thereof, a
25 synthetic steviol glycoside or combinations thereof.

32. The method of any of claims 22 to 30, wherein the substrate steviol glycoside is a mixture of stevioside and rebaudioside A.

30 **33.** The method of any of claims 22 to 32, wherein the target steviol glycoside is steviol, steviol-13-O-glucoside, steviol-19-O-glucoside, rubusoside, steviol-1,2-bioside, steviol-1,3-bioside, rubusoside, dulcoside B, dulcoside A, rebaudioside B, rebaudioside G, stevioside, rebaudioside C, rebaudioside F, rebaudioside A, rebaudioside I, rebaudioside E, rebaudioside H, rebaudioside L, rebaudioside K, rebaudioside J, rebaudioside M, rebaudioside D, rebaudioside N, rebaudioside O, rebaudioside Q, an isomer thereof, a synthetic steviol glycoside or combinations thereof.

34. The method of any of claims 22 to 32, wherein the target steviol glycoside is a mixture of rebaudioside E and rebaudioside D.
35. The method of any of claims 22 to 32, wherein the target steviol glycoside is rebaudioside D.
- 5 36. The method of any of claims 22 to 32, wherein the target steviol glycoside is rebaudioside E.
37. The method of any of claims 22 to 36, wherein the non-UDP nucleotide diphosphate is ADP, GDP, CDP, or TDP.
38. The method of any of claims 22 to 37, wherein the non-UDP nucleotide diphosphate is
10 ADP.
39. A polynucleotide encoding a polypeptide of any of claims 1-18.
40. A host microorganism heterologously expressing a polynucleotide of claim 36.

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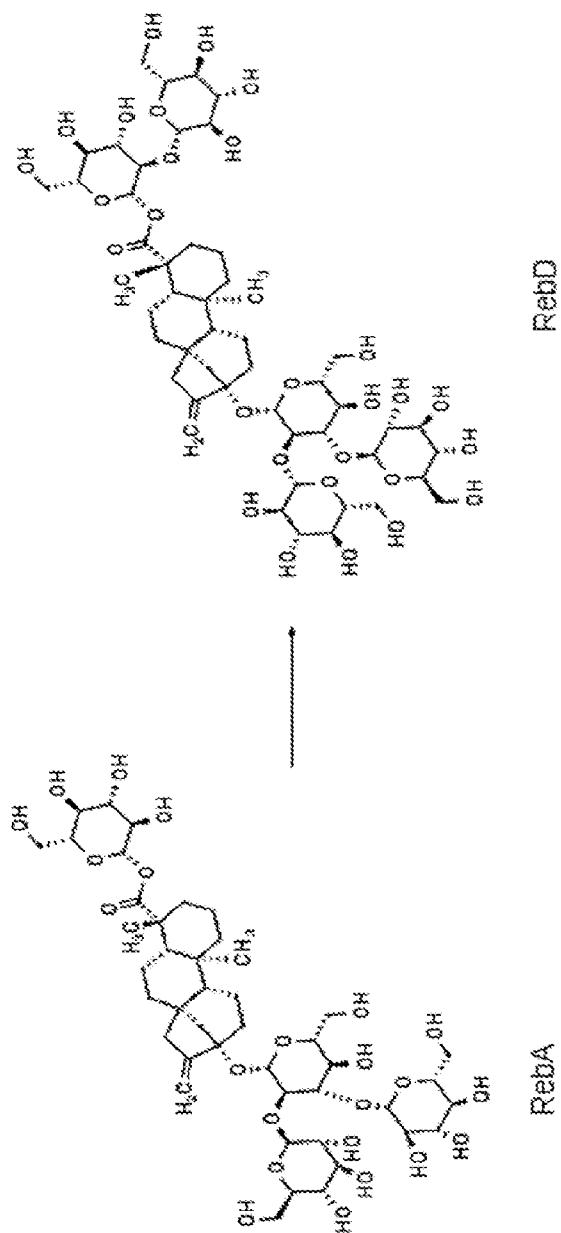


FIG. 1

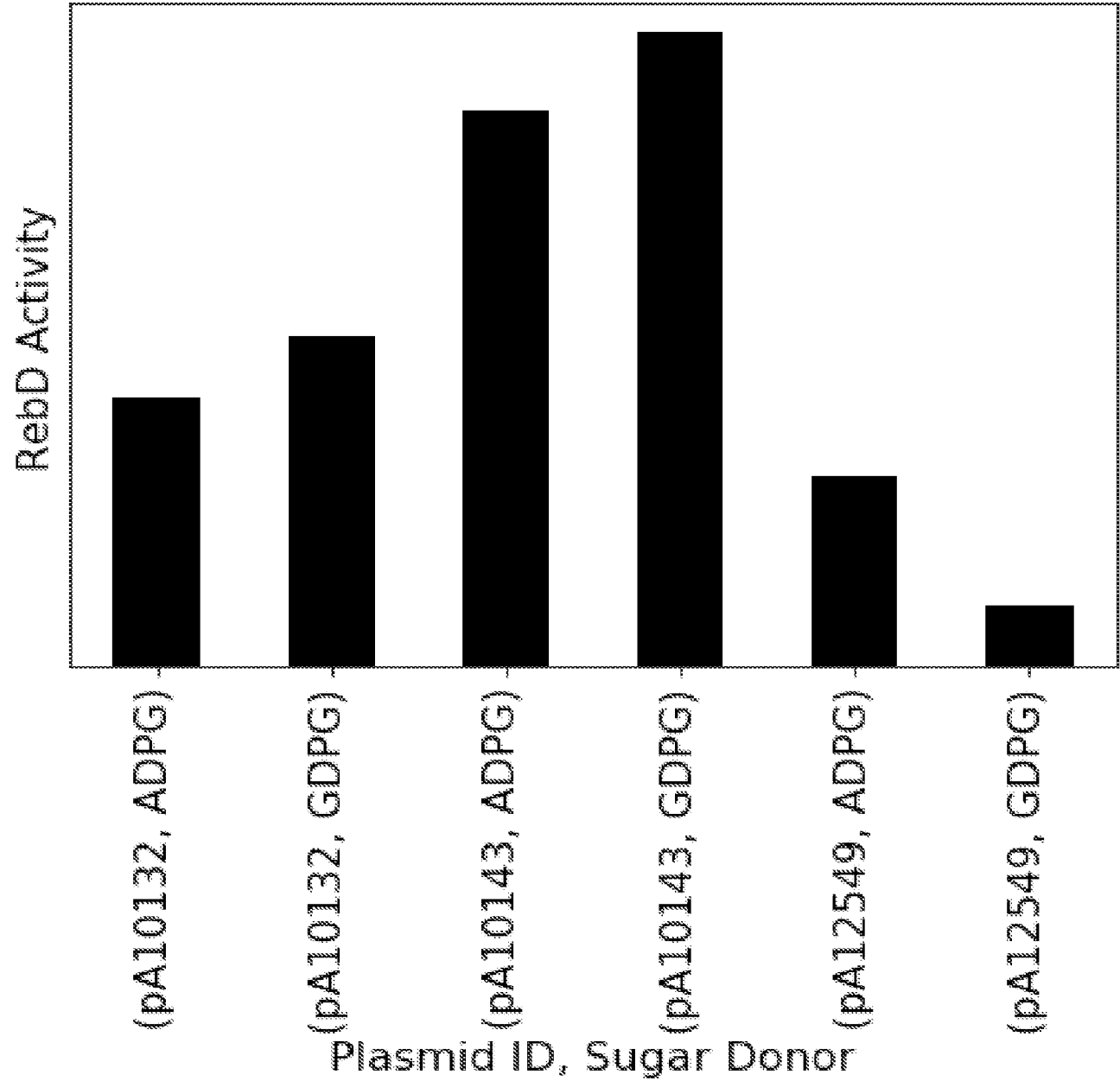


FIG. 2

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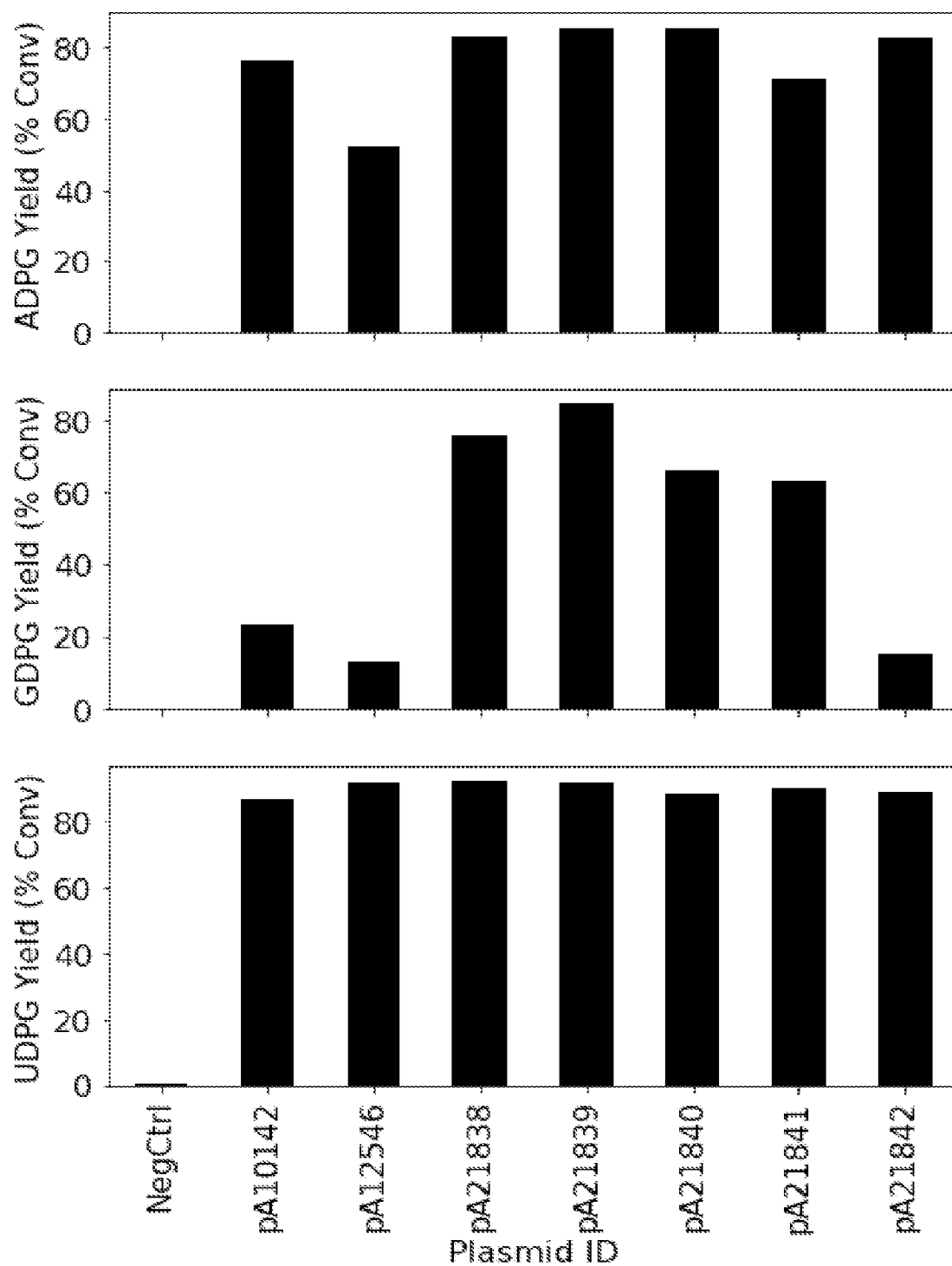


FIG. 3

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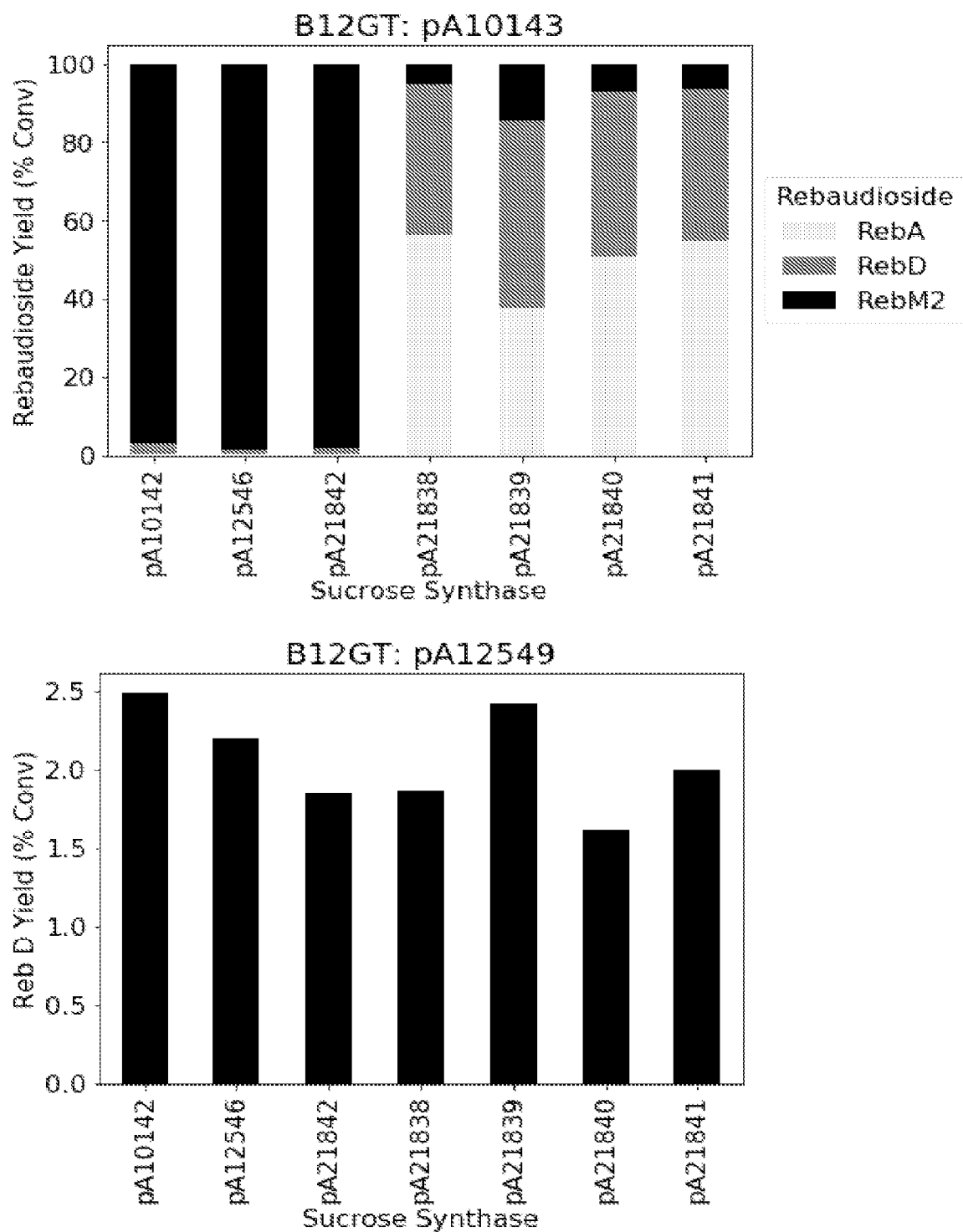


FIG. 4

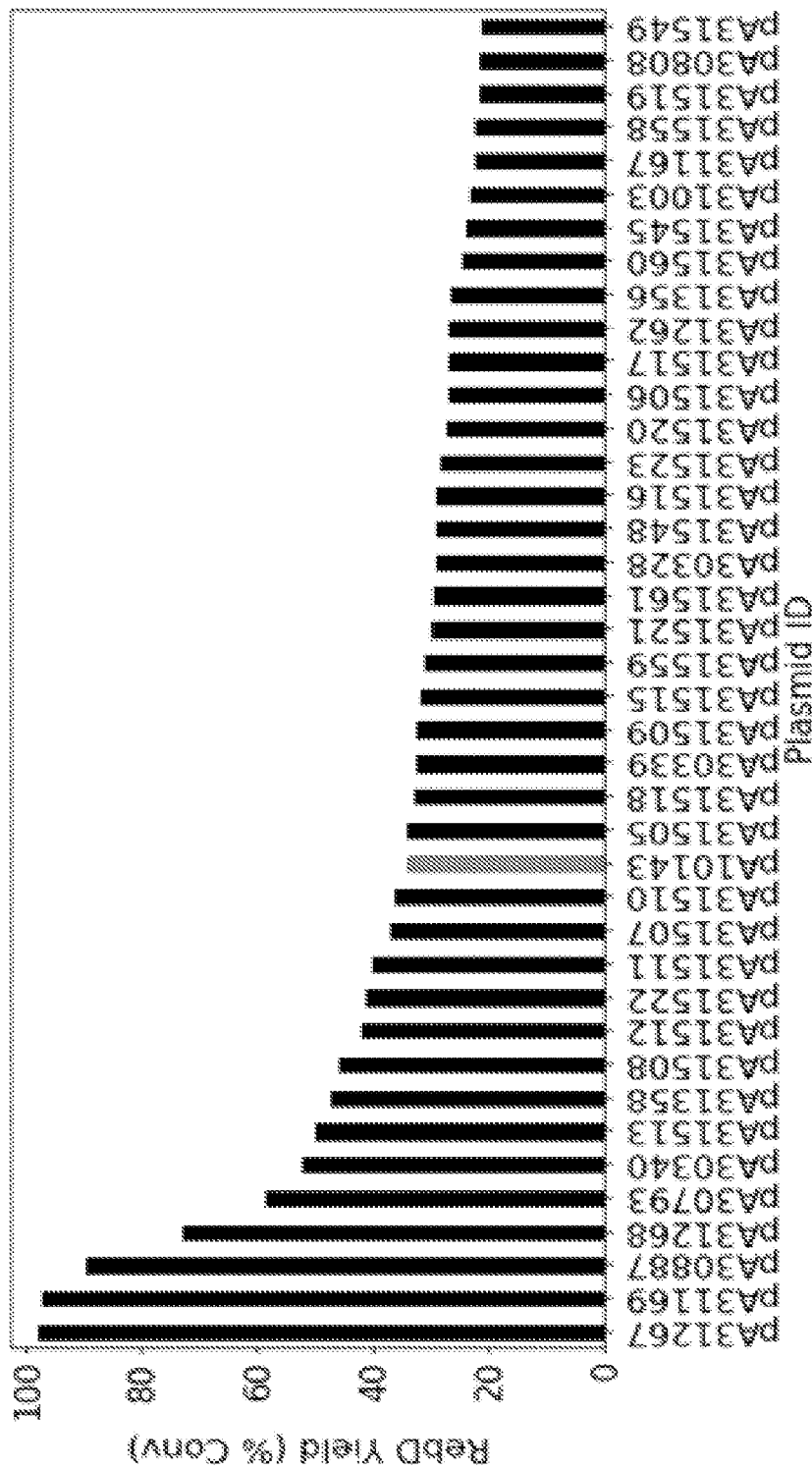


FIG. 5

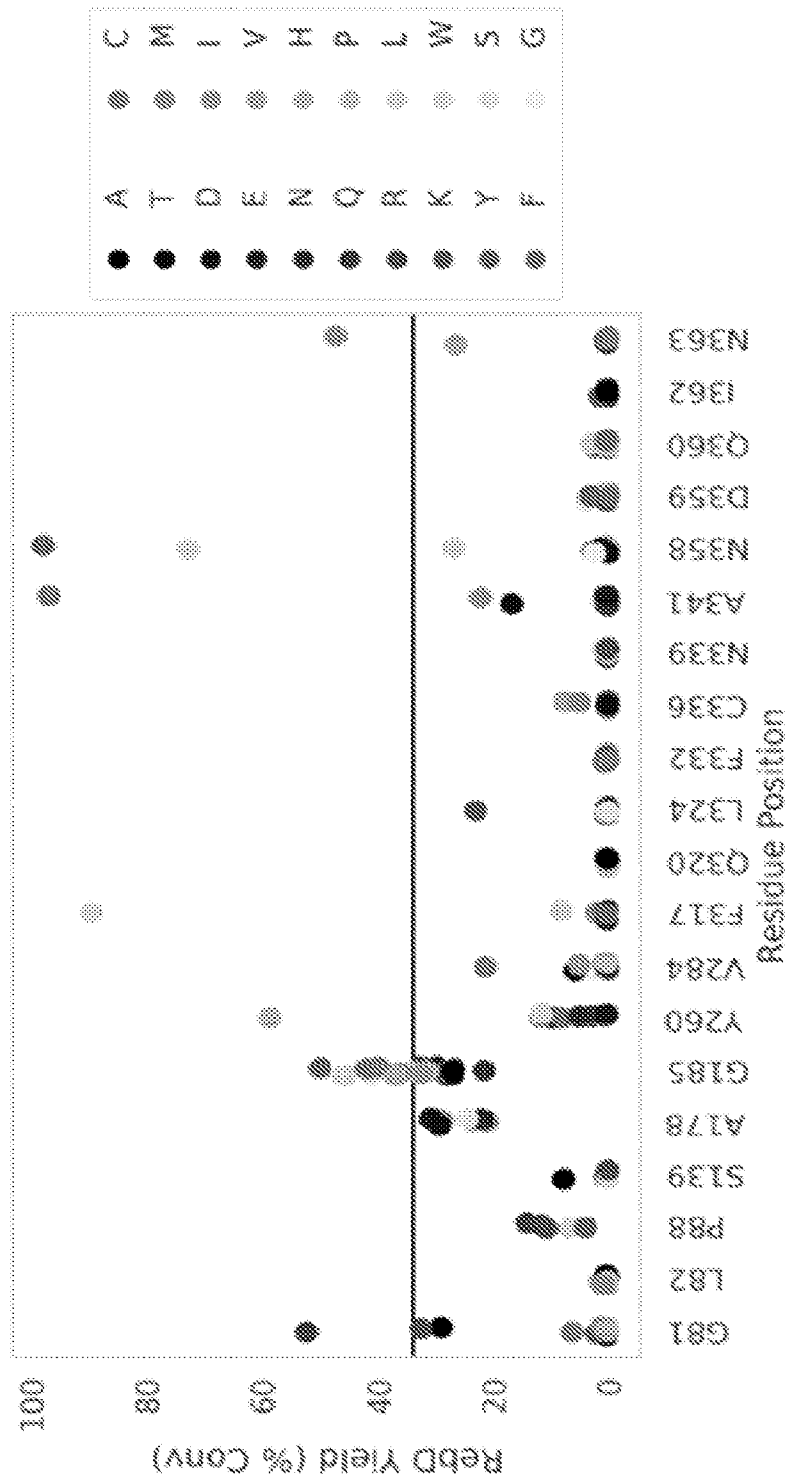


FIG. 6

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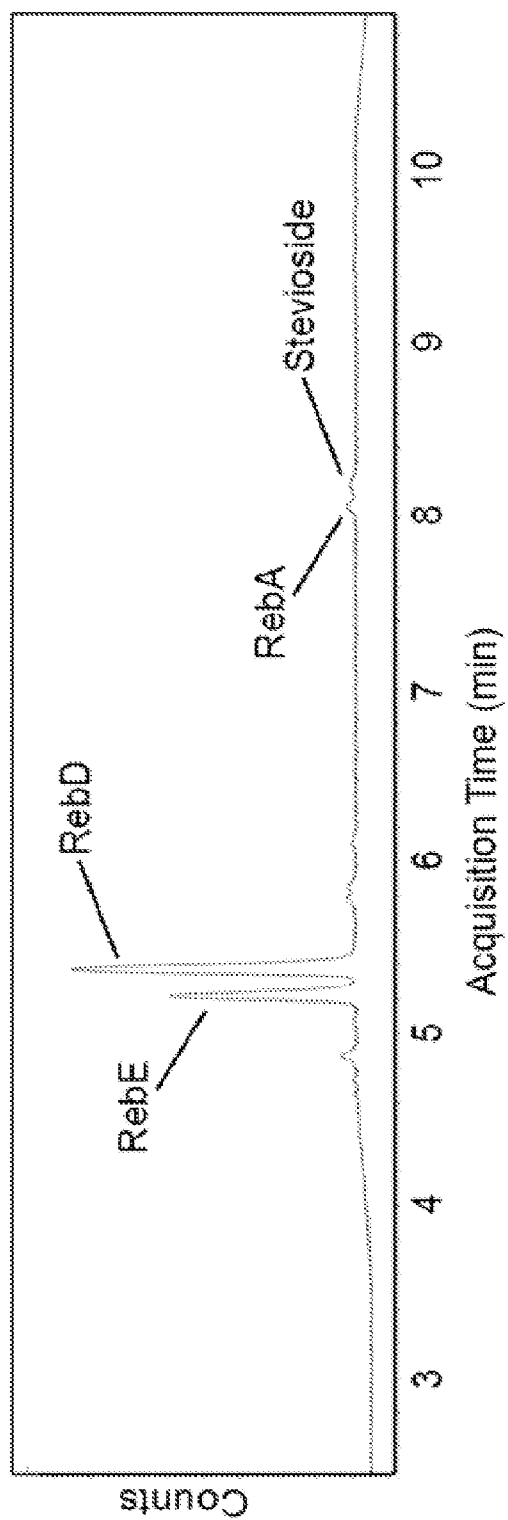


FIG. 7

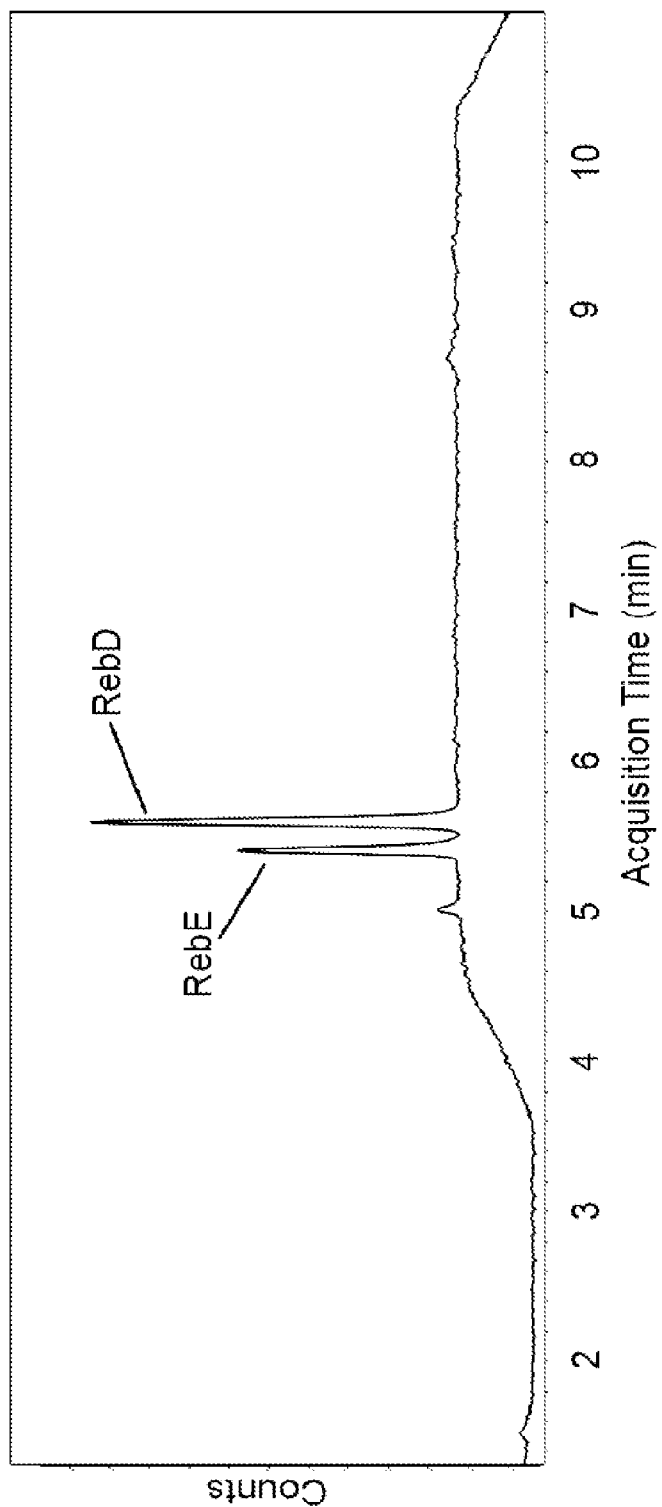


FIG. 8

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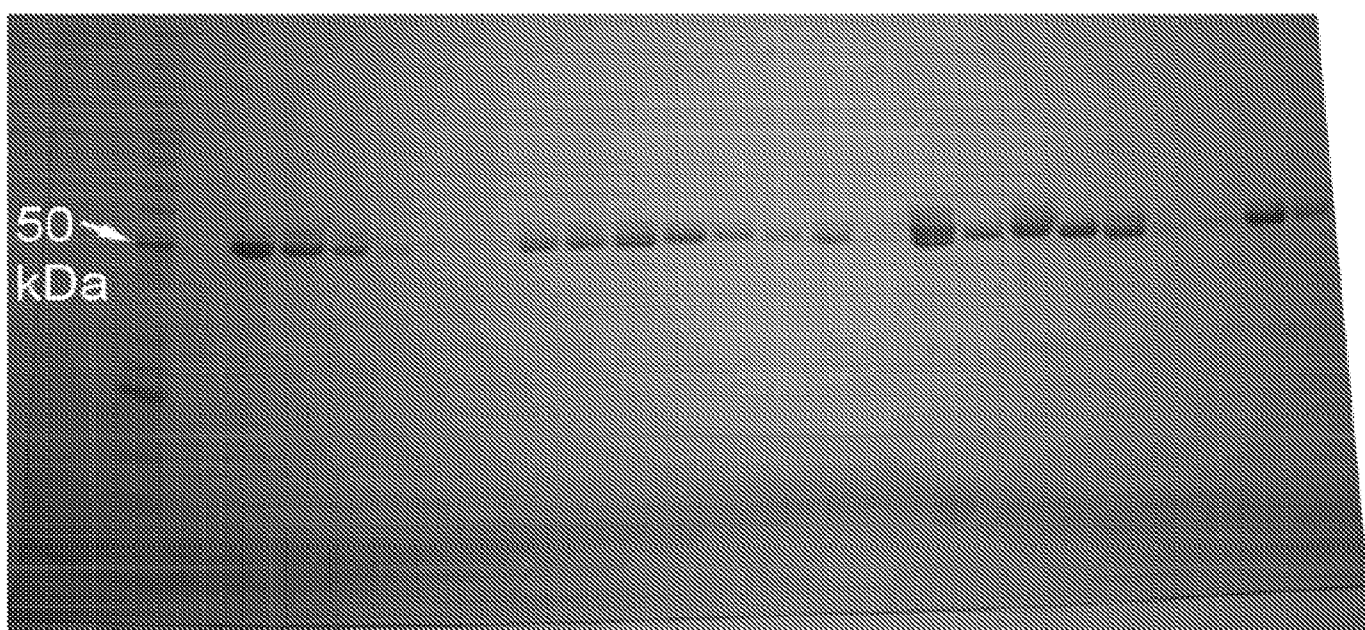


FIG. 9

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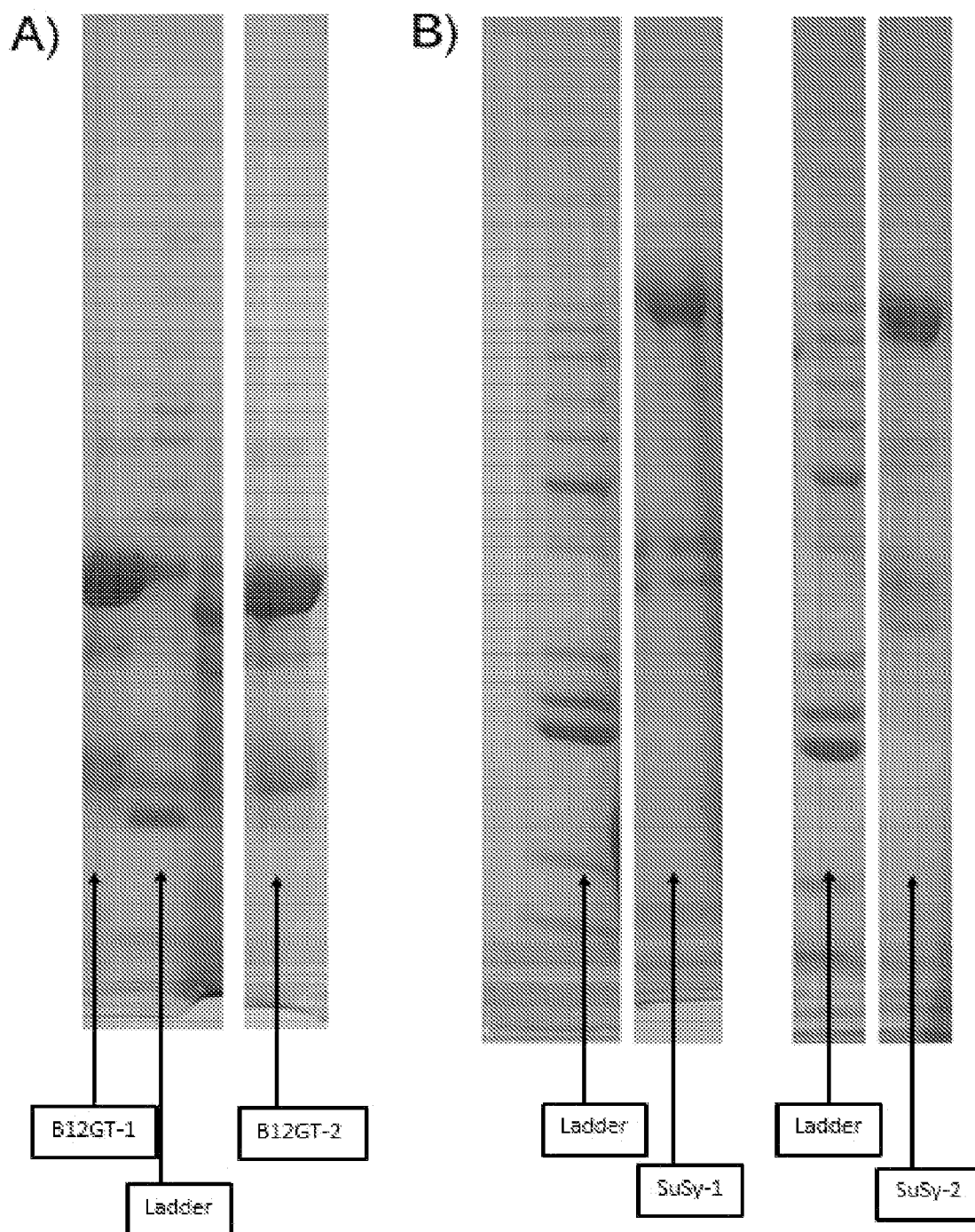


FIG. 10

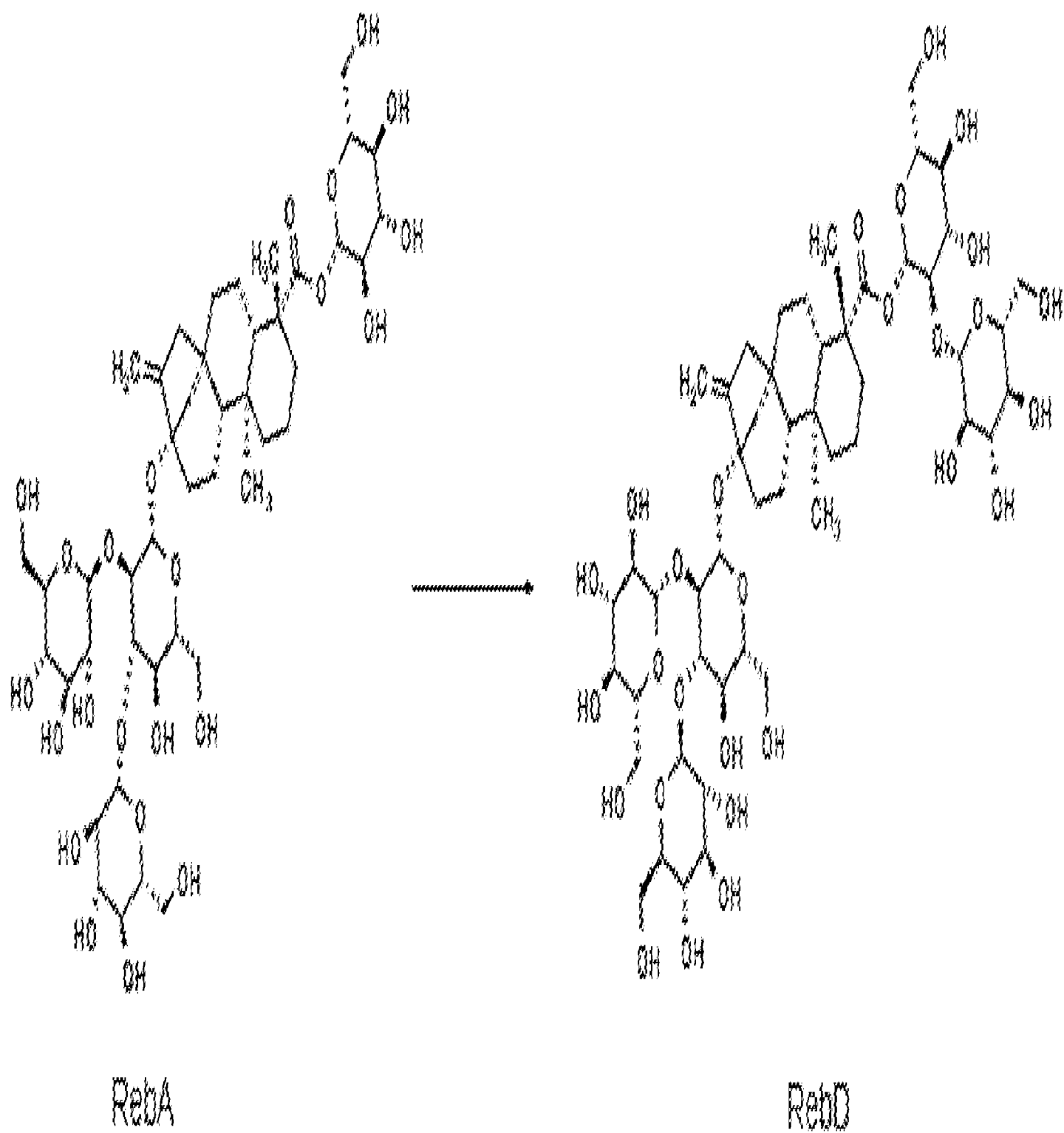


FIG. 1