FATTY ACID HYDRATASES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of Singapore provisional application no. 10202301091Q, filed 19 April 2023, the contents of it being hereby incorporated by reference in its entirety for all purposes.

FIELD OF THE INVENTION

[0002] The present invention relates generally to the field of biotechnology. In particular, the present invention relates to fatty acid hydratases and methods of producing hydroxy fatty acids from unsaturated fatty acids by a hydration reaction catalysed by one or a combination of fatty acid hydratase enzymes.

BACKGROUND OF THE INVENTION

[0003] Hydroxy fatty acids (HFAs) are saturated and unsaturated fatty acids with one or more hydroxyl functional groups attached to carbon atom/s along the carbon chain. They are essential chemical compounds for the production of biodegradable polymers, lubricants, emulsifiers, drugs, cosmetic ingredients, and flavours. Some hydroxy fatty acids and their derivatives have also been shown to possess beneficial biological activities, indicating suitability for application in the medical and functional foods sectors.

[0004] Hydroxy fatty acids can be produced from unsaturated fatty acids by the activity of a fatty acid hydratase (EC 4.2.1.53). Fatty acid hydratase is an enzyme that catalyses the hydroxylation of unsaturated fatty acids to produce hydroxy fatty acids. Fatty acid hydratases are classified into 11 homologous families based on protein sequence similarity.

[0005] However, the regioselectivity of fatty acid hydratases can be unpredictable. It has been shown that fatty acid hydratases within the same homologous families may exhibit a completely different positional selectivity, thereby resulting in different substrate and product scopes. For example, fatty acid hydratases within homologous family 2 (HFam 2) have been shown to hydroxylate unsaturated fatty acids ranging 14 to 22 carbon atoms in length, targeting carbon-carbon *cis*-double bond/s at position 9 only, at position 12 only, or at both positions. Another fatty acid hydratase within the same family, FA-HY1 from *Lactobacillus acidophilus*, has also been shown to hydroxylate unsaturated fatty acids with a carbon-carbon *cis*-double bond at position 11, 13, or 14.

[0006] Thus, there is an unmet need for fatty acid hydratases with defined regioselectivity and improved fatty acid hydroxylating activity.

SUMMARY

[0007] In one aspect, the present disclosure refers to a method of producing hydroxy fatty acids comprising contacting at least one fatty acid hydratase with one or more unsaturated fatty acids, wherein

the fatty acid hydratase comprises, or consists of, an amino acid sequence selected from the group consisting of SEQ ID NOs 1 to 8, and 11 to 23 or the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

[0008] In another aspect, the present disclosure refers to a fatty acid hydratase comprising a protein sequence with a sequence identity of at least 83% to a protein sequence selected from the group consisting of SEQ ID Nos 1 to 8, and 11 to 23.

[0009] In yet another aspect, the present disclosure refers to a fatty acid hydratase comprising a nucleic acid sequence with a sequence identity of at least 83% to a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

[0010] In one aspect, the present disclosure refers to a vector expressing a protein sequence selected from the group consisting of SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

[0011] In another aspect, the present disclosure refers to a host cell comprising the vector as disclosed herein.

[0012] In yet another aspect, the present disclosure refers to a method of producing hydroxy fatty acids, the method comprising culturing the host cell as disclosed herein under conditions suitable for culturing of the host cell.

[0013] In one aspect, the present disclosure refers to a method of producing poly-hydroxy fatty acids, the method comprising two or more of the fatty acid hydratases as disclosed herein.

[0014] In another aspect, the present disclosure refers to a method of producing hydroxy fatty acids, the method comprising use of a host cell or a native bacterial strain comprising a fatty acid hydratase as disclosed herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0015] The invention will be better understood with reference to the detailed description when considered in conjunction with the non-limiting examples and the accompanying drawings, in which:

[0016] **Fig. 1** shows the results of *in silico* gene mining and sequence similarity analysis of 108 putative fatty acid hydratases (FAHs). Fig. 1(a) shows the results of a sequence similarity analysis comparing 108 putative fatty acid hydratases with 55 described fatty acid hydratases (and among themselves) to identify 42 putative fatty acid hydratases that shared <83% sequence identity with the described fatty acid hydratases and <97% sequence identity to one another. In total, 21 of the 42 putative fatty acid hydratases were selected for the screening of fatty acid-hydroxylating activities along with two control fatty acid hydratases. Fig. 1(b) shows a phylogenetic tree based on protein sequences showing the relationship between the 21 selected putative fatty acid hydratases and the two control fatty acid hydratases (indicated with an asterisk). The maximum-likelihood tree was inferred under the LG+G4 protein substitution model (optimal log-likelihood of -11608.2102) using IQ-TREE, rooted by midpoint-rooting, and visualised using

iTOL. Ultrafast bootstrap values based on 1,000 replications are indicated at branch points. The scale bar denotes 0.1 substitutions per amino acid position. HFam, homologous family; SeqID, sequence identity.

[0017] **Fig. 2** shows the results of screening 21 identified fatty acid hydratases for fatty acid-hydroxylating activities. Fig. 2(a) shows the classification of both identified and control fatty acid hydratases into three different subtypes based on the profile of hydroxy fatty acids produced from oleic acid (OA) and linoleic acid (LA) in Wilfarin OA-7075. Fig. 2(b) shows a scatter plot illustrating the total conversion of hydroxy fatty acids from oleic acid and linoleic acid by the 21 identified fatty acid hydratases and the two control fatty acid hydratases. The graph shows the mean percentage conversion ± standard deviations of two independent replicates after 48 hours of incubation at 40°C. Fig. 2(c) shows a bar graph illustrating the percentage conversion of oleic acid into 10-hydroxystearic acid (10-HSA), and linoleic acid into (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) and 10,13-dihydroxystearic acid (10,13-dHSA) by the 21 identified fatty acid hydratases and the two control fatty acid hydratases. Bars show the mean percentage conversion ± standard deviations of two independent replicates after 24 hours of incubation at 40°C. For fatty acid abbreviations, refer to Table 2.

[0018] **Fig. 3** shows schematic illustrations of the hydroxylation reactions of unsaturated fatty acids catalysed by fatty acid hydratases. Fig. 3 (a-e) show hydroxylation of monounsaturated fatty acids. Fig. 3 (f-j) show hydroxylation of polyunsaturated fatty acids. For fatty acid abbreviations, refer to Table 2.

[0019] **Fig. 4** shows the results of characterising the regioselectivity, substrate selectivity, and product scopes of 17 identified fatty acid hydratases. The 17 identified fatty acid hydratases, representing the top performers of each subtype, were selected for characterisation with a panel of nine different unsaturated fatty acid substrates, alongside the two control fatty acid hydratases (indicated with an asterisk). The heat map shows the mean percentage conversion ± standard deviation of three independent replicates (light grey, no conversion; dark grey, 100% conversion) after 24 hours of incubation at 40°C. For fatty acid abbreviations, refer to Table 2.

[0020] **Fig. 5** shows the results of using dual-protein systems for poly-hydroxy fatty acid production. Fig. 5(a) is a schematic illustration of the dual-protein system, consisting of an identified fatty acid hydratase of the *cis*-Δ9 subtype and an identified fatty acid hydratase of the *cis*-Δ12 subtype. The protein pair was thought to work simultaneously or sequentially to convert a polyunsaturated fatty acid first into mono-hydroxy fatty acid intermediates and then into the di-hydroxy fatty acid product. Fig. 5 (b-e) are bar charts showing the efficiency of the dual-protein systems in generating di-hydroxy fatty acids from (Fig. 5b) linoleic acid (LA), (Fig. 5c) arachidonic acid (ARA), (Fig. 5d) α-linolenic acid (ALA), and (Fig. 5e) γ-linolenic acid (GLA) as compared to those produced by the top two identified fatty acid hydratases of the *cis*-Δ9/12 subtype. The bar charts show the mean percentage conversion ± standard deviation of three independent replicates after 24 hours of incubation at 40°C. The numerical values above the bars indicate the mean percentage conversion of di-hydroxy fatty acids. For fatty acid abbreviations, refer to Table 2.

[0021] **Fig. 6** shows a phylogenetic tree based on protein sequences illustrating the relationship between the 21 identified fatty acid hydratases (FAHs), the two control fatty acid hydratases, and the 55

described fatty acid hydratases (CTR0001-0055). Described fatty acid hydratases were classified into the three different subtypes based on their reported positional selectivity and hydroxy fatty acid product scopes. Inactive fatty acid hydratases, control fatty acid hydratases, and fatty acid hydratases with unknown positional selectivity are indicated with a cross (×), an asterisk (*), or as not available (NA), respectively. Uncoloured clades consist of fatty acid hydratases of the *cis*-Δ9 subtype, inactive fatty acid hydratases, and fatty acid hydratases with unknown positional selectivity (except CTR0009, which is a described fatty acid hydratase of the *cis*-Δ9/12 subtype). The maximum-likelihood tree was inferred under the LG+I+G4 protein substitution model (optimal log-likelihood of -24196.4090) using IQ-TREE, rooted by midpoint-rooting, and visualized using FigTree. Ultrafast bootstrap values based on 1,000 replications are indicated at branch points. The scale bar denotes 0.2 substitutions per amino acid position. Hybrids were synthetic fusion proteins made up of partial protein sequences of fatty acid hydratases isolated from *Lcc*. *lactis* and *Lys*. *Fusiformis*. *Alk*, *Alkaliphilus*; *Bf*, *Bifidobacterium*; *Chr*, *Chryseobacterium*; *Cl*, *Clostridium*; *Cpc*, *Coprococcus*; *Dsf*, *Desulfomicrobium*; *Elz*, *Elizabethkingia*; *Ent*, *Enterococcus*; *Fu*, *Furfurilactobacillus*; *Glc*, *Gluconobacter*; *Gml*, *Gemella*; *Hc*, *Haloarcula*; *Ht*, *Haloterrigena*; *L*, *Lactobacillus*; *Lc*, *Lacticaseibacillus*; *Lcc*, *Lactococcus*; *Lg*, *Ligilactobacillus*; *Lm*, *Limosilactobacillus*; *Lp*, *Lactiplantibacillus*; *Lq*, *Liquorilactobacillus*; *Lu*, *Leuconostoc*; *Lv*, *Levilactobacillus*; *Lys*, *Lysinibacillus*; *M*, *Mucilaginibacter*; *Mc*, *Macrococcus*; *N*, *Nectria*; *Pc*, *Pediococcus*; *Rd*, *Rhodococcus*; *Shr*, *Sharpea*; *Stn*, *Stenotrophomonas*; *Stp*, *Staphylococcus*; *Str*, *Streptococcus*; *Thr*, *Thermoanaerobacterium*.

[0022] **Fig. 7** shows the plasmid maps of vectors used herein. Fig. 7(a) shows the plasmid map of the pET-15b vector. Fig. 7(b) shows the plasmid map of the expression plasmid pET-15b-XXXX (XXX refers to the abbreviation of each identified fatty acid hydratase). pET-15b-XXXX plasmid was constructed by cloning the nucleotide sequences encoding the identified fatty acid hydratases and the control fatty acid hydratases into the region between the *BamHI* and *NdeI* restriction digestion sites of the pET-15b vector. Expression of identified fatty acid hydratases and control identified fatty acid hydratases was induced upon the addition of lactose or isopropyl β-D-1-thiogalactopyranoside (IPTG) to derepress LacI-*lac* operator inhibition on the T7 promoter.

[0023] **Fig. 8** shows the results of examining the hydroxylation efficiency of the identified fatty acid hydratases at higher substrate concentrations and larger biotransformation scales. Fig. 8(a) shows a bar chart illustrating the efficiency of converting oleic acid (OA) into 10-hydroxystearic acid (10-HSA) by identified and control fatty acid hydratases at 100g L^{-1} of Wilfarin OA-7075. Fig. 8(b) shows a bar chart illustrating the efficiency of converting linoleic acid (LA) into (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), and 10,13-dihydroxystearic acid (10,13-dHSA) by identified and control fatty acid hydratases at a 100g L^{-1} of linoleic acid. Three representative identified fatty acid hydratases of each subtype were examined along with the two control fatty acid hydratases (indicated with an asterisk). Each bar indicates the mean percentage conversion ± standard deviation of three independent replicates after 24 hours of incubation at 40°C. Fig. 8(c) shows the growth kinetic graph of a 1 L fermenter culture of a representative recombinant *E. coli* strain expressing the identified fatty acid

hydratase WIL0024-HY15.1. Fig. 8(d) is a bar chart showing the efficiency of converting oleic acid (OA) to 10-hydroxystearic acid (10-HSA). Cells harvested from the 1L fermenter culture were used to set up biotransformation reactions with 100 g L^{-1} Wilfarin OA-7075 at a larger scale of 30 and 250 mL, at 40°C for 24 hours. For fatty acid abbreviations, refer to Table 2.

[0024] **Fig. 9** shows representative overlays of liquid chromatography-tandem mass spectrometry (LC-MS/MS) extracted ion chromatograms (EIC) showing the hydroxylation products of (Fig. 9a) palmitoleic acid (PA), (Fig. 9b) (8Z)-heptadec-8-enoic acid (HA), (Fig. 9c) oleic acid (OA), (Fig. 9d) vaccenic acid (VA), and (Fig. 9e) ricinoleic acid (RA), in reaction mixtures containing induced *E. coli* cells expressing one of the identified fatty acid hydratases. The mass-to-charge ratios (m/z) used to extract the precursor ion of each compound are shown in Table 6. Peaks of monounsaturated fatty acid substrates and their hydroxylation products are labelled with arrows. For fatty acid abbreviations, refer to Table 2.

[0025] **Fig. 10** shows representative overlays of liquid chromatography-tandem mass spectrometry (LC-MS/MS) extracted ion chromatograms (EIC) showing the hydroxylation products of (Fig. 10a) linoleic acid (LA), (Fig. 10b) α-linolenic acid (ALA), (Fig. 10c) γ-linolenic acid (GLA), and (Fig. 10d) arachidonic acid (ARA), in reaction mixtures containing induced *E. coli* cells expressing one of the identified fatty acid hydratases. The mass-to-charge ratios (m/z) used to extract the precursor ion of each compound are shown in Table 6. Peaks of polyunsaturated fatty acid substrates and their hydroxylation products are labelled with arrows. For fatty acid abbreviations, refer to Table 2.

[0026] **Fig. 11** shows representative liquid chromatography-tandem mass spectrometry (LC-MS/MS) spectra of (Fig. 11a) 10-hydroxypalmitic acid (10-HPA), (Fig. 11b) 9-hydroxyheptadecanoic acid (9-HHA), (Fig. 11c) 10-hydroxystearic acid (10-HSA), (Fig. 11d) 12-hydroxystearic acid (12-HSA), (Fig. 11e) 10,12-dihydroxystearic acid (10,12-dHSA), and (Fig. 11f) 10,13-dihydroxystearic acid (10,13-dHSA) detected in reaction mixtures containing induced *E. coli* cells expressing one of the identified fatty acid hydratases and the respective unsaturated fatty acid substrates. Fragmentation is indicated by the dotted lines together with the corresponding mass-to-charge ratios (m/z) of the resulting fragment ions. For fatty acid abbreviations, refer to Table 2.

[0027] **Fig. 12** shows representative liquid chromatography-tandem mass spectrometry (LC-MS/MS) spectra of (Fig. 12a) (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (Fig. 12b) (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), (Fig. 12c) (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE), (Fig. 12d) (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE), and (Fig. 12e) (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE) detected in reaction mixtures containing induced *E. coli* cells expressing one of the identified fatty acid hydratases and the respective unsaturated fatty acid substrates. Fragmentation is indicated by the dotted lines together with the corresponding mass-to-charge ratios (m/z) of the resulting fragment ions. For fatty acid abbreviations, refer to Table 2.

[0028] **Fig. 13** shows representative liquid chromatography-tandem mass spectrometry (LC-MS/MS) spectra of (Fig. 13a) (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), (Fig. 13b) (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), (Fig. 13c) (9Z,15Z)-13-hydroxyoctadeca-

9,15-dienoic acid (α-13-HODE), (Fig. 13d) (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE), (Fig. 13e) (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), and (Fig. 13f) (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE) detected in reaction mixtures containing induced *E. coli* cells expressing one of the identified fatty acid hydratases and the respective unsaturated fatty acid substrates. Fragmentation is indicated by the dotted lines together with the corresponding mass-to-charge ratios (m/z) of the resulting fragment ions. For fatty acid abbreviations, refer to Table 2.

DEFINITIONS

[0029] As used herein, the term "fatty acid hydratases (FAHs)" refers to enzymes that catalyse the hydration of unsaturated bonds in fatty acids, leading to the formation of hydroxyl groups. In other words, fatty acid hydratases are enzymes that catalyse the addition of a hydrogen atom and a hydroxyl group from a water molecule to the carbon-carbon double bond of an unsaturated fatty acid to form a hydroxy fatty acid.

[0030] As used herein, the term "hydroxy fatty acids" refers to saturated and unsaturated fatty acids with one or more hydroxyl groups (-OH) attached to the carbon chain. The hydroxyl group/s can attach to carbon atom/s at various positions (from the carboxyl end, -COOH) along the carbon chain backbone, for example, but are not limited to, positions 9, 10, 12, 13, 15, and combinations thereof. Examples of hydroxy fatty acids are, but are not limited to, 10-hydroxypalmitic acid (10-HPA), 9-hydroxyheptadecanoic acid (9-HHA), 10-hydroxystearic acid (10-HSA), 12-hydroxystearic acid (12-HSA), 10,12-dihydroxystearic acid (10,12-dHSA), (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), 10,13-dihydroxystearic acid (10,13-dHSA), (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE), (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE), (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE), (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE), and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE).

[0031] As used herein, the term "putative fatty acid hydratases" refers to enzymes that are hypothesized to have fatty acid hydratase activity based on sequence similarity to known or previously described fatty acid hydratases. Upon experimental validation confirming their ability to convert unsaturated fatty acids into hydroxy fatty acids through hydration reactions, these enzymes are acknowledged as authentic fatty acid hydratases.

[0032] As used herein, the term "*cis*-Δ9 subtype" refers to a subtype of fatty acid hydratases that hydroxylates unsaturated fatty acids with a carbon-carbon *cis*-double bond at position 9 from the carboxyl end of the carbon chain. A fatty acid hydratase of the "*cis*-Δ9 subtype" can also hydrate alternative carbon-carbon *cis*-double bonds, for example, at positions 8 and 11. For example, when a carbon-carbon *cis*-double bond is at position 8, 9, or 11 and no other hydroxyl groups are present in the unsaturated fatty acid, a

mono-hydroxy fatty acid with a hydroxyl group at position 9, 10, or 12 can be produced. If at least two carbon-carbon *cis*-double bonds are present at any of positions 8, 9, and 11 and no other hydroxyl groups are present in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least two hydroxyl groups at positions 9, 10, and 12 can be produced. If at least one carbon-carbon *cis*-double bond is present at positions 8, 9, and 11 and at least one hydroxyl group is present at other positions in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least one additional hydroxyl group at positions 9, 10, and 12 can be produced. A fatty acid hydratase of the *cis*-Δ9 subtype can be, but is not limited to, a protein having an amino acid sequence of SEQ ID Nos: 1 to 2, 7 to 8, 15, 17 to 19, and 23; or the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs: 24 to 25, 30 to 31, 38, 40 to 42, and 46. Examples of *cis*-Δ9 fatty acid hydratase activity are, but are not limited to, the conversion of oleic acid to 10-hydroxystearic acid (10-HSA) and the conversion of linoleic acid to 10-hydroxy-12(*Z*)-octadecenoic acid (10-HOE).

[0033] As used herein, the term "*cis*-Δ12 subtype" refers to a subtype of fatty acid hydratases that hydroxylates unsaturated fatty acids with a carbon-carbon *cis*-double bond at position 12 from the carboxyl end of the carbon chain. A fatty acid hydratase of the "*cis*-Δ12 subtype" can also hydrate alternative carbon-carbon *cis*-double bonds, for example, at positions 11 and 14. If a carbon-carbon *cis*-double bond is present at position 11, 12, or 14 and no other hydroxyl groups are present in the unsaturated fatty acid, a mono-hydroxy fatty acid with a hydroxyl group at position 12, 13, or 15 can be produced. If at least two carbon-carbon *cis*-double bonds are present at any of positions 11, 12, and 14 and no other hydroxyl groups are present in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least two hydroxyl groups at positions 12, 13, and 15 can be produced. If at least one carbon-carbon *cis*-double bond is present at any of positions 11, 12, and 14 and at least one hydroxyl group is present at other position in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least one additional hydroxyl group at positions 12, 13, and 15 can be produced. A fatty acid hydratase of the *cis*-Δ12 subtype can be, but is not limited to, a protein having an amino acid sequence of SEQ ID NOs: 13 to 14, 16, and 20 to 22; or the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs: 36 to 37, 39, and 43 to 45. A non-limiting example of *cis*-Δ12 fatty acid hydratase activity is the conversion of linoleic acid to 13-hydroxy-9(*Z*)-octadecenoic acid (13-HOE).

[0034] As used herein, the term "*cis*-Δ9/12 subtype" refers to a subtype of fatty acid hydratases that hydroxylates unsaturated fatty acids with carbon-carbon *cis*-double bond/s at positions 9 and/or 12 from the carboxyl end of the carbon chain. A fatty acid hydratase of the "*cis*-Δ9/12 subtype" can also hydrate alternative carbon-carbon *cis*-double bonds at, for example, positions 8, 11, and 14. If a carbon-carbon *cis*-double bond is present at position 8, 9, 11, 12, or 14 and no other hydroxyl groups are present in the unsaturated fatty acid, a mono-hydroxy fatty acid with a hydroxyl group at position 9, 10, 12, 13, or 15 can be produced. If at least two carbon-carbon *cis*-double bonds are present at any of positions 8, 9, 11, 12, and 14 and no other hydroxyl groups are present in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least two hydroxyl groups at positions 9, 10, 12, 13, and 15 can be produced. If at least one carbon-carbon

cis-double bond is present at any of positions 8, 9, 11, 12, and 14 and at least one hydroxyl group is present at other position in the unsaturated fatty acid, a poly-hydroxy fatty acid with at least one additional hydroxyl group at positions 9, 10, 12, 13, and 15 can be produced. A fatty acid hydratase of the *cis*-Δ9/12 subtype can be, but is not limited to, a protein having an amino acid sequence of SEQ ID NOs: 3 to 6, and 11 to 12; or the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of, but not limited to SEQ ID NOs: 26 to 29, and 34 to 35. A non-limiting example of *cis*-Δ9/12 fatty acid hydratase activity is the conversion of linoleic acid first to intermediates 10-hydroxy-12(*Z*)-octadecenoic acid (10-HOE) and 13-hydroxy-9(*Z*)-octadecenoic acid (13-HOE), and then to 10,13-dihydroxystearic acid (10,13-dHSA).

[0035] As used herein, the term "regioselectivity" refers to the characteristic of a fatty acid hydratase to act on a specific chemical bond over other chemical bonds present within a molecule. An example of a specific chemical bond is, but is not limited to, a carbon-carbon *cis*-double bond at a specific position along the carbon chain. Examples of specific carbon-carbon *cis*-double bonds are, but are not limited to, *cis*-8, *cis*-9, *cis*-11, *cis*-12, and *cis*-14 double bonds. A regioselective enzyme would push a reaction in a specific direction, thereby mainly (or exclusively) producing a structural isomer (also referred to as a constitutional isomer).

[0036] As used herein, the term "regioisomers", also referred to as structural or constitutional isomers, refers to isomers with the same molecular formula presented in different chemical structures. For example (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), and (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE) all have the molecular formula $C_{18}H_{32}O_3$, but are four different structural isomers of this molecular formula.

[0037] As used herein, the term "fatty acid hydratase activity" refers to an activity that converts an unsaturated fatty acid into a hydroxy fatty acid by a hydration reaction. The "hydration reaction" refers to a reaction that hydroxylates an unsaturated fatty acid through the addition of a hydrogen atom and a hydroxyl group from a water molecule to the first carbon atom and the second carbon atom, respectively, of a carbon-carbon double bond. A particular example of fatty acid hydratase activity is the conversion of oleic acid to 10-hydroxystearic acid (10-HSA).

[0038] As used herein, the term "unsaturated fatty acids" refers to free fatty acids and their derivatives including hydroxy fatty acids that have one or more carbon-carbon double bonds in *cis* and/or *trans* configurations. These double bonds can occur at any various positions (from the carboxyl end) along the carbon chain backbone of an unsaturated fatty acid, for example, but are not limited to, positions 8, 9, 11, 12, 14, and combinations thereof. Examples of unsaturated fatty acids are, but are not limited to, palmitoleic acid (PA), (8Z)-heptadec-8-enoic acid (HA), oleic acid (OA), vaccenic acid (VA), linoleic acid (LA), α-linolenic acid (ALA), γ-linolenic acid (GLA), arachidonic acid (ARA), and ricinoleic acid (RA).

[0039] As used herein, the term "monounsaturated fatty acids" refers to unsaturated fatty acids that have one carbon-carbon double bond, for example, but is not limited to, a *cis*-double bond at position 8, 9,

11, 12, or 14. Examples of monounsaturated fatty acids are, but are not limited to, palmitoleic acid (PA), (8Z)-heptadec-8-enoic acid (HA), oleic acid (OA), vaccenic acid (VA), and ricinoleic acid (RA).

[0040] As used herein, the term "polyunsaturated fatty acids" refers to unsaturated fatty acids that have more than one carbon-carbon double bond, for example, but are not limited to, *cis*-double bonds at positions 8, 9, 11, 12, 14, and combinations thereof. Examples of polyunsaturated fatty acids are, but are not limited to, linoleic acid (LA), α-linolenic acid (ALA), γ-linolenic acid (GLA), and arachidonic acid (ARA).

[0041] As used herein, the term "mono-hydroxy fatty acids" refers to saturated and unsaturated fatty acids with one hydroxyl group attached to the carbon chain. The hydroxyl group can attach to carbon atom at various positions along the carbon chain backbone, for example, but are not limited to, positions 9, 10, 12, 13, or 15. Examples of mono-hydroxy fatty acids are, but are not limited to, 10-hydroxypalmitic acid (10-HPA), 9-hydroxyheptadecanoic acid (9-HHA), 10-hydroxystearic acid (10-HSA), 12-hydroxystearic acid (12-HSA), (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE), (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE), and (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE).

[0042] As used herein, the term "di-hydroxy fatty acid" refers to saturated and unsaturated fatty acids with two hydroxyl groups attached to the carbon chain. The hydroxyl groups can attach to carbon atoms at various positions along the carbon chain backbone, for example, but are not limited to, combinations of positions 9, 10, 12, 13, and 15. Examples of di-hydroxy fatty acids are, but are not limited to, 10,12-dihydroxystearic acid (10,12-dHSA), 10,13-dihydroxystearic acid (10,13-dHSA), (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE), and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE).

[0043] As used herein, the term "poly-hydroxy fatty acid" refers to saturated and unsaturated fatty acids with more than one hydroxyl groups attached to the carbon chain. The hydroxyl groups can attach at various positions along the carbon chain backbone, for example, but are not limited to, combinations of positions 9, 10, 12, 13, and 15. Examples of poly-hydroxy fatty acids are, but are not limited to, 10,12-dihydroxystearic acid (10,12-dHSA), 10,13-dihydroxystearic acid (10,13-dHSA), (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE), and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE).

[0044] As used herein, the term "10-hydroxy fatty acids" refers to mono-hydroxy fatty acids with one hydroxyl group attached to carbon atom at position 10 from the carboxyl end of the carbon chain. Examples of 10-hydroxy fatty acids are, but are not limited to, 10-hydroxypalmitic acid (10-HPA), 10-hydroxystearic acid (10-HSA), (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), and (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE).

[0045] As used herein, the term “12-hydroxy fatty acids” refers to mono-hydroxy fatty acids with one hydroxyl group attached to carbon atom at position 12 from the carboxyl end of the carbon chain. Examples of 12-hydroxy fatty acids are, but are not limited to, 12-hydroxystearic acid (12-HSA) and (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE).

[0046] As used herein, the term “13-hydroxy fatty acids” refers to mono-hydroxy fatty acids with one hydroxyl group attached to carbon atom at position 13 from the carboxyl end of the carbon chain. Examples of 13-hydroxy fatty acids are, but are not limited to, (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), and (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE).

[0047] As used herein, the term “15-hydroxy fatty acids” refers to mono-hydroxy fatty acids with one hydroxyl group attached to carbon atom at position 15 from the carboxyl end of the carbon chain. An example of a 15-hydroxy fatty acid is, but is not limited to, (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE).

[0048] As used herein, the term “10,13-di-hydroxy fatty acids” refers to di-hydroxy fatty acids with two hydroxyl groups attached to carbon atoms at positions 10 and 13 from the carboxyl end of the carbon chain. Examples of 10,13-dihydroxy fatty acids are, but are not limited to, 10,13-dihydroxystearic acid (10,13-dHSA), (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), and (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE).

[0049] As used herein, the term “delta (Δ)” refers to a naming system used to denote the position of carbon atoms in fatty acids. In the delta (Δ) naming system, the position of the carbon atom is counted from the carboxyl end (-COOH) of the carbon chain. The carbon atom of the carboxyl group (-COOH) is counted as the first carbon atom (C1). The position of a double bond is named according to the position of the first carbon atom of the carbon-carbon double bond. For example, a *cis*-double bond between the ninth and tenth carbon atom from the carboxyl end would be denoted as *cis*-Δ9, or *cis*-9. The position of a hydroxyl group is named according to the position of the carbon atom the hydroxyl group is attached to. For example, a hydroxyl group attached to the tenth carbon atom from the carboxyl end would be denoted as hydroxyl group at position 10 of the carbon chain, 10-hydroxyl, or 10-OH.

[0050] As used herein, the term “native bacterial strain” refers to a naturally occurring bacterial strain without having been intentionally introduced or manipulated (that is to say, without mutations).

[0051] As used herein, the term “dual-protein system” refers to a biological system or a method involving the use of two fatty acid hydratases of two different subtypes. Examples of dual-protein system are, but are not limited to, a system involving a fatty acid hydratase of the *cis*-Δ9 subtype and a fatty acid hydratase of the *cis*-Δ12 subtype, a system involving a fatty acid hydratase of the *cis*-Δ9 subtype and a fatty acid hydratase of the *cis*-Δ9/12 subtype, and a system involving a fatty acid hydratase of the *cis*-Δ12 subtype and a fatty acid hydratase of the *cis*-Δ9/12 subtype. In these examples, the two fatty acid hydratases work

simultaneously and/or sequentially to convert polyunsaturated fatty acids into di-hydroxy fatty acids and/or poly-hydroxy fatty acids.

[0052] As used herein, the term “hydroxylate” refers to the addition of a hydroxyl group (-OH) to fatty acids, while the term “hydrate” refers to the addition of a hydroxyl group and a hydrogen atom to a double bond.

[0053] As used herein, the term “promiscuity” refers to the characteristic of a fatty acid hydratase to hydrate a double bond at a specific position not typically hydrated by other fatty acid hydratases of the same subtype. The term “promiscuity” also refers to the characteristic of a fatty acid hydratase to hydroxylate an unsaturated fatty acid not typically hydroxylated by other fatty acid hydratases of the same subtype. For example, WIL0029-HY20.1 (SEQ ID NOs 20 and 43) was thought to exhibit promiscuity towards the *cis*-9 double bond of palmitoleic acid. This *cis*-double bond and unsaturated fatty acids were not hydrated and hydroxylated by other fatty acid hydratases of the *cis*-Δ12 subtype.

DETAILED DESCRIPTION OF THE PRESENT INVENTION

[0054] Fatty acid hydratases have been implicated in the hydroxylation of unsaturated fatty acids, specifically catalysing the addition of a water molecule to a carbon-carbon double bond along the carbon chain, resulting in the formation of a hydroxyl group (-OH) at the site of hydration. This process results in the formation of hydroxy fatty acids. Fatty acid hydratases are classified into 11 homologous families (HFam) based on protein sequence similarity. A fatty acid hydratase can target double bonds at different positions along the carbon chain for hydration, leading to the production of different hydroxy fatty acid products.

[0055] Fatty acid hydratases within the same homologous family (HFam) can vary in their regioselectivity, resulting in differences in the types of substrates (the molecules they act upon) they accept and the products they produce. For example, fatty acid hydratases within homologous family 2 (HFam 2) exhibit variation in regioselectivity, hydroxylating C14 to C22 unsaturated fatty acids at *cis*-double bonds of position 9 only, position 12 only, or a combination of both 9 and 12 positions, resulting in the production of mono- or di-hydroxy fatty acids (Table 3).

[0056] Furthermore, fatty acid hydratases within homologous family 2 (HFam 2) have been demonstrated to hydrate alternative *cis*-double bond positions. For example, the FA-HY1 from *Lactobacillus acidophilus*, hydrates alternative *cis*-double bonds at positions 11, 13, and 14.

[0057] This demonstrates the necessity for fatty acid hydratases with defined regioselectivity and improved fatty acid hydroxylating activity for efficient and cost-effective synthesis of specific hydroxy fatty acids for various industrial and biomedical applications.

Putative Fatty Acid Hydratase Identification by In silico Gene Mining and Sequence Similarity Analysis

[0058] Fatty acid hydratases belong to a family of highly conserved proteins known as myosin-cross-reactive antigen (MCRA; PF06100). Described herein is therefore the use of an integrated bioinformatics

workflow to identify putative fatty acid hydratases from a database of draft genomes curated from 139 bacterial strains. This workflow involves a homology search conducted through alignment with the consensus protein sequence of the hidden Markov model (HMM) of the myosin-cross-reactive antigen (MCRA) protein family. A total of 108 putative fatty acid hydratases were initially identified from the search. This number was reduced to 61 putative fatty acid hydratases by eliminating those sharing more than 83% sequence identity with 55 previously described fatty acid hydratases (Fig. 1a). Further refinement yielded 42 putative fatty acid hydratases after retaining only a single entry of each group of closely related proteins with more than 97% sequence identity to one another. Among these, 21 putative fatty acid hydratases were selected for screening fatty acid-hydroxylating activities, along with 2 control fatty acid hydratases sharing more than 90% sequence identity to the previously described fatty acid hydratases (Table 1 and 4).

[0059] Out of the 21 putative fatty acid hydratases selected, 16 were categorised under the homologous family 2 (HFam 2), while the remaining 5 were categorised under homologous family 3 (HFam 3). On a phylogenetic tree, putative fatty acid hydratases belonging to the same homologous family aggregated into the same clusters or clades. Putative fatty acid hydratases derived from related taxonomic groups clustered closer to one another than those from distantly related taxonomic groups (Figs. 1b and 6).

[0060] The lengths of the 21 putative fatty acid hydratases ranged from 557 to 645 amino acids. These putative fatty acid hydratases were identified in 20 distinct bacterial strains, all of which are proprietary bacterial strains. Among them is an isolate of a new species designated as *Limosilactobacillus* sp. WILCCON 0055. Of the 21 putative fatty acid hydratases, two putative fatty acid hydratases, WIL0055-HY35.1 (SEQ ID NOs 14 and 37) and WIL0055-HY36.4 (SEQ ID NOs 15 and 38), were identified in this isolate. None of the 21 putative fatty acid hydratases have been previously identified and characterised for their fatty acid hydroxylating activities.

Screening of Putative Fatty Acid Hydratases for Fatty Acid Hydroxylating Activities

[0061] To investigate the fatty acid hydroxylating activities of the 21 putative fatty acid hydratases, the nucleotide sequences encoding the 21 putative fatty acid hydratases, along with those of the 2 control fatty acid hydratases, were cloned into pET-15b vector, under the regulation of a *lac* operon (Fig. 7b). The expression plasmids were subsequently transformed into *E. coli* strain Acella to construct recombinant strains Acella/pET-15b-XXX (XXX referred to the abbreviation of each putative fatty acid hydratase). Recombinant protein expression was induced by cell growth in an autoinduction medium containing 1.5% (w/v) lactose and verified by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE).

[0062] A whole-cell biotransformation assay was conducted to assess the fatty acid hydroxylating activities of the 21 putative fatty acid hydratases. This assay was conducted by incubating induced recombinant *E. coli* strains with Wilfarin OA-7075, a fatty acid mixture consisting of approximately 81.0% oleic acid (OA; C18:1 $\Delta^{9(Z)}$) and 10.1% linoleic acid (LA: C18:2 $\Delta^{9(Z),12(Z)}$), at 40°C for 48 hours. The resulting reaction mixtures were analysed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) to determine their fatty acid composition and establish the profile of hydroxy fatty acids produced.

[0063] Based on this screening assay, putative fatty acid hydratases are classified as authentic fatty acid hydratases if they produce hydroxy fatty acids from the provided unsaturated fatty acid substrates (Fig. 2a). An authentic fatty acid hydratase is classified as the *cis*-Δ9 subtype if it produces 10-hydroxystearic acid (10-HSA) and (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE) from oleic acid and linoleic acid, respectively. If an authentic fatty acid hydratase produces only (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) from linoleic acid, it is classified as the *cis*-Δ12 subtype. An authentic fatty acid hydratase that produces 10-hydroxystearic acid (10-HSA) from oleic acid, (12Z)-10-hydroxyoctadec-12-enoic (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), and 10,13-dihydroxystearic acid (10,13-dHSA) from linoleic acid, is classified as the *cis*-Δ9/12 subtype.

[0064] All 21 putative fatty acid hydratases described herein, and the two control fatty acid hydratases were found to be active under the tested expression and screening conditions (Fig. 2b). This outcome confirms that the 21 putative fatty acid hydratases identified were authentic fatty acid hydratases.

[0065] Out of the 21 identified fatty acid hydratases, 9 were classified as the *cis*-Δ9 subtype, 6 were classified as the *cis*-Δ12 subtype, and 6 were classified as the *cis*-Δ9/12 subtype (Fig. 2c). Identified fatty acid hydratases of the *cis*-Δ9 subtype were found across homologous families 2 and 3 (HFam 2 and 3), while those of the *cis*-Δ12 and *cis*-Δ9/12 subtypes were exclusive to homologous family 2 (HFam 2; Fig. 1b). In terms of taxonomic distribution, there was no clear trend for fatty acid hydratases of the *cis*-Δ9 and *cis*-Δ12 subtypes, but those of the *cis*-Δ9/12 subtype were identified only in species belonging to the genera *Enterococcus* and *Leuconostoc*. The two fatty acid hydratases identified in the novel isolate *Limosilactobacillus* sp. WILCCON 0055, varied in their activity and regioselectivity. WIL0055-HY35.1 (SEQ ID NOs 14 and 37) was selective to the *cis*-12 double bond while WIL0055-HY36.4 (SEQ ID NOs 15 and 38) was selective to the *cis*-9 double bond.

[0066] The relative production levels of hydroxy fatty acids were compared among different subtypes of fatty acid hydratases. Specifically, the production levels of 10-hydroxystearic acid (10-HSA) and 10-hydroxyoctadec-12-enoic acid (10-HOE) were higher for identified fatty acid hydratases of the *cis*-Δ9/12 subtype compared to the *cis*-Δ9 subtype, while the level of production of (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) was higher for identified fatty acid hydratases of the *cis*-Δ12 subtype than the *cis*-Δ9/12 subtype (Fig. 2c).

[0067] All 15 identified fatty acid hydratases of the *cis*-Δ9 (13.4-56.2%) and *cis*-Δ9/12 (68.3-86.3%) subtypes produced higher levels of 10-hydroxystearic acid (10-HSA) compared to the control fatty acid hydratases (0-13.3%). Similarly, all 6 identified fatty acid hydratases of the *cis*-Δ12 subtype exhibited a higher production level of (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) compared to the control fatty acid hydratases (0-18.1%), with values ranging from 23.7-40.8%.

[0068] Thus, the present disclosure describes a fatty acid hydratase comprising a protein sequence with a sequence identity of at least 83% to a protein sequence selected from the group consisting of, but not limited to, SEQ ID NOs 1 to 8, and 11 to 23. In another example, the sequence identity is at least 84%, at

least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% to a protein sequence selected from the group consisting of, but not limited to, SEQ ID NOs 1 to 8, and 11 to 23.

[0069] In one example, the present disclosure describes a fatty acid hydratase comprising a nucleic acid sequence with a sequence identity of at least 83% to a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46. In another example, the sequence identity is at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% to a nucleic acid selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46.

[0070] In one example, the fatty acid hydratase is regioselective for a carbon-carbon *cis*-double bond at one position over another when the one or more unsaturated fatty acid comprises one or more than one carbon-carbon *cis*-double bond.

[0071] In one example, the fatty acid hydratase is modified. Examples of the modification as disclosed herein can be, but are not limited to, substitution, deletion, insertion, addition, and combinations thereof. In one example, the modification is C-terminal or N-terminal of the peptide, or at the 5'- or 3'- end of the nucleic acid sequence. In another example, the modification is an addition of a His-tag or a thrombin cleavage site.

[0072] In one example, the fatty acid hydratase is purified, free, immobilized, wet, or lyophilised. In another example, the fatty acid hydratase is expressed from a host cell or a native bacterial strain.

[0073] Also disclosed herein is the method of producing hydroxy fatty acids comprising contacting a fatty acid hydratase with one or more unsaturated fatty acids. In one example, the fatty acid hydratase comprises, or consists of, an amino acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs 1 to 8, and 11 to 23. In another example, the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46. Also disclosed herein is a nucleic acid sequence encoding a fatty acid hydratase. In yet another example, the nucleic acid sequence has a sequence identity of at least 83% to a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46. In one example, the sequence identity is at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% to a nucleic acid selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46. In another example, the nucleic acid sequence is selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46.

[0074] In one example, the method is performed at temperature of 30°C or higher. In another example, the method is performed at temperature of about 31°C, 32°C, 33°C, 34°C, 35°C, 36°C, 37°C, 38°C, 39°C,

40°C, 41°C, 42°C, 43°C, 44°C, 45°C, 46°C, 47°C, 48°C, 49°C, 50°C, 51°C, 52°C, 53°C, 54°C, 55°C, 56°C, 57°C, 58°C, 59°C, or 60°C.

[0075] In one example, applying the fatty acid hydratases disclosed herein, for example, in the methods disclosed herein, results in an increase in the yield of hydroxy fatty acids. In another example, the fatty acid hydratase disclosed herein has an increased activity in the production of hydroxy fatty acids compared to a control.

[0076] In one example, a vector expressing a protein sequence can be, but is not limited to, SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence comprising or consisting of SEQ ID NOs 24 to 31, and 34 to 46. In another example, the sequence identity is at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% as compared to a protein sequence selected from, but not limited to, SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence selected from, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46.

[0077] The present disclosure also describes a host cell comprising the vector expressing a protein sequence selected from the group consisting of, but not limited to, the group consisting of SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence selected from the group consisting of, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46. In another example, the sequence identity selected from the group consisting of, but not limited to, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% as compared to a protein sequence selected from the group consisting of, but not limited to, SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence selected from, but not limited to, SEQ ID NOs 24 to 31, and 34 to 46.

[0078] In one example, the host cell can be, but is not limited to, bacteria and fungi. In another example, the bacteria are Enterobacteriaceae. In yet another example, the Enterobacteriaceae can be, but are not limited to, the group consisting of *Escherichia* spp., *Escherichia coli* Acella, and *Escherichia coli* BL21 (DE3).

[0079] Also disclosed herein is a method of producing hydroxy fatty acids, the method comprising culturing the host cell under conditions suitable for culturing of the host cell. In one example, the hydroxy fatty acid is a mono- or a poly-hydroxy fatty acid. In yet another example, the fatty acid hydratase has an improved substrate specificity for one particular unsaturated fatty acid over another.

Characterization of Regioselectivity, Substrate Selectivity, and Product Scopes

[0080] Fatty acid hydratases have previously been reported to hydrate not only the *cis*-9 and *cis*-12 double bonds of unsaturated fatty acids with carbon chains other than C18. Therefore, a total of 17 identified fatty acid hydratases comprising of fatty acid hydratases of all three subtypes, along with the two control fatty acid hydratases, were further characterised by testing their activity on other unsaturated fatty acids. In one example, the fatty acid hydratase disclosed herein hydrates a carbon-carbon *cis*-double bond selected

from the group consisting of, but not limited to, a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof in the one or more unsaturated fatty acids.

[0081] Of the 17 identified fatty acid hydratases, all 6 fatty acid hydratases of the *cis*-Δ12 subtype and *cis*-Δ9/12 subtype were selected, while 5 fatty acid hydratases of the *cis*-Δ9 subtype were selected.

[0082] The induced recombinant *E. coli* cells expressing each of the 17 identified fatty acid hydratases were subjected to another series of whole-cell biotransformation reactions involving a panel of nine unsaturated fatty acid substrates (30 mM final concentration). In addition to oleic acid (OA) and linoleic acid (LA), palmitoleic acid (PA; C16:1 $\Delta^{9(Z)}$), (8*Z*)-heptadec-8-enoic acid (HA; C17:1 $\Delta^{8(Z)}$), vaccenic acid (VA; C18:1 $\Delta^{11(Z)}$), ricinoleic acid (RA; C18:1 $\Delta^{9(Z)}$, 12-OH), α-linolenic acid (ALA; C18:3 $\Delta^{9(Z),12(Z),15(Z)}$), γ-linolenic acid (GLA; C18:3 $\Delta^{6(Z),9(Z),12(Z)}$) and arachidonic acid (ARA; C20:4 $\Delta^{5(Z),8(Z),11(Z),14(Z)}$) were tested. This expanded substrate panel allowed the examination of hydration at eight different *cis*-double bond positions in a variety of even-chain (C16, C18, and C20) monounsaturated and polyunsaturated fatty acids, as well as an odd-chain (C17) monounsaturated fatty acid (Table 2 and Fig. 3).

[0083] The whole-cell biotransformation reactions of the 17 selected fatty acid hydratases revealed consistent profiles of hydroxy fatty acids produced from the nine different unsaturated fatty acid substrates across fatty acid hydratases within each subtype (Fig. 4). All 6 identified fatty acid hydratases and control fatty acid hydratases of the *cis*-Δ9 subtype were regioselective towards the *cis*-9 double bond, converting palmitoleic acid, oleic acid, ricinoleic acid, linoleic acid, α-linolenic acid, and γ-linolenic acid into 10-hydroxypalmitic acid (10-HPA), 10-hydroxystearic acid (10-HSA), 10,12-dihydroxystearic acid (10,12-dHSA), (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), and (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), respectively. While there was slight variation in substrate selectivity between fatty acid hydratases, a general trend of higher conversion efficiency was observed for oleic acid (84.4-91.7%), followed by ricinoleic acid (35.0-91.8%), palmitoleic acid (29.6-99.6%), γ-linolenic acid (9.8-55.0%), α-linolenic acid (1.6-46.7%), and linoleic acid (2.1-28.7%). This suggested a preference of the *cis*-Δ9 subtype for monounsaturated fatty acids over polyunsaturated fatty acids, and C18 over C16 carbon chain length. Additionally, the conversion of (8*Z*)-heptadec-8-enoic acid (HA) to 9-hydroxyheptadecanoic acid (9-HHA; 1.6-46.9%) and arachidonic acid to (5*Z*,8*Z*,14*Z*)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE; 0.1-0.9%) were observed, suggesting hydration of the *cis*-8 and *cis*-11 double bond of a C17 monounsaturated fatty acid and a C20 polyunsaturated fatty acid, respectively.

[0084] Similarly, all 7 identified fatty acid hydratases and control fatty acid hydratases of the *cis*-Δ12 subtype exhibited regioselectivity towards the *cis*-12 double bond, producing (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), and (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE) products from linoleic acid, α-linolenic acid, and γ-linolenic acid, respectively. In terms of substrate selectivity, although subtle variation between fatty acid hydratases existed, a trend of higher conversion efficiency was observed in the order of linoleic acid (62.4-

71.5%), γ-linolenic acid (13.1-77.7%) and α-linolenic acid (2.2-35.0%). This indicated a preference of the *cis*-Δ12 subtype for polyunsaturated fatty acids of the C18 carbon chain length with a lower degree of unsaturation. Additionally, the conversion of vaccenic acid to 12-hydroxystearic acid (12-HSA; 0.7-75.3%) and arachidonic acid to (5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE; 5.7-43.2%) were observed, indicating hydration of the *cis*-11 and *cis*-14 double bond of a C18 monounsaturated fatty acid and a C20 polyunsaturated fatty acid, respectively.

[0085] All 6 identified fatty acid hydratases of the *cis*-Δ9/12 subtype showed activity towards the *cis*-9 and/or *cis*-12 double bonds, converting palmitoleic acid into 10-hydroxypalmitic acid (10-HPA), oleic acid into 10-hydroxystearic acid (10-HSA), ricinoleic acid into 10,12-dihydroxystearic acid (10,12-dHSA), linoleic acid into (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE), (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE), and 10,13-dihydroxystearic acid (10,13-dHSA), α-linolenic acid into (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid (α-10-HODE), (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE), and (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE), and γ-linolenic acid into (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE), (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE), and (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE). A higher regioselectivity for *cis*-9 over *cis*-12 double bond was inferred, as evidenced by a higher ratio of 10-hydroxy fatty acid intermediates (mono-hydroxy fatty acids with a hydroxyl group at position 10; in this case referring to (12Z)-10-hydroxyoctadec-12-enoic acid, (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid, and (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid) over 13-hydroxy fatty acid intermediates (mono-hydroxy fatty acids with a hydroxyl group at position 13; in this case referring to (9Z)-13-hydroxyoctadec-9-enoic acid, (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid, and (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid) in reactions involving polyunsaturated fatty acids containing the two *cis*-double bonds (in this case referring to linoleic acid, α-linolenic acid, and γ-linolenic acid). The accumulation of 10-hydroxy fatty acid intermediate resulted from more efficient hydration of the *cis*-9 double bond of the polyunsaturated fatty acid substrates, coupled with less efficient hydration of the *cis*-12 double bond of the generated 10-hydroxy fatty acid intermediate to form the final 10,13-di-hydroxy fatty acid product (di-hydroxy fatty acids with two hydroxyl groups at positions 10 and 13; in this case referring to 10,13-dihydroxystearic acid, (15Z)-10,13-dihydroxyoctadec-15-enoic acid, and (6Z)-10,13-dihydroxyoctadec-6-enoic acid). Conversely, a lower level of 13-hydroxy fatty acid intermediate corresponded to less efficient hydroxylation of the *cis*-12 double bond of the polyunsaturated fatty acid substrates and higher efficiency of hydroxylating the *cis*-9 double bond of the 13-hydroxy fatty acid intermediate to form the final 10,13-di-hydroxy fatty acid product.

[0086] Thus, in one example, the fatty acid hydratase disclosed herein has an improved substrate specificity for one particular unsaturated fatty acid over another. This means that a fatty acid hydratase disclosed herein can be regioselective for a carbon-carbon *cis*-double bond at one position over another, when the one or more unsaturated fatty acid comprises one or more than one carbon-carbon *cis*-double bond. In another example, the fatty acid hydratase is promiscuous for alternative carbon-carbon *cis*-double

bond positions. In another example, the fatty acid hydratase hydrates a carbon-carbon *cis*-double bond which can be, but is not limited to, a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof in the one or more unsaturated fatty acids.

[0087] Substrate selectivity for the *cis*-Δ9/12 subtype was generally higher and comparable for C16 and C18 monounsaturated fatty acids with a *cis*-9 double bond: palmitoleic acid (>99.0%), oleic acid (86.1-88.6%), and ricinoleic acid (96.5-98.9%). For C18 polyunsaturated fatty acids containing both the *cis*-9 and *cis*-12 double bonds, a preference of the *cis*-Δ9/12 subtype for linoleic acid (88.2-99%) over α-linolenic acid (48.0-70.1%) and γ-linolenic acid (6.6-25.2%) was observed based on an overall higher conversion of the substrate into the mono-hydroxy fatty acid intermediates (10-hydroxy fatty acid and 13-hydroxy fatty acid) and the final 10,13-di-hydroxy fatty acid product. Similarly, the *cis*-Δ9/12 subtype hydrated the *cis*-8 double bond of (8Z)-heptadec-8-enoic acid (HA) to produce 9-hydroxyheptadecanoic acid (9-HHA; 12.2-23.4%), *cis*-11 double bond of vaccenic acid to produce 12-hydroxystearic acid (12-HSA; 9.7-41.0%), and *cis*-11 and *cis*-14 double bonds of arachidonic acid to produce the mono-hydroxy fatty acid intermediates (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE) and (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE), and the final di-hydroxy fatty acid product (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE; total conversion from arachidonic acid: 1.1-5.4%).

[0088] There was a lack of overlap in the regioselectivity between the *cis*-Δ9 and *cis*-Δ12 subtypes, except for the *cis*-11 double bond. In this regard, the *cis*-Δ9 subtype demonstrated hydration of the *cis*-11 double bond of arachidonic acid but not vaccenic acid, whereas the *cis*-Δ12 subtype demonstrated hydration of the *cis*-11 double bond of vaccenic acid but not arachidonic acid.

[0089] Thus, the *cis*-Δ9 subtype described in this disclosure demonstrated regioselectivity towards the *cis*-8, *cis*-9, and *cis*-11 double bonds of C16-C20 unsaturated fatty acids, producing hydroxy fatty acids with (additional) hydroxyl group attached at position 9, 10, or 12 of the carbon chain (in this case referring to 9-hydroxyheptadecanoic acid, 10-hydroxypalmitic acid, 10-hydroxystearic acid, (12Z)-10-hydroxyoctadec-12-enoic acid, (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic acid, (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid, 10,12-dihydroxystearic acid, and (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid. In contrast, the *cis*-Δ12 subtype described in this disclosure demonstrated regioselectivity towards the *cis*-11, *cis*-12, and *cis*-14 double bonds of C18 and C20 unsaturated fatty acids, generating hydroxy fatty acids with (additional) hydroxyl group attached at position 12, 13, or 15 of the carbon chain (in this case referring to 12-hydroxystearic acid, (9Z)-13-hydroxyoctadec-9-enoic acid, (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid, (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid, and (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid. The *cis*-Δ9/12 subtype described in this disclosure could hydrate all double bond positions targeted by the other two subtypes, ultimately yielding hydroxy fatty acids with (additional) hydroxyl group attached at position 9, 10, 12, 13, and/or 15 of the carbon chain (in this case referring to 10-hydroxypalmitic acid, 9-hydroxyheptadecanoic acid, 10-hydroxystearic acid, 12-hydroxystearic acid, 10,12-dihydroxystearic acid, (12Z)-10-hydroxyoctadec-12-enoic acid, (9Z)-13-hydroxyoctadec-9-enoic acid, 10,13-dihydroxystearic acid, (12Z,15Z)-10-hydroxyoctadeca-12,15-dienoic

acid, (9Z,15Z)-13-hydroxyoctadeca-9,15-dienoic acid, (15Z)-10,13-dihydroxyoctadec-15-enoic acid, (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid, (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid, (6Z)-10,13-dihydroxyoctadec-6-enoic acid, (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid, (5Z,8Z,11Z)-15-hydroxyicosa-5,8,11-trienoic acid, and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid).

[0090] Without being bound by theory, the structures of the carbon chains preceding and following or succeeding the targeted *cis*-double bond were thought to influence substrate compatibility. The *cis*-Δ9 subtype seemed to exhibit a preference for monounsaturated fatty acids with a straight and saturated alkyl chain of eight carbon atoms (including the carboxyl group) preceding the targeted *cis*-double bond. Increased unsaturation or variations in the number of carbon atoms in the preceding chain significantly impacted hydroxylation by the *cis*-Δ9 subtype, as evidenced by reduced conversion of (8Z)-heptadec-8-enoic acid (HA), γ-linolenic acid and arachidonic acid. Additionally, the *cis*-Δ9 subtype hydroxylated palmitoleic acid as efficiently as oleic acid, suggesting a preference for a straight alkyl chain of 6-8 carbon atoms succeeding the targeted *cis*-double bond. Increased unsaturation in the succeeding chain affected the hydroxylation efficiency of linoleic acid, α-linolenic acid, γ-linolenic acid, and arachidonic acid.

[0091] On the other hand, the *cis*-Δ12 subtype appeared to prefer polyunsaturated fatty acids with a preceding alkyl chain of eleven carbon atoms, with one conjugated *cis*-double bond ahead of the targeted *cis*-double bond, and a succeeding alkyl chain of five carbon atoms in straight and saturated configuration. Deviations from these preferred substrate structures appeared to lead to decreased hydroxylation of vaccenic acid, α-linolenic acid, γ-linolenic acid, and arachidonic acid by the *cis*-Δ12 subtype. Lastly, the *cis*-Δ9/12 subtype exhibited activities reminiscent of a blend of the *cis*-Δ9 and *cis*-12 subtypes. This subtype preferred monounsaturated fatty acids with straight alkyl chains of eight carbon atoms preceding and 6-8 carbon atoms succeeding the targeted *cis*-double bond, and polyunsaturated fatty acids with two targeted *cis*-double bonds conjugated to one another, preceded by a straight alkyl chain of eight carbon atoms, and succeeded by a straight alkyl chain of five carbon atoms. The presence of additional *cis*-double bonds in the preceding or the succeeding alkyl chain significantly affected the hydroxylation of α-linolenic acid, γ-linolenic acid, and arachidonic acid by the *cis*-Δ9/12 subtype. Considering that the presence of an additional *cis*-double bond results in an extra bend or "kink" in the carbon chain, without being bound by theory, it was thought that the drop in the hydroxylation of less preferred unsaturated fatty acid substrates was due to a suboptimal 3D structure that was less compatible with the substrate binding site or the active site of fatty acid hydratases.

[0092] The performance of fatty acid hydratases between and within the 3 different subtypes were compared. In terms of monounsaturated fatty acid substrates, the *cis*-Δ9/12 subtype performed better than the *cis*-Δ9 subtype in the conversion of palmitoleic acid (>99% versus 29.6-99.6%) and ricinoleic acid (96.5-98.9% versus 35.0-91.8%), but slightly less efficient than the *cis*-Δ12 subtype in the conversion of vaccenic acid (9.7-41.0% versus 0.7-75.3%; Fig. 4). The *cis*-Δ12 subtype was more efficient than the *cis*-Δ9 subtype in the conversion of most polyunsaturated fatty acids, including linoleic acid (62.4-71.5% versus 2.1-28.7%), γ-linolenic acid (13.1-77.7% versus 9.8-55.0%) and arachidonic acid (5.7-43.2% versus

0.1-0.9%). The *cis*-Δ9/12 subtype showed higher efficiency than the *cis*-Δ12 subtype in the conversion of linoleic acid and α-linolenic acid but lower efficiency in the conversion of γ-linolenic acid and arachidonic acid.

[0093] All six identified fatty acid hydratases of the *cis*-Δ9/12 subtype and the two identified fatty acid hydratases of the *cis*-Δ9 subtype, WIL0039-HY28.1 (SEQ ID NOs 18 and 41) and PA-HY29.2 (SEQ ID NOs 19 and 42) produced a higher level of 10-hydroxypalmitic acid (10-HPA) from palmitoleic acid, 9-hydroxyheptadecanoic acid (9-HHA) from (8Z)-heptadec-8-enoic acid (HA), and 10,12-dihydroxystearic acid (10,12-dHSA) from ricinoleic acid than the control fatty acid hydratases. Additionally, all 6 identified fatty acid hydratases of the *cis*-Δ9/12 subtype showed higher conversion efficiency than the control fatty acid hydratases in converting vaccenic acid to 12-hydroxystearic acid (12-HSA). Similar results were also observed for 4 identified fatty acid hydratases, WIL0076-HY48.1 (SEQ ID NOs 13 and 36), WIL0029-HY20.1 (SEQ ID NOs 20 and 43), WIL0055-HY35.1 (SEQ ID NOs 14 and 37), and WIL0075-HY05.2 (SEQ ID NOs 16 and 39), of the *cis*-Δ12 subtype, in converting vaccenic acid to 12-hydroxystearic acid (12-HSA). These four fatty acid hydratases also showed higher efficiency than the control fatty acid hydratase in the conversion of α-linolenic acid to (9*Z*,15*Z*)-13-hydroxyoctadeca-9,15-dienoic acid (α-13-HODE) and γ-linolenic acid to (9*Z*,15*Z*)-13-hydroxyoctadeca-9,15-dienoic acid (γ-13-HODE). WIL0055-HY35.1 (SEQ ID NOs 14 and 37) demonstrated high efficiency in the conversion of arachidonic acid to (5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE) (43.2%), while WIL0029-HY20.1 (SEQ ID NOs 20 and 43) demonstrated promiscuity towards the *cis*-9 double bond of palmitoleic acid (8.5% conversion). The performances of these identified fatty acid hydratases were reproducible even at a higher substrate concentration (100 g L^{-1} Wilfarin OA-7075 or linoleic acid; Fig. 8a and 8b), as well as at a larger transformation volume (30 mL or 250 mL; Fig. 8d).

[0094] The close clustering of these identified fatty acid hydratases in the phylogenetic tree (Fig. 1b) was thought to indicate a correlation between enzyme performance and their intrinsic sequence information. This association was particularly notable for the *cis*-Δ9 subtype, where identified fatty acid hydratases of homologous family 3 (HFam 3) generally showed higher substrate conversion efficiency than those of homologous family 2 (HFam 2). The synthesis of 9-hydroxyheptadecanoic acid (9-HHA; Fig. 11b), (5Z,8Z,14Z)-12-hydroxyicosa-5,8,14-trienoic acid (12-HITE; Fig. 12c), and (5*Z*,8*Z*)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE; Fig. 12e) emphasises the capability of the identified fatty acid hydratases to produce previously unknown hydroxy fatty acids, thus indicating their industrial applicability.

Dual-Protein System for Poly-Hydroxy Fatty Acid Production

[0095] The synthesis of di-hydroxy fatty acids from polyunsaturated fatty acids by the *cis*-Δ9/12 subtype was primarily hindered by a higher regioselectivity towards the *cis*-9 over the *cis*-12 double bond (in this case referring to linoleic acid, α-linolenic acid, γ-linolenic acid), as well as towards the *cis*-14 over the *cis*-11 double bond (in this case referring to arachidonic acid). This bias led to the accumulation of

mono-hydroxy fatty acid intermediates, which were less efficiently converted into the desired di-hydroxy fatty acid products.

[0096] The present disclosure describes a dual-protein system involving a fatty acid hydratase of the *cis*-Δ9 subtype and a fatty acid hydratase of the *cis*-Δ12 subtype, working simultaneously or sequentially to convert polyunsaturated fatty acids into poly-hydroxy fatty acids (Fig. 5a). The rationale behind this strategy was that each subtype would exhibit optimal regioselectivity for the assigned double bond position, thereby collectively and efficiently converting a polyunsaturated fatty acid substrate into the poly-hydroxy fatty acid product.

[0097] In one example, the dual protein system disclosed herein comprises a fatty acid hydratase of the *cis*-Δ9 subtype selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 1 to 2, 7 to 8, 15, 17 to 19, and 23; and a fatty acid hydratase of the *cis*-Δ12 subtype selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 13 to 14, 16, and 20 to 22. In another example, the method disclosed herein comprises the use of a first fatty acid hydratase and a second fatty acid hydratase. In one example, the first and the second fatty acid hydratase are used simultaneously or sequentially. In a further example, the first fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to any one of SEQ ID Nos: 1 to 2, 7 to 8, 15, 17 to 19, and 23; and the second fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to any one of SEQ ID Nos: 13 to 14, 16, and 20 to 22. In another example, the sequence identity is at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% to the respective reference sequence. In yet another example, the dual protein system disclosed herein comprises an identified fatty acid hydratase of the *cis*-Δ9 subtype, WIL0039-HY28.1 (SEQ ID NOs 18 and 41), and an identified fatty acid hydratase of the *cis*-Δ12 subtype, WIL0075-HY05.2 (SEQ ID NOs 16 and 39). In yet another example, the dual protein system disclosed herein comprises an identified fatty acid hydratase of the *cis*-Δ9 subtype, PA-HY29.2 (SEQ ID NOs 19 and 42), and an identified fatty acid hydratase of the *cis*-Δ12 subtype, WIL0055-HY35.1 (SEQ ID NOs 14 and 37).

[0098] The present disclosure also describes a dual-protein system involving a fatty acid hydratase of the *cis*-Δ9 subtype and a fatty acid hydratase of the *cis*-Δ9/12 subtype, working simultaneously or sequentially to convert polyunsaturated fatty acids into poly-hydroxy fatty acids. In one example, the *cis*-Δ9 subtype is selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 1 to 2, 7 to 8, 15, 17 to 19, and 23; and the *cis*-Δ9/12 subtype is selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 3 to 6, and 11 to 12.

[0099] In yet another example, the present disclosure describes a dual-protein system involving a fatty hydratase of the *cis*-Δ12 subtype and a fatty acid hydratase of the *cis*-Δ9/12 subtype, working simultaneously or sequentially to convert polyunsaturated fatty acids into poly-hydroxy fatty acids. In one

example, the *cis*-Δ12 subtype is selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 13 to 14, 16, and 20 to 22; and the *cis*-Δ9/12 subtype is selected from the group consisting of, but not limited to, a protein having an amino acid sequence of SEQ ID NOs: 3 to 6, and 11 to 12.

[00100] Induced recombinant *E. coli* cells expressing each identified fatty acid hydratase of the *cis*-Δ9 (for example, WIL0039-HY28.1 or PA-HY29.2) and *cis*-Δ12 (for example, WIL0075-HY05.2 or WIL0055-HY35.1) subtype were co-incubated with 30 mM of linoleic acid, α-linolenic acid, γ-linolenic acid, or arachidonic acid. The resulting fatty acid profiles were compared with those generated by the top two performing identified fatty acid hydratases of the *cis*-Δ9/12 subtype, WIL0020-HY11.1 (SEQ ID NOs 5 and 28) and WIL0024-HY15.1 (SEQ ID NOs 4 and 27). Both *cis*-Δ9 + *cis*-Δ12 pairs formed a higher level of di-hydroxy fatty acids, specifically (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE) from γ-linolenic acid (10.3-18.3% versus 0.4-0.9%; Fig. 5e) and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE) from arachidonic acid (0.2-0.7% versus 0.1%; Fig. 5c) but not 10,13-dihydroxystearic acid (10,13-dHSA) from linoleic acid (40.2-68.0% versus 68.9-85.0%; Fig. 5b) and (15Z)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE) from α-linolenic acid (1.0-2.3% versus 8.3-20.3%; Fig. 5d). The relative levels of mono-hydroxy fatty acid intermediates for each pair conformed with their individual selectivity for the polyunsaturated fatty acid substrates and their efficiency in generating the corresponding mono-hydroxy fatty acids. For instance, the higher selectivity for linoleic acid and greater conversion to (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) by WIL0075-HY05.2 (SEQ ID NOs 16 and 39) compared to (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE) by WIL0039-HY28.1 (SEQ ID NOs 18 and 41) aligned with the relatively higher proportion of (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) than (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE) intermediates in the dual-protein systems.

[00101] The observed differences in the efficiency of synthesizing di-hydroxy fatty acids from the four polyunsaturated fatty acid substrates using the dual-protein systems could be attributed to variations in the efficiency of utilizing the polyunsaturated fatty acids and their corresponding mono-hydroxy fatty acid intermediates as substrates. Without being bound by theory, it was thought that increased production of 6(*Z*)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE) and (5Z,8Z)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE) stemmed from the higher selectivity and activity of the *cis*-Δ9 + *cis*-Δ12 pair in converting γ-linolenic acid and arachidonic acid into mono-hydroxy fatty acid intermediates, and the *cis*-Δ9 subtype in converting the (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-13-HODE) and (5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE) intermediates produced by the *cis*-Δ12 subtype into the corresponding di-hydroxy fatty acid products. Both (6Z,9Z)-13-hydroxyoctadeca-6,9-dienoic acid (γ-13-HODE) and (5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE) lacked a *cis*-double bond succeeding the *cis*-double bond targeted by the *cis*-Δ9 subtype. Their straight and saturated configurations of the succeeding alkyl chain were highly preferred by the *cis*-Δ9 subtype, notably at a selectivity greater than γ-linolenic acid and arachidonic acid. In contrast, the (6Z,12Z)-10-hydroxyoctadeca-6,12-dienoic acid (γ-10-HODE) and (5*Z*,8*Z*,14*Z*)-12-hydroxyicosa-5,8,14-trienoic acid

(12-HITE) intermediates produced by the *cis*-Δ9 subtype were less compatible (than γ-linolenic acid and arachidonic acid) with the *cis*-Δ12 subtype, due to the absence of a conjugated *cis*-double bond preceding the targeted *cis*-double bonds. This differential selectivity was advantageous for the dual-protein system, as it directed the reaction first towards the *cis*-Δ12 subtype and then *cis*-Δ9 subtype, minimizing substrate competition and thereby permitting and improving the production of poly-hydroxy fatty acids. Thus, in one example, the method disclosed herein comprises the sequential use of a fatty acid hydratase of the *cis*-Δ9 subtype and a fatty acid hydratase of the *cis*-Δ12 subtype.

[00102] A similar scenario was initially theorized for the dual-protein reaction involving linoleic acid. This was because, in comparison to linoleic acid, the (9Z)-13-hydroxyoctadec-9-enoic acid (13-HOE) intermediate displayed a more favourable structure for the *cis*-Δ9 subtype, and the (12Z)-10-hydroxyoctadec-12-enoic acid (10-HOE) intermediate was less preferred by the *cis*-Δ12 subtype. However, this differential selectivity did not result in a higher level of 10,13-dihydroxystearic acid (10,13-dHSA) than that observed for the two identified fatty acid hydratases of the *cis*-Δ9/12 subtype, presumably due to a collectively lower selectivity and efficiency of the *cis*-Δ9 + *cis*-Δ12 pair than the *cis*-Δ9/12 subtype in converting linoleic acid and the mono-hydroxy fatty acid intermediates. Nonetheless, the level of 10,13-dihydroxystearic acid (10,13-dHSA) was the highest among the di-hydroxy fatty acids produced from the four polyunsaturated fatty acid substrates using the dual-protein system. Lastly, the lower production of (15*Z*)-10,13-dihydroxyoctadec-15-enoic acid (α-10,13-dHOE) from α-linolenic acid could simply be attributed to the lower selectivity and activity of the *cis*-Δ9 + *cis*-Δ12 pair in converting α-linolenic acid and its mono-hydroxy fatty acid intermediates, the structures of which were suboptimal.

[00103] The dual-protein system demonstrated the capability of producing poly-hydroxy fatty acids, by using multiple identified fatty acid hydratases of different subtypes and regiospecificities. The efficiency of this system relies on the compatibility and selectivity of the fatty acid hydratase pair with the polyunsaturated fatty acid substrates and the mono-hydroxy fatty acid intermediates. In one example, this system was shown to enhance the production of di-hydroxy fatty acids from polyunsaturated fatty acid substrates less preferred by the *cis*-Δ9/12 subtype, as evidenced by the >2-fold improvement in the production of the (6Z)-10,13-dihydroxyoctadec-6-enoic acid (γ-10,13-dHOE) and the (5*Z*,8*Z*)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE). One of these, (5*Z*,8*Z*)-12,15-dihydroxyicosa-5,8-dienoic acid (12,15-dHIDE), represented a previously uncharacterised di-hydroxy fatty acid with unknown functions.

[00104] Thus, the present disclosure describes a method of producing hydroxy fatty acids, the method comprising use of a host cell or a native bacterial strain comprising a fatty acid hydratase. In one example, the method comprises use of two or more fatty acid hydratases. In yet another example, the two or more fatty acid hydratases each hydrate a carbon-carbon *cis*-double bond selected from, but not limited to, the group consisting of a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof. In one example, the two or more fatty acid hydratases are

used simultaneously or sequentially. The use of two enzymes disclosed herein in the same method describes and shows an alternative approach for production of poly-hydroxy fatty acids.

[00105] The data provided herein highlights the use and application of the 21 identified fatty acid hydratases disclosed herein. It was shown that half of these fatty acid hydratases represent new members within the understudied *cis*-Δ12 (six identified fatty acid hydratases) and *cis*-Δ9/12 (six identified fatty acid hydratases) subtypes. It was also shown that all identified fatty acid hydratases showed greater activity compared to the control fatty acid hydratases in the production of at least one hydroxy fatty acid. In one example, WIL0055-HY35.1 (SEQ ID NOs 14 and 37) of the *cis*-Δ12 subtype demonstrated higher synthesis of (5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid (15-HITE) from arachidonic acid. In one example, the fatty acid hydratase is promiscuous for alternative carbon-carbon *cis*-double bond positions. In another example, the WIL0029-HY20.1 (SEQ ID NOs 20 and 43) of the *cis*-Δ12 subtype showed promiscuity to the *cis*-9 double bond of palmitoleic acid, producing 10-hydroxypalmitic acid (10-HPA).

[00106] The invention illustratively described herein may suitably be practiced in the absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms "comprising", "including", "containing", etc. shall be read expansively and without limitation. Additionally, the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the inventions embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention.

[00107] As used in this application, the singular form “a,” “an,” and “the” include plural references unless the context clearly dictates otherwise. For example, the term “a genetic marker” includes a plurality of genetic markers, including mixtures and combinations thereof.

[00108] As used herein, the term “about”, in the context of concentrations of components of the formulations, typically means +/- 5% of the stated value, more typically +/- 4% of the stated value, more typically +/- 3% of the stated value, more typically, +/- 2% of the stated value, even more typically +/- 1% of the stated value, and even more typically +/- 0.5% of the stated value.

[00109] Throughout this disclosure, certain embodiments may be disclosed in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the disclosed ranges. Accordingly, the description of a range should be considered to have specifically disclosed all the possible sub-ranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed sub-ranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

[00110] Certain embodiments may also be described broadly and generically herein. Each of the narrower species and sub-generic groupings falling within the generic disclosure also form part of the disclosure. This includes the generic description of the embodiments with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

[00111] The invention has been described broadly and generically herein. Each of the narrower species and sub-generic groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

[00112] Other embodiments are within the following claims and non- limiting examples. In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

EXPERIMENTAL SECTION

In silico Gene Mining and Sequence Similarity Analysis

[00113] Homology search was performed using the *tblastn* program of BLAST+ software, on a curated database made up of draft genomes of 139 bacterial strains. Putative fatty acid hydratases were identified by alignment with the consensus protein sequence of the hidden Markov model (HMM) of the myosin-cross-reactive antigen (MCRA) protein family, using an *e*-value of less than 10^{-3} as the threshold for filtering. The raw hidden Markov model of the myosin-cross-reactive antigen protein family (SEQ ID NO 47) was obtained from the Pfam database (https://pfam.xfam.org/). An all-versus-all, pairwise sequence comparison between the 108 putative fatty acid hydratases and 55 previously described fatty acid hydratases was performed using the online EFI-EST tool (https://efi.igb.illinois.edu/efi-est/). The resulting sequence similarity network was visualized and analysed using the organic layout of Cytoscape software (version 3.8.0). Classification into 11 homologous families was based on the 62% sequence identity threshold recommended by the Hydratase Engineering Database (https://hyed.biocatnet.de/). To infer phylogeny based on protein sequences, a multiple sequence alignment was first generated using the online MUSCLE tool of EMBL-EBI (https://www.ebi.ac.uk/Tools/msa/muscle/) and trimmed to remove poorly aligned or gapped positions using the "automated1" method of trimAl (version 1.3; https://vicfero.github.io/trimal/). A maximum-likelihood tree was reconstructed using IQ-TREE (version 1.6.12; http://www.iqtree.org/), based on the best protein substitution model identified by the "ModelFinder" method and supported with 1,000 ultrafast bootstrapping. Interactive Tree Of Life (version 6.8.1; https://itol.embl.de/) or FigTree (version 1.4.4; https://github.com/rambaut/figtree) was used for graphical visualisation of the resulting tree.

Expression Plasmid Construction

[00114] Genomic DNAs were extracted from pure bacterial cultures using InstaGene Matrix (Bio-Rad, Hercules, California, USA) following the manufacturer's instructions. Specific primers were designed

(Table 5) and synthesised by Integrated DNA Technologies (Coralville, Iowa, USA) to PCR-amplify the underlying nucleotide sequences of the 21 identified fatty acid hydratases and the 2 control fatty acid hydratases (without start codon) from the genomic DNAs. Polymerase chain reactions (PCR) were conducted using Q5 High-Fidelity DNA Polymerase (New England Biolabs, Ipswich, Massachusetts, USA) with the following settings: initial denaturation at 98°C for 60 seconds, followed by 35 cycles of annealing-extension at 98°C for 10 seconds, 55°C for 20 seconds, 72°C for 60 seconds, and final extension at 72°C for 120 seconds. The resulting PCR products were purified using QIAquick PCR Purification Kit (Qiagen, Hilden, Germany) and cloned into the multiple cloning site of pET-15b vector (Novagen/Merck, Kenilworth, New Jersey, USA; Fig. 7a) through Gibson assembly approach. Prior to the reaction, the pET-15b vector was linearized by digestion with *BamHI* and *NdeI* restriction enzymes and purified using QIAquick PCR Purification Kit (Qiagen, Hilden, Germany). Gibson assembly was performed using NEBuilder HiFi DNA Assembly Master Mix (New England Biolabs, Ipswich, Massachusetts, USA), with a vector-to-insert ratio of 1-to-2 (1:2) at 50°C for 1 hour. The ligation products were transformed into the competent cells of *E. coli* strain 10-beta (New England Biolabs, Ipswich, Massachusetts, USA) and selected on lysogeny broth (LB) plates by resistance to 100 µg mL^{-1} of ampicillin. Positive transformants were confirmed by colony PCR using the primer pair T7-Pro-F (SEQ ID NO 149: 5'AGAGGATCGAGATCTCGATCCCGCG3') and T7-Ter-R (SEQ ID NO 150: 5'CCTCTTGCGGGATATCCGGATATAG3'). Expression plasmids, pET-15b-XXX (XXX refers to the abbreviation of each identified fatty acid hydratase; Table 5 and Fig. 7b), were subsequently extracted from the overnight cultures of the positive transformants using QIAprep Spin Miniprep Kit (Qiagen, Hilden, Germany). Lastly, DNA sequencing (1st Base Sequencing, Singapore) was conducted to validate the nucleotide sequences inserted into the vector.

Recombinant Protein Expression in E. coli Strains

[00115] Expression plasmids, pET-15b-XXX (Table 5), were transformed into the competent cells of *E. coli* strain Acella (Edge Biosystems, San Jose, California, USA) and selected on lysogeny broth (LB) plates containing 100 µg mL^{-1} ampicillin to give recombinant strains Acella/pET-15b-XXX. To induce recombinant protein expression, seed cultures were first prepared by cultivating single colonies of the *E. coli* strains in 5 mL of SOC^{AMP} medium (20 g L^{-1} tryptone, 5 g L^{-1} yeast extract, 0.5 g L^{-1} sodium chloride, 2.5 mM potassium chloride, 20 mM magnesium chloride, 20 mM magnesium sulfate, 100 µg mL^{-1} ampicillin, pH 7.0) supplemented with 20 mM glucose, at 37°C, 220 rpm for 7 hours. The obtained seed cultures were diluted to OD_{600nm} of 0.01 in 100 mL of autoinduction medium in 500 mL Erlenmeyer flask and cultured aerobically with 160 rpm of agitation, first at 24°C for 18 hours and then 14°C for another 48 hours. The autoinduction medium was prepared by supplementing the SOC^{AMP} medium with autoinduction sugars consisting of 1.5% (w/v) lactose, 0.5% (w/v) glycerol and 0.05% (w/v) glucose. The induced recombinant *E. coli* cells were harvested by centrifugation at 4,000 × *g*, 4°C for 10 minutes. The collected cell pellets were washed, weighed, and resuspended to a wet cell mass of 70-90 g L^{-1} in 50 mM citrate-

phosphate buffer (59.9 mM citric acid, 50 mM disodium phosphate, pH 6.0). For storage at -80°C, 20% (w/v) glycerol was added to the cell suspension.

[00116] To evaluate recombinant protein expression and solubility in *E. coli* strains, sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was conducted. Whole-cell protein extracts were prepared by lysing cells harvested from 1 mL aliquot of the induced recombinant *E. coli* cultures with 200 µL of BugBuster® Protein Extraction Reagent (Merck Millipore, Burlington, Massachusetts, USA) following manufacturer's instructions. Soluble protein fractions were collected as supernatants of the whole-cell protein extracts after centrifugation at 21,000 × *g* for 10 minutes. The remaining cell pellets were further solubilized with 8 M urea for 1 hour to give insoluble protein fractions. Both soluble and insoluble protein fractions were mixed with one third volume of 4× Laemmli Sample Buffer (Bio-Rad, Hercules, California, USA) spiked with 1.42 M of 2-mercaptoethanol before denaturation at 95°C for 10 minutes. The denatured protein samples were loaded on 4-20% Mini-PROTEAN® TGX Precast Gels along with Precision Plus Protein Dual Color Standards (Bio-Rad, Hercules, California, USA). After electrophoresis at 120 V for 80 minutes with TGX buffer (25 mM Tris, 192 mM glycine, 0.1% SDS, pH 8.3), the gels were stained with InstantBlue® Coomassie Protein Stain (Abcam, Cambridge, UK) for the visualization of protein bands.

Recombinant E. coli Whole-Cell Biotransformation Assays

[00117] Induced recombinant *E. coli* cells were collected by thawing the frozen cell suspensions at room temperature followed by centrifugation at 4,000 × *g*, 4°C for 10 minutes to remove supernatant. After washing with 50 mM citrate-phosphate buffer (59.9 mM citric acid, 50 mM disodium phosphate, pH 6.0), the cells were resuspended in "anoxic" reaction medium, at a final wet cell mass of 35 g L^{-1}. "Anoxic" reaction medium was prepared by first adding to 50 mM citrate-phosphate buffer an appropriate amount of free fatty acid substrates and 0.25% (v/v) Tween 40, before anoxic conditioning inside a Coy anoxic chamber (atmosphere 4% hydrogen, 5% carbon dioxide and 91% nitrogen; Coy Laboratory Products, Grass Lake, Michigan, USA) for at least 48 hours. For the screening of fatty acid-hydroxylating activity, the cells were resuspended in 10 mL of "anoxic" reaction medium containing 100 g L^{-1} Wilfarin OA-7075 (Natural Oleochemicals Sdn. Bhd., Johor, Malaysia), in 15 mL conical tubes. The substrate Wilfarin OA-7075 consisted of 81.0% oleic acid, 10.1% linoleic acid, 7.1% palmitic acid (C16:0) and 1.8% stearic acid (C18:0). For the characterization of substrate selectivity and product scope, cells were resuspended in 1 mL of "anoxic" reaction medium supplemented with 30 mM unsaturated fatty acid substrates, in 2 mL microcentrifuge tubes. Oleic acid (C18:1; ≥99% purity), linoleic acid (C18:2; ≥95% purity) and arachidonic acid (C20:4; >95% purity) were purchased from Sigma-Aldrich (Burlington, Massachusetts, USA); vaccenic acid (C18:1; >99% purity), ricinoleic acid (C18:1, 12-OH; >99% purity) and α-linolenic acid (C18:3; >99% purity) were purchased from Larodan AB (Solna, Sweden); palmitoleic acid (C16:1; >98% purity) and γ-linolenic acid (C18:3; >98% purity) were purchased from Tokyo Chemical Industry (Tokyo, Japan). (8*Z*)-heptadec-8-enoic acid (C17:1) was produced in-house using an enzymatic approach and the purity was approximately 85%. For the examination of hydroxylation efficiency at a higher substrate

concentration, reaction mixtures were similarly prepared except for adding 100 g L^{-1} instead of 30 mM substrate (Wilfarin OA-7075 and linoleic acid),

[00118] To minimize oxygen exposure, addition of cells to the "anoxic" reaction medium was conducted inside the anoxic chamber, and the tubes were sealed with parafilm before removal from the anoxic chamber. The obtained "anoxic" reaction mixtures were incubated at 40°C with 245 rpm of agitation for 24-48 hours (outside the anoxic chamber). After the reaction, samples were diluted appropriately with acetonitrile/isopropanol mixture (1-to-1 ratio) and centrifuged to settle cell debris (21,000 × *g* for 10 minutes) when necessary, before liquid chromatography-tandem mass spectrometry analysis (LC-MS/MS) analysis.

Dual-Protein System

[00119] Recombinant *E. coli* cells were similarly prepared as for the whole-cell biotransformation assay. For reactions involving the interaction of two identified fatty acid hydratases, recombinant cells expressing each fatty acid hydratase were added to the "anoxic" reaction medium at 17.5 g L^{-1} to give a total wet cell mass of 35 g L^{-1}.

Biotransformation Scale-up and Lipid Extraction

[00120] Seed cultures of selected recombinant *E. coli* strains were inoculated at an OD_{600nm} of 0.1 into a 2 L Univessel Glass fermenter (Sartorius, Göttingen, Germany) containing 1 L of SOC^{AMP} medium supplemented with 0.5% (w/v) glucose and 1.5% (w/v) glycerol. Cultivation was initially maintained at the following conditions using a Biostat B benchtop controller (Sartorius, Göttingen, Germany): 40% oxygen saturation, 500 rpm of agitation, and 30°C. The temperature was adjusted to 20°C at 6 hours following the addition of 0.5 mM isopropyl β-D-1-thiogalactopyranoside (IPTG), a molecular mimic of lactose, to induce fatty acid hydratase expression. The stirring speed was elevated to 800 rpm at 24 hours, in parallel with the supplementation of 0.5% (w/v) glycerol. A second dose of 0.5 mM isopropyl β-D-1-thiogalactopyranoside (IPTG) was added at 30 hours, after which cells were harvested at 48 hours by centrifugation at 4,000 × *g* at 4°C for 10 minutes. The collected cell pellets were washed, weighed, and resuspended to a wet cell mass of 35 g L^{-1} in 30 or 250 mL of reaction medium containing 50 mM citrate-phosphate buffer, 100 g L^{-1} Wilfarin OA-7075, and 0.25% (v/v) Tween 40. The obtained reaction mixtures were incubated at 40°C, 245 rpm for 48 hours. Fatty acids were subsequently extracted by adding to the reaction mixture an appropriate volume (2-3× volume of reaction medium) of acetonitrile/ethyl acetate mixture (1-to-1 ratio), mixed, and heated to 80°C until a clear upper layer was observed. The upper layer was transferred to a new bottle and incubated at 50°C to evaporate the acetonitrile and ethyl acetate solvents. Finally, the remaining fatty acid fraction was diluted appropriately with an acetonitrile/isopropanol mixture (1-to-1 ratio) before liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis.

Analytical Methods

[00121] Fatty acid profiles were analysed with a Vanquish liquid chromatography (LC) system attached to a Q Exactive Plus Orbitrap mass spectrometer equipped with electrospray ionisation (Thermo Scientific, Waltham, Massachusetts, USA). For liquid chromatography, samples were injected at a volume of 0.2 µL

onto a Poroshell 120 EC-C18 (2.7 µm, 3.0 mm × 100 mm) threaded column (Agilent, Santa Clara, California, USA) at 35°C, with a flow rate of 0.4-0.5 mL min^{-1}. Mobile phase A was 0.1% formic acid with 1 mM ammonium acetate in an acetonitrile/water mixture at 6-to-4 ratio, while mobile phase B was isopropanol. The running gradient was as follows: starting solvent mixture of 25% B; 0-2.3 minutes linear gradient to 50% B; 2.3-3.0 minutes linear gradient to 85% B; 3.0-3.5 minutes linear gradient to 100% B; 3.5-6.0 minutes isocratic with 100% B; 6.0-6.1 minutes linear gradient to 10% B; and 6.1-7.0 minutes isocratic with 10% B. For tandem mass spectrometry (MS/MS), samples were run in negative full scan mode followed by parallel reaction monitoring. Representative liquid chromatography-tandem mass spectrometry (LC-MS/MS) chromatograms and mass spectra are provided in Fig. 9-13.

TABLES

[00122] Table 1. List of 21 identified fatty acid hydratases and two control fatty acid hydratases examined in this study sorted according to the families of bacterial strains from which they were derived. Their fatty acid hydratase subtype, homologous family (HFam) classification, and amino acid length are also provided. Control fatty acid hydratases are indicated with an asterisk.

Phylum; Class; Order; Family	Strain	Fatty Acid Hydratase	Sub-type	HFam	Amino Acid Length	Amino Acid SEQ ID NO	Nucleo-tide SEQ ID NO
Actinomycetota; *Actinobacteria*; *Bifidobacteriales*; *Bifidobacteriaceae*	*Bifidobacterium apri* DSM 100238^T	**DSM100238^T-HY64.1**	*cis*-Δ9	2	622	NO: 1	NO: 24
	Bifidobacterium thermophilum WILCCON 0093	**WIL0093-HY53.1**	*cis*-Δ9	2	642	NO: 2	NO: 25
Bacillota; *Bacilli*; *Lactobacillales*; *Enterococcaceae*	*Enterococcus avium* WILCCON 0019	**WIL0019-HY10.1**	*cis*-Δ9/12	2	590	NO: 3	NO: 26
	Enterococcus gallinarum WILCCON 0024	**WIL0024-HY15.1**	*cis*-Δ9/12	2	590	NO: 4	NO: 27
	Enterococcus malodoratus WILCCON 0020	**WIL0020-HY11.1**	*cis*-Δ9/12	2	590	NO: 5	NO: 28
	Enterococcus xiangfangensis WILCCON 0022	**WIL0022-HY13.1**	*cis*-Δ9/12	2	590	NO: 6	NO: 29
Bacillota; *Bacilli*; *Lactobacillales*; *Lactobacillaceae*	*Furfurilactobacillus rossiae* DSM 15814^T	**DSM15814^T-HY67.1**	*cis*-Δ9	3	559	NO: 7	NO: 30
	Lacticaseibacillus saniviri WILCCON 0041	**WIL0041-HY30.1**	*cis*-Δ9	3	558	NO: 8	NO: 31
	Lactiplantibacillus plantarum WILCCON 0012	*WIL0012-HY06.2	*cis*-Δ9	3	564	NO: 9	NO: 32
	Lactobacillus amylovorus WILCCON 0068	*WIL0068-HY41.1	*cis*-Δ12	2	590	NO: 10	NO: 33
	Leuconostoc pseudomesenteroides WILCCON 0006	**WIL0006-HY03.1**	*cis*-Δ9/12	2	590	NO: 11	NO: 34
	Leuconostoc suionicum WILCCON 0008	**WIL0008-HY04.1**	*cis*-Δ9/12	2	590	NO: 12	NO: 35
	Ligilactobacillus ubinensis WILCCON 0076	**WIL0076-HY48.1**	*cis*-Δ12	2	589	NO: 13	NO: 36
	Limosilactobacillus sp. WILCCON 0055	**WIL0055-HY35.1**	*cis*-Δ12	2	591	NO: 14	NO: 37
		WIL0055-HY36.4	*cis*-Δ9	2	605	NO: 15	NO: 38
	Liquorilactobacillus nagelii WILCCON 0075	**WIL0075-HY05.2**	*cis*-Δ12	2	589	NO: 16	NO: 39

	Pediococcus pentosaceus WILCCON 0037	**WIL0037-HY26.1**	*cis*-Δ9	3	557	NO: 17	NO: 40
	Pediococcus stilesii WILCCON 0039	**WIL0039-HY28.1**	*cis*-Δ9	3	571	NO: 18	NO: 41
	Pediococcus acidilactici PA	**PA-HY29.2**	*cis*-Δ9	3	559	NO: 19	NO: 42
Bacillota; *Bacilli*; *Lactobacillales*; *Streptococcaceae*	*Lactococcus lactis* subsp. *lactis* WILCCON 0029	**WIL0029-HY20.1**	*cis*-Δ12	2	589	NO: 20	NO: 43
Bacillota; *Clostridia*; *Eubacteriales*; *Clostridiaceae*	*Clostridium neuense* WILCCON 0114	**WIL0114-HY62.1**	*cis*-Δ12	2	564	NO: 21	NO: 44
	Candidatus Clostridium cibarium WILCCON 0042	**WIL0042-HY33.1**	*cis*-Δ12	2	564	NO: 22	NO: 45
Bacillota; *Erysipelotrichia*; *Erysipelotrichales*; *Coprobacillaceae*	*Sharpea azabuensis* WILCCON 0057	**WIL0057-HY37.1**	*cis*-Δ9	2	645	NO: 23	NO: 46

[00123] Table 2. List of fatty acid abbreviations, their common and IUPAC names, chemical formulas, PubChem Compound Identifiers (CID) and CAS registry numbers.

Abbreviation	**Common/IUPAC Name**	**Chemical formula**	**PubChem CID**	**CAS Registry No.**
PA	Palmitoleic acid; (9Z)-hexadec-9-enoic acid	C16:1 $\Delta^{9(Z)}$	445638	373-49-9
10-HPA	10-hydroxypalmitic acid; 10-hydroxyhexadecanoic acid	C16:0 , 10-OH	15569771	23048-75-1
HA	(8Z)-heptadec-8-enoic acid	C17:1 $\Delta^{8(Z)}$	5312439	NA
9-HHA	9-hydroxyheptadecanoic acid	C17:0 , 9-OH	86012010	NA
OA	Oleic acid; (9Z)-octadec-9-enoic acid	C18:1 $\Delta^{9(Z)}$	445639	112-80-1
10-HSA	10-hydroxystearic acid; 10-hydroxyoctadecanoic acid	C18:0 , 10-OH	9561835	638-26-6
VA	Vaccenic acid; (11Z)-octadec-11-enoic acid	C18:1 $\Delta^{11(Z)}$	5282761	506-17-2
12-HSA	12-hydroxystearic acid; 12-hydroxyoctadecanoic acid	C18:0 , 12-OH	7789	106-14-9
RA	Ricinoleic acid; (9Z)-12-hydroxyoctadec-9-enoic acid	C18:1 $\Delta^{9(Z)}$, 12-OH	643684	141-22-0
10,12-dHSA	10,12-dihydroxystearic acid; 10,12-dihydroxyoctadecanoic acid	C18:0 , 10,12-OH	22404576	NA
LA	Linoleic acid; (9Z,12Z)-octadeca-9,12-dienoic acid	C18:2 $\Delta^{9(Z),12(Z)}$	5280450	60-33-3
10-HOE	(12Z)-10-hydroxyoctadec-12-enoic acid	C18:1 $\Delta^{12(Z)}$, 10-OH	46186046	NA
13-HOE	(9Z)-13-hydroxyoctadec-9-enoic acid	C18:1 $\Delta^{9(Z)}$, 13-OH	88183365	NA
10,13-dHSA	10,13-dihydroxystearic acid; 10,13-dihydroxyoctadecanoic acid	C18:0 , 10,13-OH	57471641	NA

ALA	α-linolenic acid; (9*Z*,12*Z*,15*Z*)-octadeca-9,12,15-trienoic acid	C18:3 $\Delta^{9(Z),12(Z),15(Z)}$	5280934	463-40-1
α-10-HODE	(12*Z*,15*Z*)-10-hydroxyoctadeca-12,15-dienoic acid	C18:2 $\Delta^{12(Z),15(Z)}$, 10-OH	88320085	NA
α-13-HODE	(9*Z*,15*Z*)-13-hydroxyoctadeca-9,15-dienoic acid	C18:2 $\Delta^{9(Z),15(Z)}$, 13-OH	124089055	NA
α-10,13-dHOE	(15*Z*)-10,13-dihydroxyoctadec-15-enoic acid	C18:1 $\Delta^{15(Z)}$, 10,13-OH	122574238	NA
GLA	γ-linolenic acid; (6*Z*,9*Z*,12*Z*)-octadeca-6,9,12-trienoic acid	C18:3 $\Delta^{6(Z),9(Z),12(Z)}$	5280933	506-26-3
γ-10-HODE	(6*Z*,12*Z*)-10-hydroxyoctadeca-6,12-dienoic acid	C18:2 $\Delta^{6(Z),12(Z)}$, 10-OH	118046914	NA
γ-13-HODE	(6*Z*,9*Z*)-13-hydroxyoctadeca-6,9-dienoic acid	C18:2 $\Delta^{6(Z),9(Z)}$, 13-Oh	60104676	NA
γ-10,13-dHOE	(6*Z*)-10,13-dihydroxyoctadec-6-enoic acid	C18:1 $\Delta^{6(Z)}$, 10,13-OH	91826743	NA
ARA	Arachidonic acid; (5*Z*,8*Z*,11*Z*,14*Z*)-icosa-5,8,11,14-tetraenoic acid	C20:4 $\Delta^{5(Z),8(Z),11(Z),14(Z)}$	444899	506-32-1
12-HITE	(5*Z*,8*Z*,14*Z*)-12-hydroxyicosa-5,8,14-trienoic acid	C20:3 $\Delta^{5(Z),8(Z),14(Z)}$, 12-OH	60060296	NA
15-HITE	(5*Z*,8*Z*,11*Z*)-15-hydroxyicosa-5,8,11-trienoic acid	C20:3 $\Delta^{5(Z),8(Z),11(Z)}$, 15-OH	6438724	NA
12,15-dHIDE	(5*Z*,8*Z*)-12,15-dihydroxyicosa-5,8-dienoic acid	C20:2 $\Delta^{5(Z),8(Z)}$, 12,15-OH	NA	NA

[00124] Table 3. List of 55 previously described fatty acid hydratases sorted according to the families of microbial strains from which they were derived. Fatty acid hydratase subtype was deducted from their reported positional selectivity and hydroxy fatty acid product scopes. Homologous family (HFam) classification and amino acid length are also provided.

Kingdom; Phylum; Class; Order; Family	**Species**	**Fatty Acid Hydratase**	**Subtype**	**HFam**	**Amino Acid Length**
Bacteria; Actinomycetota; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae	*Bifidobacterium animalis* subsp. *lactis*	**CTR0001**	*cis*-Δ9	2	732
	Bifidobacterium breve	**CTR0002**	*cis*-Δ9	2	625
		CTR0003	*cis*-Δ9	2	625
	Bifidobacterium longum	**CTR0004**	*cis*-Δ9	2	625
Bacteria; Actinomycetota; Actinobacteria; Mycobacteriales; Nocardiaceae	*Rhodococcus erythropolis*	**CTR0005**	*cis*-Δ9	3	559
Bacteria; Bacillota; Bacilli; Caryophanales; Caryophanaceae	*Lysinibacillus fusiformis*	**CTR0006**	*cis*-Δ9	2	590
		CTR0007	*cis*-Δ9	2	590
Bacteria; Bacillota; Bacilli; Caryophanales; Staphylococcaceae	*Gemella morbillorum*	**CTR0008**	*cis*-Δ9	2	590
	Macrococcus caseolyticus	**CTR0009**	*cis*-Δ9/12	2	589
	Staphylococcus aureus	**CTR0010**	*cis*-Δ9	2	591
Bacteria; Bacillota; Bacilli;	*Lacticaseibacillus casei*	**CTR0011**	NA	3	564

Lactobacillales; Lactobacillaceae	*Lacticaseibacillus rhamnosus*	**CTR0012**	*cis*-Δ9	3	564
	Lactiplantibacillus plantarum	**CTR0013**	*cis*-Δ9	3	569
		CTR0014	*cis*-Δ9	3	569
	Lactobacillus acidophilus	**CTR0015**	*cis*-Δ9	2	591
		CTR0016	*cis*-Δ9	2	591
		CTR0017	*cis*-Δ12	2	590
	Lactobacillus crispatus	**CTR0018**	*cis*-Δ12	2	590
	Lactobacillus delbrueckii subsp. *bulgaricus*	**CTR0019**	NA	2	591
	Lactobacillus gallinarum	**CTR0020**	*cis*-Δ12	2	590
	Lactobacillus gasseri	**CTR0021**	*cis*-Δ12	2	590
	Lactobacillus hamsteri	**CTR0022**	*cis*-Δ12	2	590
	Lactobacillus johnsonii	**CTR0023**	Inactive	2	591
	Levilactobacillus hammesii	**CTR0024**	*cis*-Δ9	3	564
	Levilactobacillus spicheri	**CTR0025**	*cis*-Δ9	3	564
	Limosilactobacillus reuteri	**CTR0026**	*cis*-Δ9	2	590
	Pediococcus claussenii	**CTR0027**	*cis*-Δ12	2	590
Bacteria; Bacillota; Bacilli; Lactobacillales; Streptococcaceae	*Lactococcus garvieae*	**CTR0028**	*cis*-Δ9	2	587
	Streptococcus equinus	**CTR0029**	*cis*-Δ12	2	589
	Streptococcus mutans	**CTR0030**	*cis*-Δ12	2	589
	Streptococcus pyogenes	**CTR0031**	*cis*-Δ9/12	2	590
		CTR0032	*cis*-Δ9/12	2	590
		CTR0033	*cis*-Δ9/12	2	603
Bacteria; Bacillota; Bacilli; Hybrid fusion	*Lactococcus lactis* and *Lysinibacillus fusiformis*	**CTR0034**	*cis*-Δ9	2	590
		CTR0035	*cis*-Δ9	2	587
Bacteria; Bacillota; Clostridia; Eubacteriales; Clostridiaceae	*Alkaliphilus metalliredigens*	**CTR0036**	NA	1	554
	Clostridium botulinum	**CTR0037**	NA	2	565
Bacteria; Bacillota; Clostridia; Eubacteriales; Lachnospiraceae	*Coprococcus eutactus*	**CTR0038**	NA	2	666
Bacteria; Bacillota; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae	*Thermoanaerobacterium thermosaccharolyticum*	**CTR0039**	Inactive	1	533
		CTR0040	NA	1	525
Bacteria; Bacillota; Erysipelotrichia; Erysipelotrichales; Coprobacillaceae	*Coprobacillus* sp.	**CTR0041**	NA	1	563
	Chryseobacterium gleum	**CTR0042**	*cis*-Δ9	11	642

Bacteria; Bacteroidota; Flavobacteriia; Flavobacteriales; Weeksellaceae	*Elizabethkingia meningoseptica*	**CTR0043**	*cis*-Δ9	11	646
		CTR0044	*cis*-Δ9	11	646
Bacteria; Bacteroidota; Sphingobacteriia; Sphingobacteriales; Sphingobacteriaceae	*Mucilaginibacter paludis*	**CTR0045**	Inactive	1	515
Bacteria; Euryarchaeota; Halobacteria; Halobacteriales; Haloarculaceae	*Haloarcula marismortui*	**CTR0046**	NA	1	529
Bacteria; Euryarchaeota; Halobacteria; Natrialbales; Natrialbaceae	*Haloterrigena thermotolerans*	**CTR0047**	Inactive	1	532
Bacteria; Pseudomonadota; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae	*Gluconobacter oxydans*	**CTR0048**	NA	11	386
Bacteria; Pseudomonadota; Deltaproteobacteria; Desulfovibrionales; Desulfomicrobiaceae	*Desulfomicrobium baculatum*	**CTR0049**	*cis*-Δ9	2	611
Bacteria; *Pseudomonadota*; *Gammaproteobacteria*; *Lysobacterales*; *Lysobacteraceae*	*Stenotrophomonas maltophilia*	**CTR0050**	*cis*-Δ9	2	589
		CTR0051	*cis*-Δ9	2	589
		CTR0052	NA	2	589
		CTR0053	*cis*-Δ9	11	661
	Stenotrophomonas nitritireducens	**CTR0054**	*cis*-Δ9	11	653
Fungi; Ascomycota; Sordariomycetes; Hypocreales; Nectriaceae	*Nectria haematococca*	**CTR0055**	NA	2	585

[00125] Table 4. List of fatty acid hydratases used as controls. Control fatty acid hydratases shared >90% sequence identity with the described fatty acid hydratases. SeqID, sequence identity.

Bacterial Strain	**Fatty Acid Hydratase**	**HFam**	**Amino Acid Length**	**Closest Described FAHs**	**% SeqID**
Lactiplantibacillus plantarum WILCCON 0012	**WIL0012-HY06.2**	3	564	CTR0014	100
				CTR0013	99.8
Lactobacillus amylovorus WILCCON 0068	**WIL0068-HY41.1**	2	590	CTR0020	94.2
				CTR0017	94.1
				CTR0018	93.7

[00126] Table 5. List of expression plasmids and primer pairs used to amplify the 21 identified fatty acid hydratases and the two control fatty acid hydratases (indicated with an asterisk) from genomic DNAs.

Expression Plasmid	Primer Name	Primer Nucleotide Sequence
pET-15b-DSM100238^{T}-HY64.1	Fw (DSM100238T-HY64.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGGTGCCCGCCTCGACGTTGAGGCCCGGCTTC-3’
	Rv (DSM100238T-HY64.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTCACAACACCCCGCACGCCTTGAGCAGCTT-3’
pET-15b-WIL0093-HY53.1	Fw (WIL0093-HY53.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGCAATTGGACATGTTTCCGCCGATTGTCGAT-3’
	Rv (WIL0093-HY53.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTCACAATGCCCCGCACGCCTTGAGCAGCTT-3’
pET-15b-WIL0019-HY10.1	Fw (WIL0019-HY10.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGGAATTATGAAGCATTT-3’
	Rv (WIL0019-HY10.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCCTACAGTAAATGATTGTCCTTCAACACATC-3’
pET-15b-WIL0024-HY15.1	Fw (WIL0024-HY15.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGAGATATACAAACGGAAATTATGAAGCTTTT-3’
	Rv (WIL0024-HY15.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTTAAACTAAATGATTTTTTTCAAGGATTTC-3’
pET-15b-WIL0020-HY11.1	Fw (WIL0020-HY11.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGAAATTACGAAGCATTT-3’
	Rv (WIL0020-HY11.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTTACAACAAATGATTCTCTTTCAATACATC-3’
pET-15b-WIL0022-HY13.1	Fw (WIL0022-HY13.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGAAATTATGAAGCTTTT-3’
	Rv (WIL0022-HY13.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTTACAACAGATGGTTGTCTTTCAACACATC-3’
pET-15b-DSM15814^{T}-HY67.1	Fw (DSM15814T-HY67.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGGCACAGCATGCATACATGATTGGTACAGGC-3’
	Rv (DSM15814T-HY67.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCCTATCTGAACATTGTCTTGGTTGCACGGGC-3’
pET-15b-WIL0041-HY30.1	Fw (WIL0041-HY30.1)	5’-CCTGGTGCCGCGCGGCAGCCATATGGCACAACATGCTTATATGATCGGTACTGGT-3’
	Rv (WIL0041-HY30.1)	5’-TTCGGGCTTTGTTAGCAGCCGGATCTTAACGGAACATGGTCCGTGTTGCCCGCAG-3’
*pET-15b-WIL0012-HY06.2	Fw (WIL0012-HY06.2)	5’-CCTGGTGCCGCGCGGCAGCCATATGGTTAAAAGTAAAGCAATTATGATTGGTGCC-3’

	Rv (WIL0012-HY06.2)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTAATCAAACATCTTCTTAG TTGCCTTGAG-3’
*pET-15b-WIL0068-HY41.1	Fw (WIL0068-HY41.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGCATTATAGCAATGGTAATT ATGAAGCTTTC-3’
	Rv (WIL0068-HY41.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTAAATCAACTTGTACTTCT TAAGCAATTC-3’
pET-15b-WIL0006-HY03.1	Fw (WIL0006-HY03.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTATTATAGTAATGGTAATT ATGAGGCATTT-3’
	Rv (WIL0006-HY03.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTCACATCAAGTGTGCTTCA ACAAGCAACTC-3’
pET-15b-WIL0008-HY04.1	Fw (WIL0008-HY04.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTATTATAGTAATGGTAATT ATGAAGCATTT-3’
	Rv (WIL0008-HY04.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTATAATAAATGTGCTTCTG CCAATAATTC-3’
pET-15b-WIL0076-HY48.1	Fw (WIL0076-HY48.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTATTATAGTAGTGGTAATT ATGAAGCTTTT-3’
	Rv (WIL0076-HY48.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCCTAGATTAAGTGCTCATCT CTAAAGATTTC-3’
pET-15b-WIL0055-HY35.1	Fw (WIL0055-HY35.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGATGCATTACACAAATGGAA ACTACGAGGCG-3’
	Rv (WIL0055-HY35.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCCTAGATCAGCCGATATTCT TTTAAAAGTTC-3’
pET-15b-WIL0055-HY36.4	Fw (WIL0055-HY36.4)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTTATCGCTTTCGCAAGGAT TATTTTACACT-3’
	Rv (WIL0055-HY36.4)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTCAGTCAAGCAGATGCTGC TCTTTGAGAAT-3’
pET-15b-WIL0075-HY05.2	Fw (WIL0075-HY05.2)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTACTACAGTAGTGGTAATT ATGAAGCATTT-3’
	Rv (WIL0075-HY05.2)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTAGAGTAACTTTTGAGAT TTCAAAATTTC-3’
pET-15b-WIL0037-HY26.1	Fw (WIL0037-HY26.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGGAAAAAGCATATATGATCG GTACTGGAATT-3’
	Rv (WIL0037-HY26.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTATCTAAACATAGTCTTA GTTGCTTTTAG-3’
pET-15b-WIL0039-HY28.1	Fw (WIL0039-HY28.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGCTATGTATTTTAAATAAGA ATGAGGAGGAG-3’

	Rv (WIL0039-HY28.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTATCTAAACATTGTTTTAG TAGCTCTTAA-3’
pET-15b-PA-HY29.2	Fw (PA-HY29.2)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGATGAGAAAAGCGTTTATGA TTGGTACAGGA-3’
	Rv (PA-HY29.2)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCCTAACGGAACATGGTCCGG GTTGCCTTCAA-3’
pET-15b-WIL0029-HY20.1	Fw (WIL0029-HY20.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTATTACAGTAACGGAAATT ATGAAGCATTT-3’
	Rv (WIL0029-HY20.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCCTATAATAAGTGTTGATCG ACTAATATTTC-3’
pET-15b-WIL0114-HY62.1	Fw (WIL0114-HY62.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGAATAATTATCAAAGAATCA ATCCAATCGCA-3’
	Rv (WIL0114-HY62.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTATAATAAATTTTTTAATT CTGTGTTCTT-3’
pET-15b-WIL0042-HY33.1	Fw (WIL0042-HY33.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGAATAATTATCAAAGAATTA ATCCAATTAAA-3’
	Rv (WIL0042-HY33.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTATAGTAATTTTTCAATTT CTGTATTCTT-3’
pET-15b-WIL0057-HY37.1	Fw (WIL0057-HY37.1)	5’-CCTGGTGCCGCGCGGCAGCCAT ATGTATTACAGCAGTGGTAATT ACGAAGCTTTT-3’
	Rv (WIL0057-HY37.1)	5’-TTCGGGCTTTGTTAGCAGCCGG ATCTTAAGATTTCTTTTTATGCA ACAATGCAGC-3’

[00127] Table 6. A summary of the retention times, exact masses, mass-to-charge ratios (m/z) of the precursor ions and qualifier fragment ions of unsaturated fatty acid substrates and hydroxy fatty acid products detected and quantified in this study. For fatty acid abbreviations, refer to Table 2.

Compound	Chemical Formula	Retention time (min)	Exact mass (Da)	Precursor ion (m/z)	Qualifier fragment ion (m/z)
PA	$C_{16}H_{30}O_2$	4.43-4.45	254.2246	253.2173	- 5
10-HPA	$C_{16}H_{32}O_3$	3.01-3.04	272.2351	271.2279	113.0961
HA	$C_{17}H_{32}O_2$	4.54-4.57	268.2402	267.2330	-
9-HHA	$C_{17}H_{34}O_3$	3.54-3.59	286.2508	285.2435	141.1274
OA	$C_{18}H_{34}O_2$	4.64-4.68	282.2559	281.2486	-
10-HSA	$C_{18}H_{36}O_3$	3.84-3.86	300.2664	299.2592	141.1275
VA	$C_{18}H_{34}O_2$	4.63-4.65	282.2559	281.2486	-
12-HSA	$C_{18}H_{36}O_3$	3.71-3.74	300.2664	299.2592	113.0961
RA	$C_{18}H_{34}O_3$	3.24-3.28	298.2508	297.2435	183.1388
10,12-dHSA	$C_{18}H_{36}O_4$	2.56-2.57	316.2614	315.2541	185.1177
LA	$C_{18}H_{32}O_2$	4.49-4.51	280.2402	279.2330	-
10-HOE	$C_{18}H_{34}O_3$	3.35-3.37	298.2508	297.2435	185.1177
13-HOE	$C_{18}H_{34}O_3$	3.27-3.30	298.2508	297.2435	197.1540
10,13-dHSA	$C_{18}H_{36}O_4$	1.97-1.99	316.2614	315.2541	185.1176
ALA	$C_{18}H_{30}O_2$	4.28-4.30	278.2246	277.2173	-
α-10-HODE	$C_{18}H_{32}O_3$	2.76-2.80	296.2351	295.2279	185.1178
α-13-HODE	$C_{18}H_{32}O_3$	2.78-2.81	296.2351	295.2279	225.1493
α-10,13-dHOE	$C_{18}H_{34}O_4$	1.68-1.69	314.2457	313.2384	243.1602
GLA	$C_{18}H_{30}O_2$	4.31-4.33	278.2246	277.2173	-
γ-10-HODE	$C_{18}H_{32}O_3$	3.06-3.10	296.2351	295.2279	183.1022
γ-13-HODE	$C_{18}H_{32}O_3$	2.88-2.92	296.2351	295.2279	195.1387
γ-10,13-dHOE	$C_{18}H_{34}O_4$	1.83-1.85	314.2457	313.2384	155.1069
ARA	$C_{20}H_{32}O_2$	4.43-4.45	304.2402	303.2330	-
12-HITE	$C_{20}H_{34}O_3$	3.46-3.47	322.2508	321.2435	181.1227
15-HITE	$C_{20}H_{34}O_3$	3.29-3.31	322.2508	321.2435	221.1544
12,15-dHIDE	$C_{20}H_{36}O_4$	2.15-2.17	340.2614	339.2541	181.1229

SEQUENCE LISTING

[00128] The following sequences are disclosed in the present application.

SEQ ID NO:	Name	Sequence
1	DSM100238^{T}-HY64.1	MVPASTLRPGFIKTEMPSMKPANNDGKGVIMYYSAGNYEAFATPEKP EGIDDKYAYIVGSGLAGLSAACYLIRDAQMPGDHITVFEFLPVAGGSC DGIYDATRGYIMRGGREMDNHFEVMWDLFRSIPSIQNPGETIFSEYYK LNKHDPNFSLCRVTEKQGQDAHTDKKYGMNPKATQELLHLFMATDE ELADKTIDDVFDDDFYKTNFWVYWQTMFAFEKWHSAIEMKRYMQR YIHHIDGLPDLSALRFTRYNQYDSMIRPMVKYITDAGAKVLYDTNVTN VVCEVTRSRKAARRIEYTQGGEAKSIDLTDNDLVFITNGSQGDCTAYG DQTHAPVVSIKNGEGPSVELWKRIAAQSSDFGHPEKFFKDIEETSWES WTVDTSNKEVLDAIEAICHRDPLSGKIVTGGIVTARDSSWLLSWTINRQ GQFPDQPSDHCLIWVYGLNCWHDNGDFVKKPMAQCTGEELCEEWLY HIGIPQDRIKQLASEVCNTTAAMMPYVTSFFEPRRDGDRPKVVPDGSV NLAFVGQYAETPRDTVFTTEYSIRTGMEAVYTLCNVDRGVPEVWGSV FDVRDLLTATVKLADGKKLTEMDLPLKDRLALHELLKKVQGTEIEKL LKACGVL
2	WIL0093-HY53.1	MQLDMFPPIVDGFSPRTDPIMVFASTLRPGFAKAPSLHETGGRNDGKG VIMYYSAGNYEAFATPEKPEGIDDKYAYIVGSGLAGLSAACYLIRDAQ MPGDHITVFESLPVAGGSCDGIYDATRGYIMRGGREMDNHFEVMWDL FRSIPSIQNPGETIFSEYYKLNKHDPNFSLCRVTEKQGQDAHTDKKYGM NPKATQELLHLFMATDEELADKTIDDVFDDDFYKTNFWVYWQTMFA FEKWHSAIEMKRYMQRYIHHIDGLPDLSALRFTRYNQYDSMIRPMVK YITDAGAKVLYDTNVTNVVCEVTRSRKAARRIEYTQGGEAKSIDLTDN DLVFVTNGSQGDCTAYGDQTHAPVVSIKNGEGPSVELWKRIAAQSPD FGHPEKFFKDIEETSWESWTVDTSNKEVLDAIEAICHRDPLSGKIVTGGI VTARDSSWLLSWTINRQGQFPDQPSDHCLIWVYGLNCWHDNGDFVK KPMAQCTGEELCEEWLYHIGIPQDRIKQLASEACNTTAAMMPYVTSFF EPRRDGDRPKVVPDGSVNLAFVGQYAETPRDTVFTTEYSIRTGMEAV YTLCNVDRGVPEVWGSVFDVRDLLTATVKLADGKKLTEMDLPLKDR LALRELLKKVQGTEVEKLLKACGAL
3	WIL0019-HY10.1	MRYTNGNYEAFARPRKPAGVDDKSAYIVGAGLAGLAAAVFLIRDGQ MKGEHIHIFEELSLSGGSLDGKFIPHDGFVTRGGREMENHFECLWDLF RSVPSLEVEDASVLDEFYWLDHDDPNSSNCRIIYNRGERAEDDGDFTL SKKAQKELVELFMTSEDQLIGKKIEDVFGEEFFASNFWLYWCSMFAFE KWHSAIEMRRYVMRFIHHIKGLPDFTALKFTRYNQYESLVKPLLAFLN DHGVDFQYETKINNIEVEATPDKKVAKKILLTRSGKAEEINLTENDLVF VTNGSITESSTEGNHHTPAPITHELGGSWNLWKNLAKQSNEFGHPEVF CDNLPDESWFVSATVTWENFDIEPYISRLTQRKLRTGKVVTGGIITIKD SNWLMSFATHRQPHFKEQSDQQTVTWVYGLLSNTPGNYIKKPIEQCS GQEIVQELMYHLGVPEEDIKKFSEESCVVTPVYMPFITSYFMLREPGDR PLVIPNGSENLAFIGNFAETERDTVFTTEYSVRTAMEAVYSFLDIERGV PEVFASAYDLRMLANSVYYLSDRKKLSEMDLPFVEKKVLEHFVKKVE HTYIGDVLKDNHLL
4	WIL0024-HY15.1	MRYTNGNYEAFARSRKPKDVEKKQAYIVGGGLAGLAAAVFLIRDGH MEGKKIHVLEELSLSGGSLDGKFIPHDGFVTRGGREMENHFECLWDLF RSIPSLEVEDASVLDEFYWLDHDDPNSSNCRIIHDRGQRAADDGEFTLS AAAQKELVQLFMTSEDQLVGKRIEDVFGDEFFESNFWLYWCTMFAFE KWHSAIEMRRYVLRFIHHIDGLPDFTALKFTRYNQYESLVKPLLAYLD AQGVDFQYETKVMNIDVKITEGEKIAQSITLMKNGKAQEITLTADDLV

		FVTNGSITESSTEGDHHTPAPITHELGGSWNLWKNLAAQSPEFGRPEVF YDNLPAESWFVSATVTWQNFDIEPYISRLTKRKLRTGRVVTGGIVTIKD SNWLMSFATHRQPHFKEQGDQQTVTWVYGLLSNTPGNYIKKPIEHCS GQEIVQELLYHLGVPEDKILRISNESCSAIPVYMPFITSYFMLREPGDRP LVIPNGSRNLAFIGNFAETQRDTVFTTEYSVRTAMEAVYQLLAIERGVP EVFASAYDLRTLANAIYYLSDKKKLTEMELPFIERKLVEGFVKKTKDT YIGEILEKNHLV
5	WIL0020- HY11.1	MRYTNGNYEAFARPRKPAGVDDKSAYIVGAGLAGLAAAVFLIRDGQ MKGENIHIFEELSLSGGSLDGKFIPHDGFVTRGGREMENHFECLWDLF RSVPSLEVEDASVLDEFYWLDHDDPNSSNCRIIHNRGERAADDGDFTL SKKAQKELVELFMTSEDQLIGKKIEDVFGDEFFASNFWLYWCSMFAFE KWHSAIEMRRYVMRFIHHIKGLPDFTALKFTRYNQYESLVKPLLSFLN DHGVDFQYETKINNIQVEATPDKKVAQKILLTRAGKAEEIALTEKDLV FVTNGSITESSTEGDHHTPAPITHELGGSWNLWKNLAKQSAEFGHPEV FCDNLPDESWFVSATVTWENFDIEPYISRLTKRKLRTGKVVTGGIITIK DSNWMMSFATHRQPHFKEQKDQQTVTWVYGLLSNTPGNYIKKPIEQC SGQEIVQELMYHLGVPEDDIKKFSEESCVVVPVYMPFITSYFMLREPGD RPLVIPNGSENLAFIGNFAETERDTVFTTEYSVRTAMEAVYSFLDIERG VPEVYASAYDLRTLANSVYYLSDRKKLSEMDLPFVEKKVLEHFVKKV EDTYIGDVLKENHLL
6	WIL0022- HY13.1	MRYTNGNYEAFARPRKPAGVDEKSAYIVGAGLAGLAAAVFLIRDGQ MSGERIHIFEELSLSGGSLDGKFIPHDGFVTRGGREMENHFECLWDLFR SVPSLEVEDASVLDEFYWLDHDDPNSSNCRIIHNRGERAEDDGDFTLS KTAQKELVELFMTSENQLIGKKIEDVFGEEFFASNFWLYWCSMFAFEK WHSAIEMRRYVMRFIHHINGLPDFTALKFTRYNQYESLVKPLLAFLND HGVDFQYETKINNIEVEVTPDKKVAQKILLTRSGQATEIPLTENDLVFV TNGSITESSTEGNHHTPAPITHELGGSWNLWKNLAKQSDEFGHPAVFC ENLPAESWFVSATVTWENFDIEPYISRLTKRKLRSGKVVTGGIITIKDSN WLMSFATHRQPHFKEQNDQQTVTWVYGLLSNTPGNYIKKPIEKCSGQ EIVQELMYHLGVPEEDIKKFSEESCVVTPVYMPFITSYFMLREPGDRPL VIPNGSKNLAFIGNFAETKRDTVFTTEYSVRTAMEAVYSFLDLERGVPE VFASAYDLRTLANSVYYLSDRKKLSEMELPFVEKKVLHHFAKKIEHTY IEDVLKDNHLL
7	DSM1581 4^{T}- HY67.1	MAQHAYMIGTGIGNLAAGIYLIRDGGWHGDQITMYGLETHGANDGD TVTGYENEYGNQALKNSQGYLAKGGRMLNEETYENLWDLMRSVPSL DHPDQSVTDEILAFDHAHPTHDVARLMDKVNGIRNKGDENDYRHMQ FDNRDRYLLTKLMLMPESKEERLNDIGIDEWFASSPHFFTTNFWYMW QTTFAFKRQSSAMELRRYMNRMILEFSRINTLEGVTRTPYNQYESLILP MRKFLEDHGVTFINNRKVTALTFKDTPMRDDIIVTGFDYEEVDGDHQ AGHVDVNDDDFVFDTNGSITDSSSFGDMDTPLKENHEYAPSAALWKQ ASEHFYDLGHPDKFFNDREQSEWMSFTVTNNDHKLLNEITRITQQQPG NALNTWIDSTGLMSIVVHHQPHFHAQKENETVFWGYIMYPRRHGDYV NKPFIEMTGREILTELIGHLNEVDDSRDKIGDHIDDIMASTVNVIPVYMP YASALFNRRAVGDRPLVVPKHSHNLAFISQFAEMPFDMVFTEQYSFRC AQRAVYTFLGIPLSKLTPLHHYEKDPKVMARATKTMFR
8	WIL0041- HY30.1	MAQHAYMIGTGIGNLAAGIYLIRDGGWRGEQITMYGLDTHGANDGAP VSDYEDEYGNGPLKDSQGYLAKGGRMLNEETYENVWDILASVPSLDN PGQSVTDDILNFDHAHPTHDVARLIDRNGLRIGPDKNNYRHMQFNNK DRALLTKLMMTPEKDEQKLNDISIAEWFKNSPHIFETNFWWMWQTTF AFKKVSSAMELRRYMNRMILEFSRINTLEGVTRTPYNQYESIILPMRKY LEDRGVEFVNNRKITEFVFKDTPLQDDIIVTGLKYQDVTGDKESGEIAI NEDDFVFDTNGAITDSASIGDLNTPAVENHEYAPSAQLWKQAADKFY NLGHPDKFFNDRSQSEWASFTVTTNNHYLLDQITRITNQAPGNALNTW IDSTPTMSIVVHHQPHFKAQKPNETVFWGYFLYPRRNGDFVQKPVVE

		MTGAEMLEEFLGHLARTDKSADNIGNHHDEIMSSIVNVIPVFMPYASA LFNQRAIGDRPKVVPDHSKNLAFVSQFAEMPFDMVFTEQYSVRAAQM AVYTFLGIPLAEMTPMHHYEKDPKVMLRATRTMFR
9	WIL0012-HY06.2	MVKSKAIMIGAGLSNMAAAVYLIQDGHWDGKDITFYGVDMHGAND GGATTDFTNEYWNKNHPMANTTGYVARGGRMLNYRTYVDLMDLLD RIPSVTEPGMTAAEDTRDFDAKHRTYDIARLMQGGKGIINAGKLGFNN KDRTLLTKLIMMPDSEETKLDNVSIAEYFKDDPHMFQTNFWYMWETT FAFRTQSSAQELRRYMHQMIYEFTQIEHLVGVNRTRYNQFESMILPLIK YLQGQGVTFIDNKIVKDWQFKDTPMQDEITVTGLVIEDAQTGETEEVE VDEDTAVIFTNGSITDSATMGDYNTPAPENMDYGVSASLWKKATERF YNLGTPDKFFNDRNASEWVSFTLTTKNHLFLNEIVRITTQEPGNALNSF LSTTPITPLNQKDVNMSIVVHHQPHFTTQQPNETVLWGYFLYPRRQGE FVNKPYIKMTGKEMAQELIGQLSKVDPGPGNIKDKEKEILDSIVNNIPV YMPYASALFNNRAKSDRPEVLPKHSTNLAFTGEFAEQPYQMIFTEQSA VRSGEIAAYHFAGVPMDNLVKTPRYDKDPKTLLKATKKMFD
10	WIL0068-HY41.1	MHYSNGNYEAFVNASKPKDVDQKSAYIVGSGLAALASAVFLIRDGHM KGERIHIFEELGLPGGSMDGIYNKQKESYIIRGGREMEPHFECLWDLFR SIPSPENKDESVLDEFYRLNRRDPSYAKTRVIVNRGEALPTDGQLLLTP KAVKEIVDLCLTPEKDLQNKKINEVFTKEFFQSNFWLYWSTMFAFEPW ASAMEMRRYLMRFVQHVATLKNLSSLRFTKYNQYESLILPMVKYLKD RGVQFHYNTVVDNIFVNRSNGEKVAKQIILTENGEKKNIDLTENDLVF VTNGSITESTTYGDNLHPAPEEHELGASWQLWKNLAAQDEDFGHPEV FCKDIPKANWRMSATITFKNNDIVPFIEAVNKKDPHSGSIVTSGPTTIKD SNWLLGYSISRQPHFKAQKPNELIVWLYGLFSDTKGNYVEKTMPDCN GIELCEEWLYHMGVPEERIPEMAAAATTIPAHMPYITSYFMPRALGDR PKVVPDHSKNLAFIGNFAETPRDTVFTTEYSVRTAMEAVYTLLDIDRG VPEVFASAFDVRMLMNAMYYLNDQKKLEELDLPIPEKMAIKGMLKK VKGTYVEELLKKYKLI
11	WIL0006-HY03.1	MYYSNGNYEAFATPRKPKGVDQKSAYIVGSGLAGLSAAVFLIRDGQM KGEAIHILEELPLAGGSLDGIARPNVGFVTRGGREMENHFECLWDLYR SIPSLEIPGASYLDEYYWLDKDDPNSSNCRLIYDRGNRVPDDGDYTLG KSSQEIIKLIMTPEAKLGTQTIEDYFSDAFFESNFWTYWATMFAFEKWH SAVEMRRYAMRFIHHIDGLPDFSALKFNKYNQYDSMVLPLIHYLEDH GVDVQFDTTVDNIIVDFDNGQKVAKSIELTVSGQHETRPLTANDLVFV TNGSITESTTYGSHFEPAPVTNEPGGSWQLWENLAAQSDEFGHPSVFY QDLPAKSWFVSATATIENTEIDPYIERLTKRDLHDGKINTGGIITITDSN WLMSFAVHRQPHFKTQKPNETTVWIYGLYSDVPGNYVKKTIVDCSGE EITQELLYHLGVPESKIQQLSKQESINTVPVYMPFITSYFMPRVMGDRP KVVPDGSVNLAFIGNFAESPSRDTVFTTEYSVRTAMEAVYSLLDVERG VPEVFNSIYDIRELLRAMYYMNDKKAITDMDLPIPKLIQKVGMKKIKG TWLEELLVEAHLM
12	WIL0008-HY04.1	MYYSNGNYEAFATPRKPKNVDQKSAYIVGSGLAGLAAAVFLIRDGHM KGESIHIFEELPLAGGSLDGIQRPNVGFVTRGGREMENHFECLWDLYRS VPSLEIPGASYLDEYYWLDKDDPNSSNCRLIYDRGNRVPNDGDYTLGK SSEEIIKLIMTPEAKLGTTTIEDYFSEDFFKSNFWIYWATMFAFEKWHS AIEMRRYAMRFIHHIDGLPDFSALKFNKYNQYDSMVLPLIKYLEDHGV DVQFDSTVDNVIVNFDHGNKVVKELQLTVAGKPETKQLTANDLVFIT NGSITESTTYGSHFEPAPVTNEPGGSWRLWEKLAEQSDEFGHPGVFYQ NLPAKSWFVSATATIKNTEIDPYIERLTKRDIHDGKINTGGIVTITDSNW LMSFAVHRQPHFKQQKPNETTVWIYGLYSDVPGNYVKKTIVESSGQEI TQEFLYHLGVPKSKINQLAQQESINTVPVYMPFITSYFMPRVMGDRPK VIPDGSVNLAFIGNFAESPSRDTVFTTEYSVRTAMEAVYSLLDVERGVP EVFNSIYDIRELLRAMYYMNDKKPLSEMDLPIPKLIQKIGLKKIKGTWL EELLAEAHLL

13	WIL0076-HY48.1	MYYSSGNYEAFAHPKKPANADKKSAYIVGSGLAGLAAAVFLIRDGQV PGNQIHILEELKLPGGSMDGILNEQRGYIIRGGREMEPHFETLWDLFRSI PTLENPDVSVLDEFYWLNKKDPSYSKTRAIENRGQKIATDGQLTLSRK AVEEIAKLVLTSEEKLGDIKINEVFGSEFFKSNFWLYWSTMFAFEPWAS AIEMRRYLLRFVHHVGTLQNMSALKFTKYNQYESLVKPMVKYLEDK GVQFQYDTIVNNVIVNRTAGQKIATELDMTVAGEKETLSLTPDDFVFV TNGSITESTTYGDNNHPAPTEHAIGASWQLWEKLAEQDPSFGHPAKFY KNIPEANWVISATCTFTDNRIVPYIKKITGKDPHSGSIVTSGPVSIKDSN WLLGISISRQPHFKQQNPNELIVWLYGLFSDQPGNYIQKKITDCNGQEL CEEFLYHIGVPEDQIADIAKDANSIPIHMPYITSYFMPRKTGDRPLVVPE GSQNLAFIGNFAETKKDTVFTTEYSVRTAMEAVYQLLDIDRGVPEVFA SSYDIRTILSSIYYLNDKKSLEELPLNKVEQIGLEAFLKKIKGTYLEEIFR DEHLI
14	WIL0055-HY35.1	MMHYTNGNYEAFVNADKPADIEKKSAYIIGAGLAGLATAVFLIRDGQ MPGKKIHILEELSVPGGSMDGIYSVQRNSYIIRGGREMEPHFETLWDLF RSIPSLEVPGASVLDEFYRLNRKDPCYAKTRVIQNRGEALPTDGQLLLT PKAVKEIVDLVLTPEEKLQDVKINEVFDKEFFQSNFWLYWCTMFAFEP WASAMEMRRYLMRFIQHVGTLKNLSSLRFTKFNQYESLILPMVKFLK DHEVQFHQETTVDNIIVNRSGDDKLATKIEMKVAGEPQNIELTPNDLV FVTNGSITESTTYGDNDHPAPIDHPLGASWQLWKNLAAQDSDFGHPEK FCEQIPNANWTMSATITFKNNDIVPFIEKVNKKDPHSGSIVTSGPTTIKD SNWLLGYSISRQPHFHQQKPNELIVWLYGLFSDKGGNYVKKTMPECT GIELCEEWLYHMGVPENDIPAMAKAATTIPAHMPYITSYFMPRSLGDR PLVVPKHSKNLAFIGNFAETPRDTVFTTEYSVRTAMEAVYTLLDIDRG VPEVFASAFDVRLMMNAMYYLNDQKKLTELDLPLSQKLLVKEGLKK VKGTYIEELLKEYRLI
15	WIL0055-HY36.4	MLSLSQGLFYTGGVFMYYSNGNYEAFARPRKPEGIEQKHAYIIGGGLA GLAAAVFMVRDAQMPGENIHILEELPVAGGSLDGEKRPGVGYVIRGG REMENHFECLWDMYRSIPSLEIPGASYLDEYYWLDKDDPNSSNCRLIH NRGDRVPSDGKYGVEKFSKYIVKLVLTSEDELEGKTIGDWFPDEFFDT NFWMYWSTMFAFEKWHSLIEMRRYCMRYIHHIDGLPTLSALKFNKYN QYESMTKPILAYLQDHNVDIQYDTVVNNVLVDTSNDKKIAKKILLTKD GKDEEIVLTDNDYVFVTNGSITESSTYGDQNTPAPITHSLGPSWKLWE NLSYQDADFGHPDVFCKNVPDRAWFISATATLKNRKLAPYFERLTKRS LYDGKVNTGGIITVTDSNWMLSFTIHRQPHFKDQKPDETVVWIYALYS DTEGNYIKKRVVDCSGKEITEELLYHLGVPVDDIEGYAENDVNTVPVY MPYVTSYFQLRKKGDRPAVVPKGSQNLAFLGNFAESPTRDTVFTTEYS VRTAMEAVYTLFNVDRGVPEVFDSVFDIRQELRALYYLSDKKTLPEM DLPVPKLAAKTALRKLKGTWIEEILKEQHLLD
16	WIL0075-HY05.2	MYYSSGNYEAFARPKKPANATKKSAYIVGAGLAGLAAAAFLVRDGQ VPGNQIHVFEELGLPGGSMDGILNEQRGYIIRGGREMEPHFETLWDLFR SIPTLEDASVSVLDEFYWLNKADPSNSHTRVIEKRGNQLASDGQLTLSR KAIEEIAKLVLTPESQLDNVKINQVFSDDFFKSNFWLYWSTMFAFEPW ASAMEMRRYLLRFVHHVGTLQNMSALKFTKYNQYESLIKPLIKYLED HDVKFQYNTTVDNIIVEQTGEQKQAVKIELTIDGNQQSLDLTPDDLVF VTNGSITESTTYGDNEHSAPATHPTGASWELWEKLAAQDPAFGHPAK FYQDIPAANWVMSATCTFKDDRIVPYIQKITGKDPYSGSIVTSGPVSIR DSNWLLGISISRQPHFQQQKPNELIVWLYGLFSDQPGNYIHKKITDCSG AEICQEFLYHIGVPENQIAEIAQTANSIPIHMPYITSYFMPRQAGDRPLV VPEGSSNLAFIGNFAETERDTVFTTEYSVRTAMEAVYRLLDIDRGIPEV FDSAFDIRTILSALYYLNDKKSLTELPLNQIEKIGLNAFLKRVHGTYLEE ILKSQKLL
17	WIL0037-HY26.1	MEKAYMIGTGIANLAAGIYLIRDGGWSGNQITMFGLEKHGANDGAAV ADYEQEYGNQSLSNNRGYLAKGGRMLNEETYENLWDILRSVPSLDNP

		GQSVTDDILNFDHAHPTHDVARLMDKKNGIRNNGGADDYNRMQFNN KDRYLLSKLMMMPESKEDKLNDISIAEWFAESPHIFSTNFWYMWETTF AFKKESSAMELRRYMNRMILEFSRINTLEGVTRTPYNQFESIILPMRKY LADQGVEFVNNRKITAFNFKDTPLRDDIIVTGLEYEDVESGETGKIEVD ENDLVFDINGAITDSSSMGDFNTPVKENMEYAPSAALWKQATEHFYN LGNPDKFFNDRAQSEWMSFTVTTNNHYLVNEISRITQQEPGNALNTW VDSNNLLSIVVHHQPHFHAQKENETVFWGYFMFPRKNGDYVDKPVIE MTGKEMLQELLGHLSEVDRAADNIINHEEEIMDSIVNVIPVYMPYASA LFNQRAVGDRPDVVPKNSKNLAFVSQFAEMPFDMVFTEQYSIRAAQK AVYHFMGIPESQMTPVHHYEKDPKVLLKATKTMFR
18	WIL0039-HY28.1	MLCILNKNEEEHTMEKAYMIGTGIANLAAGIYLIRDGGWTGDQITMFG LEKHGANDGAPVSDYESEYGNQRLSDNRGFLAKGGRMLNEETYENL WDLFRSVPSLDNPGQSVTDDILNFDHAHPTHDVARLMDKKNGIRNNG GADDYYHMQFNNKDRLLLSKLMMMPESKEEKLNDISIEEWFKDSPHI FKTNFWYMWETTFAFKKESSAMELRRYMNRMILEFSRINTLEGVTRTP YNQYESLILPMRKYLEDQGVKFINNRKITAFEFKDTALRDDIIVTGLQY EDVDGSDEKGTIPVNENDLVFDINGAITDSSSFGDFNTPIKENMEYAPS AALWKQATEHFYSLGNPDKFFNDRAQSEWMSFTVTTNNHFLVNEISRI TQQEPGNALNTWVDSNNLLSIVVHHQPHFHAQKENETVFWGYFMFPR KHGDYVDKPVIEMTGKEILQELLGHLAEVDTATDNIRNHESEIMDSIIN VIPVYMPYASALFNRRAVGDRPDVVPKNSKNLAFVSQFAEMPFDMVF TEQYSIRAAQKAVYHFMGIPEDEMTPVHHYEKDPKVMLRATKTMFR
19	PA-HY29.2	MMRKAFMIGTGVANLAAGVYLIRDGGWSGNQITMFGLDKHGANDG AAVADYETEYGNQRLSNDRGFLAKGGRMLNEETYENLWDVLRSVPS LDHPGQSVTDDILNFDHAHPTHDVARLMDKRNGIRNNGGADDYSHM QFNNQDRKLLTKLMVMPESQEAKLNDVSIAEWFKDSPHIFTTNFWYM WETTFAFKKESSAMELRRYMNRMILEFSRINTLEGVTRTPYNQYESIIL PMRKYLSDHGVTFINNRKITAFQFKDTPLRDDIIVTGLEYEDVGENKQT GTIPVDENDLVFDINGAITDSSSIGDFNTPIKENMEYAPSAALWKQATE HFYNLGNPDKFFNDRAQSEWMSFTVTTKNHYLVNQISRITQQEPGNAL NTWVDSNNLLSIVVHHQPHFHAQKENETVFWGYFMFPRKNGDYVDK PVIEMTGKEMLQELLGHLAEVDQATDSIVYHEEEIMDSIVNVIPVYMP YASALFNTRAVGDRPEVVPKHSKNLAFVSQFAEMPFDMVFTEQYSFR AAQRAVYHFLGIPEEKMTPVHHYEKNPKVLLKATRTMFR
20	WIL0029-HY20.1	MYYSNGNYEAFAKPKKPKNVENKSAYIVGSGLAGLASAIFLIRDGQM PGENIHIFEELSLAGGSMDGIYNESRGYIIRGGREMEAHFETLWDLFRSI PTLENPEISVLDEFYWLNKEDPSYSKTRVIEKCGKQLENDGELTLSRKA IDEMLKLVLTSESQLDDVKINEVFSDEFFESNFWLYWSTMFAFEPWAS AMEMRRYLLRFVQHVGTLKDMSALKFTKFNQYESLVKPMIHYLEGH NVHFQYDTVVNNIIVNRSDSQKIATEIQLTESGQTKVLPLTIDDLVIVTN GSITESTTYGDTEHPAPQEHEVGQSWQLWENIAKQDTSFGRPWKFYR NVPVANWVNSTTLTFSDDQVVPFLESITGKDPHSGSLVTSGPITIRDSN WLLGISISRQPHFEQQKDNELIVWLYGLFSDLPGNYIPKKITDCTGREIC EEFLYHIGVPKNKISEIAATVKAVPTNMPYITSYFMPRAAGDRPKVVPD GSANLAFVGNFAETERDTVFTTEYSVRTAMEAVYQLLDVDRGIPEVFD SSFDMRMILNAIYYLNDKKGLRDLPLTKVEKFGLEAFLKKIKGTYIEEI LVDQHLL
21	WIL0114-HY62.1	MNNYQRINPIAPKNIEKRNAYLLGGGIGSLAAAAFLIRDAHMPGKNIHI LEQLDVVGGSMDGAGTAEKGYTARGGREIEEHFECFMELYSFIPSLKD KNRSVLDEFRELNIEEPIESHCRLVENQGEKADFSSLGLSTANAMELAK LHMATEEALGATTIGQFFSPSFFKTNFWYFWATMFAFEKWHSVVEVK RYMERFMHLIGGMNKLKGILHTEYNQYDSLILPVIVWLKDHEVNFDS GCKVTDIDFDFSNNEKIATKICYTKAGKDEVISVNKDDLVLFTNGSMT ENTTRGDLDHPAIINRSEDKGCFSVWEKLAKKSPDFGHPEKFCSDIDKS

		KWMSFTVTLKDDDIVFPYLYKLTGDKPGMGGLVTIKDSSWFMSWVV PKHPHFANQPDNVKVLWAYALNLDTPGDYVKKTFSDCTGREMFEELL YHMGLKDRIPEILSHTVNAIPSMMPYITSQFMPRIPGDRPDVIPKGSKNF GFLGQYAEVPHDCVFTVEYSVRSAMMAVYGLMGLEKEVDQVYPSQY DIRVLTNAAKTCLGIDKLPLENIPLGALLKNTELKNLL
22	WIL0042- HY33.1	MNNYQRINPIKPKNIESRKAYLIGGGIGSLSAAAFLIKDGHMPGNNIHVI EQLDILGGSMDGAGTAEKGYTARGGREIEEHFECFMELYSFIPSLTDKN RSVLDEFRELNIEEPIESHCRLVHNQGEKSDFSTLGLSKGHAMELTKLH LSTEEALGSTTIEEFFTPSFFNTNFWYFWATMFAFEKWHSVVEVKRYM ERFMHLIGGMNKLKGILHTEYNQYDSLILPLITWLKDQGVCFDSCCKA TDIDFDFTNNQKIAKAIHYTKDGKNEIINVNEDDIVLFTNGSMTENTTR GDIDHPAIINRSEDKGCFSLWEKLAKKSPDFGHPEKFCTNIDKSKWMSF TVTLKDDDIVFPHIYNLTGDKPGMGGLVTIKDSNWFMSWVVPKHPHFI NQPDNVKVLWAYALNLDVPGNYIKKTYSDCTGREMFEELLYHMGLE DKIPEILSHTVNVIPSMMPYITAQFMPRVPGDRPNVIPEGSKNFGFLGQF AEVPEDCVFTVEYSVRSALMAVYGLLGLEKTLDPVYPSKYDIRVLINA AKTCLGIDKLPLKNIPLGEFFKNTEIEKLL
23	WIL0057- HY37.1	MYYSSGNYEAFAKPEKPEGIEKKHAYIVGSGLAGLAAACFLIRDAQMP GENITVFESLPIAGGSCDGLHDPQKGYIMRGGREMDNHFECMWDLFR SIPSIVNPGETIFSEYYKLNKEDPNYSLCRVTEKQGQDAHTDRQYGLNK NAEKQILKLMLSTDEELADKKIDDVFDEDFYKTNFWIYWQTMFAFEK WHSALEMKLYMQRYIHHIDGLPDLSALRFTRYNQYESMILPMLKYIED AGGKIAYNTQVTDIQCETSPTRKAARYIAYVQDGVEKHLELTDDDFVF ITNGSQGDGSAYGDQTHAPEITIKNGQGPSIELWKKLAAQDDAFGHPD KFFKDIKETSWESWTVDTANKQILSAIEKICHRDPLSGKVVTGGIVTAK DSSWLMSWTINRQGQFVDQPDDHCLIWVYGLNCWDDDGDYVHKPM YKCTGEELCQEWLYHIGIPVDEIDELAKQCNTTPCMMPYVTSFFEPRA YGDRPLVVPVGSVNIAFVGQYAETPRDTVFTTEYSIRTAMEAVYTLCN VDRGVPEVWGSVFDVRELIKAGVKMNDGKMIKEWPLPASQKAAIAA AFKLINNTEISKLLIRLGAAEKKDFAPIVEMPKVKVEVTSRVSELKDSK TAKIGAGVTVASLMAIAALLHKKKS
24	DSM1002 38^{T}- HY64.1	ATGGTGCCCGCCTCGACGTTGAGGCCCGGCTTCATCAAGACGGAAA TGCCTTCAATGAAACCGGCGAACAATGACGGCAAAGGAGTCATCA TGTACTACTCGGCTGGAAACTATGAAGCCTTCGCAACCCCGGAGAA GCCTGAAGGCATCGACGACAAGTACGCGTATATCGTCGGGTCCGGT CTTGCCGGCCTGTCGGCGGCATGCTACCTGATCCGCGACGCCCAGA TGCCCGGCGACCATATCACGGTCTTCGAATTCCTGCCGGTGGCCGG CGGCTCCTGCGACGGCATCTACGATGCGACACGCGGCTACATCATG CGCGGCGGTCGTGAGATGGACAACCATTTCGAAGTCATGTGGGACC TGTTCCGTTCCATCCCGTCCATCCAGAACCCCGGGGAGACGATCTT CTCCGAATACTACAAGCTCAACAAGCACGACCCGAACTTCTCCCTG TGTCGCGTCACCGAAAAGCAAGGCCAGGATGCGCACACCGACAAG AAGTACGGGATGAACCCGAAGGCCACGCAGGAACTGCTGCACCTG TTCATGGCCACGGACGAGGAGCTCGCCGACAAGACCATCGATGAC GTGTTCGACGACGATTTTTACAAGACGAACTTCTGGGTGTACTGGC AGACGATGTTCGCGTTCGAGAAATGGCACAGCGCCATCGAGATGA AACGCTACATGCAGCGTTACATCCATCACATCGACGGCTTGCCCGA TTTGTCTGCCCTGCGTTTCACGCGCTACAACCAGTATGATTCCATGA TCCGCCCGATGGTCAAGTACATCACGGACGCCGGGGCGAAGGTGCT GTACGACACCAATGTGACCAACGTGGTGTGCGAGGTGACGCGCAG CCGCAAAGCGGCCCGCCGCATCGAATACACGCAGGGCGGTGAGGC CAAGAGCATCGACTTGACCGACAACGACCTCGTGTTCATCACCAAC GGCTCGCAAGGCGATTGCACCGCCTACGGCGACCAGACACACGCG CCGGTCGTGTCCATCAAGAACGGCGAAGGCCCATCGGTTGAACTGT

		GGAAGCGGATCGCCGCCCAATCCTCGGACTTCGGGCACCCTGAGAA GTTCTTCAAGGACATCGAGGAAACCAGCTGGGAATCGTGGACGGTC GACACGTCCAACAAGGAGGTGCTCGACGCAATCGAGGCGATCTGC CACCGCGACCCGCTGTCCGGCAAGATCGTGACCGGCGGCATCGTGA CCGCCAGGGATTCGAGCTGGCTGCTGTCGTGGACCATCAACAGGCA AGGCCAGTTCCCTGACCAGCCGTCCGACCATTGCCTGATCTGGGTG TACGGCCTCAACTGCTGGCATGACAACGGCGATTTCGTCAAGAAGC CGATGGCACAATGCACCGGTGAGGAATTGTGCGAGGAATGGTTGT ACCACATCGGCATCCCGCAGGACAGGATCAAGCAGCTGGCGAGCG AAGTATGCAACACGACCGCCGCGATGATGCCGTATGTGACGAGTTT CTTCGAACCGCGCCGCGACGGGGACCGGCCGAAGGTCGTGCCCGA CGGCTCTGTGAACCTCGCCTTCGTCGGCCAGTACGCCGAAACGCCG CGCGACACCGTGTTCACCACGGAGTATTCAATCCGCACTGGCATGG AAGCGGTGTACACGCTGTGCAATGTCGACCGTGGCGTGCCGGAGGT ATGGGGTAGCGTCTTCGACGTGCGCGACCTGCTGACCGCGACGGTC AAACTCGCCGACGGCAAGAAACTCACAGAAATGGACCTGCCGCTC AAAGACCGTCTCGCTCTGCATGAACTGCTCAAGAAAGTACAGGGCA CCGAGATCGAGAAGCTGCTCAAGGCGTGCGGGGTGTTGTGA
25	WIL0093-HY53.1	ATGCAATTGGACATGTTTCCGCCGATTGTCGATGGTTTTTCCCCTCG AACCGATCCTATAATGGTGTTCGCCTCGACGTTGAGGCCCGGTTTC GCAAAGGCGCCAAGCCTGCACGAGACCGGCGGACGAAATGACGGC AAAGGAGTCATCATGTACTACTCGGCTGGAAACTATGAAGCCTTCG CGACCCCGGAGAAGCCTGAAGGCATCGACGACAAGTACGCGTATA TCGTCGGGTCCGGTCTTGCCGGTCTGTCGGCGGCATGCTACCTGATC CGCGACGCCCAGATGCCCGGCGACCATATCACAGTCTTCGAATCCC TGCCGGTGGCCGGTGGCTCCTGTGACGGCATCTACGATGCGACACG CGGCTACATCATGCGCGGCGGCCGTGAGATGGACAACCATTTCGAG GTCATGTGGGACCTGTTCCGTTCCATTCCGTCCATCCAGAACCCCGG AGAGACGATTTTTTCTGAATACTACAAGCTCAACAAGCACGACCCG AACTTCTCCCTGTGTCGCGTCACCGAGAAGCAAGGTCAGGACGCGC ACACCGACAAGAAGTACGGGATGAACCCGAAGGCGACGCAGGAGC TGCTGCACCTGTTCATGGCCACGGACGAGGAGCTCGCCGACAAGAC CATCGATGACGTGTTCGACGACGATTTCTACAAGACGAACTTCTGG GTGTACTGGCAGACGATGTTCGCGTTTGAGAAATGGCACAGTGCCA TCGAGATGAAGCGATATATGCAGCGTTACATCCATCACATCGACGG ATTGCCCGATTTGTCCGCGCTGCGCTTCACCCGCTATAACCAGTATG ATTCCATGATCCGCCCGATGGTCAAGTACATCACGGACGCCGGGGC GAAGGTGCTGTACGACACTAATGTGACCAACGTGGTGTGCGAGGTG ACGCGCAGCCGCAAAGCGGCCCGCCGCATCGAATACACGCAGGGC GGCGAGGCCAAGAGCATCGACCTGACCGACAACGACCTTGTGTTCG TCACCAACGGCTCGCAGGGCGATTGCACCGCGTACGGCGACCAGA CGCATGCGCCGGTCGTATCCATCAAGAACGGCGAAGGGCCGTCGGT CGAACTGTGGAAGAGGATCGCCGCCCAATCCCCGGATTTCGGGCAC CCAGAGAAGTTCTTCAAGGACATCGAGGAAACCAGCTGGGAGTCG TGGACGGTCGACACGTCCAACAAGGAGGTGCTCGACGCAATCGAA GCGATTTGCCACCGCGACCCGCTGTCCGGCAAGATTGTGACCGGCG GCATCGTGACCGCTAGGGATTCGAGCTGGCTGCTGTCGTGGACCAT CAACCGGCAAGGCCAGTTCCCCGATCAGCCGTCCGACCACTGCCTG ATCTGGGTGTACGGCCTCAACTGCTGGCATGATAACGGCGATTTCG TCAAGAAGCCGATGGCGCAATGCACCGGCGAAGAACTGTGCGAGG AATGGCTGTACCATATCGGCATCCCGCAGGACAGGATCAAGCAGTT GGCGAGCGAGGCATGCAATACGACCGCCGCGATGATGCCGTATGT GACGAGCTTCTTCGAACCGCGTCGCGACGGGGACCGGCCGAAGGT CGTGCCCGACGGCTCCGTGAATCTCGCCTTCGTCGGCCAGTACGCC

		GAAACGCCGCGCGACACCGTGTTCACCACGGAGTATTCAATTCGCA CCGGCATGGAAGCGGTGTACACGCTGTGCAATGTCGACCGTGGCGT GCCGGAAGTATGGGGCAGCGTCTTCGACGTGCGTGACCTGCTGACC GCGACGGTCAAACTCGCCGACGGCAAGAAACTCACCGAAATGGAC CTGCCGCTCAAAGATCGTCTCGCCCTGCGTGAACTGCTCAAGAAGG TGCAGGGCACCGAGGTCGAGAAGCTGCTCAAGGCGTGCGGGGCAT TGTGA
26	WIL0019-HY10.1	ATGAGATATACGAATGGGAATTATGAAGCATTTGCTAGACCAAGA AAACCGGCAGGCGTGGACGACAAGAGTGCCTATATCGTCGGAGCA GGTCTGGCAGGCTTAGCTGCAGCTGTTTTTTTAATTCGGGATGGAC AAATGAAAGGCGAACACATCCATATTTTTGAAGAGCTTTCCTTGTC TGGCGGTTCATTAGATGGAAAATTTATTCCTCATGACGGCTTTGTAA CTCGTGGCGGACGAGAAATGGAAAATCACTTTGAATGCTTGTGGGA TTTATTCCGCTCAGTGCCTTCATTGGAAGTAGAGGATGCTTCGGTTT TAGATGAGTTCTATTGGTTGGATCATGATGATCCGAATTCATCAAA TTGCCGGATCATCTACAATCGTGGAGAACGTGCAGAGGATGATGGT GATTTTACATTGTCGAAAAAAGCACAAAAAGAATTGGTTGAGCTTT TCATGACTTCAGAAGATCAACTGATTGGTAAAAAAATCGAAGACGT TTTTGGAGAAGAATTTTTTGCATCGAACTTCTGGTTGTACTGGTGTT CAATGTTTGCCTTTGAAAAATGGCATTCAGCGATTGAAATGCGCCG TTATGTGATGCGTTTCATTCACCATATTAAGGGCTTACCAGATTTTA CAGCATTGAAATTTACTCGCTACAATCAATATGAATCTTTAGTGAA ACCATTATTGGCCTTCTTAAATGACCATGGAGTAGATTTCCAATATG AAACGAAAATCAATAATATTGAAGTCGAAGCCACTCCTGATAAAA AAGTAGCGAAAAAGATTCTGTTGACACGTTCAGGCAAAGCTGAAG AGATCAACTTAACAGAAAATGATTTGGTTTTCGTTACGAACGGATC AATCACGGAGAGCTCTACAGAAGGCAATCATCATACCCCAGCACC GATTACTCATGAATTAGGCGGCAGCTGGAATCTTTGGAAAAACTTG GCAAAACAATCGAATGAATTTGGTCACCCTGAAGTTTTTTGTGACA ACCTGCCAGATGAAAGCTGGTTTGTTTCTGCTACAGTGACTTGGGA AAACTTTGATATTGAACCGTATATTTCACGCTTAACTCAACGTAAAT TGCGAACTGGGAAAGTGGTAACAGGCGGAATCATTACCATCAAGG ATTCGAATTGGCTGATGAGCTTTGCGACACACCGTCAACCACATTT CAAAGAGCAAAGTGATCAACAAACGGTGACTTGGGTCTATGGTTTA TTATCTAATACGCCTGGAAATTACATCAAAAAACCGATCGAACAAT GCAGCGGGCAAGAGATCGTTCAAGAACTGATGTATCATTTAGGGGT TCCAGAAGAAGACATCAAGAAATTCTCTGAAGAATCATGCGTGGTA ACACCAGTTTATATGCCGTTTATCACCTCGTATTTTATGTTGCGAGA ACCTGGTGATCGTCCATTAGTCATTCCAAATGGCTCAGAGAACCTT GCCTTCATCGGCAACTTTGCTGAAACCGAACGTGATACTGTCTTTAC GACAGAGTATTCAGTCCGAACAGCGATGGAAGCTGTTTATTCATTC TTAGATATCGAACGCGGTGTGCCAGAAGTATTTGCCTCGGCCTATG ATCTTCGGATGTTAGCCAATTCAGTCTATTATTTAAGTGATCGTAAG AAGCTTTCGGAAATGGATCTGCCATTTGTTGAGAAAAAAGTGTTGG AGCATTTTGTGAAGAAAGTGGAACATACCTATATTGGCGATGTGTT GAAGGACAATCATTTACTGTAG
27	WIL0024-HY15.1	ATGAGATATACAAACGGAAATTATGAAGCTTTTGCAAGAAGCAGA AAACCGAAAGATGTCGAAAAGAAACAGGCCTATATTGTTGGTGGC GGATTAGCTGGATTAGCAGCAGCAGTCTTTTTGATTCGTGACGGAC ACATGGAGGGAAAGAAAATCCATGTGCTGGAGGAGCTGTCTCTTTC AGGCGGCTCACTCGACGGCAAATTTATTCCTCATGATGGCTTTGTC ACTCGAGGCGGCCGTGAAATGGAAAATCATTTTGAATGTTTATGGG ATTTATTCCGTTCGATTCCATCATTGGAGGTAGAAGATGCCTCCGTC TTAGATGAATTTTATTGGTTGGATCATGACGATCCAAACTCATCCA

		ATTGTCGGATCATTCATGATCGTGGCCAACGAGCAGCAGATGACGG AGAATTCACTTTATCAGCAGCAGCCCAAAAAGAGTTGGTCCAACTA TTTATGACTTCAGAAGATCAGCTTGTTGGCAAACGGATCGAGGATG TTTTTGGAGACGAGTTCTTTGAATCAAACTTTTGGCTTTATTGGTGT ACGATGTTTGCTTTTGAAAAATGGCATTCTGCCATCGAAATGCGTA GATATGTTTTAAGATTCATTCACCATATCGATGGATTGCCTGATTTC ACGGCTTTGAAATTTACTCGTTACAATCAATATGAATCGTTAGTTAA ACCATTATTAGCTTACCTTGATGCACAAGGTGTCGATTTCCAATATG AAACCAAAGTCATGAATATTGACGTGAAGATCACTGAAGGAGAGA AAATCGCCCAAAGTATCACACTGATGAAAAATGGCAAAGCCCAAG AAATCACTTTGACAGCAGATGATCTGGTGTTTGTAACAAACGGCTC AATCACGGAGAGTTCGACTGAAGGGGATCACCATACACCTGCCCCT ATTACTCATGAATTAGGTGGCAGTTGGAATCTTTGGAAGAACTTGG CTGCTCAATCTCCTGAATTTGGTCGCCCAGAAGTCTTTTATGACAAT CTGCCAGCAGAAAGCTGGTTTGTATCAGCGACAGTCACATGGCAAA ACTTTGATATTGAACCTTATATTTCTCGTTTGACAAAACGGAAATTA CGGACAGGAAGAGTAGTGACCGGTGGGATCGTCACTATCAAAGAT TCAAATTGGCTGATGAGTTTTGCGACCCATCGTCAACCTCATTTCAA AGAGCAAGGCGATCAACAAACGGTGACTTGGGTTTATGGTCTATTG TCTAATACACCAGGAAATTATATCAAAAAACCGATTGAACACTGTT CCGGACAAGAAATCGTTCAAGAACTATTGTATCACTTAGGTGTTCC AGAAGATAAAATTCTACGGATCTCTAATGAATCATGTTCAGCGATC CCTGTGTATATGCCTTTCATCACTTCTTACTTCATGTTGCGGGAACC TGGAGATCGTCCGCTTGTGATACCGAATGGTTCACGAAACTTAGCC TTCATCGGCAACTTTGCCGAAACGCAACGTGATACCGTCTTTACGA CTGAATATTCTGTACGAACGGCGATGGAAGCTGTCTACCAATTGTT AGCTATTGAACGAGGCGTTCCAGAAGTCTTTGCTTCCGCCTATGAT CTGCGTACATTGGCCAATGCGATTTACTATTTATCGGACAAGAAAA AATTGACTGAGATGGAGCTGCCATTTATCGAACGCAAATTAGTAGA AGGATTTGTTAAGAAGACGAAAGATACCTATATCGGCGAAATCCTT GAAAAAAATCATTTAGTTTAA
28	WIL0020- HY11.1	ATGAGATATACGAATGGAAATTACGAAGCATTTGCTAGACCGAGA AAACCAGCGGGCGTTGATGATAAGAGCGCTTATATCGTGGGTGCAG GCTTAGCCGGATTAGCAGCAGCAGTTTTTCTGATCAGAGATGGCCA AATGAAGGGTGAAAATATCCACATTTTTGAGGAACTATCTTTATCC GGCGGATCATTGGATGGAAAATTTATTCCTCACGATGGCTTTGTTA CACGCGGCGGACGTGAAATGGAAAATCATTTTGAGTGTCTATGGGA CTTGTTCCGCTCTGTGCCATCACTGGAAGTCGAAGATGCCTCAGTCT TAGATGAATTTTATTGGTTGGACCATGATGATCCCAACTCATCAAA TTGTCGGATCATTCATAACCGCGGTGAACGTGCGGCGGATGATGGC GACTTCACGTTATCGAAAAAAGCGCAAAAAGAACTAGTCGAACTCT TCATGACTTCGGAAGATCAATTGATCGGCAAGAAAATCGAAGACGT TTTTGGCGATGAATTCTTTGCCTCAAACTTTTGGTTGTATTGGTGCT CGATGTTTGCCTTTGAAAAATGGCATTCAGCGATCGAAATGCGCCG TTATGTGATGCGTTTTATCCATCACATCAAAGGGCTGCCAGACTTCA CGGCATTGAAGTTCACGCGTTACAATCAATATGAATCCTTAGTAAA ACCACTATTATCATTTTTAAATGATCACGGAGTGGATTTCCAATACG AAACGAAGATCAACAATATTCAAGTTGAAGCAACACCAGATAAAA AGGTTGCGCAAAAGATCTTGCTGACGCGTGCAGGCAAAGCAGAAG AAATCGCGTTGACAGAAAAGGATTTGGTCTTTGTTACAAACGGCTC AATCACGGAAAGTTCTACTGAAGGCGACCATCATACACCAGCACCG ATCACTCATGAATTGGGCGGCAGCTGGAACCTATGGAAAAATTTAG CGAAACAATCAGCTGAGTTTGGTCATCCAGAAGTCTTTTGCGATAA TTTGCCAGACGAAAGCTGGTTTGTTTCAGCGACTGTAACTTGGGAA

		AACTTTGACATTGAACCGTATATCTCACGCTTAACTAAACGGAAAC TACGGACAGGTAAAGTTGTGACCGGTGGGATCATTACGATCAAGG ATTCCAATTGGATGATGAGCTTCGCGACACATCGTCAACCGCATTT CAAAGAACAAAAAGACCAACAAACAGTAACTTGGGTCTACGGACT TTTGTCTAACACACCCGGAAACTATATCAAGAAACCGATCGAACAA TGCAGCGGGCAAGAAATCGTTCAAGAATTGATGTATCACTTAGGTG TCCCAGAAGACGACATTAAGAAATTCTCTGAAGAATCTTGTGTAGT GGTTCCTGTCTACATGCCATTTATCACATCGTACTTTATGCTACGCG AACCTGGCGATCGTCCTTTAGTGATTCCGAATGGTTCAGAAAATCT AGCCTTCATCGGAAACTTTGCCGAGACAGAACGTGATACGGTCTTC ACCACAGAATATTCTGTTCGGACAGCAATGGAAGCTGTTTACTCAT TCTTGGATATTGAACGAGGCGTACCAGAAGTTTATGCTTCCGCCTA TGATCTAAGAACTTTAGCTAACTCGGTCTACTATTTAAGCGATCGC AAAAAACTTTCCGAAATGGATCTGCCTTTTGTTGAGAAAAAAGTGT TGGAACACTTTGTGAAGAAAGTCGAAGATACGTATATTGGTGATGT ATTGAAAGAGAATCATTTGTTGTAA
29	WIL0022-HY13.1	ATGAGATATACGAATGGAAATTATGAAGCTTTTGCTAGACCAAGAA AACCAGCGGGTGTTGATGAGAAAAGTGCTTATATTGTCGGCGCGGG ATTAGCTGGATTAGCGGCAGCAGTTTTTCTAATCAGAGATGGCCAA ATGAGTGGTGAACGTATCCATATTTTTGAGGAACTTTCCTTATCCGG CGGTTCATTAGATGGAAAATTCATTCCTCATGATGGTTTCGTGACGC GCGGCGGTCGTGAAATGGAAAATCATTTTGAATGTTTATGGGATCT GTTTCGCTCCGTTCCTTCACTGGAAGTAGAAGATGCCTCAGTTTTAG ATGAGTTTTATTGGTTAGATCACGATGATCCTAATTCATCAAATTGC CGGATTATCCATAATCGGGGGGAACGTGCGGAAGATGATGGCGAT TTTACCTTATCAAAAACGGCACAAAAAGAATTAGTCGAATTATTTA TGACCTCAGAAAATCAATTGATCGGTAAAAAAATTGAAGATGTTTT TGGGGAAGAGTTCTTCGCTTCAAACTTTTGGTTGTATTGGTGTTCGA TGTTTGCTTTTGAAAAATGGCATTCAGCAATTGAAATGCGCCGCTA TGTCATGCGTTTTATCCATCATATCAATGGCTTACCAGATTTTACCG CTTTGAAATTCACACGGTACAATCAATACGAATCATTAGTAAAACC GCTCTTAGCGTTTTTGAATGATCATGGTGTGGATTTCCAGTATGAAA CGAAAATCAATAATATTGAAGTCGAAGTGACACCGGATAAAAAAG TGGCGCAAAAAATCTTACTGACACGTTCAGGCCAAGCAACAGAGA TTCCTTTGACAGAAAATGATTTGGTCTTTGTGACGAATGGTTCGATT ACGGAAAGCTCAACGGAAGGAAATCATCATACACCAGCACCGATT ACTCATGAATTGGGCGGCAGCTGGAATTTATGGAAAAATTTAGCGA AACAATCGGATGAATTTGGTCATCCCGCTGTTTTTTGCGAAAACCT GCCGGCAGAAAGCTGGTTCGTTTCAGCGACTGTTACTTGGGAAAAT TTTGATATAGAACCATATATTTCACGGTTGACGAAACGTAAATTAC GTTCTGGAAAAGTTGTTACTGGCGGGATTATTACGATCAAAGATTC CAATTGGCTGATGAGTTTTGCGACCCATCGCCAACCACATTTCAAA GAACAAAACGATCAACAAACAGTGACTTGGGTCTACGGATTATTGT CCAATACACCAGGAAATTATATCAAGAAACCAATTGAAAAATGCA GCGGGCAAGAAATCGTGCAAGAATTGATGTATCATCTAGGCGTGCC GGAAGAAGACATTAAGAAATTTTCTGAAGAATCTTGTGTTGTGACC CCTGTGTATATGCCGTTTATTACGTCATATTTTATGCTGCGGGAACC TGGGGATCGCCCATTAGTCATTCCAAATGGCTCTAAGAACTTAGCC TTCATCGGAAACTTTGCTGAAACAAAACGCGATACAGTCTTCACAA CAGAATATTCAGTTCGAACGGCGATGGAAGCTGTGTACTCATTTTT AGATCTTGAACGCGGCGTACCAGAAGTTTTTGCATCGGCGTATGAT CTGCGGACATTAGCCAATTCGGTTTATTATTTAAGCGATCGTAAAA AACTTTCTGAAATGGAATTGCCTTTTGTAGAGAAAAAAGTATTGCA

		TCATTTTGCTAAGAAAATCGAACATACGTATATTGAAGATGTGTTG AAAGACAACCATCTGTTGTAA
30	DSM1581 4^T- HY67.1	ATGGCACAGCATGCATACATGATTGGTACAGGCATTGGTAACTTAG CAGCAGGAATTTACCTCATTCGCGATGGTGGTTGGCACGGTGACCA GATCACCATGTACGGTCTTGAAACCCACGGTGCAAACGATGGTGAC ACAGTAACTGGCTACGAAAATGAGTACGGTAACCAAGCTCTTAAA AACAGTCAAGGTTACCTTGCCAAAGGTGGTCGGATGCTCAACGAGG AAACGTATGAAAACTTATGGGATCTCATGCGCTCCGTTCCATCACT AGATCACCCTGATCAATCTGTGACTGATGAGATTTTAGCCTTCGAC CACGCACACCCAACTCACGATGTTGCCCGGTTGATGGATAAAGTAA ACGGCATTCGCAACAAAGGCGACGAAAATGATTACCGCCACATGC AGTTTGACAACCGTGACCGCTACCTTCTGACAAAACTAATGTTGAT GCCGGAAAGCAAAGAAGAACGCCTGAATGATATCGGGATTGATGA ATGGTTTGCCAGTTCACCACACTTCTTCACCACTAACTTCTGGTACA TGTGGCAAACAACTTTTGCATTCAAACGTCAAAGTTCAGCGATGGA ACTGCGTCGCTACATGAACCGTATGATCCTTGAATTTAGTCGTATTA ACACACTCGAGGGTGTTACTCGCACACCTTACAACCAGTACGAAAG TCTCATTTTGCCGATGCGCAAGTTCTTAGAGGATCATGGTGTAACTT TCATTAATAATCGTAAAGTTACGGCGCTCACCTTCAAGGACACGCC AATGCGCGACGATATTATCGTAACCGGTTTCGATTACGAAGAAGTT GATGGCGATCATCAAGCTGGCCACGTTGACGTTAATGACGATGATT TTGTCTTCGACACTAATGGCTCTATCACCGACAGTTCTTCGTTTGGG GACATGGATACCCCACTGAAGGAAAACCACGAATATGCGCCAAGT GCAGCTCTATGGAAACAAGCTTCCGAGCACTTCTATGACCTTGGTC ATCCAGATAAATTCTTTAATGACCGGGAACAAAGTGAGTGGATGAG TTTCACGGTCACAAACAATGATCACAAACTACTTAATGAAATCACC CGAATCACTCAACAACAACCTGGTAATGCATTGAATACTTGGATCG ACAGTACTGGATTAATGTCAATCGTTGTTCATCATCAACCTCATTTT CACGCACAAAAGGAAAACGAAACCGTCTTCTGGGGATACATTATGT ACCCTCGACGGCATGGTGATTACGTCAATAAACCATTCATTGAAAT GACTGGTCGTGAAATTCTCACCGAACTTATTGGTCACTTGAACGAA GTTGATGATAGCCGCGACAAGATTGGTGACCACATTGACGATATTA TGGCATCAACCGTCAATGTCATTCCTGTTTACATGCCTTATGCCAGC GCCCTCTTCAACCGACGGGCAGTTGGTGACCGTCCATTAGTGGTTC CAAAGCACAGTCACAACCTCGCCTTTATCAGTCAATTTGCTGAAAT GCCATTTGACATGGTATTTACAGAACAATATTCATTCCGCTGCGCG CAGCGTGCTGTATACACGTTCTTGGGCATTCCATTGAGCAAACTAA CACCGCTTCACCACTATGAAAAAGATCCGAAAGTCATGGCCCGTGC AACCAAGACAATGTTCAGATAG
31	WIL0041- HY30.1	ATGGCACAACATGCTTATATGATCGGTACTGGTATTGGTAACTTGG CAGCAGGGATCTATTTGATTCGCGATGGTGGCTGGCGTGGTGAACA AATTACAATGTACGGCTTGGATACGCACGGGGCCAATGATGGTGCC CCCGTATCAGATTATGAAGATGAATACGGCAACGGCCCATTGAAAG ATAGTCAAGGTTACTTGGCTAAGGGCGGCCGGATGTTAAATGAAGA AACGTACGAGAATGTCTGGGACATCTTGGCTTCAGTGCCATCACTC GATAATCCAGGCCAAAGCGTCACCGACGATATTTTGAACTTTGACC ACGCGCATCCAACTCACGACGTTGCGCGGTTGATCGATCGCAACGG CTTGCGTATCGGACCGGACAAAAACAACTATCGGCACATGCAGTTC AACAACAAGGATCGGGCGTTGCTTACCAAGTTGATGATGACACCTG AAAAGGATGAACAGAAGTTAAACGACATCAGTATCGCTGAATGGT TCAAGAACAGTCCACATATTTTTGAAACCAACTTCTGGTGGATGTG GCAGACCACTTTCGCTTTCAAGAAGGTCAGCAGCGCTATGGAGTTG CGGCGTTACATGAACCGGATGATTTTGGAATTCAGTCGGATCAATA CGCTTGAAGGGGTTACTCGGACACCTTACAACCAGTACGAAAGCAT

		TATTTTGCCAATGCGCAAGTACCTGGAAGACCGTGGCGTCGAATTC GTCAATAACCGTAAGATTACCGAATTCGTCTTTAAGGACACGCCGC TACAAGACGACATTATTGTGACTGGATTGAAATATCAAGATGTGAC CGGCGACAAGGAGAGTGGCGAGATTGCCATCAACGAAGATGATTT TGTCTTCGATACCAATGGCGCCATCACGGATTCTGCCTCAATTGGG GACTTAAACACACCCGCTGTGGAAAACCATGAGTACGCACCAAGC GCACAGTTGTGGAAGCAAGCGGCCGATAAGTTCTACAATTTAGGCC ATCCAGACAAGTTCTTCAATGATCGGTCGCAGAGTGAATGGGCGAG TTTCACGGTGACAACGAACAATCACTATCTGCTAGATCAAATCACC CGGATCACGAATCAAGCACCCGGGAACGCGTTGAATACATGGATT GACAGTACACCAACGATGTCGATTGTTGTGCACCATCAACCACACT TCAAGGCGCAAAAGCCAAACGAAACCGTCTTCTGGGGTTACTTCTT GTACCCACGGCGCAACGGTGACTTCGTTCAAAAGCCAGTCGTTGAA ATGACAGGGGCAGAGATGCTTGAAGAATTCTTGGGCCACCTGGCTC GCACCGACAAGAGCGCCGACAATATCGGTAATCACCACGATGAAA TTATGTCTTCAATCGTCAATGTCATTCCTGTCTTCATGCCATACGCT TCCGCACTCTTCAATCAGCGGGCCATCGGTGACCGGCCTAAGGTAG TGCCTGATCACAGTAAGAACCTGGCCTTTGTCAGTCAGTTCGCTGA AATGCCGTTTGACATGGTTTTCACTGAACAATATTCCGTTCGCGCAG CTCAGATGGCGGTTTACACCTTCTTAGGGATTCCATTGGCAGAGAT GACACCAATGCATCACTACGAAAAAGATCCTAAGGTCATGCTGCGG GCAACACGGACCATGTTCCGTTAA
32	WIL0012-HY06.2	ATGGTTAAAAGTAAAGCAATTATGATTGGTGCCGGGCTATCAAATA TGGCTGCGGCGGTCTACTTGATTCAAGATGGTCATTGGGATGGTAA GGACATCACATTCTATGGTGTTGATATGCACGGTGCGAATGATGGT GGTGCCACGACTGATTTTACCAATGAGTATTGGAATAAGAATCATC CGATGGCTAACACGACTGGGTATGTTGCCCGGGGTGGTCGGATGCT GAATTACCGGACGTACGTTGACTTAATGGATTTATTGGACCGGATT CCATCGGTAACTGAACCGGGGATGACGGCGGCCGAAGATACGCGT GATTTTGATGCGAAACATCGGACGTATGATATTGCCCGCTTGATGC AGGGTGGTAAAGGCATTATTAATGCTGGTAAGTTAGGATTCAATAA TAAGGATCGGACTTTGCTGACTAAGTTGATCATGATGCCAGATAGT GAAGAAACGAAGCTCGACAACGTTTCGATTGCTGAGTACTTCAAGG ATGATCCGCATATGTTCCAAACGAATTTCTGGTATATGTGGGAAAC AACCTTTGCCTTTAGAACGCAAAGCTCTGCTCAAGAACTGCGGCGT TACATGCATCAAATGATTTATGAATTTACACAAATTGAACACTTAG TTGGTGTCAACCGGACGCGTTACAATCAATTCGAAAGCATGATTTT GCCATTAATTAAGTACTTGCAAGGGCAAGGTGTGACTTTCATTGAT AATAAGATTGTTAAGGATTGGCAATTTAAAGACACGCCAATGCAAG ACGAAATTACGGTGACTGGCTTAGTCATTGAGGATGCGCAGACTGG CGAAACGGAAGAAGTTGAAGTTGATGAGGACACAGCGGTGATCTT CACTAACGGTTCAATTACCGATTCTGCAACGATGGGTGATTACAAC ACGCCTGCTCCTGAAAATATGGATTATGGTGTTAGTGCTAGTTTGTG GAAGAAGGCTACTGAGCGGTTCTATAACTTAGGGACGCCAGATAA GTTCTTCAACGATCGGAATGCTAGCGAATGGGTCAGCTTCACGTTG ACGACTAAGAATCATTTATTCTTAAATGAAATCGTTCGGATCACCA CCCAGGAACCCGGGAATGCGTTGAACTCCTTCTTATCAACTACGCC AATTACGCCGTTGAACCAAAAGGATGTTAATATGTCGATCGTGGTG CACCACCAACCACACTTTACGACACAGCAACCAAACGAAACAGTTC TGTGGGGCTACTTCTTGTATCCACGGCGTCAAGGTGAGTTTGTTAAC AAGCCGTATATCAAGATGACGGGTAAGGAAATGGCTCAAGAATTA ATTGGTCAACTTTCCAAAGTAGATCCGGGTCCAGGCAATATTAAGG ACAAGGAAAAGGAAATTTTAGACAGTATCGTGAACAATATTCCGGT ATACATGCCATATGCTTCCGCACTCTTTAATAACCGGGCTAAGTCTG

		ATCGGCCAGAAGTCTTACCAAAGCACTCAACGAACCTAGCCTTTAC GGGTGAATTTGCGGAACAACCATACCAGATGATCTTCACGGAACAG AGTGCGGTCCGCTCTGGTGAGATTGCCGCTTATCACTTTGCTGGGGT CCCAATGGATAACTTGGTCAAGACACCACGGTACGATAAGGATCCA AAGACCTTGCTCAAGGCAACTAAGAAGATGTTTGATTAA
33	WIL0068-HY41.1	ATGCATTATAGCAATGGTAATTATGAAGCTTTCGTAAACGCAAGTA AGCCAAAAGACGTTGATCAAAAATCAGCATATATCGTCGGTTCAGG TTTGGCCGCACTTGCTAGTGCTGTATTTTTAATCCGTGACGGTCACA TGAAGGGTGAGAGAATTCATATCTTTGAAGAATTAGGTCTGCCTGG TGGCTCAATGGACGGTATTTATAATAAACAAAAAGAAAGTTACATC ATCCGTGGTGGTCGTGAAATGGAGCCACACTTTGAATGTTTGTGGG ACCTATTTAGATCAATTCCATCACCAGAAAACAAAGACGAATCTGT CCTTGATGAATTTTACCGCTTGAACAGAAGAGATCCAAGTTACGCT AAGACTCGTGTCATCGTTAACCGCGGCGAAGCTCTCCCAACAGATG GCCAATTGCTCCTTACTCCAAAGGCTGTCAAAGAAATCGTTGATCT TTGCTTAACTCCAGAAAAAGATTTGCAAAACAAGAAGATTAACGA AGTCTTTACCAAAGAATTCTTCCAATCCAACTTCTGGCTTTACTGGT CAACTATGTTTGCCTTTGAACCGTGGGCAAGTGCAATGGAAATGCG TCGTTACTTGATGCGTTTCGTTCAACACGTTGCTACTCTTAAGAACT TGTCATCACTACGCTTTACCAAGTATAACCAATACGAATCATTGATT TTGCCAATGGTTAAATACTTGAAAGACCGTGGTGTTCAATTCCACT ACAACACTGTTGTTGACAACATCTTTGTTAACCGTTCAAACGGTGA AAAGGTTGCTAAACAAATTATTTTAACCGAAAATGGTGAAAAGAA GAATATTGATTTAACTGAAAACGACCTTGTCTTTGTTACTAACGGTT CAATTACTGAAAGCACCACTTATGGTGACAACCTCCACCCAGCTCC AGAAGAGCATGAATTAGGTGCGAGCTGGCAATTATGGAAGAATTT AGCTGCTCAAGATGAAGACTTTGGTCATCCAGAGGTCTTCTGCAAG GATATTCCAAAGGCTAACTGGAGAATGTCAGCTACGATTACCTTTA AGAATAATGATATCGTGCCATTTATTGAAGCAGTTAATAAGAAGGA TCCACATAGTGGCTCAATTGTTACTAGTGGTCCAACTACGATTAAG GATTCTAACTGGTTATTAGGTTACTCAATTAGTCGTCAACCACACTT TAAGGCACAAAAGCCAAATGAATTGATTGTTTGGCTTTATGGTTTG TTCTCAGACACTAAGGGTAATTATGTAGAAAAGACCATGCCTGACT GTAATGGCATTGAATTGTGTGAAGAATGGCTTTACCACATGGGTGT TCCTGAAGAAAGAATTCCTGAAATGGCTGCAGCTGCAACTACTATT CCAGCACACATGCCATATATTACTTCATATTTTATGCCAAGAGCATT AGGCGACAGACCGAAGGTAGTTCCAGATCATTCAAAGAACTTAGC CTTCATTGGTAACTTTGCTGAGACTCCAAGAGACACTGTCTTCACCA CTGAATACTCTGTCAGAACTGCCATGGAAGCTGTTTATACCTTGCTT GATATTGATCGTGGTGTGCCAGAAGTATTCGCATCCGCATTCGATG TCAGAATGCTCATGAACGCAATGTACTACTTGAACGATCAAAAGAA GCTTGAAGAACTTGATTTGCCTATACCTGAAAAAATGGCAATTAAG GGGATGCTCAAGAAGGTTAAAGGCACCTACGTAGAAGAATTGCTT AAGAAGTACAAGTTGATTTAA
34	WIL0006-HY03.1	ATGTATTATAGTAATGGTAATTATGAGGCATTTGCCACACCACGAA AGCCAAAGGGGGTCGATCAAAAGTCAGCTTATATTGTCGGTTCTGG GTTGGCTGGGTTGTCGGCTGCGGTATTTTTGATTAGAGATGGTCAA ATGAAAGGTGAGGCAATTCATATTTTAGAAGAACTACCGTTAGCTG GCGGTTCATTAGATGGCATAGCACGCCCAAATGTGGGTTTCGTAAC GCGTGGTGGTCGTGAAATGGAAAATCATTTTGAGTGCTTATGGGAT TTGTATCGATCAATTCCATCACTTGAAATTCCGGGTGCTTCATATCT TGATGAATATTATTGGTTAGACAAAGATGATCCCAATTCTTCAAAT TGCCGATTGATTTACGATCGCGGTAATCGTGTGCCAGATGACGGTG ACTATACTTTGGGTAAATCATCACAAGAAATTATCAAACTGATTAT

		GACACCAGAAGCCAAGCTGGGTACCCAAACGATTGAAGATTACTTC TCAGATGCTTTCTTTGAAAGCAATTTTTGGACTTACTGGGCAACAAT GTTCGCCTTTGAAAAATGGCATTCTGCTGTTGAAATGCGTCGCTATG CCATGCGATTTATTCACCATATTGATGGATTACCAGATTTTTCAGCT TTGAAATTCAATAAATACAATCAATATGACTCGATGGTTTTGCCCTT GATTCATTACTTAGAGGATCATGGTGTTGATGTACAATTTGATACC ACGGTCGATAACATTATTGTGGATTTTGATAATGGTCAAAAGGTGG CTAAATCAATAGAATTAACCGTTAGCGGGCAACACGAAACAAGAC CATTAACTGCCAATGATTTGGTGTTTGTAACCAACGGATCTATCACC GAAAGTACAACTTATGGCAGCCACTTTGAACCAGCACCAGTAACCA ATGAGCCGGGTGGATCATGGCAATTATGGGAAAATTTGGCGGCAC AATCTGATGAATTTGGTCATCCATCGGTCTTTTACCAAGATTTACCT GCAAAAAGTTGGTTTGTGTCAGCGACCGCCACAATTGAAAATACAG AAATTGATCCCTATATTGAACGTTTGACGAAACGTGATTTGCATGA TGGTAAAATCAATACTGGCGGCATTATTACAATTACAGATTCTAAT TGGTTAATGAGTTTTGCTGTACATCGTCAGCCACATTTCAAAACAC AAAAGCCAAATGAAACAACTGTCTGGATTTATGGCTTGTATTCTGA TGTGCCTGGCAATTATGTAAAAAAGACGATTGTTGATTGCTCCGGC GAAGAAATTACGCAAGAATTACTTTATCATCTTGGCGTGCCAGAAA GTAAAATTCAGCAATTATCCAAGCAAGAGTCGATTAATACTGTGCC GGTTTACATGCCGTTTATCACAAGTTACTTCATGCCACGTGTAATGG GCGATCGACCAAAAGTCGTTCCTGACGGGTCGGTTAATTTGGCATT CATTGGTAACTTTGCGGAGTCGCCATCACGCGATACAGTGTTTACG ACTGAATACTCAGTCCGTACAGCAATGGAAGCCGTGTATAGTCTGC TAGATGTTGAACGCGGTGTGCCGGAAGTGTTTAATTCAATTTATGA TATTCGTGAATTATTACGCGCCATGTATTATATGAACGACAAAAAA GCTATTACGGATATGGATTTGCCAATTCCTAAGTTAATTCAAAAAG TTGGTATGAAAAAAATTAAAGGGACATGGTTAGAAGAGTTGCTTGT TGAAGCACACTTGATGTGA
35	WIL0008-HY04.1	ATGTATTATAGTAATGGTAATTATGAAGCATTTGCAACACCACGCA AGCCGAAGAATGTAGATCAGAAATCAGCATATATTGTCGGTTCGGG GCTAGCAGGATTGGCTGCTGCAGTATTTCTTATTCGTGACGGTCATA TGAAAGGAGAGTCAATTCATATATTTGAAGAACTCCCATTGGCTGG TGGTTCATTGGATGGTATTCAACGACCAAATGTTGGTTTTGTCACAC GTGGCGGCCGTGAAATGGAAAATCATTTTGAGTGTTTATGGGATCT ATATCGCTCAGTGCCATCATTGGAAATCCCCGGAGCTTCTTACCTCG ATGAGTATTATTGGCTAGATAAGGATGATCCTAACTCATCAAATTG TCGGTTGATCTATGATCGAGGAAATCGTGTGCCAAACGACGGTGAT TATACGTTAGGTAAATCATCTGAAGAAATTATTAAATTGATTATGA CGCCTGAAGCAAAGTTAGGCACAACGACGATTGAAGATTATTTTTC AGAAGACTTTTTCAAAAGCAATTTTTGGATATATTGGGCAACAATG TTTGCTTTTGAAAAGTGGCATTCAGCAATCGAGATGAGGCGTTACG CAATGCGCTTTATTCACCATATTGATGGGCTACCGGATTTTTCAGCA TTGAAGTTCAATAAATACAATCAATATGATTCGATGGTCTTGCCTTT GATCAAGTATCTCGAAGATCATGGTGTTGACGTACAGTTTGATTCT ACAGTTGATAATGTCATTGTGAATTTCGATCATGGCAATAAAGTTG TTAAAGAATTACAGCTCACTGTTGCAGGAAAGCCAGAAACTAAAC AACTTACAGCAAATGATTTAGTTTTCATAACGAACGGTTCCATTACT GAAAGTACGACCTATGGGAGCCATTTTGAACCAGCGCCAGTTACAA ACGAACCCGGCGGATCGTGGCGTTTATGGGAAAAATTAGCTGAAC AATCAGACGAATTTGGTCATCCAGGTGTGTTTTACCAAAACTTACC AGCAAAAAGTTGGTTTGTTTCAGCAACAGCAACAATTAAAAATACT GAAATTGATCCCTATATTGAACGACTTACCAAGAGGGACATACATG ACGGTAAAATTAATACAGGTGGCATTGTAACCATTACCGATTCAAA

		TTGGTTGATGAGTTTTGCTGTCCATCGTCAACCACATTTTAAGCAAC AAAAGCCAAATGAAACAACAGTTTGGATCTACGGACTATATTCTGA TGTTCCTGGCAACTATGTTAAGAAGACTATTGTAGAGTCTTCTGGTC AAGAAATTACACAAGAATTTTTGTACCACCTAGGTGTCCCTAAAAG TAAAATTAATCAACTAGCACAGCAAGAATCAATTAACACTGTTCCA GTGTACATGCCGTTTATTACAAGTTATTTTATGCCACGTGTCATGGG TGATCGTCCAAAAGTAATTCCGGATGGCTCTGTCAATTTGGCATTTA TTGGAAACTTTGCTGAGTCGCCTTCGCGAGATACAGTCTTTACTACG GAATATTCAGTACGTACTGCTATGGAGGCTGTATATAGCTTGCTAG ATGTTGAGCGTGGTGTACCAGAAGTCTTTAATTCAATCTACGATATT AGAGAATTATTGCGAGCTATGTACTATATGAATGATAAAAAGCCAC TGAGCGAAATGGATTTGCCAATTCCTAAGCTAATACAAAAAATTGG GCTTAAAAAAATTAAAGGTACTTGGCTAGAAGAATTATTGGCAGAA GCACATTTATTATAA
36	WIL0076-HY48.1	ATGTATTATAGTAGTGGTAATTATGAAGCTTTTGCTCATCCTAAAAA GCCAGCAAATGCAGACAAAAAATCTGCTTACATCGTTGGTTCTGGA TTAGCCGGACTGGCAGCTGCTGTCTTTTTAATTCGTGATGGTCAAGT TCCCGGTAATCAAATTCACATCCTAGAAGAATTAAAGCTTCCGGGC GGTAGTATGGATGGTATTTTAAACGAGCAACGTGGTTATATTATTC GTGGTGGTCGTGAAATGGAACCCCATTTTGAAACTTTATGGGACTT ATTCCGTTCTATTCCAACTCTAGAAAACCCTGATGTTTCAGTTCTTG ACGAGTTTTATTGGCTCAATAAAAAAGACCCTAGTTACTCAAAAAC ACGCGCCATTGAAAATCGTGGGCAAAAAATTGCAACTGATGGTCA ACTAACGCTTTCAAGAAAAGCAGTTGAAGAAATTGCTAAATTAGTT TTAACCTCTGAAGAAAAACTAGGAGATATTAAAATTAACGAAGTTT TTGGAAGCGAATTCTTCAAATCAAATTTTTGGCTATATTGGTCCACA ATGTTTGCTTTTGAGCCATGGGCTAGCGCAATAGAAATGCGACGCT ATTTATTACGTTTTGTTCACCATGTTGGCACATTGCAAAACATGTCC GCTCTAAAATTCACTAAATATAATCAATACGAATCTTTGGTTAAAC CTATGGTTAAATACCTTGAAGACAAGGGAGTTCAGTTTCAATACGA CACAATAGTTAATAATGTTATTGTTAATCGTACTGCTGGGCAAAAA ATTGCGACTGAGTTAGATATGACTGTTGCTGGCGAAAAGGAAACCT TATCCCTTACTCCTGATGACTTTGTTTTTGTTACAAACGGCTCCATC ACAGAAAGCACAACTTATGGTGATAACAATCATCCAGCCCCAACA GAACATGCAATCGGAGCAAGTTGGCAACTTTGGGAAAAATTAGCT GAACAAGATCCGTCATTTGGTCATCCTGCTAAATTCTACAAAAATA TTCCTGAAGCAAATTGGGTAATTTCAGCTACATGTACCTTTACTGAT AACCGTATTGTTCCTTATATCAAAAAAATTACCGGCAAAGATCCAC ATAGTGGCTCAATTGTTACTAGTGGTCCTGTATCAATTAAAGACTC AAATTGGCTTTTAGGTATTTCAATCAGTCGTCAACCACACTTTAAAC AACAAAACCCAAATGAATTAATTGTCTGGCTTTACGGTTTATTCTCT GATCAACCTGGAAATTACATTCAAAAGAAAATTACAGATTGCAATG GACAAGAATTATGCGAAGAATTTCTTTATCATATTGGTGTTCCAGA AGATCAAATCGCTGATATTGCTAAAGATGCAAATTCAATTCCTATT CATATGCCATATATTACTTCTTATTTCATGCCAAGAAAAACAGGGG ATCGGCCTTTAGTTGTCCCTGAGGGTTCTCAAAATCTTGCTTTTATT GGTAACTTTGCTGAAACTAAAAAAGATACTGTTTTTACGACTGAAT ACTCAGTTAGAACTGCTATGGAAGCTGTTTATCAATTATTAGATATT GATCGTGGTGTCCCTGAAGTTTTTGCATCATCATATGATATTCGAAC TATCCTAAGCTCTATTTACTACTTAAACGATAAAAAAAGTTTAGAA GAACTACCATTAAATAAAGTTGAACAAATAGGACTTGAAGCCTTTT TGAAGAAAATTAAAGGTACTTATTTAGAAGAAATCTTTAGAGATGA GCACTTAATCTAG

37	WIL0055-HY35.1	ATGATGCATTACACAAATGGAAACTACGAGGCGTTCGTTAATGCTG ACAAGCCAGCCGATATCGAAAAAAAATCGGCATATATCATTGGAG CAGGTCTAGCTGGATTAGCCACAGCCGTCTTTTTGATTCGTGACGG ACAGATGCCAGGTAAAAAAATCCATATTCTTGAAGAATTGTCAGTT CCAGGCGGCAGCATGGATGGAATTTACAGCGTTCAGCGCAATTCCT ATATTATTCGTGGCGGCCGTGAAATGGAACCGCATTTTGAGACGCT CTGGGATCTGTTTCGTTCGATTCCGTCACTGGAAGTCCCCGGCGCTT CAGTATTGGATGAGTTCTATCGTCTAAACCGTAAAGACCCCTGCTA TGCTAAAACTCGTGTCATTCAGAATCGCGGTGAAGCTTTGCCAACC GATGGACAGCTGCTGCTGACGCCAAAAGCGGTCAAAGAGATCGTT GACCTGGTTTTAACGCCAGAAGAAAAACTCCAGGACGTCAAAATC AATGAAGTCTTTGACAAGGAGTTCTTCCAATCCAATTTCTGGCTCTA CTGGTGTACGATGTTTGCCTTTGAGCCATGGGCCAGCGCCATGGAA ATGCGTCGTTATCTGATGCGGTTCATTCAACACGTTGGTACGCTCAA AAATCTTTCATCACTGCGTTTTACCAAATTCAACCAATATGAGTCAT TGATTCTCCCAATGGTTAAATTCTTAAAGGATCATGAGGTTCAATTC CATCAAGAAACCACCGTCGACAACATCATCGTTAACCGCTCCGGTG ACGACAAGCTTGCCACCAAGATCGAGATGAAAGTTGCTGGTGAGC CGCAAAACATCGAACTGACACCAAATGATCTGGTCTTTGTAACAAA TGGTTCGATCACCGAAAGCACCACGTACGGCGACAATGATCACCCT GCACCAATTGATCATCCGCTTGGCGCTAGCTGGCAGCTATGGAAGA ACCTGGCAGCCCAAGACAGTGATTTTGGTCATCCAGAAAAGTTCTG CGAGCAGATTCCAAATGCAAACTGGACTATGTCGGCTACGATTACT TTTAAAAACAATGATATCGTACCATTTATTGAAAAAGTAAATAAAA AAGATCCGCACAGTGGCTCAATCGTAACCAGCGGCCCTACAACAAT CAAAGACTCCAACTGGCTCTTAGGCTATTCGATCAGTCGGCAGCCT CATTTTCACCAGCAGAAGCCTAATGAACTGATCGTCTGGCTGTACG GCCTCTTCTCTGACAAAGGCGGCAACTACGTTAAAAAAACGATGCC CGAATGTACCGGTATCGAACTATGTGAGGAGTGGCTATATCATATG GGCGTACCAGAAAATGATATTCCGGCCATGGCAAAAGCAGCAACA ACGATTCCTGCTCACATGCCGTATATCACATCCTACTTCATGCCGCG ATCCTTGGGTGACCGCCCATTAGTCGTACCAAAGCATTCCAAGAAT CTAGCCTTTATCGGCAATTTTGCTGAAACGCCACGTGATACGGTCTT TACAACTGAATACTCCGTTCGTACCGCCATGGAAGCCGTTTATACT CTGCTTGACATTGACCGGGGCGTTCCCGAAGTCTTTGCCTCAGCCTT TGACGTTCGTTTGATGATGAATGCCATGTACTATCTTAATGATCAAA AGAAATTAACTGAACTGGACCTGCCATTGTCCCAGAAACTATTAGT TAAAGAGGGACTCAAAAAAGTCAAGGGAACCTATATCGAAGAACT TTTAAAAGAATATCGGCTGATCTAG
38	WIL0055-HY36.4	ATGTTATCGCTTTCGCAAGGATTATTTTACACTGGAGGGGTTTTTAT GTATTATTCCAACGGTAATTATGAAGCATTTGCACGTCCTCGCAAG CCTGAGGGAATCGAACAAAAACACGCCTATATTATTGGCGGGGGG CTGGCTGGTTTGGCAGCGGCCGTCTTCATGGTTCGTGATGCTCAGAT GCCTGGCGAAAACATTCATATCTTAGAAGAGCTGCCGGTTGCGGGT GGCTCACTGGATGGCGAGAAGCGTCCTGGCGTTGGATATGTCATTC GGGGTGGCCGTGAAATGGAAAACCACTTTGAATGTCTCTGGGATAT GTACCGCTCAATTCCTTCCCTGGAGATTCCAGGCGCTTCTTATCTGG ATGAATACTACTGGCTGGACAAGGATGATCCCAACTCGTCAAACTG CCGCCTGATTCATAATCGCGGTGATCGGGTACCTAGTGATGGCAAG TATGGTGTCGAGAAGTTTTCAAAGTATATCGTCAAGCTGGTTTTGA CCTCAGAAGATGAATTAGAGGGCAAGACGATTGGCGACTGGTTCCC AGATGAATTCTTCGACACCAATTTCTGGATGTACTGGTCAACCATG TTTGCCTTTGAAAAGTGGCACTCCTTGATTGAAATGCGGCGCTACT GCATGCGCTATATTCACCATATTGATGGTCTGCCAACGCTGAGCGC

		CCTCAAATTCAATAAATACAACCAGTATGAGTCAATGACTAAGCCA ATCTTGGCATATCTGCAGGATCACAACGTCGACATTCAATACGACA CGGTGGTCAACAATGTTTTGGTTGATACCAGCAACGACAAGAAGAT TGCCAAAAAGATTCTGCTGACCAAGGATGGCAAGGATGAAGAAAT CGTCTTGACGGACAACGATTATGTCTTCGTTACCAATGGCTCAATTA CCGAAAGTTCAACCTATGGCGATCAGAACACGCCGGCACCGATCAC GCACAGCTTAGGGCCTAGTTGGAAACTGTGGGAGAATCTTTCCTAT CAGGATGCCGATTTTGGTCACCCCGATGTCTTCTGCAAGAACGTTC CTGACCGTGCCTGGTTCATCTCGGCTACGGCAACGCTCAAGAACCG TAAGCTGGCGCCATACTTTGAACGGCTGACCAAGCGCAGTCTTTAT GATGGCAAGGTCAATACTGGTGGGATCATCACGGTTACCGACTCGA ACTGGATGCTGAGCTTTACGATTCACAGACAGCCGCACTTTAAGGA CCAAAAGCCGGACGAAACGGTTGTCTGGATCTACGCGCTTTATTCC GACACGGAAGGCAACTACATCAAGAAACGGGTCGTGGACTGCTCA GGCAAAGAGATTACTGAAGAATTGCTCTACCACCTGGGCGTTCCAG TTGACGACATTGAAGGCTATGCAGAAAACGACGTCAATACCGTACC AGTCTACATGCCTTACGTTACCAGCTACTTCCAGCTGCGTAAAAAG GGTGACCGGCCGGCAGTCGTGCCAAAGGGGTCGCAAAACCTGGCC TTTTTGGGCAACTTTGCCGAATCGCCAACCCGCGACACGGTCTTTAC CACGGAATACTCGGTTCGGACCGCGATGGAAGCCGTCTACACGCTC TTTAACGTTGATCGTGGCGTTCCAGAAGTCTTTGATTCCGTCTTTGA CATTCGCCAAGAGCTGCGGGCACTGTACTACTTAAGCGACAAGAAG ACGTTGCCGGAGATGGATCTGCCGGTGCCAAAGCTGGCTGCCAAGA CTGCGCTGCGCAAACTGAAGGGAACCTGGATCGAAGAAATTCTCA AAGAGCAGCATCTGCTTGACTGA
39	WIL0075-HY05.2	ATGTACTACAGTAGTGGTAATTATGAAGCATTTGCTCGGCCTAAAA AACCAGCAAACGCCACCAAGAAATCAGCCTATATTGTTGGGGCCG GTTTAGCCGGTTTAGCTGCCGCCGCTTTTTTAGTGCGCGATGGTCAG GTTCCTGGAAACCAAATTCATGTTTTTGAAGAACTTGGACTTCCCG GTGGCAGCATGGATGGGATTTTAAATGAACAACGTGGCTATATTAT TCGTGGTGGGCGTGAAATGGAACCTCACTTTGAAACTCTTTGGGAT CTTTTTCGTTCAATTCCTACCTTAGAAGATGCCAGTGTTTCGGTACT TGACGAATTCTATTGGCTAAATAAAGCCGATCCAAGTAATTCACAC ACCCGCGTAATCGAAAAACGTGGTAATCAGTTAGCCAGTGATGGTC AGTTGACGCTTTCCCGAAAAGCAATTGAAGAAATCGCCAAATTAGT GCTAACACCGGAAAGCCAACTTGACAATGTCAAAATCAATCAAGTT TTCAGCGATGACTTCTTTAAATCAAATTTCTGGCTCTATTGGTCCAC CATGTTTGCTTTCGAGCCTTGGGCAAGTGCAATGGAAATGCGCCGT TATTTATTACGCTTTGTCCATCATGTTGGCACCTTGCAAAATATGTC AGCATTGAAATTTACCAAATATAATCAATATGAGTCATTAATCAAA CCACTGATTAAATATCTTGAAGATCACGACGTTAAATTCCAATACA ATACCACCGTTGACAATATTATTGTTGAACAAACCGGTGAACAAAA ACAAGCTGTTAAAATTGAGCTAACGATCGATGGTAATCAGCAAAGC CTCGACCTAACACCTGACGATTTGGTTTTCGTTACAAATGGATCAAT TACTGAAAGCACTACTTATGGTGACAATGAACATTCAGCACCAGCA ACGCATCCAACCGGTGCTAGCTGGGAATTATGGGAAAAATTAGCG GCTCAAGACCCAGCTTTCGGACATCCAGCTAAATTTTATCAAGATA TTCCAGCGGCTAACTGGGTCATGTCGGCAACTTGCACCTTTAAAGA CGATCGAATCGTACCCTATATTCAAAAAATTACTGGTAAAGATCCG TATAGTGGTTCAATTGTTACCAGTGGCCCAGTCTCCATTAGGGACTC AAACTGGTTATTAGGAATTTCCATCAGCCGTCAACCACATTTTCAA CAACAAAAGCCAAATGAATTAATCGTATGGTTATATGGTCTCTTTT CCGATCAGCCCGGAAATTATATTCACAAAAAAATTACTGATTGCAG TGGCGCAGAAATCTGTCAAGAATTTCTTTATCACATTGGTGTCCCA

		GAAAATCAAATTGCTGAGATCGCGCAAACAGCTAATTCAATTCCAA TTCATATGCCATACATTACTTCATACTTTATGCCACGCCAAGCTGGT GATCGTCCCTTAGTTGTCCCTGAAGGTTCAAGCAATTTGGCTTTTAT TGGGAACTTTGCCGAAACTGAGCGAGACACCGTCTTTACAACTGAA TACTCTGTCAGAACTGCTATGGAAGCTGTCTACCGACTGCTTGACA TTGATCGTGGCATCCCAGAAGTCTTTGATTCCGCCTTTGACATACGA ACAATCTTAAGTGCCTTATATTATTTGAATGATAAAAAGAGCTTGA CCGAATTGCCTTTAAATCAAATTGAAAAAATTGGTCTAAATGCCTT TTTGAAAAGGGTTCATGGCACCTATCTTGAAGAAATTTTGAAATCT CAAAAGTTACTCTAA
40	WIL0037-HY26.1	ATGGAAAAAGCATATATGATCGGTACTGGAATTGCCAATTTAGCAG CAGGTATTTATTTGATTCGCGATGGTGGGTGGTCTGGTAACCAGAT TACGATGTTTGGTTTAGAAAAACATGGTGCCAATGATGGGGCTGCC GTTGCCGACTATGAGCAAGAATATGGAAATCAAAGTCTGTCTAACA ACCGAGGCTATTTAGCCAAGGGTGGACGGATGTTAAACGAAGAAA CTTACGAAAATCTCTGGGACATTCTGCGGAGTGTCCCATCTTTGGA CAATCCGGGCCAATCGGTTACGGATGATATATTGAATTTCGACCAT GCACATCCCACTCATGATGTTGCCAGATTGATGGATAAGAAGAATG GAATTCGTAACAATGGTGGAGCAGACGACTATAATCGGATGCAGTT TAATAATAAAGATCGCTACTTACTATCTAAATTAATGATGATGCCA GAGAGTAAGGAAGATAAATTAAACGATATTAGCATTGCAGAATGG TTCGCTGAAAGTCCTCATATTTTTTCAACTAACTTCTGGTATATGTG GGAAACTACTTTTGCCTTCAAGAAGGAAAGCTCGGCCATGGAGCTT CGGCGCTATATGAATCGGATGATTCTAGAATTCAGTCGAATCAACA CTTTGGAAGGGGTAACTCGTACACCATACAATCAGTTTGAAAGTAT TATCTTACCTATGAGAAAATACCTTGCGGATCAAGGCGTTGAATTT GTTAATAACCGAAAAATTACGGCATTTAACTTCAAAGACACTCCGC TCCGTGATGATATTATCGTTACGGGACTCGAATACGAAGATGTTGA GAGCGGTGAAACTGGAAAAATCGAAGTTGATGAAAATGATTTAGT ATTTGATATTAATGGAGCAATTACGGATAGTTCATCAATGGGTGAT TTCAACACGCCAGTTAAAGAAAATATGGAATACGCTCCAAGTGCAG CCCTTTGGAAACAAGCTACAGAACATTTTTATAACCTTGGAAATCC TGATAAATTCTTTAATGATCGAGCCCAAAGTGAATGGATGAGTTTC ACGGTTACTACTAATAACCACTACTTGGTAAATGAAATTAGTCGAA TTACCCAACAAGAACCGGGGAATGCGCTAAATACTTGGGTAGATA GTAACAACCTCCTATCCATTGTGGTGCATCACCAACCTCATTTCCAT GCCCAAAAGGAAAATGAAACGGTCTTCTGGGGTTACTTCATGTTCC CACGTAAAAATGGGGATTATGTTGATAAACCAGTGATTGAAATGAC GGGTAAAGAAATGCTTCAAGAACTTCTAGGACATCTATCAGAAGTT GACCGAGCAGCTGATAACATCATCAATCATGAAGAAGAAATCATG GATAGTATCGTGAATGTTATTCCAGTTTACATGCCATATGCTAGTGC TTTGTTCAACCAACGGGCAGTGGGAGATCGTCCAGACGTTGTACCA AAGAACTCTAAGAACTTGGCTTTTGTTAGTCAATTTGCTGAAATGC CATTTGATATGGTCTTTACGGAACAATACTCAATCAGAGCCGCTCA AAAGGCGGTTTACCACTTCATGGGTATTCCAGAATCACAAATGACG CCGGTTCATCACTATGAAAAAGATCCAAAAGTCTTGCTAAAAGCAA CTAAGACTATGTTTAGATAA
41	WIL0039-HY28.1	ATGCTATGTATTTTAAATAAGAATGAGGAGGAGCATACTATGGAAA AAGCATATATGATTGGAACAGGAATTGCTAATCTTGCCGCAGGAAT TTATTTGATTCGTGATGGCGGTTGGACCGGTGATCAAATTACGATG TTCGGTCTTGAAAAACACGGAGCTAACGATGGTGCACCCGTCTCCG ACTACGAAAGTGAATATGGAAATCAACGTCTATCTGATAATCGAGG ATTTCTGGCTAAAGGTGGTCGAATGTTAAATGAAGAAACATACGAA AATCTTTGGGATCTTTTCCGTAGTGTGCCTTCATTGGATAATCCGGG

		ACAATCGGTTACCGATGATATCTTAAACTTTGATCATGCTCATCCGA CACATGATGTTGCGCGTTTAATGGACAAGAAAAATGGAATTCGCAA TAACGGTGGTGCGGATGATTATTATCATATGCAGTTTAACAATAAA GATCGTCTTTTACTATCAAAATTAATGATGATGCCTGAAAGTAAGG AAGAAAAACTTAATGACATTAGCATTGAAGAATGGTTTAAAGACA GTCCGCATATTTTTAAAACTAATTTTTGGTATATGTGGGAAACAACT TTTGCTTTCAAAAAGGAAAGTTCTGCCATGGAACTCCGACGTTACA TGAATCGGATGATTCTCGAATTTAGTAGAATTAACACGCTTGAAGG AGTTACCAGAACGCCGTATAATCAGTACGAAAGTCTTATCCTACCG ATGCGCAAGTATTTGGAAGATCAGGGAGTTAAGTTTATCAATAATC GTAAAATTACTGCCTTTGAATTTAAAGATACGGCACTTCGGGATGA CATTATTGTGACTGGTCTTCAATACGAAGACGTTGATGGTAGCGAT GAAAAGGGAACGATCCCGGTTAATGAAAATGACTTAGTATTTGATA TCAATGGAGCAATTACCGATAGTTCATCCTTTGGTGATTTTAATACA CCAATCAAAGAAAATATGGAATACGCTCCAAGTGCGGCATTGTGG AAGCAAGCAACTGAACATTTTTATAGTTTAGGTAATCCAGACAAAT TCTTTAACGATCGAGCTCAAAGTGAGTGGATGAGCTTCACGGTAAC AACTAATAATCATTTTCTAGTAAATGAAATTAGTCGAATCACACAA CAAGAACCTGGTAATGCTTTGAATACTTGGGTTGATAGTAATAATT TATTATCAATTGTTGTGCATCATCAACCACATTTTCATGCACAAAAG GAAAATGAAACCGTATTTTGGGGATACTTCATGTTCCCACGTAAAC ATGGTGACTATGTTGATAAACCCGTGATCGAAATGACCGGAAAAG AGATTTTACAAGAACTTTTGGGTCATCTTGCGGAAGTTGATACTGC AACCGATAATATTCGAAATCATGAGTCTGAAATCATGGATAGCATT ATTAACGTCATTCCAGTTTATATGCCATATGCGAGTGCCTTGTTCAA CCGTCGTGCAGTGGGTGATCGCCCAGACGTTGTTCCTAAGAATTCT AAAAATTTGGCTTTTGTCAGTCAATTTGCTGAGATGCCATTTGATAT GGTATTTACTGAACAGTATTCAATTCGAGCAGCTCAAAAGGCCGTT TATCACTTTATGGGAATTCCAGAAGATGAGATGACACCCGTCCATC ACTATGAAAAGGATCCAAAAGTGATGTTAAGAGCTACTAAAACAA TGTTTAGATAA
42	PA- HY29.2	ATGATGAGAAAAGCGTTTATGATTGGTACAGGAGTTGCAAATTTAG CTGCCGGCGTATATTTGATTCGTGATGGTGGTTGGAGCGGTAATCA AATTACCATGTTCGGACTCGATAAACACGGGGCTAACGATGGGGCA GCGGTTGCGGATTACGAGACGGAATACGGCAACCAGCGGCTATCT AACGATCGGGGCTTTTTAGCCAAGGGCGGTCGGATGCTTAACGAAG AGACCTACGAAAACTTGTGGGACGTTTTGCGGAGTGTGCCGTCTTT GGATCACCCAGGGCAATCGGTTACGGATGACATTTTAAACTTTGAC CATGCTCATCCAACCCATGACGTGGCCCGGCTAATGGATAAGCGTA ACGGGATCCGGAATAATGGCGGTGCGGACGACTATTCGCATATGCA ATTTAATAACCAAGACCGGAAGTTGTTAACCAAATTAATGGTGATG CCTGAAAGCCAAGAAGCAAAGCTTAACGACGTCAGCATTGCGGAA TGGTTTAAGGATAGTCCGCACATTTTCACTACTAACTTCTGGTACAT GTGGGAAACTACCTTTGCGTTTAAGAAGGAAAGCTCCGCAATGGAA TTGCGGCGTTACATGAACCGGATGATTCTGGAATTTAGTCGGATTA ACACCCTTGAAGGGGTTACCAGAACGCCGTATAACCAATACGAAA GTATCATTCTACCGATGCGTAAGTACTTGAGCGATCACGGGGTTAC CTTTATCAACAACCGTAAGATTACCGCCTTCCAATTCAAGGACACT CCGTTGCGCGATGATATCATCGTTACTGGCTTAGAGTACGAAGACG TAGGGGAAAATAAGCAAACCGGCACAATCCCGGTTGACGAAAATG ACCTCGTTTTCGATATCAACGGCGCGATTACCGATAGTTCATCGATT GGTGATTTCAACACCCCAATTAAGGAAAATATGGAATACGCTCCTA GCGCAGCATTATGGAAACAAGCTACCGAACATTTCTATAATCTAGG AAATCCGGACAAGTTCTTTAACGACCGTGCCCAAAGTGAATGGATG

		AGCTTTACGGTAACCACGAAGAACCACTATTTGGTAAACCAAATTA GCCGGATTACCCAACAAGAACCGGGGAATGCTTTAAATACTTGGGT AGACAGTAATAATTTGTTATCCATCGTGGTTCATCATCAGCCGCATT TCCACGCTCAAAAGGAAAACGAAACGGTCTTCTGGGGCTACTTCAT GTTCCCACGTAAAAATGGGGATTATGTGGACAAACCGGTAATTGAA ATGACCGGAAAAGAAATGCTGCAAGAATTACTAGGTCATTTGGCA GAAGTTGATCAAGCAACGGATAGCATTGTTTATCATGAAGAGGAA ATTATGGATAGCATCGTTAACGTAATTCCGGTTTACATGCCGTACG CTAGCGCACTGTTCAATACGCGAGCTGTCGGAGACCGTCCTGAAGT AGTGCCAAAGCATTCGAAAAACTTGGCATTTGTCAGCCAGTTCGCA GAAATGCCATTTGATATGGTCTTTACCGAACAATACTCGTTCCGGG CGGCACAACGGGCAGTCTACCATTTCTTAGGAATTCCTGAAGAAAA AATGACCCCAGTGCACCACTACGAGAAGAATCCAAAGGTGCTTTTG AAGGCAACCCGGACCATGTTCCGTTAG
43	WIL0029-HY20.1	ATGTATTACAGTAACGGAAATTATGAAGCATTTGCAAAACCTAAAA AACCAAAAAATGTAGAAAATAAATCAGCTTATATTGTTGGTTCAGG TCTTGCTGGATTAGCATCGGCAATTTTTTTAATTAGAGATGGTCAAA TGCCCGGAGAAAATATTCATATTTTTGAAGAACTCTCTTTAGCTGGT GGTAGTATGGATGGAATATATAATGAATCACGTGGTTACATCATTC GTGGTGGTCGTGAAATGGAAGCCCATTTTGAAACCCTTTGGGATTT ATTCCGTTCAATTCCAACTCTTGAAAATCCAGAAATTTCAGTATTAG ATGAGTTTTATTGGTTAAATAAAGAAGACCCAAGTTATTCTAAAAC ACGTGTAATTGAAAAATGCGGAAAACAATTAGAAAATGACGGAGA ATTAACGTTATCTCGTAAAGCTATTGATGAAATGTTAAAACTAGTC TTAACATCAGAAAGTCAATTAGATGATGTTAAAATCAATGAAGTCT TTTCTGATGAATTTTTTGAATCTAACTTTTGGTTATACTGGTCTACA ATGTTTGCTTTTGAACCATGGGCAAGTGCGATGGAAATGCGCCGTT ACTTACTACGTTTCGTACAGCATGTAGGTACACTAAAAGATATGTC AGCGTTAAAATTTACTAAATTTAATCAATATGAATCTTTAGTAAAA CCAATGATCCATTACTTAGAAGGGCATAATGTACATTTCCAATACG ATACAGTTGTCAATAATATTATAGTGAACCGTTCGGACAGTCAAAA AATCGCCACAGAAATTCAACTTACTGAATCTGGTCAAACAAAAGTG TTACCTTTGACAATAGATGATTTGGTCATTGTAACTAATGGTTCAAT TACTGAAAGTACAACGTATGGAGATACCGAACATCCTGCACCTCAA GAGCATGAAGTAGGACAAAGTTGGCAATTATGGGAAAATATAGCC AAACAAGATACATCTTTTGGTCGTCCTTGGAAATTTTATCGTAATGT TCCCGTTGCAAATTGGGTAAATTCAACAACTTTAACGTTCTCAGAT GATCAAGTTGTTCCATTTTTAGAATCTATTACTGGTAAAGATCCGCA TAGTGGTTCTCTAGTAACAAGTGGTCCTATAACAATTCGTGACTCTA ATTGGTTATTAGGAATTTCCATTAGTCGTCAGCCTCACTTTGAGCAA CAAAAAGACAATGAATTAATTGTTTGGTTGTACGGTCTATTTTCAG ATTTACCTGGAAATTATATTCCTAAAAAAATTACTGACTGTACTGGT CGTGAAATATGCGAAGAATTCTTATATCACATTGGAGTTCCTAAAA ATAAAATTTCAGAAATTGCAGCAACAGTGAAAGCTGTTCCTACAAA CATGCCTTATATTACTTCTTACTTTATGCCTAGAGCAGCTGGAGATC GTCCAAAAGTGGTACCGGATGGTTCAGCTAATCTTGCATTCGTTGG AAACTTTGCTGAAACAGAACGCGATACAGTCTTCACTACTGAATAT TCTGTTCGTACAGCCATGGAAGCTGTTTATCAATTACTAGATGTAG ACCGTGGAATTCCAGAAGTATTTGATTCTTCTTTTGATATGCGCATG ATTCTAAATGCTATCTATTATCTTAATGATAAAAAAGGATTACGTG ACTTACCTTTAACAAAAGTTGAAAAATTTGGATTAGAAGCATTTCT TAAGAAAATTAAAGGAACATACATTGAAGAAATATTAGTCGATCA ACACTTATTATAG

44	WIL0114-HY62.1	ATGAATAATTATCAAAGAATCAATCCAATCGCACCTAAGAATATTG AAAAGAGAAATGCATACCTACTTGGAGGTGGAATAGGTTCCCTAGC TGCTGCTGCCTTTTTAATAAGAGATGCTCATATGCCTGGTAAAAAC ATTCATATACTTGAACAACTCGATGTTGTTGGAGGCTCAATGGATG GAGCTGGCACAGCAGAAAAAGGCTACACAGCAAGGGGCGGCAGA GAAATAGAAGAACATTTTGAATGCTTTATGGAGCTTTATAGTTTTAT CCCATCTTTAAAGGATAAGAATAGAAGTGTATTAGATGAATTCCGC GAACTTAATATAGAAGAACCAATTGAATCTCACTGCAGATTAGTAG AAAATCAAGGAGAAAAAGCTGATTTTTCAAGTCTTGGACTATCAAC TGCCAATGCTATGGAACTTGCAAAACTTCATATGGCAACAGAAGAA GCACTTGGAGCAACAACAATAGGACAATTTTTCTCTCCTAGCTTCTT TAAGACAAACTTCTGGTATTTCTGGGCAACAATGTTTGCTTTTGAAA AGTGGCACAGTGTAGTTGAAGTTAAGCGTTATATGGAAAGATTCAT GCACTTAATCGGCGGTATGAATAAATTAAAAGGAATACTTCACACT GAATATAATCAATACGATTCTTTAATTCTTCCTGTTATTGTATGGCT AAAGGATCATGAAGTAAACTTTGACAGTGGCTGCAAGGTTACAGA CATTGATTTTGATTTTTCTAATAATGAAAAAATAGCTACTAAAATTT GCTATACTAAGGCTGGTAAAGATGAAGTTATAAGTGTAAATAAAG ACGATTTAGTGTTATTTACAAATGGTTCTATGACAGAAAACACAAC TAGAGGTGATCTTGATCATCCTGCTATTATAAATAGATCAGAAGAT AAAGGCTGCTTTAGCGTATGGGAAAAGCTTGCTAAAAAATCACCAG ACTTTGGTCACCCAGAAAAATTCTGCAGTGATATTGATAAATCAAA ATGGATGTCCTTTACTGTAACTTTAAAAGATGATGATATTGTGTTCC CTTATCTTTATAAACTTACAGGAGATAAACCTGGAATGGGCGGACT TGTTACAATAAAAGATTCAAGCTGGTTTATGAGCTGGGTTGTTCCA AAACATCCTCACTTTGCTAATCAACCTGACAACGTAAAAGTTCTTT GGGCATATGCTTTGAACTTAGATACACCAGGCGATTATGTAAAAAA GACTTTTTCAGATTGTACAGGTCGTGAGATGTTTGAAGAACTTCTTT ATCATATGGGCTTAAAAGATAGAATTCCTGAAATTCTTTCACATAC AGTAAATGCAATACCTAGCATGATGCCTTATATTACTTCACAATTTA TGCCTCGTATACCAGGAGATAGACCAGATGTAATTCCAAAAGGAA GCAAAAACTTTGGTTTCCTTGGACAATATGCAGAGGTTCCTCATGA TTGCGTATTCACTGTAGAATACTCAGTAAGAAGTGCAATGATGGCT GTATATGGACTAATGGGCTTAGAAAAGGAAGTAGATCAAGTATATC CAAGCCAATATGATATTCGTGTACTGACAAATGCAGCAAAAACTTG CCTTGGTATTGATAAGCTTCCATTAGAAAATATACCATTAGGTGCA CTACTCAAGAACACAGAATTAAAAAATTTATTATAA
45	WIL0042-HY33.1	ATGAATAATTATCAAAGAATTAATCCAATTAAACCAAAGAATATTG AATCAAGAAAAGCATACTTAATAGGAGGTGGAATAGGTTCCTTATC AGCAGCAGCTTTTTTAATAAAAGACGGCCATATGCCAGGAAATAAC ATTCATGTGATTGAACAGCTTGATATCCTTGGAGGTTCAATGGATG GCGCAGGAACTGCAGAAAAAGGCTATACTGCAAGAGGCGGTAGAG AAATAGAAGAACATTTTGAATGCTTTATGGAGCTTTATAGTTTCATT CCTTCTTTAACTGATAAAAACAGAAGCGTATTAGATGAATTTCGCG AACTTAATATAGAAGAACCAATTGAATCCCACTGCAGATTAGTACA CAATCAAGGAGAGAAGTCAGACTTTTCAACTCTTGGATTATCAAAG GGACATGCTATGGAGCTTACAAAACTTCATTTGTCTACAGAGGAAG CCCTAGGTTCAACTACTATAGAAGAATTTTTTACTCCTAGTTTCTTC AATACAAACTTCTGGTATTTCTGGGCAACCATGTTTGCATTTGAAA AATGGCATAGTGTCGTTGAAGTAAAACGTTATATGGAAAGATTCAT GCATTTAATAGGTGGTATGAATAAATTAAAAGGTATACTTCACACT GAATATAATCAATATGATTCTTTAATACTTCCTCTTATTACATGGCT TAAAGATCAAGGTGTATGCTTTGATAGCTGCTGTAAAGCTACAGAT ATTGATTTTGATTTTACAAATAATCAAAAGATTGCAAAAGCAATTC

		ACTATACTAAAGATGGTAAAAATGAAATCATTAATGTAAATGAAG ATGATATTGTATTATTTACTAACGGATCTATGACAGAAAACACAAC AAGGGGCGACATTGATCATCCTGCTATTATAAATAGATCAGAAGAT AAAGGTTGTTTTAGTTTATGGGAAAAGCTAGCAAAGAAGTCACCTG ACTTTGGACACCCTGAAAAATTCTGTACTAATATAGATAAATCAAA ATGGATGTCCTTTACTGTTACCTTAAAGGATGATGACATTGTCTTCC CTCATATTTATAATCTTACAGGAGATAAGCCTGGTATGGGTGGTTT AGTTACAATAAAGGATTCTAACTGGTTTATGAGCTGGGTTGTACCA AAACATCCACACTTTATTAATCAACCTGATAACGTAAAAGTTCTTT GGGCATATGCATTAAATCTTGATGTACCAGGAAACTATATTAAAAA GACATATTCAGATTGTACAGGCCGTGAAATGTTTGAAGAACTCCTT TACCACATGGGATTAGAAGATAAGATTCCTGAAATTCTATCTCATA CAGTAAACGTAATTCCTAGCATGATGCCTTACATCACTGCACAATT TATGCCTCGTGTTCCAGGCGATAGACCTAATGTAATTCCAGAAGGA AGTAAAAACTTTGGTTTCCTAGGACAATTTGCAGAAGTTCCTGAAG ACTGCGTATTCACAGTAGAATATTCAGTAAGAAGTGCACTTATGGC TGTATATGGATTACTAGGTCTTGAGAAAACATTAGATCCTGTATAT CCAAGCAAATATGATATTCGTGTATTAATTAATGCAGCAAAAACTT GTCTTGGTATTGATAAACTTCCACTTAAGAATATACCACTAGGTGA ATTTTTTAAGAATACAGAAATTGAAAAATTACTATAA
46	WIL0057-HY37.1	ATGTATTACAGCAGTGGTAATTACGAAGCTTTTGCGAAACCTGAAA AGCCTGAAGGCATCGAGAAGAAGCATGCCTATATTGTTGGCTCTGG TCTGGCAGGTTTAGCTGCAGCTTGTTTTCTTATCAGGGATGCACAAA TGCCTGGTGAAAACATCACAGTCTTTGAATCTCTTCCAATAGCTGGT GGCTCTTGTGATGGTCTCCATGATCCACAAAAAGGCTATATTATGC GTGGTGGCAGAGAGATGGATAATCACTTTGAATGTATGTGGGATCT CTTTAGATCTATTCCATCCATTGTCAATCCAGGTGAAACCATTTTCT CTGAATACTACAAGCTCAACAAAGAAGATCCAAACTATTCCCTCTG TCGTGTGACAGAAAAACAAGGTCAGGATGCCCATACTGATCGCCA ATATGGATTAAACAAGAATGCTGAAAAACAGATTTTAAAGCTCATG CTTTCAACTGATGAAGAACTTGCCGACAAGAAGATTGATGATGTCT TTGATGAAGATTTCTATAAGACAAACTTCTGGATTTACTGGCAGAC AATGTTTGCCTTTGAAAAATGGCATTCCGCACTTGAAATGAAACTC TATATGCAAAGATATATTCATCATATCGATGGGTTACCAGACTTAA GTGCACTTCGCTTTACACGCTATAATCAGTATGAATCCATGATTCTT CCAATGTTGAAATATATTGAAGATGCTGGTGGAAAGATTGCCTATA ATACACAAGTGACTGATATCCAGTGTGAAACATCACCTACAAGAAA AGCTGCTCGTTATATTGCCTATGTGCAGGATGGTGTAGAAAAACAT CTTGAATTAACTGATGATGATTTTGTATTCATTACCAATGGTTCACA GGGAGATGGCAGTGCTTATGGTGATCAGACACATGCCCCAGAAATC ACAATCAAGAATGGTCAGGGACCTTCTATTGAACTCTGGAAGAAAT TGGCTGCTCAGGATGATGCTTTTGGACATCCTGATAAATTCTTCAAA GATATCAAGGAAACAAGCTGGGAAAGCTGGACTGTTGATACCGCA AATAAGCAGATCTTAAGTGCAATTGAGAAGATATGTCATCGTGATC CATTGAGCGGCAAGGTTGTTACTGGTGGTATTGTTACGGCAAAAGA TTCATCATGGCTTATGAGCTGGACAATTAATCGTCAGGGTCAATTC GTTGATCAGCCTGATGATCATTGCTTAATCTGGGTTTATGGCTTGAA TTGCTGGGATGATGATGGTGATTATGTACATAAGCCAATGTACAAA TGTACAGGTGAAGAATTATGTCAAGAATGGCTCTATCATATTGGTA TTCCAGTCGATGAGATTGATGAACTAGCCAAGCAATGTAATACAAC ACCATGTATGATGCCTTATGTCACATCTTTCTTTGAACCACGTGCTT ATGGCGATCGTCCATTAGTTGTACCTGTTGGCTCCGTCAATATCGCT TTTGTCGGCCAGTATGCCGAAACACCAAGAGATACAGTCTTTACAA CAGAATACTCCATTCGTACAGCCATGGAAGCTGTCTATACATTATG

		TAATGTTGATAGAGGCGTTCCTGAAGTATGGGGCTCAGTATTCGAT GTCCGTGAACTGATTAAGGCTGGCGTAAAGATGAATGATGGCAAG ATGATCAAAGAATGGCCATTACCAGCTAGTCAGAAGGCTGCCATAG CCGCCGCTTTCAAGCTGATCAATAATACAGAAATCTCTAAGCTACT GATTCGCTTAGGTGCAGCAGAGAAGAAAGATTTTGCCCCAATTGTT GAGATGCCAAAAGTCAAAGTAGAAGTGACTTCTAGAGTCTCTGAAC TCAAAGATTCTAAGACAGCTAAGATTGGTGCTGGTGTTACAGTTGC CTCCTTGATGGCTATTGCTGCATTGTTGCATAAAAAGAAATCTTAA
47	HMM consensus sequence of MCRA family	KKKAYLVGSGIASLAAAVYLIRDAKVPGENIHILEELKVAGGSLDGAG DPEKGYVLRGGRELEEHYECLWDLLSSIPSLEEPGASVLDEIEELNKED KNKSKARLVEKRGEEAVDDKKLGLSKKDRLELLKLLLTKEEKLEDKR IEDVFSEEFFESNFWLLWSTTFAFQKWHSALELRRYLRRFIHEISGLEDL SGLKRTKYNQYESLILPLVKYLKEQGVDFQFNTKVTDIEFEEEEEDKKT VTEIELEKEEGEEETIELEEDDLVFVTNGSITESSSLGDNDTPAKLEEKE ADESWELWKKLAAKSPKFGNPEKFCSDIEESKWESFTVTLKDEKLLER IEKLTKNEPGTGGLVTLKDSNWLLSIVVNRQPHFKEQPEDVTVLWGY GLFPEKEGDYVKKPMLECTGEEILEELLYHLGVPEEKIEELLKSSVNTIP CVMPYITALFLPRAKGDRPKVVPEGSKNLALIGQFVEIPRDTVFTVEYS VRTAQEAVY
48	CTR0001	MDTRAPKVGAGKSSRERARARGGAMYYSAGNFEAFAHPKKPEGLEN KSAYIIGTGLAALTAAFYLVRDAQMPGKNIHVFDKDVVPGGALDGAFI KGEGYVMRGGREMDNHFEVMWDVYRDVPSIEDPNVSMLDHYYWLN KEDPNYSKCRATKARGHNAHTDNKFNLSDKGCMEILKLYLASEDELA NKKITDYFDDEVLNSNFWLYWRTMFAFENWDSALEMHRYIHRFIHHI GGLPDFSALRFTRYNQYESMILPLMNYLKAHDVQFHMGTAVDDVTFA ISDHENGPVRNVFTNVSMDEAQRAQAENGAFPRNPYSTPNKKVAKTL VITDLVKNERKTIELTEDDFVFITNGGLVESTTEGDQNTPAGFDPTLKP GNGWDMWNRIAAVDPSFGHPEKFIYDPNLTKWMSATATTLDDTIPAY IEKITGRSPFGGHTVTGGIVTVEDSNWLMSWTVNRQQQFRNQPKDMIS AWIYGLFPDKPGNYIRKPMQDCTGMEICEEWLYHMGVPEEQIEELAK NHCNTVPVMMPYVDAFFMPRELGDRPDVVPDGAVNFAFIGQFAEEPR DTIFTTEYSMRTGMEAVYTLCDVDRGVPEVWNSEYDVRDMLNAAVK LRDGQPLTTFGRNNVERKAIAFALGRTRGTYIYDMLKVYGAIADPKHP VDMKPGMRFDESFNEADEQRLMQHAKEAEAEAFATPCSADAPVAAD TVDTVDTVAPAAAPDGALEPGENDSAK
49	CTR0002	MYYSSGNYEAFARPKKPAGVDSKHAYIIGTGLAALSSACYLVRDGQM PGDHIHILEKDPVPGGACDGLDIPGLGYVMRGGREMDNHFEVMWDLF RSIPSIETEGVSVLDEYYWLNKEDPNYSLCRATKDLGKDAGLKGKFGL SDKASMEIMKLFFTPDEDLYDKPITDFFDDEVLNSNFWLYWRTMFAFE NWHSALEMKLYIKRYIHHIGGLPDFSALRFTRYNQYESMILPMVKYLE SHGVEFRYNTKVENVEFAIGGGDGPKREHTGIGQDTIQKIQATSGFFKR NPASTPTKKLAVRIDVSQEGEKSSIDLTENDLVFITNGGCVENSTMGSQ NSPAAWNPDLKPGGGWDMWRRIAEQDPSFGHPEKFCSDPNATKWMS ATVTTLDDEIPPYIQKICKRDPFSGKVVTGGIVTVQDSNWLMSWTLNR QQQFRDQPKDQLCVWVYGLFPDKPGNYVKKPMTECTGEEICEEWLY HMGVPTDKIEPLAKHHANTVPVMMPYITAFFMPRAAGDRPDVVPDGA VNFAFLGQFAETPRDTIFTTEYSMRTGMEAVYTLLGVDRGVPEVWGS VYDVRNLLNATVKLRDGAPVTDMKLNFIEKAVVKKVLKKLDGTDIAT LLREYHVI
50	CTR0003	MYYSSGNYEAFARPKKPAGVDSKHAYIIGTGLAALSSACYLVRDGQM PGDHIHILEKDPVPGGACDGLDIPGLGYVMRGGREMDNHFEVMWDLF RSIPSIETEGVSVLDEYYWLNKEDPNYSLCRATKDLGKDAGLKGKFGL SDKASMEIMKLFFTPDEDLYDKPITDFFDDEVLNSNFWLYWRTMFAFE NWHSALEMKLYIKRYIHHIGGLPDFSALRFTRYNQYESMILPMVKYLE

		SHGVEFRYNTKVENVEFAIGGGDGPKREHTGVGQDTIQKIQATSGFFK RNPASTPTKKLAVRIDVSQEGEKSSIDLTENDLVFITNGGCVENSTMGS QNSPAAWNPDLKPGGGWDMWRRIAEQDPSFGHPEKFCSDPNATKWM SATVTTLDDEIPPYIQKICKRDPFSGKVVTGGIVTVQDSNWLMSWTLN RQQQFRDQPKDQLCVWVYGLFPDKPGNYVKKPMTECTGEEICEEWL YHMGVPTDKIESLAKHHANTVPVMMPYITAFFMPRAAGDRPDVVPDG AVNFAFLGQFAETPRDTIFTTEYSMRTGMEAVYTLLGVDRGVPEVWG SVYDVRNLLNATVKLRDGAPVTDMKLNFIEKAVVKKVLKKLDGTDIA TLLREYHVI
51	CTR0004	MYYSSGNYEAFARPKKPADVDNKHAYIIGTGLAALSAACYLVRDGQ MPGENIHILEKDPVPGGACDGLDIPGLGYVMRGGREMDNHFEVMWD LFRSIPSIETEGVSVLDEYYWLNKEDPNYSLCRATKNLGKDAGLKGKF GLSDKASMEIMKLFFTPDEDLYDKPITDFFDDEVLNSNFWLYWRTMF AFENWHSALEMKLYIKRYIHHIGGLPDFSALRFTRYNQYESMILPMVK YLESHGVEFRYNTKVENVEFAIGGGAGPKREHTGVGQDTIQKIQATSG FFKRNPASTPTKKLAVRIDVDHEGDKSSIDLTENDLVFITNGGCVENST MGSQNSPAAWNPDLKPGGGWDMWKRIADQDPSFGHPEKFCSDPNAT KWMSATVTTLDGEIPPYIQKICKRDPFSGKVVTGGIVTVQDSNWLMS WTLNRQQQFRDQPKDQLCVWVYGLFPDKPGNYVKKPMTECTGEEIC EEWLYHMGVPTDKIEALAKHHANTVPVMMPYITAFFMPRAAGDRPD VVPDGAVNFAFLGQFAETPRDTIFTTEYSMRTGMEAVYTLLGVDRGV PEVWGSVYDVRNLLNATVKLRDGAPVTDMKLNFIEKAVVKKVLKKL DGTDIATLLREYRVI
52	CTR0005	MSSNLSHKAYMIGAGIGNLSAAVYLIRDGEWNGEDITIMGLDMHGAN DGESAATFQHQYGHRELGNDAGFINRGGRMLNEETYENLWDVLSAV PSLDNPGKSVTDDILDFDHAHPTHDVARLIDRDGIRNKGENDYKHMQF DNKDRYLLTKLMTMPESDEAKLDDISIEQWFEETPHFFTTNFWYMWE TTFAFKRVSSAMELRRYMNRMILEFSRIQTLAGVTRSPYNQYESIILPM RTFLEGKGVKFVNELKITEFVFKDTPLRDEIIVTGLDYENVRTGEKGRI DVAEGDFVFDTNGSITDSSSIGDLDTPIVEDMRYAPSALLWKQATEHF YDLGNPDKFFGDRAQSEWTSFTVTTSSHELINEISRITKQLPGNALNTF VDSNVLLSIVVHHQPHYHAQKENEGVFWGYCLFPRKDGDYVKKPFIE MTGREMLEETLGHLEALDESGTLAARRQEIMDSVVNSIPSHMPYASAL FNRRAVGDRPLVVPKHSKNLAFISQFAELPFDMVFTEQYSVRCAQVAV YKFLGIPEDKLTKMHHYEKDPKVLAKAAVTMFR
53	CTR0006	MYYSNGNYEAFARPKKPEGVDGKSAYLIGSGLASLSAACFLIRDGQM KGENIHILEELDISGGSLDGILNPTRGFIIRGGREMEDHFECLWDLFRSIP SLEVDNASVLDEFYWLNKEDPNYSKCRLIKDRGQRLEDDGKFTLSDQ SSEEMIKLFFTPEEKLEDKKITDVFSEEFFESNFWLYWSTMFAFEKWHS AMEMRRYIMRFIHHIGGLPDLSALKFTKYNQYESLVLPMIKYLEGHDV DFQYNTVVENVLVDKVGDKKVAHTLVLRKNGVKENIELTENELVFVT NGSITESTTYGDNYTPAPVNKELGGSWSLWKNIAAQDTDFGRPEKFCD NLPKESWFVSATLTTLDDRVAPYIEKISKRDPYAGKVVTGGIVTATDS NWMLSYTLNRQPHFKHQPKDQLVVWIYGLLSNKPGDFIKKSITECSGI EIAQEWLYHMGVPVDEIPDIAQNSCNTIPCYMPYITSYFMPRAMGDRP LVVPEGSANLAFIGNFSETVRDTVFTTEYSVRTAMEAVYQLLNIDRGV PEVFASSFDVRTLLASTARLLDGKKLTDIDAPFILKQIGKLGIHKTKDTII YDLLKESKLI
54	CTR0007	MYYSNGNYEAFARPKKPEGVDEKSAYLIGSGLASLSAACFLIRDGQM KGENIHILEELDISGGSLDGILNPTRGFIIRGGREMEDHFECLWDLFRSIP SLEVENASVLDEFYWLNKEDPNYSKCRLMKDRGQRLEDDGKFTLSDK SSEEMIKLFFTPEEKLEDKKITDVFSDEFFESNFWLYWSTMFAFEKWHS AMEMRRYIMRFIHHIGGLPDLSALKFTKYNQYESLVLPMIKYLESHDV DFQYNTVVENVLVDKVGDKKVAHTLVLRKDGVKKNIELTENELVFV

		TNGSITESTTYGDNNTPAPINKDLGGSWSLWKNIAAQGEEFGRPEKFC DNLPEESWFVSATLTTLDDRVAPYIEKISKRDPYAGKVVTGGIVTATDS NWMLSYTLNRQPHFRNQPKDQLVVWIYGLLSNKPGDFIKKSITECTGI EIAQEWLYHMGVPVDEIPDIAQNSCNTIPCYMPYITSYFMPRAMGDRP LVVPEGSANLAFIGNFSETARDTVFTTEYSVRTAMEAVYQLLRIDRGV PEVFASAFDVRTLLASTARLLDGKKLTDIEAPFILKQIGKLGIHKTKDTII YDLLKESKLI
55	CTR0008	MYYSNGNYEAFAKPKKPAGVDKKSAYLVGSGLASLAAAAFLVRDGQ MKGERIHILEELPIAGGSLDGIMNPTRGFIIRGGREMEDHFECLWDLFRS IPSLEVEDASVLDEFYWLNKEDPNFSKCRVIENRGQQIPNDGLFALSDK SSQELVKLYLTSESELQGMKITDFFSSEFFESNFWTYWATMFAFEKWH SVAEMRRYMLRFIHHIKGLPDLSALKFTKYNQYESLVLPLVKYLESHG VTFEYNTVVKDIKVEKQGKDLVAKHLILEVNGEPVVRELTEDDLVFVT NGSITASTTYGNNDTSAPVSKELGGAWQLWKNLAKQDERFGRPEVFC ENLPDQSWFVSATTTVTDKRIAEYIEKICKRDPYAGKVVTGGIVTARD SNWMMSFTLNRQPHFKSQSKDELVVWIYGLYSNISGNYIKKPIEACTGI EIAEEWLYHIGVPEQFIHEFASKGCSTVPCYMPYITSYFMPRHDGDRPL VIPEGSKNLAFIGNFSETPRDTVFTTEYSVRTAMEAVYTLLDVDRGVPE VFNSAYDLRVMTKSTNRLMDGKKLEEVKLPFFAKAISKRVLKKIKGT YIEEILKDAGLI
56	CTR0009	MYYSNGNYEAFARPKKPEGVDNKSAYLVGSGLASLAAASFLIRDGQM KGENIHILEELDLPGGSLDGILNPERGYIMRGGREMENHFECLWDLFRS VPSLEVEDASVLDEFYWLNKEDPNYSKCRVIENRGQRLESDGKMTLT KKANKEIIQLCLMKEEQLNDVKISDVFSKDFLDSNFWIYWKTMFAFEP WHSAMEMRRYLMRFIHHIGGLADFSALKFTKFNQFESLVMPLIEHLKA KNVTFEYGVTVKNIQVECSKESKVAKAIDIVRRGNEESIPLTENDLVFV TNGSITESTTYGDNDTPAPPTSKPGGAWQLWENLSTQCEEFGNPAKFY KDLPEKSWFVSATATTNNKEVIDYIQKICKRDPLSGRTVTGGIVTVDDS NWQLSFTLNRQQQFKNQPDDQVSVWIYALYSDERGERTNKTIVECSG KEICEEWLYHMGVPEEKISALAAECNTIPSYMPYITAYFMPRKEGDRPL VVPHGSKNIAFIGNFAETERDTVFTTEYSVRTAMEAVYKLLEVDRGVP EVFASVYDVRILLHALSVLNDGKKLDEIDMPFYERLVEKRLLKKASGT FIEELLEEANLI
57	CTR0010	MYYSYGNYEAFARPKKPENVENKSAYLIGSGLASLAAACFLIRDGQM EGSKIHILEELPKAGGSLDGENMPLKGYVVRGGREMENHFECLWDLF RSIPSLEIDNASVLDEFYWLNKEDPNYSRCRVIEKQGQRLVTDGDFTLT KTAIKEILDLCLTNEEDLDDVKITDVFSDDFFNSNFWIYWKTMFAFEP WHSAMEMRRYLMRFVHHIGGLADFSALKFTKYNQYESLVLPMVEYL KSHGVQFEYDVKVEDIKVDVTTSQKIAREILIHRHGKAESIKLTVDDLV FVTNGSITESSTYGDNDTPAPPTDELGGSWTLWKNLARQSPEFGNPDK FCQNIPKKSWFVSATSTTNNKEIIDTIESICKRDPLAGKTVTGGIITINDS AWQMSFTINRQQQFKDQPENEISTWIYALYSDVNGDYIKKPITECSGN EICQEWLYHLGVSTDKIEDLAKHVSNTIPVYMPYITSYFMTRAIGDRPL VVPHQSQNLSFIGNFAETERDTVFTTEYSVRTAMEAVYQLLNIDRGIPE VINSTFDLRVLMDAVYELNDHQDLREITKDSKMQKLALAGFLKKIKG TYIETLLKEHKLL
58	CTR0011	MIKHKAIMIGAGLANMAAAVYLIQEAHWQGDQITFYSLDDHGSNDGA PTVDTVDEYWNKNHPMENTKGYVARGGRMLNYRTYVDLMDLLSRIP SATEPGLTAEEDTRQFDAQHRTFDKARLMEGGIGIIQAGHLGLNNTDR LLLTKLIMMPDSEEEKLDNVSIADYFKDDPHMFQTNFWYMWETTFAF RTQSSAQELRRYMHMMIYEFTQIEHLVGVNRTRYNQFESIMLPLINYL KEQGCKIILNRRVTAFEFEDTAMTDEITVTGLTILNTETDDEEHVTVDD DTAVFFTNGSITDSATQGDFDHAAVENMDYGAAASLWKQATEHFYN LGNPDKFFADRSASEWVSFTLTTKDHLLLNEIERITTQVPGNALNSFMS

		TQPITALGQKDVMMSIVVHHQPHFTTQKPNETVLWGYFLYPRRYGEF VNKPYIEMTGKEMALELIGQLAKVDPGPGNIRDHQDEIMASIINNIPVY MPYASALFNNRAKVDRPDVIPAHSTNLAFTGEFAEQPFQMVFTEQSAV RSGEIAAYHFTGIPMSHLVKTPRYDKDIKTLMRATKKMFE
59	CTR0012	MIKHKAIMIGAGLANMAAAVYLIQEGHWQGDQITFYSLDDHGSNDGA PAEETADEYWNKYHPMENTKGYVARGGRMLNYRTYVDLMDLLSRIP SATEPGLTAEEDTRQFDAQHRTFDKARLMEGGIGIIQAGHLGLNNKDR LLLTKLIMMPDSEEEKLDNVSIADYFKDDPHMFQTNFWYMWETTFAF RVESSAQELRRYMHMMIYEFTQIEHLVGVNRTRYNQFESIMLPLINYL KDQGCRIILNRRVTAFEFKDTAMTDEITVTGLKMLNTETDKPEHVVVD DDTAVFFTNGSITDSATQGDFDHPAVENMDYGAAASLWKQATDHFY NLGNPDKFFADRAASEWVSFTLTTKDHLLLNEIERITTQIPGNALNSFL STQPITALGQKDVMMSIVVHHQPHFTTQKPNETVLWGYFLYPRRYGE FVNKPYIKMTGKEMALELIGQLAKVDPGPGNIRDRQDEIMASIINNIPV YMPYASALFNNRAKVDRPEVIPAHSTNLAFTGEFAEQPFQMVFTEQSA VRSGEIAAYHFTGIPMSHLVHTPRYDKDIKTLMRATKKMFE
60	CTR0013	MGALFMVKSKAIMIGAGLSNMAAAVYLIQDGHWDGKDITFYGVDMH GANDGGATTDFTNEYWNKNHPMANTTGYVARGGRMLNYRTYVDL MDLLDRIPSVTEPGMTAAEDTRDFDAKHRTYDIARLMQGGKGIINAG KLGFNNKDRTLLTKLIMMPDSEETKLDNVSIAEYFKDDPHMFQTNFW YMWETTFAFRTQSSAQELRRYMHQMIYEFTQIEHLVGVNRTRYNQFE SMILPLIKYLQGQGVTFIDNKIVKDWQFKDTPMQDEITVTGLVIEDAQT GETEEVEVDEDTAVIFTNGSITDSATMGDYNTPAPENMDYGVSASLW KKATERFYNLGTPDKFFNDRNASEWVSFTLTTKNHLFLNEIVRITTQEP GNALNSFLSTTPITPLNQKDVNMSIVVHHQPHFTTQQPNETVLWGYFL YPRRQGEFVNKPYIKMTGKEMAQELIGQLSKVDPGPGNIKDKEKENL DSIVNNIPVYMPYASALFNNRAKSDRPEVLPKHSTNLAFTGEFAEQPY QMIFTEQSAVRSGEIAAYHFAGVPMDNLVKTPRYDKDPKTLLKATKK MFD
61	CTR0014	MGALFMVKSKAIMIGAGLSNMAAAVYLIQDGHWDGKDITFYGVDMH GANDGGATTDFTNEYWNKNHPMANTTGYVARGGRMLNYRTYVDL MDLLDRIPSVTEPGMTAAEDTRDFDAKHRTYDIARLMQGGKGIINAG KLGFNNKDRTLLTKLIMMPDSEETKLDNVSIAEYFKDDPHMFQTNFW YMWETTFAFRTQSSAQELRRYMHQMIYEFTQIEHLVGVNRTRYNQFE SMILPLIKYLQGQGVTFIDNKIVKDWQFKDTPMQDEITVTGLVIEDAQT GETEEVEVDEDTAVIFTNGSITDSATMGDYNTPAPENMDYGVSASLW KKATERFYNLGTPDKFFNDRNASEWVSFTLTTKNHLFLNEIVRITTQEP GNALNSFLSTTPITPLNQKDVNMSIVVHHQPHFTTQQPNETVLWGYFL YPRRQGEFVNKPYIKMTGKEMAQELIGQLSKVDPGPGNIKDKEKEILD SIVNNIPVYMPYASALFNNRAKSDRPEVLPKHSTNLAFTGEFAEQPYQ MIFTEQSAVRSGEIAAYHFAGVPMDNLVKTPRYDKDPKTLLKATKKM FD
62	CTR0015	MYYSNGNYEAFADPKKPAGVDKKSAYIIGSGLAGLSTAVFLVRDAQM KGENIHILEELPVAGGSLDGADRPNAGFVVRGGREMENHFECLWDMY RSIPSLEVPGASYLDEYYWLDKEDPNSSNCRLIYNRGDRLPSDGQYGL GKCANEIVKLIMTPEKEIEGQTIEEFFSDEFFKTNFWTYWSTMFAFEKW HSLAEMRRYAMRFIHHIDGLPDFTALKFNKYNQYESMVKPLLAYLKD HGVQFEYDCHVKNVEVDHEGDSKIAKKIVMTQNGKDKEIDLTHNDIV FVTNGSITESSTYGDQNTPAPITNAKGDSWKLWENLAKQDPAFGHPDV FCENLPERSWFVSATATLENKKLAPYFERLTKRSLYDGKVNTGGIITIV DSNWELSFTIHRQPHFKSQNPDQIVVWIYALYSDTEGNYIKKRIVDCTG KEIAEELLYHLGVPESQISELASEENMNTVPVYMPYITSYFMPRRDGDR PDVVPEGSINLAFIGNFAESPTRDTVFTTEYSVRTAMEAVYTLLNVDRG

		VPEVFDSIYDIRQLLRAMYYMSDKKKLADQDMPLPEKLAVKTGMRKI KKTWVEELLKEANLV
63	CTR0016	MYYSNGNYEAFADPKKPAGVDKKSAYIIGSGLAGLSTAVFLVRDAQM KGENIHILEELPVAGGSLDGADRPNAGFVVRGGREMENHFECLWDMY RSIPSLEVPGASYLDEYYWLDKEDPNSSNCRLIYNRGDRLPSDGQYGL GKCANEIVKLIMTPEKEIEGQTIEEFFSDEFFKTNFWTYWSTMFAFEKW HSLAEMRRYAMRFIHHIDGLPDFTALKFNKYNQYESMVEPLLAYLKD HGVQFEYDCHVKNVEVDHEGDSKIAKKIVMTQNGKDKEIDLTHNDIV FVTNGSITESSTYGDQNTPAPITNAKGDSWKLWENLAKQDPAFGHPDV FCENLPERSWFVSATATLENKKLAPYFERLTKRSLYDGKVNTGGIITIV DSNWELSFTIHRQPHFKSQNPDQIVVWIYALYSDTEGNYIKKRIVDCTG KEIAEELLYHLGVPESQISELASEENMNTVPVYMPYITSYFMPRRDGDR PDVVPEGSINLAFIGNFAESPTRDTVFTTEYSVRTAMEAVYTLLNVDRG VPEVFDSIYDIRQLLRAMYYMSDKKKLADQDMPLPEKLAVKTGMRKI KKTWVEELLKEANLV
64	CTR0017	MHYSSGNYEAFVNASKPKDVDQKSAYLVGSGLASLASAVFLIRDGHM KGDRIHILEELSLPGGSMDGIYNKQKESYIIRGGREMEAHFECLWDLFR SIPSAENKDESVLDEFYRLNRKDPSFAKTRVIVNRGHELPTDGQLLLTP KAVKEIIDLCLTPEKDLQNKKINEVFSKEFFESNFWLYWSTMFAFEPW ASAMEMRRYLMRFVQHVSTLKNLSSLRFTKYNQYESLILPMVKYLKD RGVQFHYNTVVDNIFVNRSNGEKIAKQILLTENGEKKSIDLTENDLVFV TNGSITESTTYGDNLHPASEEHKLGATWKLWQNLAAQDDDFGHPDVF CKDIPKANWVMSATITFKNNDIVPFIEAVNKKDPHSGSIVTSGPTTIKDS NWLLGYSISRQPHFEAQKPNELIVWLYGLFSDTKGNYVEKTMPDCNGI ELCEEWLYHMGVPEERIPEMASAATTIPAHMPYITSYFMPRALGDRPK VVPDHSKNLAFIGNFAETPRDTVFTTEYSVRTAMEAVYTLLNIDRGVP EVFASAFDVRMLMNAMYYLNDQKKLEDLDLPIAEKLAIKGMLKKVK GTYIEELLKKYKLV
65	CTR0018	MHYSNGNYEAFVKADKPKDVDQKSAYIVGSGLAALATAVFLIRDGQ MKGEKIHIFEELGLPGGSMDGIYNKEKESYIIRGGREMEPHFECLWDLF RSIPSPDHEGESILDSFYRLNRKDPSYAKTRVIVNRGQALPTDGQLLLTP KAVKEIVDLCLTPEKDLQNKKINEVFTKEFFESNFWLYWSTMFAFEPW ASAMEMRRYLMRFVQHVATLKNLSSLRFTKYNQYESLILPLVKYLKD RGVIFHYNTVVDNIFVNRSDGEKVAKQIILTEDGEKKTIDLTPNDLVFV TNGSITESTTYGDQLHPAPAEHELGASWQLWKNLAAQDEDFGHPDVF CKDIPKANWRMSATITFKNDDVVPFIEAVNKKDPHSGSIVTSGPTTIKD SNWLLGYSISRQPHFKAQKPNELIVWLYGLFSDTKGNYVEKTMPDCN GLEMCEEWLYHMGVPEERIPEIAAAATTIPVHMPYITSYFMPRALGDR PKVVPEHSKNLAFIGNFAETPRDTVFTTEYSVRTAMEAVYTLLDIDRG VPEVFASAFDVRMLMNAMYYLNDQKKLVDLDLPMPEKLAIKGMLKK VKGTYIEELMKKYKLI
66	CTR0019	MYYSNGNYEAFTDARKPKDADKKSAYVIGGGLAGLAACVFMIRDGH MDGKKIHLLEEEALAGGSLDGTKRPEYGYIIRGGREMENHFECLWDM YRSIPSLEIPGASYLDEYAWLDKDDPNSSNCRLIHHRGDRVPTDGQYG LGKCAGEIVKLIMTPEDKLEGISIEDFFSDEFFETNFWAYWATMFAFEK WHSVIEMRRYAMRFIHHIDGLPDLSALKFNKYNQYESMTKPLLAYLES HDVDICYNTQVENVVVDTSNGEKVAKKLILTRDGEHQEIDLTPDDLV YVTNGSIVESSTYGTHHTPAPITHKLGGSWHLWQNLAEQDEAFGHPEV FCENIPERAWFVSATMTMKDATLEPYFERLTKRDIHQHRVNTGGIITVT DSNWMLSFTIHRQPHFKDQKENETVVWIYALYSDTPGNYIKKRVVDC TGEEITEELLYHLGVPDDLIKKYAGDDYVNTVPVYMPYITAYFQMRK KGDRPAVVPAGSVNLAFIGNFAESPTRDTVFTTEYSVRTAMEAVYTLL NVDRGVPEVFDSVYDIRELLKATYYLNDKKPIDQMDLPLPKIVVKGA MKKVQGTWLEELLKEAKLLE

67	CTR0020	MHYSNGNYEAFVKAEKPKDVDQKSAYIVGSGLAALASAVFLIRDGQ MKGNRIHIFEELALPGGSMDGIYNKEKESYIIRGGREMEPHFECLWDLF RSIPSTEHEGESILDEFYRLNRKDPSYAKTRVIINRGEALPTDGQLLLTP KAVKEIIDLCLTPEKDLQNKKINEVFTKEFFQSNFWLYWSTMFAFEPW ASAMEMRRYLMRFVQHVATLKNLSSLRFTKYNQYESLILPMVKYLKG HGVQFHYDTVVDNIFVNRSDGKKVAKQIVLTEKGERKTIDLTENDLVF VTNGSITESTTYGDNFHPAPAEHELGASWQLWKNLAAQDEDFGHPEV FCRDIPKANWRMSATITFKNDDIVPFIEAVNKKDPHSGSIVTSGPTTIKD SNWLLGYSISRQPHFKAQKPNELIVWLYGLFSDTKGNYVEKTMPDCN GIELCEEWLYHMGVPEERIPEMAAAATTIPAHMPYITSYFMPRALGDR PKVVPDHSKNLAFIGNFAETPRDTVFTTEYSVRTAMEAVYTLLDIDRG VPEVFASAFDVRMLMNAMYYLNDQKKLEDFDLPMPEKLVIKGILKKV KGTYVEELMKKYKLI
68	CTR0021	MHYSNGNYEAFINAEKPKDVDNKSAYIVGSGLAALAAAVFLIRDGHM KGDKIHVLEELALPGGSMDAIYNVADQAYVMRGGREMEPHFETLWD LFRSIPSLDYPDQSVLDEFYRENRKDPCYSKTRVIENRGQELPTDGDLL LSPKAVKEILNLVMTPEKDLQDKKINEVFDDEFFKSNFWLYWQTMFA FMPWASAMEMRRYLMRFVQHVATLKNLSSLRFTKYNQYEDLIMPLIS YLKKHGVKFHYDTIVDNIIVNRTEDEKVATEIKMTEKGEPKVIKLTPN DLVFVTNGSITESTTYGDNTHPAEQKHELGPSWQLWKNLAAQDEDFG HPEKFCENIPAANWVISATVTFTNDDIVPYIEKVNKKDPHSGSIVTSGPT TIKDSNWLLGYSISRQPQFHKQKPNELIVWLYGLYSNTKGNYVKKTM PECDGIELCEEWLYHMGVPESEIKKMAIDATTIPNHMPYITSYFMPRAL GDRPKVVPKNSKNLAFIGNFAETERDTVFTTEYSVRTAMEAVYTLLNV DRGVPEVFASAFDVRMLMNAMYYLNDRKKLTELDLPLPEKLMVKEG LKKVKGTYVEELLKKYKLI
69	CTR0022	MHYSNGNYEAFVHASKPKDVDKKSAYIVGSGLASLATATFLLRDAQ MKGEKIHILEELSLPGGSMDGIYDQVKQSYIIRGGREMETHFETLWDLF RSIPSLDNPGETVLDEFYRLNRKDPSFSKTRVIVNRGEELPTDGQLLLTP KAVKEIVNLCLTPERDLQDKKINEVFSREFFESNFWLYWATMFAFEPW ASAMEMRRYLMRFVQHVATLKDLSSLRFTKYNQYESLILPMVKFLKD HGVQFHYDTVVNNIIVNRSNGAKVAEEIKMTENGEEKSIKLSPDDLVF VTNGSITESTTYGDNLHPADEHHEFGASWQLWKNLAAQDSDFGHPEK FCENIPKANWVMSATVTFKNDDIVPFIEKINKKDPHSGSIVTSGPTTIKD SNWMLGYSISRQPHFHKQKPNELIVWLYGLYSDTNGNYVKKTMPECN GIELCEEWLYHMGVPDEKISEMAHAAVTIPAHMPYITSYFMPRALGDR PKVVPEKSKNLAFIGNFAETERDTVFTTEYSVRTAMEAVYTLLDIDRGI PEVFASAFDVRMLMNAMYYLNDQKKLTELDLPLPEKLAIKGMLKKV KGTYIEDLLKEYRLM
70	CTR0023	MYYSKGNYEAFADTKKPAGVDKKSAYIIGSGLAGLSAAFFLVRDAKM SGDKIHILEELDVAGGSLDGTNRPNAGFVVRGGREMEDHFECMWDM YRSVPSLRIPGASYLDEYYWLDKEDPNSSNCRLIHKRGNELPTDGLYQ LGSHASEIVKLVLTPESELQGKTIEEWFSPEFFETNFWTYWSTMFAFEK WHSLAEMRRYCMRFIHHIDGLPDFTALKFNKYDQYDSMVKPLLKYLK DHGVKFEYGVQVENVLVDHEGNEKVAKKIVMKKNGKQEDIDLTEDD IVFVTNGSITESSTYGNQTTPAPITHAKGGSWKLWENLAKQDPAFGHP DVFSENLPEKSWFVSATTTLKNKKVAPYFERLTKRSLYDGKVNTGGII TVTDSNWGLSFTIHRQPHFPTQKPNEIVVWIYALYSDTEGNYIKKKVID CTGQEIAEEMLYHLGVPESEIKELSSEENMNTVPVYMPYITSYFMPRH DGDRPAVVPEGSKNLAFIGNFAESPTRDTVFTTEYSVRTAMESVYTLL NVDRGVPEVWSSVYDIRELLRAMYYMSDKKKLADQEMPLPEKLAVK AGMKKIKGTWIEELLEEANLI
71	CTR0024	MVKTKAVMIGAGLSNMAAAVYLIQEGHWRGENITFYGADMHGAND GGETSEFSDEYWNKAHPLANSTGYVARGGRMLNYRTYVDLMDLLDR

		IPSATEAGMTAAEDTRDFDAHHRTYDIARLMEGGKGIIDGGKLGLNNK DRVLLSKLVLMPDEEETKLDNITIAEYFKDDPHMFQTNFWYMWETTF AFRIQSSVQELRRYMHQMIYEFTQIEHLVGVNRTRYNQFESMMLPLIN YLKDEGVTFISNRIVTDWEFADSAMQDEITVTGLHVKNVEDDTEEVV KIDDDTAVIFTNGSITDSATMGDYNTPAPENMEYGISAALWKKATERF YNLGTPDKFFDDRKNSEWVSFTLTTKIHLLLNEITRITTQVPGNALNSF LSTTPITPLGQKDVNMSIVVHHQPHFTTQKPNESVIWGYFLYPRRQGEF VHKQYIKMTGKEMAQELIGQLSKVDPGPNNIKNHEAEILDSIINNIPVY MPYASALFNNRAKSDRPEVIPAHSTNLAFTGEFVEQPYQMIFTEQSATR SGEIAAFLFAGVPMDNLVDTPRYDKDPQTLLKATKRMFS
72	CTR0025	MVKTKAVMIGAGLANMAAAVYLIQEAHWQGDQITFYGADMHGAND GGPTGDFTNEYWNKAHPMDNQTGYVARGGRMLNYRTYVDLMDLLD RIPSVTESGMTAAEDTHDFDAHHRTYDKARLLQGGKGIIDGGKLGLN NKDRVLLSKLVMMPDDEETKLDNVSIADYFKDDPHMFQTNFWYMW ETTFAFRVQSSAQELRRYMHQMIYEFTQIEHLVGVNRTRYNQFESMM LPLIKYLEGQGVTFLDNRIVTDWDFANSELQDEITVTGLHVKNLETGD EDVVPIDGDTAVIFTNGSITDSATMGDYNTPAPENMEYGISAALWKKA TEHFYNLGTPDKFFNDRKSSEWVSFTLTTKNHLLLNEITRITTQVPGNA LNSFLSTTPITPLGHKDVNMSIVVHHQPHFTTQKPNESVIWGYFLYPRR TGEFVHKPYIKMTGKEMAQELIGQLAKVDPGPNNIKDKEPEILDSIINNI PVYMPYASALFNNRAKTDRPEVIPAHSTNLAFTGEFAEQPYQMIFTEQ SAVRSGEIAAYHFAGISMDNLVDTPRYDKDPKTLLRATKKMFS
73	CTR0026	MYYSNGNYEAFARPRKPAGVDKKHAYIVGAGLAGLSAAVFLIRDAQ MPGENIHIFEELPIAGGSLDGQDRPDVGFVTRGGREMENHFECMWDM YRSIPSLEIPGASYLDEYYWLDKDDPNSSNCRLTYKRGNEVPTDGKYL LGKSTKELMKLILTPEDQLGDLTIGDYFSEDFFKSNFWIYWSTMFAFEK WHSLAEMRRYAMRFIHHIDGLPDFTALKFNKYNQYESMTKPLLAYLK DHGVKFEYDTQVQNVLVDTKNGEKHAKKIILKQGGEDKTINLTDDDL VFVTNGSITESSNYGSHHQVAQPTRALGGSWKLWENLAKQSPAFGHP DVFCKNIPNRSWFISATATVKNPQIEPYIERLTKRDLHDGKVNTGGIITV TDSNWMMSWTILRQPHFKSQKPNETIVWIYGLYSDTEGNYIKKRIVDC TGEEITKEWLYHLGVPEALIDDLAKEESVNTVPVYMPFVTSYFMPRVK GDRPDVVPKGSANLAFIGNFAESPTRDTVFTTEYSVRTAMEAVYSLLN VDRGVPEVFNSIYDIRELMRAMYYMNDKKPLEEMDLPIPKIVEKPLLK KIKKNWIGELMEEQHLL
74	CTR0027	MYYSNGNYEAFARPKKPANVDQKSAYLVGSGLASLAAATFLVRDGQ MAGDRIHVLEELGLPGGSMDGIWNEQKGYIIRGGREMEPHFETLWDL FRSIPSLENEDVSVLDEYYWLNKEDPSFSKARVIENRGQRMASDGKLT LSRKAINEIIKVALTPEDQLQDKQIDEVFSQEFFDSNFWLYWSTMFAFE PWASALEMRRYLLRFVHHIATLSDLSSLRFTKYNQYESLIIPMVKFLES KGVHFQYNTTVDNILVNRVGTGKVATKLEMTVDGKHESKKLTADDL VFVTNGSITESTTYGDNTHAAPVEHELGATWQLWKNLAAQDPDFGHP EKFYDNIPDANWTISGTITFNDDRVTPYIEKISQKDPHSGSIVTSGPVSIK DSNWLLGYSISRQPHFKAQKPNELVVWVYGLFSDKPGNFVDKKITECT GIELCEEWLYHIGVPEDQIVDIATNSASTIPAHMPYITSYFMPRALGDRP LVVPEGSVNLAFIGNFAETERDTVFTTEYSVRTAMEAVYTLLNVDRGV PEVFDSAFDARVLMNAIYYLNDKKKLEDIQLPFAEKAIEKQVLRKIKG TYIEELLKNAHLL
75	CTR0028	MRYTNGNYEAFVRPRKPQEADKKSAYIVGAGLAGLAAAVFLIRDGQV PGNRIHILEELSLSGGSLDGSFIPHDGFVIRGGREMENHFECLWDLFHSI PSLEVENASVLDEFYYLDKDDPNSSNCRIIANRGERVADDGQFTLSRQ AQDEIVKLFMAQEESLVGKKIEDVFSEEFFESNFWLYWCSMFAFEKW HSAIEMRRYIMRFIHHIKGLPDFTALKFTKYNQYESLVKPLLAFLKDQG VIFQYEAQVENIEVDFSNNKKVAKKIIFADGKVQDLTEDDLVFVTNGSI

		TESSTQGSPTEAAPITKDLGGSWKLWKNLAAQSPEFGKPEVFYDNLPD ESWFVSATVTWKNLKIQPYFEKLTHRELRSGKVLTGGIITIKDSNWLM SFTTHRQPHFKEQKEGETVTWVYGLLSNTPGNYIKKPIEKCTGEEITQE LLYHLGMPESEIEEFVKENTNTIPVYMPFITSYFMLREPGDRPQVLPENS VNLAFIGNFAETERDTVFTTEYSVRTAMEAVYQFLNVERGVPEVFASA YDLRTLARSVYYLSDKKKLMEMDLPLLKKESLKFGLKKIKGTYLEDIL KDAGLL
76	CTR0029	MYYSNGNYEAFARPKKPENVDQKSAYIVGSGLAALSTAVFLVRDAQ MPGDHIHILEELKLPGGSMDGIKNDRLGYIIRGGREMEPHFEVLWDLF RSIPSLENPENSILDEFYWLNKEDPCYAKTRVIHDRGKAIPNDGQLTLS EKAIKEIISLILTPESKLANVQIDQVFTDEFFKSNFWLYWCTMFAFEPWS SAMEMRRYLMRFIQHVGCLKNLSSLRFTKYNQYESLILPIVHYLTEHG VDFSYNTTVTNILVNRKGQDKVATKIEFSKDGQAKELFLTPDDLVFVT NGSITESTTYGDNDHPAPVEHDLGASWELWKKLAAQDDSFGHPEVFC QNIPDANWTISATITFKDKRIAPYIEAVNHKDPYSGSIVTSGPTSIKDSN WLLGYSISRQPHFKTQKDNELVVWLYPLYTDRKGNFVDKRPDQCSGK ELCQEWLYHMGVPEADIKEMAESASTIPCHMPYITTYFMPRGLNDRPL VVPEHSKNLAFIGNYAETPRDTVFTTEYSVRTAMEAVYTLLKVDRGVP EVFASAFDVRMILNALYYLNDQKSLTEIDIPWTEKAVLKESLKKIHGT YIEELLKEYHLL
77	CTR0030	MYYSNGNYEAFAHSQKPENVDGKSAYIVGSGLAALSTAVFLIRDGQM AGERIHILEELSLPGGSMDGIRNERLGYIIRGGREMEPHFEVLWDLFRSI PSLENPKHSILDEFYWLNKKDPSFAKTRAIYERGKAIPDDGQLTLSQKA VKEIFDLVLTPESHLQDVQIDQVFSEDFFNSNFWLYWSTMFAFEPWAS AMEMRRYLMRFIQHVGTLKNLSSLKFTQYNQYESLILPLVAFLKDHN VNFSYQTVVTNILVNRSGSDKLATKIEMTVNGQEKSIALSRDDLVFVT NGSITESSTYGNNNHPAPLTHDLGASWQLWKNLAAQDSDFGCPEKFC ENIPDANWTMSATITFTDQRIAKYIEQINQKDPYSGSIVTSGPTSIKDSS WLLGYSISRQPHFKEQKKNELVIWLYALYTDRKGDYVAKRPDECTGIE MCEEWLYHIGVPENTIHELACSASTIPCHMPYITTYFMPRTTNDRPLVV PKHSKNLAFIGNYAETPRDTVFTTEYSVRTAMEAVYTLLEVDRGVPEV FASTFDIRMLLNALYYLNGQKSLIEIDFPWVEKAALKEALKKVKGTYI EELLKDYHLI
78	CTR0031	MYYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGLAAAVFLIRDGHM AGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGREMENHFECMWDMY RSIPSLEIPGASYLDEFYWLDKDDPNSSNCRLIHKRGNRVDDDGQYTL GKQSKELVHLIMKTEESLGDQTIEEFFSEDFFKSNFWVYWATMFAFEK WHSAVEMRRYAMRFIHHIDGLPDFTSLKFNKYNQYDSMVKPIIAYLES HDVDIQFDTKVTDIQVEQTAGKKVAKTIHMTVSGEAKAIELTPDDLVF VTNGSITESSTYGSHHEVAKPTKALGGSWNLWENLAAQSDDFGHPKV FYQDLPAESWFVSATATIKHPAIEPYIERLTHRDLHDGKVNTGGIITITD SNWMMSFAIHRQPHFKEQKDNETTVWIYGLYSNSEGNYVHKKIEECT GQEITEEWLYHLGVPVDKIKDLASQDYINTVPVYMPYITSYFMPRVKG DRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYSFLNVE RGIPEVFNSAYDIRELLKAFYYLNDKKAIKDMDLPIPALIEKIGHKKIKD TFIEELLKDANLM
79	CTR0032	MYYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGLAAAVFLIRDGHM AGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGREMENHFECMWDMY RSIPSLEIPGASYLDEFYWLDKDDPNSSNCRLIHKRGNRVDDDGQYTL GKQSKELVHLIMKTEESLGDQTIEEFFSEDFFKSNFWIYWATMFAFEK WQFCCRNAGYAMRFIHHIDGLPDFTSLKFNKYNQYDSMVKPIIAYLES HDVDIQFDTKVTDIQVEQTAGKKVAKTIHMTVSGEAKAIELTPDDLVF VTNGSITESSTYGSHHEVAKPTKALGGSWNLWENLAAQSDDFGHPKV FYQDLPAESWFVSATATIKHPAIEPYIERLTHRDLHDGKVNTGGIITITD

		SNWMMSFAIHRQPHFKEQKDNETTVWIYGLYSNSEGNYVHKKIEECT GQEITEEWLYHLGVPVDKIKDLASQDYINTVPVYMPYITSYFMPRVKG DRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYSFLNVE RGIPEVFNSAYDIRELLKAFYYLNDKKAIKDMDLPIPALIEKIGHKKIKD TFIEELLKDANLM
80	CTR0033	MISLCLTIQGGLEMYYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGL AAAVFLIRDGHMAGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGREM ENHFECMWDMYRSIPSLEIPGASYLDEFYWLDKDDPNSSNCRLIHKRG NRVDDDGQYTLGKQSKELIHLIMKTEESLGDQTIEEFFSEDFFKSNFWV YWATMFAFEKWHSAVEMRRYAMRFIHHIDGLPDFTSLKFNKYNQYD SMVKPIIAYLESHDVDIQFDTKVTDIQVEQTAGKKVAKTIHMTVSGEA KAIELTPDDLVFVTNGSITESSTYGSHHEVAKPTKALGGSWNLWENLA AQSDDFGHPKVFYQDLPAESWFVSATATIKHPAIEPYIERLTHRDLHDG KVNTGGIITITDSNWMMSFAIHRQPHFKEQKENETTVWIYGLYSNSEG NYVHKKIEECTGQEITEEWLYHLGVPVDKIKDLASQEYINTVPVYMPY ITSYFMPRVKGDRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAM EAVYSFLNGERGIPQGFNSAYDIRELLKAFYYLNDKKAIKDMDLPIPAL IEKIGHKKIKDTFIEELLKDANLM
81	CTR0034	MRYTNGNYEAFVHPRKPENVDQKSAYIIGAGLAGLATAVFLIRDGQM SGDRIHILEELPLSGGSLDGSFIPHDGFVVRGGREMENHFECLWDLFRTI PSLEVDNASVLDEFYRIDRDDPNSSNCRIIHNRGERVDDDGKFTLSPKA QEEIIKLFMTKEELLVGKTIEDCFTDEFFESNFWLYWCSMFAFEKWHS AMEMRRYIMRFIHHIGGLPDLSALKFTKYNQYESLVLPMIKYLEGHDV DFQYNTVVENVLVDKVGDKKVAHTLVLRKNGVKENIELTENELVFVT NGSITESTTYGDNYTPAPVNKELGGSWSLWKNIAAQDTDFGRPEKFCD NLPKESWFVSATLTTLDDRVAPYIEKISKRDPYAGKVVTGGIVTATDS NWMLSYTLNRQPHFKHQPKDQLVVWIYGLLSNKPGDFIKKSITECSGI EIAQEWLYHMGVPVDEIPDIAQNSCNTIPCYMPYITSYFMPRAMGDRP LVVPEGSANLAFIGNFSETVRDTVFTTEYSVRTAMEAVYQLLNIDRGV PEVFASSFDVRTLLASTARLLDGKKLTDIDAPFILKQIGKLGIHKTKDTII YDLLKESELI
82	CTR0035	MYYSNGNYEAFARPKKPEGVDGKSAYLIGSGLASLSAACFLIRDGQM KGENIHILEELDISGGSLDGILNPTRGFIIRGGREMEDHFECLWDLFRSIP SLEVDNASVLDEFYWLNKEDPNYSKCRLIKDRGQRLEDDGKFTLSDQ SSEEMIKLFFTPEEKLEDKKITDVFSEEFFESNFWLYWSTMFAFEKWHS AIEMRRYIMRFIHHIEGLPDFSALKFTKYNQYESLVKPLISYLKDHGVD FKYGAQVENVEVDFSNGKKVAKAIVFADKKIKELTGNDLVFVTNGSIT ESSTQGSPTQVAPKTSELGGSWKLWQNLAKQSEEFGHPDVFCKDIPKE AWVVSATVTWKNLKIQPYFEKLTHRQLRSGKVVTGGIVTVKDSNWLL SFTTHRQPHFKEQNDQETVTWVYGLLSNTPGNYIKKPIEDCTGEEITQE LLYHLGMPEEEIEAFVKENTNTIPVYMPFITSYFMLREPGDRPLVVPEQ SVNLAFLGNFAETERDTVFTTEYSVRTAMEAVYQLLNVDRGVPEVYA SAYDLRTLASSAYYLSDKQKLEDLELSFIKKQALKVGLKKIKGTYIEEL LEDAGLI
83	CTR0036	MCLNRIVYNGVTRKNLVNNILLEGITMKKDYGNKQVYFVGGGIASLA GAAYLIRDCHFKGENIHILEGMHILGGSNDGMGTPEDGFVCRGGRML NEETYENFWELFSSIPSIEHEGMSVTDEILAFDHAHPTHANARLINKDG EVLDVMSMGFDKEDQMAMGKLLLTPEEKLDHLKISDWFGPHFFETNF WYMWQTTFAFQKWSSLFEFQRYMFRMIFEFSRIQTLEGVTRTPYNQY ESIILPMKAYLDDHGVDFTIKCTVTDLDFKEGEGITVTTIHYQDQDGDG IIRLQEDDICIVTNGCMTDGATLGDLYTPAPLKPEHPISGDLWANIAAK KSGLGDPKPFFGNAEETNWESFTVTMKGNKLLKMIEKYSRNVPGSGA LMTFKDSSWLMSMVVAAQPHFKAQTADETIFWGYALHTNKVGDYV KKPMRDCTGEEMLIELLHHLHFDEEMDEIMKDVVNVIPCMMPYIISQF

		QPRAMTDRPQVVPEGSTNLAMISQFVEIPEDMVFTEEFSVRAARIAVY TLMGLDKKICPVTPHRYDVRTLLKALNTCYR
84	CTR0037	MGNYQRNNTIPPQNIKRQKAYLVGGGIASLAAAFYLIRDGHIDGKNITI FEELNIEGGAMDGAGNAETGYIIRGGREMEEHYECTWDLFADIPSLEN YGYSVLDEFKELNDNDPNISKCRLIHNCGQKKNSDSMELSPAHAKRLT ELFLATEDALGNTTVEQFFDESFLDTNFWYLWRSMFAFENWHGVVE MKRYMHRFIHLLPGFNKMKGLVFPKYNQYDSFILPLSKHLESKGVKFQ YGTQVIDLDIDIKDKEKTVTGIHIIHDNKEQVINIRSTDIVMVTNGSMTE CSEYADNKTVPKLRKDLGGVWSLWKNISEKDPAFGHPEVFCGDVDRS KWESFTITCKDSKLVDKIRELSGNEPHSGKTVTGGIITMTDSNWLLSVT CNRQPHFPDQPDDVIVLWAYGLLLDNEGNYIKKKMTECTGEELLKEL LYHLGLEKDIPEILKTDKVIPAMMPYITAQFMPRVKGDRPNVVPEGSK NLAFLGQFAEVPGDCVFTVEYSIRSAIMATYKLLNLNKKVPEVHPSQY DIRVIANAVKTLNSGRPLPAETIIKKLLKDTSMEGLI
85	CTR0038	MDIDGKLKGELLMSKKKLGIGIAAVAVAGAGAAALTVKNHNKAKVQ KEKAAAEHAEYRNTERGKHEKNSKGIYYTNGNYEAFARPRKPEGVDD KNAYIVGSGLASLAAACFLVRDGQMPGSHIHILEAMDIAGGACDGIFD PARGYVMRGGREMENHFECLWDLFRSIPSIETPGVSVLDEYYWLNKE DPNYSLCRATVNRGKDAHTDGKFNLSQKGCMEIMKLFMTKDEDLYD KTIEDVFDDEVFDSTFWLYWRTMFAFENWHSALEMKLYFQRFIHHISG LPDFSALKFTKYNQYESLILPMVKYLEAAGVTFQYNTEVTNVIFDMRD GKKIAKTIECRVNGTEKGIPLTENDLVFVTNGSCTEGTIYGDQNHAPNG DAEVRTSGCWSLWKNIAAQDPSFGHPEKFCSDISKTNWESATVTTLDD KIIPYIVDICKRDPRTGKVVTGGIVSCQDSSWLLSWTINRQGQFKTQDK DKVCVWVYGLFTDVPGDYIKKPMKDCTGKEITEEWLYHLGVPEDEIE ELATNSAVCVPTMMPYITAFFMPRAKGDRPDVIPDGCTNFAFLGQFAD TPRDTVFTTEYSVRTAMEAVYGLLGVDRGVPEVWGSVYDIRELLDSS VKLMDGKSPLEINLGPLNKLKRPILKKIQGTVIEKVLRDHDIIKEGML
86	CTR0039	MIIKELIFMRDYKNTHAYFVGGGIASLAGACYLIRDCSFPGDHIHIFEEL NVLGGSNDGAGNPETGYVIRGGRMLNDETYENTWELLLSIPSIDNPEK SVREEIIEFDTQHPTHSNARLVNNNGEVVDVSSMGFDNDDRIALAKLIV TPEEKLNMLKISDWFKPHFFETNFWYMWATTFAFQPWHSLAELRRYM IRFMHEFPRIHTLEGVTRTPYNQYDSLILPIKKFLENHNVDFKLKCAVT DLDFKDTDKITVTRIYYKEEGMEKTIEVNESDVVFVTNGSMTEGYSLG SMTKPPVLNDKGASWKLWDKISKKKQGLGNPTVFDDNIQGSKWESFT VTCHNSKFFDLMEKFSRNKAGTGALVTFKDSNWFMSIVLAHQPHFRN QPDNVKVFWGYGLFPDNPGNYVKKKMSECVGEEILIELLHHLKFEKE MDDIIKSANCIPCMMPFITAQFMPRSIGDRPQVVPEGSTNLAFIGQFCEI PDDVVFTEEYSVRSARIAVYKLFGITRPVEPINQYQYDVRTLFKSFVTM FK
87	CTR0040	MRDYKNTHAYFVGGGIASLAGACYLIRDCSFPGDHIHIFEELNVLGGS NDGAGNPETGYVIRGGRMLNDETYENTWELLLSIPSIDNPEKSVREEII EFDTQHPTHSNARLVNNNGEVVDVSSMGFDNDDRIALAKLIVTPEEKL NMLKISDWFKPHFFETNFWYMWATTFAFQPWHSLAELRRYMIRFMH EFPRIHTLEGVTRTPYNQYDSLILPIKKFLENHNVDFKLKCAVTDLDFK DTDKITVTRIYYKEEGMEKTIEVNESDVVFVTNGSMTEGYSLGSMTKP PVLNDKGASWKLWDKISKKKQGLGNPTVFDDNIQGSKWESFTVTCHN SKFFDLMEKFSRNKAGTGALVTFKDSNWFMSIVLAHQPHFRNQPDNV KVFWGYGLFPDNPGNYVKKKMSECVGEEILIELLHHLKFEKEMDDIIK SANCIPCMMPFITAQFMPRSIGDRPQVVPEGSTNLAFIGQFCEIPDDVVF TEEYSVRSARIAVYKLFGITRPVEPINQYQYDVRTLFKSFVTMFK
88	CTR0041	MKTKTKLLTGAALLAGAGAVAAKKYADNKDTVRKPVEITNQQFYLI GGGLASMAAAAYLIQDGHVDGKNIHIFEGMKILGGSNDGAGSIKDGF VCRGGRMLNEETYENFWELFDRIPSLDHPGQSVTKEILDFDHLHPTEA

		RARLIDRHGKILDVKSMGFDNNDRLTLGKLMITPESKLDDITIEQWFK DAPHFFTTNFWYMWQTTFAFQKWSSVFELKRYMNRMIFEFPRIETLA GVTRTPYNQFESVILPIKKYLDSHHVNFVTNTTVTDIDFKDDDTITVKA LYLNKDGKDEKIILNDNDICIMTNACMTDSATLGDYKTPAPKPVEKPIS GELWYKVAQKKPNLGNPEPFFGNIKETNWESITVTFKGNKFLKIIEEFS TNIPGSGALMTFKDSSWLMSMVVAAQPHFKAQDANTTIFWAYGLYT DRLGDYIKKPMKDCTGEEIFDELLYHLHLIDRKEEIKKDIINVIPCMMP YVDAQFQPRKMSDRPHVVPKGSTNFAMISQFVEIPEDMVFTEEYSVRA ARIAVYTLLGINKPICKVTPYNKDPKVLKKALETAYR
89	CTR0042	MSTINSKFDKVLNASDQFGNVNHEPDSSKEVQINTPEKTMPFSDQIGN YQRNKGIPLQSYENSKIYIVGSGIAGMSAAYYFIRDGRVPGKNIIFLDQL NVEGGSLDGAGNAKDGYIIRGGREMDMTYENLWDMFQDIPALELPAP YSVLDEYRLVNDNDPNYSKARLIHNQGQIKDFSKFGLEKKDQLAIVKL LLKKKEELDDLTIEDYFSESFLNSNFWFFWRSMFAFENWHSLLELKLY MHRFLHAIDGMKDFSCLVFPKYNQYDTYVTPLKNFLVEKGVQIQFNT LVKDLDIHINTEGKTVEGIITEQNGEEVKIPISKEDYVIVTTGSMTESTFY GDNNTVPEVTIDNSSAGQSAGWKLWKNLAAKSEVFGKPEKFCSHIEK SSWESATLTCRPSAFTEKLKELCVNDPYSGRTATGGIITITDSNWVMSF TCNRQPHFPTQPDDILVVWVYALLMDKEGNYIKKTMPQCTGNEILAE LCYHLGITDQLDNVTENTIVRTAFMPYITSMFMPRAMGDRPRVVPEGC TNLGLVGQFVETNNDVVFTMESSVRTARIAVYNLLNLNKQVPDINPLQ YDIRHLLKATQALNDYKPFLGEGILRKILKGTYFEHILVNRPEEKEEHE SFLTRFQEWVKGVKD
90	CTR0043	MNPITSKFDKVLNASSEYGHVNHEPDSSKEQQRNTPQKSMPFSDQIGN YQRNKGIPVQSYDNSKIYIIGSGIAGMSAAYYFIRDGHVPAKNITFLEQL HIDGGSLDGAGNPTDGYIIRGGREMDMTYENLWDMFQDIPALEMPAP YSVLDEYRLINDNDSNYSKARLINNKGEIKDFSKFGLNKMDQLAIIRLL LKNKEELDDLTIEDYFSESFLKSNFWTFWRTMFAFENWHSLLELKLYM HRFLHAIDGLNDLSSLVFPKYNQYDTFVTPLRKFLQEKGVNIHLNTLV KDLDIHINTEGKVVEGIITEQDGKEVKIPVGKNDYVIVTTGSMTEDTFY GNNKTAPIIGIDNSTSGQSAGWKLWKNLAAKSEIFGKPEKFCSNIEKSA WESATLTCKPSALIDKLKEYSVNDPYSGKTVTGGIITITDSNWLMSFTC NRQPHFPEQPDDVLVLWVYALFMDKEGNYIKKTMLECTGDEILAELC YHLGIEDQLENVQKNTIVRTAFMPYITSMFMPRAKGDRPRVVPEGCKN LGLVGQFVETNNDVVFTMESSVRTARIAVYKLLNLNKQVPDINPLQY DIRHLLKAAKTLNDDKPFVGEGLLRKVLKGTYFEHVLPAGAAEEEEH ESFIAEHVNKFREWVKGIRG
91	CTR0044	MNPITSKFDKVLNASSEYGHVNHEPDSSKEQQRNTPQKSMPFSDQIGN YQRNKGIPVQSYDNSKIYIIGSGIAGMSAAYYFIRDGHVPAKNITFLEQL HIDGGSLDGAGNPTDGYIIRGGREMDMTYENLWDMFQDIPALEMPAP YSVLDEYRLINDNDSNYSKARLINNKGEIKDFSKFGLNKMDQLAIIRLL LKNKEELDDLTIEDYFSESFLKSNFWTFWRTMFAFENWHSLLELKLYM HRFLHAIDGLNDLSSLVFPKYNQYDTFVTPLRKFLQEKGVNIHLNTLV KDLDIHINTEGKVVEGIITEQDGKEVKIPVGKNDYVIVTTGSMTEDTFY GNNKTAPIIGIDNSTSGQSAGWKLWKNLAAKSEIFGKPEKFCSNIEKSA WESATLTCKSSALIDKLKEYSVNDPYSGKTVTGGIITITDSNWLMSFTC NRQPHFPEQPDDVLVLWVYALFMDKEGNYIKKTMPECTGDEILAELC YHLGIEDQLENVQKNTIVRTAFMPYITSMFMPRAKGDRPRVVPEGCKN LGLVGQFVETNNDVVFTMESSVRTARIAVYKLLNLNKQVPDINPLQY DIRHLLKAAKTLNDDKPFVGEGLLRKVLKGTYFEHVLPAGAAEEEEH ESFIAEHVNKFREWVKGIRG
92	CTR0045	MGGGIASLASAAYFIRDGQINPDNIIIYEELNVAGGSLDSAGNPEDGYV MRGGRMLNFSYLCTYDLFSFIPSLSDPGIMVLDEIKAFNRNIKTHSQAR VVENGHILDVSSMGFSNKDRLDLIEMMAVGENHLGIKRINEWFAPEFF

		KTNFWFMWDTMFAFQPWHSAVEFKRYLHRFIHEFKRINTLAGVDRTP YNQFDSLAKPLINWLKQQGVHFQIGVSVTDLDFSLTGEKLTVQQIHLID GGKKKSVKIGVNDMVLVTIGSMTADSSLGSMHAAPELITDKRDGSWK LWEAIAKHSDQFGHPSVFDNHVDESKWESFTVTCQGTDFFERMKTFS GNDAGTGGLVTFKDSNWLMSIVLAYQPHFIGQPDDVTVFWGYGLFPD NEGNFVKKKMADCTGTEILTELFSHLQFDTLNDRLLKTANCIPCMLPYI TSQFLIRAPGDRPQVIPEISENMAFIGQFAEVPDDVVFTVEYSVRTAQT AVYGLLELDKKTIPMYKGDHHIDVLFDAMKTMIS
93	CTR0046	MTIHQHPHVTDRDAHFVGGGIASLAGAAFLVRDGNMPGENIHVYEKL DVVGGAMDGAGDPDEAYLIRGGRMFNYPAYECTWDLFETIPSLEDDS RSVKAVMDEFNETHPSYAKTRLMHEGERIDAGEYGLTRQHRQSIARL LLTPEPRLGDTRIEEWFDESFLETNFWYVWATIFAFQPWHSVAEVRRY MYRFLHEFPQLHTMEGIDRTKYNQYDSMILPLRRWLEDRGVSFEYGH EVTDMDIVPSRTGRTVERLYCETDSGTETVPVEPSDLVFVTNGSMTDG SSIGGMDEAPELNETGASWELWKSIAEDNPQFGNPSVFADNVTETKW ESFTVTLHNTDLFDHIVDFTNEEPGNGLVTYLGSNWLLSTVVAAQPHF ANQPDDVKVFWGYALFPDREGNYVEKPMSECTGREILQELCYHLQCE ERLPEILDDVTCIPAMMPFITAHFQPREPGDRPDVVPDGSNNLAFLGQY AEQPRDVVFTVEYSVRSAMTAVYEMLDLDREVPPVSKHYRKPGVIAD TVRAAYR
94	CTR0047	MSNEQPQRQDGSEREAYFVGGGIASLAGAAFLVRDSELPGENVHVLE KLDVMGGALDGAGSPEEGYVIRGGRMLNFPTYECTWDLLETIPSLEDR ERSIKDVMDEFNEEHQTYAVARLVGDEQEVLDVSSYGLEMDHRLSLL QLVLTPEEQLGDTRIEEWFSDSFFETTFWYIWATTFAFQPWHSVAEMR RYMHRFMHEFPRLNTMEGIHRTKYNQYDSMVRPIRRWLEDHGVEFR GGCEVTDMDIVPGRDGKTVETIHYEADGVAETIDVEPTDLVFVTNGS MTDGSDLGSMTEAPDLNTTGASFELWKNIAEDNPEFGTPSAFADHVQ ETKWPSYTVTLDEPDLLEHIVEVTGEAPGNGLITFTESNWLMSIVVAA QPHFANQPDDVKIFWGYGLFPEEEGNYVEKKMGNCTGEEILEELCYH LGYLDELPSVLEDANCIPCNMPFITSHFMPRTPGDRPDVVPPGSNNLAF IGQFAEQPRDVVFTVEYSVRSAMTAVYDQLDVDRDVPPVSTHQYEPE VLVDAAKAAFR
95	CTR0048	MRDKGVKIQFNTRVHDVDLQIRGDEKTVTGLRAMVDGQETTIPVHPN DLVFALTGSMTEGTAYGDMDTVPVLERGLHEPGEESDWTLWRNLAR KSPVFGRPDKFYGDVKGSMWESATLTCRPSPFVDKLKELSVNDPYSG KTVTGGVITFTDSNWVLSFTCNRQPHFPTQPDDVLVIWVYALLMDKE GNYVKKPMPACTGREILAELCYHLGIVEQLDAIALNTKVRLALMPYIT AQFMPRAAGDRPHVVPEGCTNLGLLGQFVETSNDIIFTMESSVRTARIA VYTLLKLPKQVPDISPTQYDIRTIFKAARAINNGEPFPGERLLHRLLDKT YFSHILPTLPKKEEADGDDFGNDLSGLFGKGSEALHKVTDWLEKFRAN LGWK
96	CTR0049	MTWQKTDRPVMSTPLGKQKESVMYYSSGNYEAFARPRKPKGVENKT AWFVGAGLAALAGAAFLIRDGQMPGNRITILEQQQLPGGALDGIKEPN KGFVIRGGREMEEHFECLWDLYRSIPSLEIEGASVLDEFYWLDKDDPN SSLQRATVKRGEDAHTDGLFTLSEQAQKEIVKLFLATGEEMENKRISE VFGKEFLDSNFWLYWRTMFAFEEWHSALEMKRYLHRFIHQIKGMPDF STLKFTKFNQYESLVLPLVKWLQEHGVVFEYGTEVTDVDFDIAPGRKQ ATRIHWRKDAGEGGVDLGPDDLVFMTIGSLTENSDNGDHHTPAKLNE GPAPAWDLWRRIAAKDPAFGRPDVFGAHIPETKWESATVTTLDQRIPK YIQKIAKRDPFSGKVVTGGIVTAKDSSWLLSWTVNRQPHFKEQPKDQI VVWVYALFVEQPGDYVKKPMQDCSGEEITQEWLYHLGVPVEDIPELA ATGAITVPVMMPYVTAFFMPRQAGDRPDVVPEGAVNFAFIGQFAESR ERDCIFTTEYSVRTPMEAVYTLLDVERGVPEVFNSTYDIRTLLSATGRL RDGKEIDIPGPAFVRNLLMKKLDKTQIGALLREFGIVGDD

97	CTR0050	MYYSSGNYEAFARPRKPAGVDGKRAWFVGSGLASLAGAAFLVRDGH MAGECITILEQQQIPGGALDGLKVPEKGFVIRGGREMEDHFECLWDLF RSIPSLEIEDASVLDEFYWLNKDDPNYSLQRATINRGEDAHTDGLFTLT EQAQRDIVALFLATRQEMENKRINEVLGRDFLDSNFWLYWRTMFAFE EWHSALEMKLYLHRFIHHIGGLPDFSALKFTKYNQYESLVLPLVKWLQ DQGVVFQYGTEVTDVDFDLQPDRKQATRIHWMHDGVAGGVELGAD DLLFMTIGSLTENSDNGDHHTAARLNEGPAPAWDLWRRIAAKDDAFG RPDVFGAHIPETKWESATVTTLDARIPAYIQKIAKRDPFSGKVVTGGIV SVRDSRWLMSWTVNRQPHFKNQPKDQIVVWVYSLFVDTPGDYVKKP MQDCTGEEITREWLYHLGVPVEEIDELAATGAKTVPVMMPYITAFFM PRQAGDRPDVVPEGAVNFAFIGQFAESKQRDCIFTTEYSVRTPMEAVY TLLGIERGVPEVFNSTYDVRSLLAATGRLRDGKELDIPGPAFLRNLLMN KLDKTQIGGLLREFKLVQED
98	CTR0051	MYYSSGNYEAFARPRKPAGVDGKRAWFVGSGLASLAGAAFLIRDGR MAGERITILEQQHIPGGALDGLKVPEKGFVIRGGREMEDHFECLWDLF RSIPSLEIEDASVLDEFYWLNKDDPNYSLQRATINRGEDAHTDGLFTLT EQAQKDIIALFLATRQEMENKRINEVLGRDFLDSNFWLYWRTMFAFEE WHSALEMKLYLHRFIHHIGGLPDFSALKFTKYNQYESLVLPLVKWLQ DQGVVFQYGTEVTDVDFDLQPDRKQATRIHWMHDGVAGGVDLGAD DLLFMTIGSLTENSDNGDHHTAARLNEGPAPAWDLWRRIAAKDDAFG RPDVFGAHIPETKWESATVTTLDARIPAYIQKIAKRDPFSGKVVTGGIV SVRDSRWLMSWTVNRQPHFKNQPKDQIVVWVYSLFVDTPGDYVKKP MQDCTGEEITREWLYHLGVPVEEIDELAATGAKTVPVMMPYITAFFM PRQAGDRPDVVPDGAVNFAFIGQFAESKQRDCIFTTEYSVRTPMEAVY TLLDIERGVPEVFNSTYDVRSLLAATGRLRDGKELGIPGPVFLRNLLMN KLDKTQIGGLLREFKLVQED
99	CTR0052	MYYSSGNYEAFARPRKPAGVDGKRAWFVGSGLASLAGAAFLVRDGR MAGEHITVLEQQQIAGGALDGLKVPEKGFVIRGGREMEDHFECLWDL FRSIPSLEIEDASVLDEFYWLNKDDPNYSLQRATINRGEDAHTDGLFTL TEQAQKDIIALFLATRQEMENKRIDEVLGRDFLDSNFWLYWRTMFAFE EWHSALEMKLYLHRFIHHIGGLPDFSALKFTKYNQYESLVLPLVRWLQ DQGVVFQYGTEVTDVDFDLAAGRKQATRIHWTRDGVAGGVDLSADD LVFMTIGSLTENSDNGDHHTAARLNEGPAPAWDLWRRIAARDPAFGR PDVFGAHIPQTKWESATVTTLDARIPAYIQTIAKRDPFSGKVVTGGIVS VRDSRWLMSWTVNRQPHFKNQPKDQIVVWVYSLFVDTPGDYVKKP MKECTGEEITREWLYHLGVPVEEIDELAATGAKTVPVMMPYITAFFMP RQAGDRPDVVPDGAVNFAFIGQFAESKQRDCIFTTEYSVRTPMEAVYT LLGIERGVPEVFNSTYDVRSLLAATGRLRDGKELDIPGPAFLRNLLMN KLDKTQIGGLLREFKLVQED
100	CTR0053	MSQPTAPGRNAGATPAFEHEPDSTGGYWSNRPENTLPPPDMMGAYM RNRPLPPEDVAQRKAYIIGTGIAGLAAAFYLIRDGGMPPANITLLDSLEI EGGSLDGAGDAEQGYLIRGGREMNWNYDNFWDLFQDVPALELPAGF SVLDEYRAVNDNDPNWSKARLLHQQGKVKDFATFGLSRGQQWELVK LLLKRKEDLDDVTIEDYFSEGFLQSNFWFFWRSMFAFENWQSLLEMK LYMHRFLDAIDGLNDMSALVFPKYNQYESFVVPLSRMLRAQGVNVQF DTRVHDLEMAVDGQSRTVTALRCRVAGNETTLPVAAGDLVFALTGS MTEGTAYGDMDTVPPLARDRRDPGEDSDWALWRNLARQSPIFGKPE KFYGDVDRSMWESATLTCRPSPLVDKIRTLSVNDPYSGRTVTGGVITIT DSNWVLSFTVNRQPHFVDQPKDVLVVWVYALLMDQDGNHIKKPMPA CTGREVLAELCHHLGIGDQIDAVAAATRVRLALMPYITAQFMPRAAG DRPHVVPAGCTNLGLLGQFVETRNDVIFTMESSIRTARVAVYTLLGLR KQVPDLSPTQYDIRNLIKAARALNNNAPFPGERLLHRLLGNSYYAHILP PLPQPEKGREAFLEEELSWLSGKGSVVLKDLSARLDRLGETLGRRRAP

101	CTR0054	MEEVSYPKAGPSIEANVGDGHWRKGPSDTLPPPDTVGPYMRNRPLPV DQVEGRKAWIIGSGIAGLASAFYLIRDGRMKGQDITILDAVGTPGGSLD GSGNAEDGYLIRGGREMNWNYDHFWDLFQDIPALEYPSPYSVLDEYR AVNDNDPNWSKSRLMHKQGQIRDFSTLGLSSAHQWELIKLLLKRKED LDDITIEQYFSDSFLETNFWYLWRSMFAFQNWQSLLEVKLYMHRFLD AIDGLTDMSALVFPKYNQYDSFVVPLVNYLKGQGVNVEFGTRVYDLD MTDNNGERTVTSILAKVDGRDQKIDIGAKDVVFALTGSMTEGTAYGD LDTAPDLTRATTPPGDSSDWALWQNLAKKSHVFGKPEKFCGQPSRSM WESATLTCKPSPLTERLKDLSINDPYSGKTVTGGIITFTDSNWVLSFTC NRQPHFPTQPDDVLVLWVYALVMDSKGNHVLKPMPECTGREILAELC YHLGIVDQVDEVARQTKVRLALMPFITAQFMPRAAGDRPRVVPAGCT NLALLGQFVETSNDIIFTMESSVRTARIGVYTLLGLRKQVADISPTQYD VRNLIKGARALNNNEPFMGERLLHRLLDNTYFAHILPPLPAGDGGSSD QAASSRMKANHTAAAALGAVSDWIHHVRDKLKPGA
102	CTR0055	MYYSKGNYEAFARPLKPEGIEKKKAWIVGSGLSGLSTAAFLVRDAQM PGKNITILEELNISGGALDGIHDSEKGFVMRGGREMESHFECLWDLFRS VPSLEENEASVLDEFYWLNKRDPNFSLQRATIKQGQDAETGTLFTLSE KAQAEVTKLFLATRKEVENVRIDQVFSQEFFDSNFWMYWQTMFAFQT WHSALEMKLYLHRFVNHIRGMPDFSTLKFTRYNQYESLVVPLHTWLE EKGVVFQYSTEVQDVDFDIKEDKKTATYIHWIKDGKKSGQALSPDDL VFMTIGSLTENTGYGDHHTVPKLLEGPAPAWDLWRRIAAKDPAFGRP EVFCGDIKATKWESATFQTLDARIPEYIQKVCKRDPLSGKVVTGGIVT VRDSSWIMSWTVNRQPHFKNQPKGSVVGWIYGLLVEKPGDYVKKPM QECTGEEIVQEWLYHLGVPTSEIATLAADAVKCVPTMMPYITAFFMPR QAGDRPDVVPAGSQNFAFIGQFAETTRDCIFTTEYAVRTGMESVYQLT GVDRAVPEVFGSTYDVRVLLDAMSQLRDGKELAPWLPERIRAFLMSK LQGSQIGQMLHEYHLV
103	Fw (DSM100 238T-HY64.1)	CCTGGTGCCGCGCGGCAGCCATATGGTGCCCGCCTCGACGTTGAGG CCCGGCTTC
104	Rv (DSM100 238T-HY64.1)	TTCGGGCTTTGTTAGCAGCCGGATCTCACAACACCCCGCACGCCTT GAGCAGCTT
105	Fw (WIL0093 -HY53.1)	CCTGGTGCCGCGCGGCAGCCATATGCAATTGGACATGTTTCCGCCG ATTGTCGAT
106	Rv (WIL0093 -HY53.1)	TTCGGGCTTTGTTAGCAGCCGGATCTCACAATGCCCCGCACGCCTT GAGCAGCTT
107	Fw (WIL0019 -HY10.1)	CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGGAATTAT GAAGCATTT
108	Rv (WIL0019 -HY10.1)	TTCGGGCTTTGTTAGCAGCCGGATCCTACAGTAAATGATTGTCCTTC AACACATC
109	Fw (WIL0024 -HY15.1)	CCTGGTGCCGCGCGGCAGCCATATGAGATATACAAACGGAAATTAT GAAGCTTTT
110	Rv (WIL0024 -HY15.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTAAACTAAATGATTTTTTTCA AGGATTTC

111	Fw (WIL0020-HY11.1)	CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGAAATTACGAAGCATTT
112	Rv (WIL0020-HY11.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTACAACAAATGATTCTCTTTCAATACATC
113	Fw (WIL0022-HY13.1)	CCTGGTGCCGCGCGGCAGCCATATGAGATATACGAATGGAAATTATGAAGCTTTT
114	Rv (WIL0022-HY13.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTACAACAGATGGTTGTCTTTCAACACATC
115	Fw (DSM15814T-HY67.1)	CCTGGTGCCGCGCGGCAGCCATATGGCACAGCATGCATACATGATTGGTACAGGC
116	Rv (DSM15814T-HY67.1)	TTCGGGCTTTGTTAGCAGCCGGATCCTATCTGAACATTGTCTTGGTTGCACGGGC
117	Fw (WIL0041-HY30.1)	CCTGGTGCCGCGCGGCAGCCATATGGCACAACATGCTTATATGATCGGTACTGGT
118	Rv (WIL0041-HY30.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTAACGGAACATGGTCCGTGTTGCCCGCAG
119	Fw (WIL0012-HY06.2)	CCTGGTGCCGCGCGGCAGCCATATGGTTAAAAGTAAAGCAATTATGATTGGTGCC
120	Rv (WIL0012-HY06.2)	TTCGGGCTTTGTTAGCAGCCGGATCTTAATCAAACATCTTCTTAGTTGCCTTGAG
121	Fw (WIL0068-HY41.1)	CCTGGTGCCGCGCGGCAGCCATATGCATTATAGCAATGGTAATTATGAAGCTTTC
122	Rv (WIL0068-HY41.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTAAATCAACTTGTACTTCTTAAGCAATTC
123	Fw (WIL0006-HY03.1)	CCTGGTGCCGCGCGGCAGCCATATGTATTATAGTAATGGTAATTATGAGGCATTT
124	Rv (WIL0006-HY03.1)	TTCGGGCTTTGTTAGCAGCCGGATCTCACATCAAGTGTGCTTCAACAAGCAACTC
125	Fw (WIL0008-HY04.1)	CCTGGTGCCGCGCGGCAGCCATATGTATTATAGTAATGGTAATTATGAAGCATTT
126	Rv (WIL0008-HY04.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTATAATAAATGTGCTTCTGCCAATAATTC
127	Fw (WIL0076-HY48.1)	CCTGGTGCCGCGCGGCAGCCATATGTATTATAGTAGTGGTAATTATGAAGCTTTT

128	Rv (WIL0076-HY48.1)	TTCGGGCTTTGTTAGCAGCCGGATCCTAGATTAAGTGCTCATCTCTAAAGATTTC
129	Fw (WIL0055-HY35.1)	CCTGGTGCCGCGCGGCAGCCATATGATGCATTACACAAATGGAAACTACGAGGCG
130	Rv (WIL0055-HY35.1)	TTCGGGCTTTGTTAGCAGCCGGATCCTAGATCAGCCGATATTCTTTTAAAAGTTC
131	Fw (WIL0055-HY36.4)	CCTGGTGCCGCGCGGCAGCCATATGTTATCGCTTTCGCAAGGATTATTTTACACT
132	Rv (WIL0055-HY36.4)	TTCGGGCTTTGTTAGCAGCCGGATCTCAGTCAAGCAGATGCTGCTCTTTGAGAAT
133	Fw (WIL0075-HY05.2)	CCTGGTGCCGCGCGGCAGCCATATGTACTACAGTAGTGGTAATTATGAAGCATTT
134	Rv (WIL0075-HY05.2)	TTCGGGCTTTGTTAGCAGCCGGATCTTAGAGTAACTTTTGAGATTTCAAAATTTC
135	Fw (WIL0037-HY26.1)	CCTGGTGCCGCGCGGCAGCCATATGGAAAAAGCATATATGATCGGTACTGGAATT
136	Rv (WIL0037-HY26.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTATCTAAACATAGTCTTAGTTGCTTTTAG
137	Fw (WIL0039-HY28.1)	CCTGGTGCCGCGCGGCAGCCATATGCTATGTATTTTAAATAAGAATGAGGAGGAG
138	Rv (WIL0039-HY28.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTATCTAAACATTGTTTTAGTAGCTCTTAA
139	Fw (PA-HY29.2)	CCTGGTGCCGCGCGGCAGCCATATGATGAGAAAAGCGTTTATGATTGGTACAGGA
140	Rv (PA-HY29.2)	TTCGGGCTTTGTTAGCAGCCGGATCCTAACGGAACATGGTCCGGGTTGCCTTCAA
141	Fw (WIL0029-HY20.1)	CCTGGTGCCGCGCGGCAGCCATATGTATTACAGTAACGGAAATTATGAAGCATTT
142	Rv (WIL0029-HY20.1)	TTCGGGCTTTGTTAGCAGCCGGATCCTATAATAAGTGTTGATCGACTAATATTTC
143	Fw (WIL0114-HY62.1)	CCTGGTGCCGCGCGGCAGCCATATGAATAATTATCAAAGAATCAATCCAATCGCA
144	Rv (WIL0114-HY62.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTATAATAAATTTTTTAATTCTGTGTTCTT
145	Fw (WIL0042-HY33.1)	CCTGGTGCCGCGCGGCAGCCATATGAATAATTATCAAAGAATTAATCCAATTAAA

146	Rv (WIL0042 -HY33.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTATAGTAATTTTTCAATTTCT GTATTCTT
147	Fw (WIL0057 -HY37.1)	CCTGGTGCCGCGCGGCAGCCATATGTATTACAGCAGTGGTAATTAC GAAGCTTTT
148	Rv (WIL0057 -HY37.1)	TTCGGGCTTTGTTAGCAGCCGGATCTTAAGATTTCTTTTTATGCAAC AATGCAGC
149	T7-Pro-F	AGAGGATCGAGATCTCGATCCCGCG
150	T7-Ter-R	CCTCTTGCGGGATATCCGGATATAG

CLAIMS

1. A method of producing hydroxy fatty acids comprising contacting at least one fatty acid hydratase with one or more unsaturated fatty acids, wherein the fatty acid hydratase comprises an amino acid sequence selected from the group consisting of SEQ ID NOs 1 to 8, and 11 to 23 or the fatty acid hydratase is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

2. The method of claim 1, wherein the method is performed at temperature of 30°C or higher.

3. The method of any one of the preceding claims, wherein the fatty acid hydratase is regioselective for a carbon-carbon *cis*-double bond at one position over another when the one or more unsaturated fatty acid comprises one or more than one carbon-carbon *cis*-double bonds.

4. The method of any one of the preceding claims, wherein the fatty acid hydratase is promiscuous for alternative carbon-carbon *cis*-double bond positions.

5. The method of any one of the preceding claims, wherein the fatty acid hydratase hydrates a carbon-carbon *cis*-double bond in the one or more unsaturated fatty acids selected from the group consisting of a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof.

6. The method of any one of the preceding claims, wherein the method comprises a first fatty acid hydratase and a second fatty acid hydratase.

7. The method of claim 6, wherein the first and the second fatty acid hydratase are used simultaneously or sequentially.

8. The method of any one of claims 6 to 7, wherein the first fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to any one of SEQ ID Nos: 1 to 2, 7 to 8, 15, 17 to 19, and 23; and the second fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to any one of SEQ ID Nos: 13 to 14, 16, and 20 to 22.

9. The method of claim 8, wherein the first fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to SEQ ID NO 18; and the second fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to SEQ ID NO 16.

10. The method of claim 8 or 9, wherein the first fatty acid hydratase is a protein according to SEQ ID NO 18, and the second fatty acid hydratase is a protein according to SEQ ID NO 16.

11. The method of claim 8, wherein the first fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to SEQ ID NO 19, and the second fatty acid hydratase is a protein sequence with a sequence identity of at least 83% to SEQ ID NO 14.

12. The method of claim 8 or 11, wherein the first fatty acid hydratase is a protein according to SEQ ID NO 19, and the second fatty acid hydratase is a protein according to SEQ ID NO 14.

13. A fatty acid hydratase comprising a protein sequence with a sequence identity of at least 83% to a protein sequence selected from the group consisting of SEQ ID Nos 1 to 8, and 11 to 23.

14. A fatty acid hydratase encoded by a nucleic acid sequence with a sequence identity of at least 83% to a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

15. The fatty acid hydratase of claims 13 to 14, wherein the sequence identity is at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

16. The fatty acid hydratase of any one of claims 13 to 15, wherein the fatty acid hydratase is regioselective for a carbon-carbon *cis*-double bond at one position over another when the one or more unsaturated fatty acid comprises one or more than one carbon-carbon *cis*-double bond.

17. The fatty acid hydratase of any one of claims 13 to 16, wherein the fatty acid hydratase is promiscuous for alternative carbon-carbon *cis*-double bond positions.

18. The fatty acid hydratase of any one of claims 13 to 17, wherein the fatty acid hydratase hydrates a carbon-carbon *cis*-double bond selected from the group consisting of a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof in the one or more unsaturated fatty acids.

19. The fatty acid hydratase of any one of claims 13 to 18, wherein the fatty acid hydratase is modified.

20. The fatty acid hydratase of claim 19, wherein the modification is selected from the group consisting of substitution, deletion, insertion, addition and combinations thereof.

21. The fatty acid hydratase of any one of claims 19 to 20, wherein the modification is C-terminal or N-terminal of the peptide, or at the 5'- or 3'- end of the nucleic acid sequence.

22. The fatty acid hydratase of any one of claims 19 to 21, wherein the modification is an addition of a His-tag or a thrombin cleavage site.

23. The fatty acid hydratase of any one of claims 19 to 22, wherein the fatty acid hydratase is purified, free, immobilized, wet, or lyophilised.

24. A vector expressing a protein sequence selected from the group consisting of SEQ ID NOs 1 to 8, and 11 to 23 or a nucleic acid sequence selected from the group consisting of SEQ ID NOs 24 to 31, and 34 to 46.

25. A host cell comprising the vector according to claim 24.

26. The host cell of claim 25, wherein the host cell is selected from the group consisting of bacteria and fungi.

27. The host cell of claim 26, wherein the bacteria are Enterobacteriaceae.

28. The host cell of claim 27, wherein the Enterobacteriaceae are selected from the group consisting of *Escherichia* spp., *Escherichia coli* Acella, and *Escherichia coli* BL21 (DE3).

29. A method of producing hydroxy fatty acids, the method comprising culturing the host cell of any one of claims 25 to 28 under conditions suitable for culturing of the host cell.

30. The method of any one of claims 1 to 12 or 29, wherein the hydroxy fatty acid is a mono- or a poly-hydroxy fatty acid.

31. The method of any one of claims 1 to 12, or claims 29 to 30, or the fatty acid hydratase of any one of claims 13 to 23, wherein the fatty acid hydratase has an improved substrate specificity and/or conversion efficiency for one particular unsaturated fatty acid over another.

32. A method of producing poly-hydroxy fatty acids, the method comprising two or more of the fatty acid hydratases as described in any one of claims 13 to 23 or 30.

33. The method of claim 32, wherein the fatty acid hydratases have different regioselectivities and promiscuities.

34. The method of claim 33, wherein the fatty acid hydratases each hydrate a different carbon-carbon *cis*-double bond position.

35. A method of producing hydroxy fatty acids, the method comprising use of a host cell or a native bacterial strain comprising a fatty acid hydratase of any one of claims 13 to 23.

36. The methods of any one of claims 29 to 35, wherein the method comprises use of two or more fatty acid hydratases.

37. The method of claim 36, wherein the two or more fatty acid hydratases each hydrate a carbon-carbon *cis*-double bond selected from the group consisting of a *cis*-9 double bond, a *cis*-12 double bond, a *cis*-8 double bond, a *cis*-11 double bond, a *cis*-14 double bond, and combinations thereof.

38. The method of any one of claims 36 to 37, wherein the two or more fatty acid hydratases are used simultaneously or sequentially.