

KETOREDUCTASE POLYPEPTIDES AND USES THEREOF**1. CROSS REFERENCES TO RELATED APPLICATIONS**

[0001] This application claims benefit under 35 U.S.C. § 119(e) of application Serial No. 60/976,345, filed September 28, 2007, the contents of which are incorporated herein by reference.

2. REFERENCE TO SEQUENCE LISTING, TABLE OR COMPUTER PROGRAM

[0002] The Sequence Listing concurrently submitted herewith under 37 C.F.R. 1.821 in a computer readable form (CRF) via EFS-Web as file name 376247-018.txt is herein incorporated by reference. The electronic copy of the Sequence Listing was created on September 28, 2008, with a file size of 254 Kbytes.

3. BACKGROUND

[0003] Enzymes belonging to the ketoreductase (KRED) or carbonyl reductase class (EC1.1.1.184) are useful for the synthesis of optically active alcohols from the corresponding prostereoisomeric ketone substrate or from the corresponding racemic aldehyde substrate. KREDs typically convert a ketone or aldehyde to the corresponding alcohol product, but may also catalyze the reverse reaction, oxidation of an alcohol substrate to the corresponding ketone/aldehyde product. The reduction of ketones and aldehydes and the oxidation of alcohols by enzymes such as KRED requires a co-factor, most commonly reduced nicotinamide adenine dinucleotide (NADH) or reduced nicotinamide adenine dinucleotide phosphate (NADPH), and nicotinamide adenine dinucleotide (NAD) or nicotinamide adenine dinucleotide phosphate (NADP) for the oxidation reaction. NADH and NADPH serve as electron donors, while NAD and NADP serve as electron acceptors. It is frequently observed that ketoreductases and alcohol dehydrogenases accept either the phosphorylated or the non-phosphorylated co-factor (in its oxidized and reduced state).

[0004] KRED enzymes can be found in a wide range of bacteria and yeasts (for reviews, see Kraus and Waldman, 1995, *Enzyme catalysis in organic synthesis*, Vols. 1&2.VCH Weinheim; Faber, K., *Biotransformations in organic chemistry*, 4th Ed. Springer, Berlin Heidelberg New York. 2000; and Hummel and Kula, 1989, *Eur. J. Biochem.* 184:1-13). Several KRED gene and enzyme sequences have been reported, e.g., *Candida magnoliae* (Genbank Acc. No. JC7338; GI:11360538) *Candida parapsilosis* (Genbank Acc. No. BAA24528.1; GI:2815409), *Sporobolomyces salmonicolor* (Genbank Acc. No. AF160799; GI:6539734).

[0005] In order to circumvent many chemical synthetic procedures for the production of key compounds, ketoreductases are being increasingly employed for the enzymatic conversion of different keto and aldehyde substrates to chiral alcohol products. These applications can employ whole cells expressing the ketoreductase for biocatalytic ketone reductions, or use purified enzymes in those instances where presence of multiple ketoreductases in whole cells would adversely affect the stereopurity and yield of the desired product. For *in vitro* applications, a co-factor (NADH or NADPH) regenerating enzyme such as glucose dehydrogenase (GDH), formate dehydrogenase etc. is used in conjunction with the ketoreductase. Examples using ketoreductases to generate useful chemical compounds include asymmetric reduction of 4-chloroacetoacetate esters (Zhou, 1983, *J. Am. Chem. Soc.* 105:5925-5926; Santaniello, *J. Chem. Res. (S)* 1984:132-133; US Patent No. 5,559,030; US Patent No. 5,700,670 and US Patent No. 5,891,685), reduction of dioxocarboxylic acids (*e.g.*, US Patent No. 6,399,339), reduction of tert-butyl (*S*) chloro-5-hydroxy-3-oxohexanoate (*e.g.*, US Patent No. 6,645,746 and WO 01/40450), reduction pyrrolotriazine-based compounds (*e.g.*, US application No. 2006/0286646); reduction of substituted acetophenones (*e.g.*, US Patent No. 6,800,477); and reduction of ketothiolanes (WO 2005/054491).

[0006] It is desirable to identify other ketoreductase enzymes that can be used to carryout conversion of various keto and aldehyde substrates to its corresponding chiral alcohol products.

4. SUMMARY

[0007] In one aspect, the present disclosure provides ketoreductase polypeptides that are capable of reducing or converting 2-[3-[3-[2-(7-chloro-2-quinoliny)] ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester ("the substrate") to (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate ("the product"), polynucleotides encoding such polypeptides, and methods for using the polypeptides. By comparison, naturally occurring ketoreductases do not display significant activity in reducing or converting the specific ketone substrate to the corresponding alcohol product.

[0008] The engineered ketoreductase polypeptides of the disclosure are derived from *Lactobacillus* species ketoreductase. As such, in some embodiments, the engineered ketoreductase polypeptides of the disclosure have an increased activity in converting the specific ketone substrate to the corresponding alcohol product as compared to the naturally-occurring wild-type ketoreductase enzymes obtained from *Lactobacillus* sp., *e.g.*, *Lactobacillus kefir* ("L. kefir"; SEQ ID NO:4), *Lactobacillus brevis* ("L. brevis"; SEQ ID NO:2), and *Lactobacillus minor* ("L. minor", SEQ ID NO:114). In some embodiments, the engineered ketoreductases have, as compared to the sequences of SEQ ID NO:2, 4, or 114, at least the following features: (1) residue corresponding to position 190 (*i.e.*, X190) is a constrained residue, and (2) residue corresponding to position 202 (*i.e.* X202) is an

aromatic residue. In some embodiments, the ketoreductases of the disclosure have, as compared to the sequences of SEQ ID NO:2, 4, or 114, at least the following features: (1) residue corresponding to position 190 (*i.e.*, X190) is a constrained residue; (2) residue corresponding to position 195 (*i.e.*, X195) is a basic, acidic, non-polar or polar residue; and (3) residue corresponding to position 202 (X202) is an aromatic residue.

[0009] In addition to the features described above, the ketoreductases can have one or more residue differences at other residue positions as compared to the sequences of SEQ ID NO:2, 4, or 114. In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: residue corresponding to X190 is a constrained residue, particularly proline; and residue corresponding to X202 is an aromatic residue, particularly tryptophan; with the proviso that the ketoreductase polypeptide has at least the preceding features, *i.e.*, residue corresponding to X190 is a constrained residue; and residue corresponding to X202 is an aromatic residue. In some embodiments, the ketoreductase polypeptide has at least the following features: residue corresponding to X190 is proline; and the residue corresponding to X202 is tryptophan.

[0010] In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: residue corresponding to X190 is a constrained residue, particularly proline; residue corresponding to X195 is a basic, acidic, non-polar or polar residue, particularly proline, arginine, lysine, aspartic acid, or asparagine; and residue corresponding to X202 is an aromatic residue, particularly tryptophan; with the proviso that the ketoreductase polypeptide has at least the preceding features, *i.e.*, residue corresponding to X190 is a constrained residue; residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and residue corresponding to X202 is an aromatic residue. In some embodiments, the ketoreductase polypeptide has at least the following features: residue corresponding to X190 is proline; the residue corresponding to X195 is proline, arginine, lysine, aspartic acid, or asparagine; and the residue corresponding to X202 is tryptophan.

[0011] In some embodiments, such as where the improved property is from a single residue difference or a specific combination of residue differences, the engineered ketoreductases may optionally include one or more conservative residue differences at other positions in the polypeptide as compared to the reference sequence. In some embodiments, the additional residue differences at other residue positions can be incorporated to produce further improvements in enzyme properties.

These improvements can be further increases in enzymatic activity for the defined substrate, but can also include increases in stereoselectivity, thermostability, solvent stability, and/or reduced product inhibition. Various residue differences that can result in one or more improved enzyme properties are provided in the detailed description. In some embodiments, these engineered ketoreductase polypeptides are based on the sequence formulas as laid out in SEQ ID NO:111, 112 and 139, or a region thereof, such as residues corresponding to residues 90 to 211. SEQ ID NO:112 is based on the wild-type amino acid sequence of the *L. kefir* ketoreductase (SEQ ID NO:4); SEQ ID NO:111 is based on the wild-type amino acid sequence of the *L. brevis* ketoreductase (SEQ ID NO:2); and SEQ ID NO:139 is based on the wild-type amino acid sequence of the *L. minor* ketoreductase (SEQ ID NO:114). The sequence formulas specify that residue corresponding to X190 is a constrained residue; residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and residue corresponding to X202 is an aromatic residue. The sequence formulas further specify features at other residue positions, as provided in the detailed description.

[0012] In some embodiments, the ketoreductase polypeptides of the disclosure are improved as compared to SEQ ID NO:2, 4, or 114 with respect to their rate of enzymatic activity, *i.e.*, their rate of converting the substrate to the product. The amount of the improvement can range from 1.5 times (or fold) the enzymatic activity of the corresponding wild-type or reference ketoreductase enzyme, to as much as 2 times, 5 times, 10 times, 20 times, 25 times, 50 times, 75 times, 100 times, or more. In some embodiments, the ketoreductase polypeptides are capable of converting the substrate to the product at a rate that is at least 5-fold, 10-fold, 25-fold, 50-fold, 75-fold, 100-fold, 150-fold, 200-fold, 250-fold, 300-fold, 500-fold, or 1000-fold over the rate displayed by the polypeptide of SEQ ID NO:4 or SEQ ID NO:90.

[0013] In some embodiments, the engineered ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinoliny)] ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, at a rate that is improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90 and capable of converting the substrate to the product with a percent stereomeric excess of at least about 95%. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110.

[0014] In some embodiments, the ketoreductase polypeptides are also capable of converting the substrate to the product with a percent stereomeric excess of at least about 99%. Exemplary

polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110. Because the reference polypeptide having the amino acid sequence of SEQ ID NO:90 is capable of converting the substrate to the product at a rate (for example, 10-20% of 1 g/L substrate converted to product in 24 hours with about 10 g/L of the KRED) and with a stereoselectivity (99% stereomeric excess) that is improved over wild-type (SEQ ID NO:4), the polypeptides herein that are improved over SEQ ID NO:90 are also improved over wild-type.

[0015] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 1-50 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 42, 44, 46, 48, 86, 88, 92, 94, 96, 100 or 102.

[0016] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 50-250 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90.

Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 10, 32, 34, 36, 50, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 98, 104, 106, and 108.

[0017] In some embodiments, the ketoreductase polypeptide is capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 250-1000 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90.

Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 12, 18, 22, 24, 26, 28, 30, 38, 40, 52, 54, 56, 58, 60, 62, and 110.

[0018] In some embodiments, the invention provides a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic

acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 1000 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

[0019] In some embodiments, the improved ketoreductase polypeptides of the disclosure also have an increased resistance to acetone as a competitive inhibitor to the conversion of the substrate to the product as compared to the reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides that have this improved acetone resistance include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 98, 104, 106, 108, and 110.

[0020] In some embodiments, the ketoreductase polypeptides are capable of converting at least about 95% of the substrate to the product in less than about 24 hours when carried out with greater than about 100 g/L of substrate and less than about 5 g/L of the polypeptide. Exemplary polypeptides that have this capability include, but are not limited to, polypeptides which comprise an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

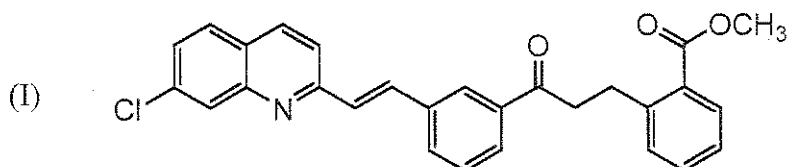
[0021] In some embodiments, the ketoreductases of the disclosure are highly stereoselective, and thus capable of reducing the substrate to the product in greater than about 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% stereomeric excess. Exemplary ketoreductase polypeptides with such high stereoselectivity include, but are not limited to, the polypeptides comprising an amino acid sequence corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110.

[0022] In another aspect, the present disclosure provides polynucleotides encoding the engineered ketoreductases described herein or polynucleotides that hybridize to such polynucleotides under highly stringent conditions. The polynucleotide can include promoters and other regulatory elements useful for expression of the encoded engineered ketoreductase, and can utilize codons optimized for specific desired expression systems. Exemplary polynucleotides include, but are not limited to, SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, or 109. Exemplary polynucleotides also include polynucleotides encoding polypeptides that correspond to the sequence formulas of SEQ ID NO: 111, 112 and 139.

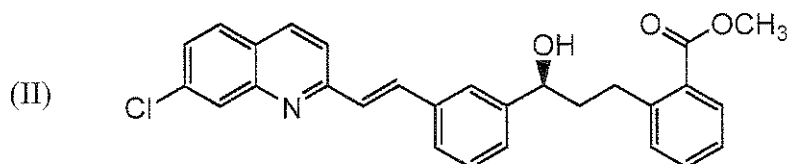
[0023] In another aspect, the present disclosure provides host cells comprising the polynucleotides and/or expression vectors described herein. The host cells may be *L. kefir* or *L. brevis* or *L. minor*, or they may be a different organism. The host cells can be used for the expression and isolation of the engineered ketoreductase enzymes described herein, or, alternatively, they can be used directly for the conversion of the substrate to the stereoisomeric product.

[0024] Whether carrying out the method with whole cells, cell extracts or purified ketoreductase enzymes, a single ketoreductase enzyme may be used or, alternatively, mixtures of two or more ketoreductase enzymes may be used.

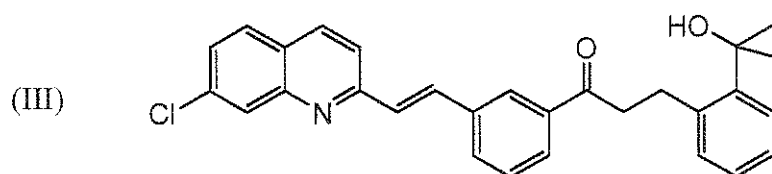
[0025] The ketoreductase enzymes described herein are capable catalyzing the reduction reaction of the keto group in the compound of structural formula (I), 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester ("the substrate"):



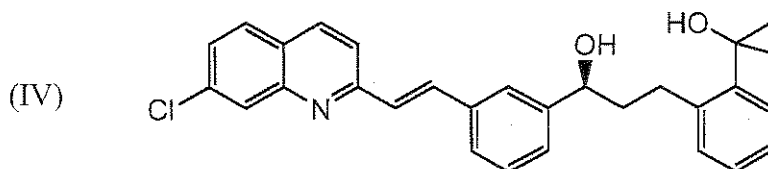
to the corresponding stereoisomeric alcohol product of structural formula (II), (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate ("the product"):



[0026] In some embodiments, the ketoreductase enzymes described herein are capable of catalyzing the reduction reaction of the keto group in the compound of structural formula (III), 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] phenyl]-2-propanol (also a "substrate"),

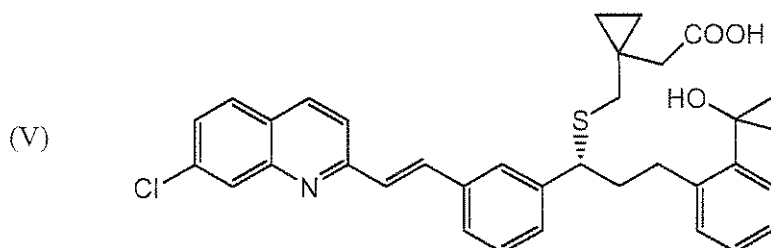


to the corresponding stereoisomeric alcohol product of structural formula (IV), (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol (also a “product” with respect to the substrate of formula (III)):



[0027] Accordingly, in some embodiments, provide herein are methods for reducing the substrate of the structural formula (I) or structural formula (III) to the corresponding alcohol product, which comprises contacting or incubating the substrate with a ketoreductase polypeptide of the disclosure under reaction conditions suitable for reducing or converting the substrate to the product of structural formula (II) or structural formula (IV), respectively.

[0028] In some embodiments, the ketoreductase polypeptides provided herein can be used in the production of intermediates for the synthesis of the compound 2-[1-[[[(1R)-1-[3-[(E)-2-(7-chloroquinolin-2-yl)ethenyl]phenyl]-3-[2-(2-hydroxypropan-2-yl)phenyl]propyl]sulfanylmethyl]cyclopropyl]acetic acid of structural formula (V):



including solvates, hydrates, and pharmaceutically acceptable salts thereof. In some embodiments, in a method for the synthesis of the compound of formula (V), a step in the method can comprise reducing or converting the substrate of formula (I) to the product of formula (II) using a ketoreductase polypeptide of the disclosure under reaction conditions suitable for reducing or converting the substrate to the product of formula (II).

[0029] In some embodiments, the intermediate of formula (IV) can also be used in the synthesis of the compound of structural formula (V). Accordingly, in some embodiments, in a method for the synthesis of the compound of formula (V), a step in the method can comprise reducing or converting the substrate of formula (III) to the product of formula (IV) by contacting the substrate with the ketoreductases disclosed herein under reaction conditions suitable for reducing or converting the substrate to the product of structural formula (IV).

[0030] In some embodiments of the method for reducing the substrate to the product, the substrate is reduced to the product in greater than about 99% stereomeric excess, wherein the ketoreductase polypeptide comprises a sequence that corresponds to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 111, or 112.

[0031] In some embodiments of the method for reducing the substrate to the product, at least about 95% of the substrate is converted to the product in less than about 24 hours when carried out with greater than about 100 g/L of substrate and less than about 5 g/L of the polypeptide, wherein the polypeptide comprises an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, or 20.

[0032] In some embodiments of this method for reducing the substrate to the product, at least about 10-20% of 1 g/L substrate is converted to the product in less than about 24 hours with about 10 g/L of the polypeptide, wherein the polypeptide comprises an amino acid sequence corresponding to 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 111, or 112.

5. BRIEF DESCRIPTION OF THE FIGURES

[0033] FIG.1 illustrates the role of ketoreductases (KRED) in the conversion of the substrate compound of formula (I) to the corresponding product of formula (II). This reduction uses a KRED described herein and a co-factor such as NADPH. A glucose dehydrogenase (GDH) is used to convert/recycle NAD(P)^+ to NAD(P)H . Glucose is converted to gluconic acid, which in turn is converted to its sodium salt (sodium gluconate) with the addition of sodium hydroxide. Alternatively, a secondary alcohol dehydrogenase (*e.g.*, a KRED) can be used to convert isopropanol to acetone and convert/recycle NAD(P)^+ to NAD(P)H .

6. DETAILED DESCRIPTION

6.1 Definitions

[0034] As used herein, the following terms are intended to have the following meanings.

[0035] “Ketoreductase” and “KRED” are used interchangeably herein to refer to a polypeptide having an enzymatic capability of reducing a carbonyl group to its corresponding alcohol. More specifically, the ketoreductase polypeptides of the invention are capable of stereoselectively reducing the compound of formula (I), *supra* to the corresponding product of formula (II), *supra*. The polypeptide typically utilizes a cofactor reduced nicotinamide adenine dinucleotide (NADH) or reduced nicotinamide adenine dinucleotide phosphate (NADPH) as the reducing agent.

Ketoreductases as used herein include naturally occurring (wild type) ketoreductases as well as non-naturally occurring engineered polypeptides generated by human manipulation.

[0036] “Coding sequence” refers to that portion of a nucleic acid (*e.g.*, a gene) that encodes an amino acid sequence of a protein.

[0037] “Naturally-occurring” or “wild-type” refers to the form found in nature. For example, a naturally occurring or wild-type polypeptide or polynucleotide sequence is a sequence present in an organism that can be isolated from a source in nature and which has not been intentionally modified by human manipulation.

[0038] “Recombinant” when used with reference to, *e.g.*, a cell, nucleic acid, or polypeptide, refers to a material, or a material corresponding to the natural or native form of the material, that has been modified in a manner that would not otherwise exist in nature, or is identical thereto but produced or derived from synthetic materials and/or by manipulation using recombinant techniques. Non-limiting examples include, among others, recombinant cells expressing genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise expressed at a different level.

[0039] “Percentage of sequence identity” and “percentage homology” are used interchangeably herein to refer to comparisons among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage may be calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Alternatively, the percentage may be calculated by determining the number of positions at which either the identical nucleic acid base or amino acid residue occurs in both sequences or a nucleic acid base or amino acid residue is aligned with a gap to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Those of skill in the art appreciate that there are many established algorithms available to align two sequences. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85:2444, by

computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the GCG Wisconsin Software Package), or by visual inspection (see generally, *Current Protocols in Molecular Biology*, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (1995 Supplement) (Ausubel)). Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., 1990, *J. Mol. Biol.* 215: 403-410 and Altschul et al., 1977, *Nucleic Acids Res.* 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as, the neighborhood word score threshold (Altschul et al, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, 1989, *Proc Natl Acad Sci USA* 89:10915). Exemplary determination of sequence alignment and % sequence identity can employ the BESTFIT or GAP programs in the GCG Wisconsin Software package (Accelrys, Madison WI), using default parameters provided.

[0040] “Reference sequence” refers to a defined sequence used as a basis for a sequence comparison. A reference sequence may be a subset of a larger sequence, for example, a segment of a full-length gene or polypeptide sequence. Generally, a reference sequence is at least 20 nucleotide or amino acid residues in length, at least 25 residues in length, at least 50 residues in length, or the full length of the nucleic acid or polypeptide. Since two polynucleotides or polypeptides may each (1) comprise a sequence (*i.e.*, a portion of the complete sequence) that is similar between the two sequences, and (2) may further comprise a sequence that is divergent between the two sequences, sequence comparisons

between two (or more) polynucleotides or polypeptide are typically performed by comparing sequences of the two polynucleotides over a “comparison window” to identify and compare local regions of sequence similarity.

[0041] In some embodiments, a “reference sequence” can be based on a primary amino acid sequence, where the reference sequence is a sequence that can have one or more changes in the primary sequence. For instance, a “reference sequence based on SEQ ID NO:4 having at the residue corresponding to X190 a proline” refers to a reference sequence in which the corresponding residue at X190 in SEQ ID NO:4 has been changed to a proline.

[0042] “Comparison window” refers to a conceptual segment of at least about 20 contiguous nucleotide positions or amino acids residues wherein a sequence may be compared to a reference sequence of at least 20 contiguous nucleotides or amino acids and wherein the portion of the sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The comparison window can be longer than 20 contiguous residues, and includes, optionally 30, 40, 50, 100, or longer windows.

[0043] “Substantial identity” refers to a polynucleotide or polypeptide sequence that has at least 80 percent sequence identity, at least 85 percent identity and 89 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 residue positions, frequently over a window of at least 30-50 residues, wherein the percentage of sequence identity is calculated by comparing the reference sequence to a sequence that includes deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. In specific embodiments applied to polypeptides, the term “substantial identity” means that two polypeptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 89 percent sequence identity, at least 95 percent sequence identity or more (*e.g.*, 99 percent sequence identity). Preferably, residue positions which are not identical differ by conservative amino acid substitutions.

[0044] “Corresponding to”, “reference to” or “relative to” when used in the context of the numbering of a given amino acid or polynucleotide sequence refers to the numbering of the residues of a specified reference sequence when the given amino acid or polynucleotide sequence is compared to the reference sequence. In other words, the residue number or residue position of a given polymer is designated with respect to the reference sequence rather than by the actual numerical position of the residue within the given amino acid or polynucleotide sequence. For example, a given amino acid sequence, such as that of an engineered ketoreductase, can be aligned to a reference sequence by

introducing gaps to optimize residue matches between the two sequences. In these cases, although the gaps are present, the numbering of the residue in the given amino acid or polynucleotide sequence is made with respect to the reference sequence to which it has been aligned.

[0045] “Stereoselectivity” refers to the preferential formation in a chemical or enzymatic reaction of one stereoisomer over another. Stereoselectivity can be partial, where the formation of one stereoisomer is favored over the other, or it may be complete where only one stereoisomer is formed. When the stereoisomers are enantiomers, the stereoselectivity is referred to as enantioselectivity, the fraction (typically reported as a percentage) of one enantiomer in the sum of both. It is commonly alternatively reported in the art (typically as a percentage) as the enantiomeric excess (e.e.) calculated therefrom according to the formula $[\text{major enantiomer} - \text{minor enantiomer}] / [\text{major enantiomer} + \text{minor enantiomer}]$. Where the stereoisomers are diastereoisomers, the stereoselectivity is referred to as diastereoselectivity, the fraction (typically reported as a percentage) of one diastereomer in a mixture of two diastereomers, commonly alternatively reported as the diastereomeric excess (d.e.). Enantiomeric excess and diastereomeric excess are types of stereomeric excess.

[0046] “Highly stereoselective” refers to a ketoreductase polypeptide that is capable of converting or reducing the substrate to the corresponding (*S*)-product with at least about 99% stereomeric excess.

[0047] “Stereospecificity” refers to the preferential conversion in a chemical or enzymatic reaction of one stereoisomer over another. Stereospecificity can be partial, where the conversion of one stereoisomer is favored over the other, or it may be complete where only one stereoisomer is converted.

[0048] “Chemoselectivity” refers to the preferential formation in a chemical or enzymatic reaction of one product over another.

[0049] “Improved enzyme property” refers to a ketoreductase polypeptide that exhibits an improvement in any enzyme property as compared to a reference ketoreductase. For the engineered ketoreductase polypeptides described herein, the comparison is generally made to the wild-type ketoreductase enzyme, although in some embodiments, the reference ketoreductase can be another improved engineered ketoreductase. Enzyme properties for which improvement is desirable include, but are not limited to, enzymatic activity (which can be expressed in terms of percent conversion of the substrate), thermal stability, solvent stability, pH activity profile, cofactor requirements, refractoriness to inhibitors (e.g., product inhibition), stereospecificity, and stereoselectivity (including enantioselectivity).

[0050] “Increased enzymatic activity” refers to an improved property of the engineered ketoreductase polypeptides, which can be represented by an increase in specific activity (e.g., product

produced/time/weight protein) or an increase in percent conversion of the substrate to the product (e.g., percent conversion of starting amount of substrate to product in a specified time period using a specified amount of KRED) as compared to the reference ketoreductase enzyme. Exemplary methods to determine enzyme activity are provided in the Examples. Any property relating to enzyme activity may be affected, including the classical enzyme properties of K_m , V_{max} or k_{cat} , changes of which can lead to increased enzymatic activity. Improvements in enzyme activity can be from about 1.5 times the enzymatic activity of the corresponding wild-type ketoreductase enzyme, to as much as 2 times, 5 times, 10 times, 20 times, 25 times, 50 times, 75 times, 100 times, or more enzymatic activity than the naturally occurring ketoreductase or another engineered ketoreductase from which the ketoreductase polypeptides were derived. In specific embodiments, the engineered ketoreductase enzyme exhibits improved enzymatic activity in the range of 1.5 to 50 times, 1.5 to 100 times greater than that of the parent ketoreductase enzyme. It is understood by the skilled artisan that the activity of any enzyme is diffusion limited such that the catalytic turnover rate cannot exceed the diffusion rate of the substrate, including any required cofactors. The theoretical maximum of the diffusion limit, or k_{cat}/K_m , is generally about 10^8 to 10^9 ($M^{-1} s^{-1}$). Hence, any improvements in the enzyme activity of the ketoreductase will have an upper limit related to the diffusion rate of the substrates acted on by the ketoreductase enzyme. Ketoreductase activity can be measured by any one of standard assays used for measuring ketoreductase, such as a decrease in absorbance or fluorescence of NADPH due to its oxidation with the concomitant reduction of a ketone to an alcohol, or by product produced in a coupled assay. Comparisons of enzyme activities are made using a defined preparation of enzyme, a defined assay under a set condition, and one or more defined substrates, as further described in detail herein. Generally, when lysates are compared, the numbers of cells and the amount of protein assayed are determined as well as use of identical expression systems and identical host cells to minimize variations in amount of enzyme produced by the host cells and present in the lysates.

[0051] “Conversion” refers to the enzymatic reduction of the substrate to the corresponding product. “Percent conversion” refers to the percent of the substrate that is reduced to the product within a period of time under specified conditions. Thus, the “enzymatic activity” or “activity” of a ketoreductase polypeptide can be expressed as “percent conversion” of the substrate to the product.

[0052] “Thermostable” refers to a ketoreductase polypeptide that maintains similar activity (more than 60% to 80% for example) after exposure to elevated temperatures (e.g., 40-80°C) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme.

[0053] “Solvent stable” refers to a ketoreductase polypeptide that maintains similar activity (more than e.g., 60% to 80%) after exposure to varying concentrations (e.g., 5-99%) of solvent

(isopropylalcohol, tetrahydrofuran, 2-methyltetrahydrofuran, acetone, toluene, butylacetate, methyl tert-butylether, etc.) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme.

[0054] "pH stable" refers to a ketoreductase polypeptide that maintains similar activity (more than e.g., 60% to 80%) after exposure to high or low pH (e.g., 4.5-6 or 8 to 12) for a period of time (e.g., 0.5-24 hrs) compared to the untreated enzyme.

[0055] "Thermo- and solvent stable" refers to a ketoreductase polypeptide that are both thermostable and solvent stable.

[0056] "Derived from" as used herein in the context of engineered ketoreductase enzymes, identifies the originating ketoreductase enzyme, and/or the gene encoding such ketoreductase enzyme, upon which the engineering was based. For example, the engineered ketoreductase enzyme of SEQ ID NO: 90 was obtained by artificially evolving, over multiple generations the gene encoding the *Lactobacillus kefir* ketoreductase enzyme of SEQ ID NO:4. Thus, this engineered ketoreductase enzyme is "derived from" the wild-type ketoreductase of SEQ ID NO: 4.

[0057] "Hydrophilic amino acid or residue" refers to an amino acid or residue having a side chain exhibiting a hydrophobicity of less than zero according to the normalized consensus hydrophobicity scale of Eisenberg *et al.*, 1984, *J. Mol. Biol.* 179:125-142. Genetically encoded hydrophilic amino acids include L-Thr (T), L-Ser (S), L-His (H), L-Glu (E), L-Asn (N), L-Gln (Q), L-Asp (D), L-Lys (K) and L-Arg (R).

[0058] "Acidic amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain exhibiting a pK value of less than about 6 when the amino acid is included in a peptide or polypeptide. Acidic amino acids typically have negatively charged side chains at physiological pH due to loss of a hydrogen ion. Genetically encoded acidic amino acids include L-Glu (E) and L-Asp (D).

[0059] "Basic amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain exhibiting a pK value of greater than about 6 when the amino acid is included in a peptide or polypeptide. Basic amino acids typically have positively charged side chains at physiological pH due to association with hydronium ion. Genetically encoded basic amino acids include L-Arg (R) and L-Lys (K).

[0060] "Polar amino acid or residue" refers to a hydrophilic amino acid or residue having a side chain that is uncharged at physiological pH, but which has at least one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Genetically encoded polar amino acids include L-Asn (N), L-Gln (Q), L-Ser (S) and L-Thr (T).

[0061] “Hydrophobic amino acid or residue” refers to an amino acid or residue having a side chain exhibiting a hydrophobicity of greater than zero according to the normalized consensus hydrophobicity scale of Eisenberg *et al.*, 1984, *J. Mol. Biol.* 179:125-142. Genetically encoded hydrophobic amino acids include L-Pro (P), L-Ile (I), L-Phe (F), L-Val (V), L-Leu (L), L-Trp (W), L-Met (M), L-Ala (A) and L-Tyr (Y).

[0062] “Aromatic amino acid or residue” refers to a hydrophilic or hydrophobic amino acid or residue having a side chain that includes at least one aromatic or heteroaromatic ring. Genetically encoded aromatic amino acids include L-Phe (F), L-Tyr (Y) and L-Trp (W). Although owing to the pKa of its heteroaromatic nitrogen atom L-His (H) it is sometimes classified as a basic residue, or as an aromatic residue as its side chain includes a heteroaromatic ring, herein histidine is classified as a hydrophilic residue or as a “constrained residue” (see below).

[0063] “Constrained amino acid or residue” refers to an amino acid or residue that has a constrained geometry. Herein, constrained residues include L-pro (P) and L-his (H). Histidine has a constrained geometry because it has a relatively small imidazole ring. Proline has a constrained geometry because it also has a five membered ring.

[0064] “Non-polar amino acid or residue” refers to a hydrophobic amino acid or residue having a side chain that is uncharged at physiological pH and which has bonds in which the pair of electrons shared in common by two atoms is generally held equally by each of the two atoms (*i.e.*, the side chain is not polar). Genetically encoded non-polar amino acids include L-Gly (G), L-Leu (L), L-Val (V), L-Ile (I), L-Met (M) and L-Ala (A).

[0065] “Aliphatic amino acid or residue” refers to a hydrophobic amino acid or residue having an aliphatic hydrocarbon side chain. Genetically encoded aliphatic amino acids include L-Ala (A), L-Val (V), L-Leu (L) and L-Ile (I).

[0066] “Cysteine” or L-Cys (C) is unusual in that it can form disulfide bridges with other L-Cys (C) amino acids or other sulfanyl- or sulfhydryl-containing amino acids. The “cysteine-like residues” include cysteine and other amino acids that contain sulfhydryl moieties that are available for formation of disulfide bridges. The ability of L-Cys (C) (and other amino acids with -SH containing side chains) to exist in a peptide in either the reduced free -SH or oxidized disulfide-bridged form affects whether L-Cys (C) contributes net hydrophobic or hydrophilic character to a peptide. While L-Cys (C) exhibits a hydrophobicity of 0.29 according to the normalized consensus scale of Eisenberg (Eisenberg *et al.*, 1984, *supra*), it is to be understood that for purposes of the present disclosure L-Cys (C) is categorized into its own unique group.

[0067] “Small amino acid or residue” refers to an amino acid or residue having a side chain that is composed of a total three or fewer carbon and/or heteroatoms (excluding the α -carbon and hydrogens). The small amino acids or residues may be further categorized as aliphatic, non-polar, polar or acidic small amino acids or residues, in accordance with the above definitions. Genetically-encoded small amino acids include L-Ala (A), L-Val (V), L-Cys (C), L-Asn (N), L-Ser (S), L-Thr (T) and L-Asp (D).

[0068] “Hydroxyl-containing amino acid or residue” refers to an amino acid containing a hydroxyl (-OH) moiety. Genetically-encoded hydroxyl-containing amino acids include L-Ser (S) L-Thr (T) and L-Tyr (Y).

[0069] “Conservative” amino acid substitutions or mutations refer to the interchangeability of residues having similar side chains, and thus typically involves substitution of the amino acid in the polypeptide with amino acids within the same or similar defined class of amino acids. However, as used herein, in some embodiments, conservative mutations do not include substitutions from a hydrophilic to hydrophilic, hydrophobic to hydrophobic, hydroxyl-containing to hydroxyl-containing, or small to small residue, if the conservative mutation can instead be a substitution from an aliphatic to an aliphatic, non-polar to non-polar, polar to polar, acidic to acidic, basic to basic, aromatic to aromatic, or constrained to constrained residue. Further, as used herein, A, V, L, or I can be conservatively mutated to either another aliphatic residue or to another non-polar residue. Table 1 below shows exemplary conservative substitutions.

Table 1: Conservative Substitutions

Residue	Possible Conservative Mutations
A, L, V, I	Other aliphatic (A, L, V, I) Other non-polar (A, L, V, I, G, M)
G, M	Other non-polar (A, L, V, I, G, M)
D, E	Other acidic (D, E)
K, R	Other basic (K, R)
P, H	Other constrained (P, H)
N, Q, S, T	Other polar
Y, W, F	Other aromatic (Y, W, F)
C	None

[0070] “Non-conservative substitution” refers to substitution or mutation of an amino acid in the polypeptide with an amino acid with significantly differing side chain properties. Non-conservative substitutions may use amino acids between, rather than within, the defined groups listed above. In one embodiment, a non-conservative mutation affects (a) the structure of the peptide backbone in the area of the substitution (*e.g.*, proline for glycine) (b) the charge or hydrophobicity, or (c) the bulk of the side chain.

[0071] “Deletion” refers to modification to the polypeptide by removal of one or more amino acids from the reference polypeptide. Deletions can comprise removal of 1 or more amino acids, 2 or more amino acids, 5 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids making up the polypeptide while retaining enzymatic activity and/or retaining the improved properties of an engineered ketoreductase enzyme. Deletions can be directed to the internal portions and/or terminal portions of the polypeptide. In various embodiments, the deletion can comprise a continuous segment or can be discontinuous.

[0072] “Insertion” refers to modification to the polypeptide by addition of one or more amino acids from the reference polypeptide. In some embodiments, the improved engineered ketoreductase enzymes comprise insertions of one or more amino acids to the naturally occurring ketoreductase polypeptide as well as insertions of one or more amino acids to other improved ketoreductase polypeptides. Insertions can be in the internal portions of the polypeptide, or to the carboxy or amino terminus. Insertions as used herein include fusion proteins as is known in the art. The insertion can be a contiguous segment of amino acids or separated by one or more of the amino acids in the naturally occurring polypeptide.

[0073] “Fragment” as used herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion, but where the remaining amino acid sequence is identical to the corresponding positions in the sequence. Fragments can be at least 14 amino acids long, at least 20 amino acids long, at least 50 amino acids long or longer, and up to 70%, 80%, 90%, 95%, 98%, and 99% of the full-length naturally-occurring ketoreductase polypeptide of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:114.

[0074] “Isolated polypeptide” refers to a polypeptide which is substantially separated from other contaminants that naturally accompany it, *e.g.*, protein, lipids, and polynucleotides. The term embraces polypeptides which have been removed or purified from their naturally-occurring environment or expression system (*e.g.*, host cell or *in vitro* synthesis). The improved ketoreductase enzymes may be present within a cell, present in the cellular medium, or prepared in various forms, such as lysates or isolated preparations. As such, in some embodiments, the improved ketoreductase enzyme can be an isolated polypeptide.

[0075] “Substantially pure polypeptide” refers to a composition in which the polypeptide species is the predominant species present (*i.e.*, on a molar or weight basis it is more abundant than any other individual macromolecular species in the composition), and is generally a substantially purified composition when the object species comprises at least about 50 percent of the macromolecular species present by mole or % weight. Generally, a substantially pure ketoreductase composition will

comprise about 60 % or more, about 70% or more, about 80% or more, about 90% or more, about 95% or more, and about 98% or more of all macromolecular species by mole or % weight present in the composition. In some embodiments, the object species is purified to essential homogeneity (*i.e.*, contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species. Solvent species, small molecules (<500 Daltons), and elemental ion species are not considered macromolecular species. In some embodiments, the isolated improved ketoreductases polypeptide is a substantially pure polypeptide composition.

[0076] “Stringent hybridization” is used herein to refer to conditions under which nucleic acid hybrids are stable. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_m) of the hybrids. In general, the stability of a hybrid is a function of ion strength, temperature, G/C content, and the presence of chaotropic agents. The T_m values for polynucleotides can be calculated using known methods for predicting melting temperatures (see, *e.g.*, Baldino et al., *Methods Enzymology* 168:761-777; Bolton et al., 1962, *Proc. Natl. Acad. Sci. USA* 48:1390; Bresslauer et al., 1986, *Proc. Natl. Acad. Sci. USA* 83:8893-8897; Freier et al., 1986, *Proc. Natl. Acad. Sci. USA* 83:9373-9377; Kierzek et al., *Biochemistry* 25:7840-7846; Rychlik et al., 1990, *Nucleic Acids Res* 18:6409-6412 (erratum, 1991, *Nucleic Acids Res* 19:698); Sambrook et al., *supra*); Suggs et al., 1981, In *Developmental Biology Using Purified Genes* (Brown et al., eds.), pp. 683-693, Academic Press; and Wetmur, 1991, *Crit Rev Biochem Mol Biol* 26:227-259. All publications incorporate herein by reference). In some embodiments, the polynucleotide encodes the polypeptide disclosed herein and hybridizes under defined conditions, such as moderately stringent or highly stringent conditions, to the complement of a sequence encoding an engineered ketoreductase enzyme of the present disclosure.

[0077] “Hybridization stringency” relates to hybridization conditions, such as washing conditions, in the hybridization of nucleic acids. Generally, hybridization reactions are performed under conditions of lower stringency, followed by washes of varying but higher stringency. The term “moderately stringent hybridization” refers to conditions that permit target-DNA to bind a complementary nucleic acid that has about 60% identity, preferably about 75% identity, about 85% identity to the target DNA; with greater than about 90% identity to target-polynucleotide. Exemplary moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C., followed by washing in 0.2×SSPE, 0.2% SDS, at 42°C. “High stringency hybridization” refers generally to conditions that are about 10°C or less from the thermal melting temperature T_m as determined under the solution condition for a defined polynucleotide sequence. In some embodiments, a high stringency condition refers to conditions that permit

hybridization of only those nucleic acid sequences that form stable hybrids in 0.018M NaCl at 65°C. (*i.e.*, if a hybrid is not stable in 0.018M NaCl at 65°C, it will not be stable under high stringency conditions, as contemplated herein). High stringency conditions can be provided, for example, by hybridization in conditions equivalent to 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C, followed by washing in 0.1×SSPE, and 0.1% SDS at 65°C. Another high stringency condition is hybridizing in conditions equivalent to hybridizing in 5X SSC containing 0.1% (w:v) SDS at 65°C and washing in 0.1x SSC containing 0.1% SDS at 65°C. Other high stringency hybridization conditions, as well as moderately stringent conditions, are described in the references cited above.

[0078] “Heterologous” polynucleotide refers to any polynucleotide that is introduced into a host cell by laboratory techniques, and includes polynucleotides that are removed from a host cell, subjected to laboratory manipulation, and then reintroduced into a host cell.

[0079] “Codon optimized” refers to changes in the codons of the polynucleotide encoding a protein to those preferentially used in a particular organism such that the encoded protein is efficiently expressed in the organism of interest. Although the genetic code is degenerate in that most amino acids are represented by several codons, called “synonyms” or “synonymous” codons, it is well known that codon usage by particular organisms is nonrandom and biased towards particular codon triplets. This codon usage bias may be higher in reference to a given gene, genes of common function or ancestral origin, highly expressed proteins versus low copy number proteins, and the aggregate protein coding regions of an organism's genome. In some embodiments, the polynucleotides encoding the ketoreductases enzymes may be codon optimized for optimal production from the host organism selected for expression.

[0080] “Preferred,” “optimal,” or “high codon usage bias codons” refers interchangeably to codons that are used at higher frequency in the protein coding regions than other codons that code for the same amino acid. The preferred codons may be determined in relation to codon usage in a single gene, a set of genes of common function or origin, highly expressed genes, the codon frequency in the aggregate protein coding regions of the whole organism, codon frequency in the aggregate protein coding regions of related organisms, or combinations thereof. Codons whose frequency increases with the level of gene expression are typically optimal codons for expression. A variety of methods are known for determining the codon frequency (*e.g.*, codon usage, relative synonymous codon usage) and codon preference in specific organisms, including multivariate analysis, for example, using cluster analysis or correspondence analysis, and the effective number of codons used in a gene (see GCG CodonPreference, Genetics Computer Group Wisconsin Package; CodonW, John Peden, University of Nottingham; McInerney, J. O, 1998, *Bioinformatics* 14:372-73; Stenico et al., 1994, *Nucleic Acids*

Res. 222437-46; Wright, F., 1990, *Gene* 87:23-29). Codon usage tables are available for a growing list of organisms (see for example, Wada et al., 1992, *Nucleic Acids Res.* 20:2111-2118; Nakamura et al., 2000, *Nucl. Acids Res.* 28:292; Duret, et al., *supra*; Henaut and Danchin, "Escherichia coli and Salmonella," 1996, Neidhardt, et al. Eds., ASM Press, Washington D.C., p. 2047-2066. The data source for obtaining codon usage may rely on any available nucleotide sequence capable of coding for a protein. These data sets include nucleic acid sequences actually known to encode expressed proteins (e.g., complete protein coding sequences-CDS), expressed sequence tags (ESTS), or predicted coding regions of genomic sequences (see for example, Mount, D., *Bioinformatics: Sequence and Genome Analysis*, Chapter 8, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; Uberbacher, E. C., 1996, *Methods Enzymol.* 266:259-281; Tiwari et al., 1997, *Comput. Appl. Biosci.* 13:263-270).

[0081] "Control sequence" is defined herein to include all components, which are necessary or advantageous for the expression of a polynucleotide and/or polypeptide of interest. Each control sequence may be native or foreign to the nucleic acid sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleic acid sequence encoding a polypeptide.

[0082] "Operably linked" is defined herein as a configuration in which a control sequence is appropriately placed (*i.e.*, in a functional relationship) at a position relative to a polynucleotide of interest such that the control sequence directs or regulates the expression of the polynucleotide and/or polypeptide of interest.

[0083] "Promoter sequence" is a nucleic acid sequence that is recognized by a host cell for expression of a polynucleotide of interest, such as a coding sequence. The control sequence may comprise an appropriate promoter sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of a polynucleotide of interest. The promoter may be any nucleic acid sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

6.2 Ketoreductase Enzymes

[0084] The present disclosure provides engineered ketoreductase (“KRED”) enzymes that are capable of stereoselectively reducing or converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate and having an improved property when compared with the naturally-occurring, wild-type KRED enzyme obtained from *L. kefir* (SEQ ID NO:4) or *L. brevis* (SEQ ID NO:2) or *L. minor* (SEQ ID NO:114) or when compared with other engineered ketoreductase enzymes. The product compound is useful in the synthesis of Montelukast, also known under the name Singulair®, a leukotriene receptor antagonist used as a therapeutic for treatment of allergies and in the management of asthma. As shown herein, the wild-type enzyme from *L. kefir* does not reduce or convert 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at any significant rate. In contrast, the ketoreductases of the disclosure are capable of reducing or converting the specified substrate to the product at appreciable levels. In some embodiments, the ketoreductase polypeptides of the disclosure have the requirement that: (1) the residue corresponding to position 190 (*i.e.*, X190) of SEQ ID NO:2, 4 or 114 is a constrained residue; and (2) the residue corresponding to position 202 (*i.e.*, X202) of SEQ ID NO:2, 4 or 114 is an aromatic residue. In some embodiments, the improved ketoreductase polypeptides have the requirement that: (1) the residue corresponding to position 190 (*i.e.*, X190) of SEQ ID NO:2, 4 or 114 is a constrained residue; (2) the residue corresponding to position 195 (*i.e.*, X195) of SEQ ID NO:2, 4 or 114 is a basic, acidic, non-polar or polar residue; and (3) the residue corresponding to position 202 (*i.e.*, X202) of SEQ ID NO:2, 4 or 114 is an aromatic residue.

[0085] As noted above, the ketoreductases of the disclosure can be described in reference to the amino acid sequence of a naturally occurring ketoreductase of *Lactobacillus kefir*, *Lactobacillus brevis*, or *Lactobacillus minor* (also referred to as “ADH” or “alcohol dehydrogenase”) or another engineered ketoreductase. As such, the amino acid residue position is determined in the ketoreductases beginning from the initiating methionine (M) residue (*i.e.*, M represents residue position 1), although it will be understood by the skilled artisan that this initiating methionine residue may be removed by biological processing machinery, such as in a host cell or *in vitro* translation system, to generate a mature protein lacking the initiating methionine residue. The amino acid residue position at which a particular amino acid or amino acid change is present in an amino acid sequence is sometimes describe herein in terms “Xn”, or “position n”, where n refers to the residue position. Where the amino acid residues at the same residue position differ between the ketoreductases, the different residues may be denoted by an “/” with the arrangement being “kefir residue/brevis

residue/minor residue". A substitution mutation, which is a replacement of an amino acid residue in a reference sequence, for example the wild-type ketoreductases of SEQ ID NO:2 and SEQ ID NO:4 and SEQ ID NO:114, with a different amino acid residue may be denoted by the symbol "→". Herein, mutations are sometimes described as a mutation "to a" type of amino acid. For example, residue 96 of SEQ ID NO:4 can be mutated "to an" aliphatic residue. But the use of the phrase "to a" does not exclude mutations from one amino acid of a class to another amino acid of the same class. For example, residue 96 of SEQ ID NO:4 is a polar residue, serine, but it can be mutated to a different polar residue; for example, the mutation can be a "S96T" (96→T) mutation. The amino acid sequence of the naturally occurring ketoreductase (also referred to as "ADH" or "alcohol dehydrogenase") of *Lactobacillus kefir*, *Lactobacillus brevis*, or of *Lactobacillus minor*, can be obtained from the polynucleotide known to encode the ketoreductase activity (e.g., Genbank accession no. AAP94029 GI:33112056 or SEQ ID NO:3 for *Lactobacillus kefir*; Genbank accession no. CAD66648 GI:28400789 or SEQ ID NO:1 for *Lactobacillus brevis*; and SEQ ID NO:113 for *Lactobacillus minor*).

[0086] In some embodiments, the improved property of the ketoreductase polypeptide, as compared to wild-type or another engineered polypeptide, is with respect to an increase in its activity for reducing or converting the substrate of formula (I), 2-[3-[3-[2-(7-chloro-2-quinoliny) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester, to its corresponding (S)-alcohol product of formula (II), (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate. In some embodiments, the increases in enzymatic activity can be manifested in an increase in its rate of conversion of the substrate to the product or manifested by the ability to use less of the improved polypeptide as compared to the wild-type or another reference sequence (for example, SEQ ID NO:90) to reduce or convert the same amount of product. In some embodiments, the improved property of the ketoreductase property is with respect to an increase in stereoselectivity in reducing the substrate to product, i.e., herein, an increase in the stereomeric excess of the product. In some embodiments, the improved property of the ketoreductase polypeptide is with respect to its stability or thermostability. In some embodiments, the ketoreductase polypeptide has more than one improved property, such as increased enzymatic activity and increased stereoselectivity.

[0087] In some embodiments, the ketoreductase polypeptides herein can have a number of modifications to the reference sequence (e.g., naturally occurring polypeptide or an engineered polypeptide), which in some embodiments can result in an improved ketoreductase property. As used herein, "modifications" include amino acid substitutions, deletions, and insertions. Any one or a combination of modifications can be introduced into the naturally occurring or engineered polypeptide to generate engineered enzymes. In such embodiments, the number of modifications to

the amino acid sequence can comprise one or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acids, 5 or more amino acids, 6 or more amino acids, 8 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 10% of the total number of amino acids, up to 15% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids of the reference polypeptide sequence. In some embodiments, the number of modifications to the naturally occurring polypeptide or an engineered polypeptide that produces an improved ketoreductase property may comprise from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 modifications of the reference sequence. In some embodiments, the number of modifications can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 amino acid residues. The modifications can comprise insertions, deletions, substitutions, or combinations thereof.

[0088] In some embodiments, the modifications comprise amino acid substitutions to the reference sequence. Substitutions that can produce an improved ketoreductase property may be at one or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acids, 5 or more amino acids, 6 or more amino acids, 8 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 10% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids of the reference enzyme sequence. In some embodiments, the number of substitutions to the naturally occurring polypeptide or an engineered polypeptide that produces an improved ketoreductase property can comprise from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 amino acid substitutions of the reference sequence. In some embodiments, the number of substitutions can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 amino acid residues.

[0089] In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: residue corresponding to position X190 is a constrained residue, particularly proline; and residue corresponding to X202 is an aromatic residue, particularly tryptophan, with the proviso that the ketoreductase polypeptide has an amino sequence in which the residue corresponding to X190 is a constrained residue, and the residue corresponding to X202 is an aromatic residue. In some embodiments, the residue corresponding to X190 is proline. In some embodiments, the residue corresponding to X202 is tryptophan. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is

proline, and the residue corresponding to X202 is tryptophan. In some embodiments, these ketoreductase polypeptides can have one or more residue differences at other residue positions as compared to the reference amino acid sequence. The differences can include various modifications, such as substitutions, deletions, and insertions. The substitutions can be non-conservative substitutions, conservative substitutions, or a combination of non-conservative and conservative substitutions. In some embodiments, these ketoreductase polypeptides can have optionally from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, or about 1-50 residue differences at other amino acid residue positions as compared to the reference sequence. In some embodiments, the number of difference can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35, 40, 45, or 50 residue differences at other amino acid residues as compared to the reference sequence.

[0090] In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: residue corresponding to position X190 is a constrained residue, particularly proline; residue corresponding to X195 is a basic, acidic, non-polar, or polar residue, particularly proline, arginine, lysine, aspartic acid, or asparagine; and residue corresponding to X202 is an aromatic residue, particularly tryptophan; with the proviso that the ketoreductase polypeptide comprises an amino acid sequence having at least the preceding features, *i.e.*, the residue corresponding to position X190 is a constrained residue; the residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and the residue corresponding to X202 is an aromatic residue. In some embodiments, the residue corresponding to X190 is proline. In some embodiments, the residue corresponding to X195 is arginine. In some embodiments, the residue corresponding to X202 is tryptophan. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is proline; the residue corresponding to X195 is proline, arginine, lysine, aspartic acid, or asparagine, particularly arginine; and the residue corresponding to X202 is tryptophan. In some embodiments, these ketoreductase polypeptides can have one or more residue differences at other residue positions as compared to the reference amino acid sequence. The differences can include various modifications, such as substitutions, deletions, and insertions. The substitutions can be non-conservative substitutions, conservative substitutions, or a combination of non-conservative and conservative substitutions. In some embodiments, these ketoreductase polypeptides can have optionally from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35, 1-40, 1-45, or about 1-50 residue differences at other amino acid residue positions as compared to the reference sequence. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30,

35, 40, 45 or 50 residue differences at other amino acid residue positions as compared to the reference sequence.

[0091] In some embodiments, an improved ketoreductase polypeptide comprises an amino acid sequence based on a sequence formula as laid out in SEQ ID NO:111 or SEQ ID NO:112 or SEQ ID NO:139, or a region thereof, such as residues corresponding to 90-211. SEQ ID NO:112 is based on the wild-type amino acid sequence of the *Lactobacillus kefir* ketoreductase (SEQ ID NO:4); SEQ ID NO:111 is based on the wild-type amino acid sequence of the *Lactobacillus brevis* ketoreductase (SEQ ID NO:2); and SEQ ID NO:139 is based on the wild-type amino acid sequence of the *Lactobacillus minor* ketoreductase (SEQ ID NO:114). The ketoreductases based on the sequence formula of SEQ ID NO: 111, 112, or 139 specify that the residue corresponding to X190 is a constrained residue; residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and X202 is an aromatic residue. In some embodiments of the sequence formula of SEQ ID NO:111, 112, or 139, the residue corresponding to X190 is proline; and the residue corresponding to X202 is tryptophan. In some embodiments of the sequence formula of SEQ ID NO:111, 112, or 139, the residue corresponding to X190 is proline; the residue corresponding to X195 is proline, arginine, lysine, aspartic acid, or asparagine, particularly arginine; and the residue corresponding to X202 is tryptophan. The sequence formula further specifies features for various residue positions, as described below.

[0092] In some embodiments, the ketoreductase polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, and having the specified features for the residues corresponding to X190 and X202 or the specified features for the residues corresponding to X190, X195 and X202 as described herein, can further include one or more of the features selected from the following, as provided in the sequence formulas: residue corresponding to X7 is a constrained or non-polar residue; residue corresponding to X17 is a non-polar or aliphatic residue; residue corresponding to X25 is a polar or acidic residue; residue corresponding to X27 is an aromatic residue; residue corresponding to X41 is a polar, aliphatic, or non-polar residue; residue corresponding to X53 is a polar, non-polar, or acidic residue; residue corresponding to X57 is a non-polar or aliphatic residue; residue corresponding to X64 is a polar, aliphatic, or non-polar residue; residue corresponding to X66 is an acidic residue; residue corresponding to X68 is a polar, acidic, aliphatic, or non-polar residue; residue corresponding to X72 is a basic residue; residue corresponding to X76 is an aliphatic, non-polar, or polar residue; residue corresponding to X80 is an aliphatic, non-polar, or polar residue; residue corresponding to X93 is a polar, aliphatic, or non-polar residue; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue; residue corresponding to X95 is an aliphatic, non-polar, or acidic residue; residue

corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue; residue corresponding to X97 is a basic, constrained or polar residue; residue corresponding to X100 is a basic, acidic, polar, aliphatic, or non-polar residue; residue corresponding to X108 is a basic or constrained residue; residue corresponding to X111 is a non-polar or aliphatic residue; residue corresponding to X139 is a non-polar or aliphatic residue; residue corresponding to X145 is an acidic, aliphatic, or non-polar residue; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue; residue corresponding to X148 is a non-polar or aliphatic residue; residue corresponding to X151 is a constrained, non-polar or aliphatic residue; residue corresponding to X152 is a polar, aromatic, aliphatic, or non-polar residue; residue corresponding to X163 is a non-polar or aliphatic residue; residue corresponding to X165 is a polar, non-polar or aliphatic residue; residue corresponding to X173 is an acidic, non-polar or aliphatic residue; residue corresponding to X179 is an aromatic, basic, aliphatic, or non-polar residue; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue; residue corresponding to X196 is a non-polar or aliphatic residue; residue corresponding to X197 is an acidic residue; residue corresponding to X198 is an acidic or polar residue; residue corresponding to X210 is a polar or basic residue; residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue; residue corresponding to X212 is a polar, aliphatic, or non-polar residue; residue corresponding to X216 is a constrained or basic residue; residue corresponding to X223 is a non-polar or aliphatic residue; residue corresponding to X226 is a non-polar or polar residue; residue corresponding to X233 is a polar or acidic residue; residue corresponding to X235 is a polar or aromatic residue; residue corresponding to X248 is a non-polar or aromatic residue; and residue corresponding to X249 is an aromatic residue. In some embodiments, the amino acid sequence can have at least two, three, four, five, six or more of the features. In some embodiments, the polypeptides comprising an amino acid sequence that is based on the sequence formula of SEQ ID NO: 111, 112, or 139 (or region thereof) can have additionally one or more residue differences at residue positions not specified by X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions not defined by X above. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0093] In some embodiments, the polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or region thereof, such as residues 90-211, can have one or more conservative mutations as compared to the amino acid sequences of SEQ ID NO: 2, 4 or 114. Exemplary conservative mutations include amino acid replacements such as, but not limited

to: replacement of residue corresponding to X27 phenylalanine (F) with another aromatic residue, *e.g.*, tyrosine; replacement of residue corresponding to X57 isoleucine (I) with another non-polar or aliphatic residue, *e.g.*, valine; replacement of residue corresponding to X64 alanine (A) with another non-polar or aliphatic residue, *e.g.*, valine; replacement of residue corresponding to X66 aspartic acid (D) with another acidic residue, *e.g.*, glutamic acid; replacement of residue X72 lysine (K) with another basic residue, *e.g.*, arginine; replacement of residue corresponding to X80 alanine (V) with another non-polar or aliphatic residue, *e.g.*, valine; replacement of residue corresponding to X93 isoleucine (I) with another polar residue, *e.g.*, serine; replacement of residue corresponding to X94 alanine (A) with another non-polar residue, *e.g.*, glycine; replacement of residue corresponding to X95 valine (V) with another non-polar or aliphatic residue, *e.g.*, leucine; and replacement of residue corresponding to X96 serine (S) with another polar residue, *e.g.*, threonine; replacement of residue corresponding to X148 valine (V) with another non-polar or aliphatic residue, *e.g.*, isoleucine; replacement of residue corresponding to X152 threonine with another polar residue, *e.g.*, serine; replacement of residue corresponding to X163 valine (V) with another non-polar or aliphatic residue, *e.g.*, isoleucine; replacement of corresponding to X179 tyrosine (Y) with another aromatic residue, *e.g.*, phenylalanine; replacement of residue X196 valine (V) with another aliphatic residue, *e.g.*, leucine; replacement of residue X198 aspartic acid (D) with another acidic residue, *e.g.*, glutamic acid; replacement of residue X223 isoleucine (I) with another non-polar or aliphatic residue, *e.g.*, valine; and replacement of residue corresponding to X249 tyrosine (Y) with another aromatic residue, *e.g.*, tryptophan.

[0094] In some embodiments, the ketoreductase polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features for the residues corresponding to X190 and X202, or the specified features for the residues corresponding to X190, X195 and X202, as described herein, can further include one or more of the features selected from the following: residue corresponding to X7 is histidine, proline, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glycine or histidine; residue corresponding to X17 is glycine, methionine, alanine, valine, leucine, isoleucine, particularly methionine; residue corresponding to X25 is glutamic acid, aspartic acid, serine, threonine, glutamine, or asparagine, particularly threonine or aspartic acid; residue corresponding to X27 is tyrosine, phenylalanine, tryptophan, particularly tyrosine; residue corresponding to X41 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly serine or alanine; residue corresponding to X53 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, isoleucine, aspartic acid, or glutamic acid, particularly threonine, glycine, or aspartic acid; residue corresponding to X57 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine; residue corresponding to X64 is serine,

threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly serine, alanine, or valine; residue corresponding to X66 is aspartic acid or glutamic acid; residue corresponding to X68 is serine, threonine, glutamine, asparagine, aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly threonine, aspartic acid, alanine, valine, or glutamic acid; residue corresponding to X72 is lysine or arginine, particularly arginine; residue corresponding to X76 is serine, threonine, glutamine, asparagine, glycine, alanine, valine, leucine, or isoleucine, particularly alanine or threonine; residue corresponding to X80 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine or isoleucine, particularly alanine, threonine, or valine; residue corresponding to X93 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine or isoleucine, particularly isoleucine, serine, alanine, or glycine; residue corresponding to X94 is cysteine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly cysteine, glycine, or alanine; residue corresponding to X95 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine, leucine, or glutamic acid; residue corresponding to X96 is cysteine, serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X97 is lysine, arginine, histidine, proline, serine, threonine, glutamine, or asparagine, particularly lysine, histidine, or serine; residue corresponding to X100 is lysine, arginine, serine, threonine, glutamine, asparagine, glycine, alanine, valine, leucine, or isoleucine, particularly glutamic acid, lysine, glutamine, or alanine; residue corresponding to X108 is arginine, lysine, histidine or proline, particularly arginine or histidine; residue corresponding to X111 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly methionine; residue corresponding to X139 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly leucine; residue corresponding to X145 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glutamic acid or leucine; residue corresponding to X147 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly phenylalanine or leucine; residue corresponding to X148 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly isoleucine; residue corresponding to X151 is proline, histidine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine; residue corresponding to X152 is serine, threonine, glutamine, asparagine, tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly threonine, tryptophan, alanine or serine; residue corresponding to X163 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly isoleucine; residue corresponding to X165 is serine, threonine, glutamine asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly asparagine; residue corresponding to X173 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, isoleucine, particularly valine; residue

corresponding to X179 is tyrosine, phenylalanine, tryptophan, arginine, lysine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly tyrosine, phenylalanine, lysine, or leucine; residue corresponding to X194 is proline, histidine, serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly proline, glutamine, serine, or leucine; residue corresponding to X196 is glycine, methionine, alanine, valine, leucine or isoleucine, particularly leucine; residue corresponding to X197 is aspartic acid or glutamic acid, particularly glutamic acid; residue corresponding to X198 is aspartic acid, glutamic acid, serine, threonine, glutamine, or asparagine, particularly aspartic acid, glutamic acid, or glutamine; residue corresponding to X210 is arginine, lysine, serine, threonine, glutamine, or asparagine, particularly threonine or arginine; residue corresponding to X211 is lysine, arginine, aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, or asparagine, particularly lysine, valine, leucine, arginine, threonine, aspartic acid, or isoleucine; residue corresponding to X212 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly threonine, serine, or valine; residue corresponding to X216 is proline, histidine, arginine or lysine, particularly histidine or arginine; residue corresponding to X223 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine; residue corresponding to X226 is glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, or asparagine, particularly threonine; residue corresponding to X233 is serine, threonine, glutamine, asparagine, aspartic acid, glutamic acid, particularly asparagine or aspartic acid; residue corresponding to X235 is serine, threonine, glutamine, asparagine, tyrosine, phenylalanine, tryptophan, particularly serine or tryptophan; residue corresponding to X248 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, or tryptophan, particularly glycine or tryptophan; and residue corresponding to X249 is tyrosine, phenylalanine, or tryptophan, particularly tryptophan. In some embodiments, the amino acid sequence can have at least two, three, four, five, six or more of the additional features defined by X above. In some embodiments, the ketoreductase polypeptides comprising an amino acid sequence that is based on the sequence formula of SEQ ID NO: 111, 112, or 139 (or region thereof) can have additionally one or more residue differences at residue positions not specified by an X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions not defined by X above. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or 40 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0095] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; and residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine. In some embodiments, the ketoreductase polypeptide can have in addition to the foregoing features, one or more of the following features: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptide can have in addition to the foregoing features, one or more of the following features: residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X64 is a polar, non-polar or aliphatic residue, particularly valine; residue corresponding to X80 is an aliphatic, non-polar or polar residue, particularly threonine; residue corresponding to X100 is a basic, acidic, polar, aliphatic or non-polar residue, particularly lysine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptide can have in addition to the foregoing features, one or more of the following features: residue corresponding to X25 is a polar or acidic residue, particularly threonine; residue corresponding to X41 is a polar, aliphatic, or non-polar residue, particularly serine or alanine; residue corresponding to X53 is a polar, non-polar, or acidic residue, particularly aspartic acid; residue corresponding to X57 is a non-polar or aliphatic residue, particularly valine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X68 is a polar, acidic, aliphatic, or non-polar residue, particularly valine; residue corresponding to X72 is a basic residue, particularly arginine; residue corresponding to X76 is an aliphatic, non-polar, or polar residue, particularly alanine; residue corresponding to X95 is an aliphatic, non-polar, or acidic residue, particularly leucine or glutamic acid; residue corresponding to X97 is a basic, constrained or polar residue, particularly histidine; residue corresponding to X108 is a basic or constrained residue, particularly histidine; residue corresponding to X111 is a non-polar or aliphatic residue, particularly

methionine; residue corresponding to X139 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X145 is an acidic, aliphatic, or non-polar residue, particularly leucine or glutamine; residue corresponding to X148 is a non-polar or aliphatic residue, particularly isoleucine; residue corresponding to X151 is a constrained, non-polar or aliphatic residue, particularly alanine; residue corresponding to X152 is a polar, aromatic, aliphatic, or non-polar residue, particularly serine; residue corresponding to X163 is a non-polar or aliphatic residue, particularly isoleucine; residue corresponding to X165 is a polar, non-polar or aliphatic residue, particularly asparagine; residue corresponding to X173 is an acidic, non-polar or aliphatic residue, particularly valine; residue corresponding to X179 is an aromatic, basic, aliphatic, or non-polar residue, particularly phenylalanine; residue corresponding to X197 is an acidic residue, particularly glutamic acid; residue corresponding to X210 is a polar or basic residue, particularly arginine; residue corresponding to X212 is a polar, aliphatic, or non-polar residue, particularly valine or serine; residue corresponding to X223 is a non-polar or aliphatic residue, particularly valine; residue corresponding to X226 is a non-polar or polar residue, particularly threonine; residue corresponding to X233 is a polar or acidic residue, particularly asparagine or aspartic acid; residue corresponding to X235 is a polar or aromatic residue, particularly tryptophan; residue corresponding to X248 is a non-polar or aromatic residue, particularly glycine or tryptophan; and residue corresponding to X249 is an aromatic residue, particularly tryptophan. As will be apparent to the skilled artisan, various combinations of the features in the foregoing groups can be used to form the ketoreductases of the disclosure.

[0096] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0097] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; and residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0098] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid

residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0100] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0101] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a

cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0102] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine or leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, isoleucine, leucine, or valine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0103] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic or non-polar residue, particularly cysteine, threonine, valine, leucine, or isoleucine; residue corresponding to X100 is a basic, acidic, polar, aliphatic or non-polar residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; residue corresponding to X152 is a polar, aromatic, aliphatic, or non-polar residue, particularly serine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0104] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine or glycine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly isoleucine, leucine or threonine; residue corresponding to X147 is an

aromatic, aliphatic or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, valine, leucine, or isoleucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0105] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes one or more or at least all of the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X64 is a polar, non-polar or aliphatic residue, particularly valine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X80 is an aliphatic, non-polar or polar residue, particularly threonine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine or glycine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly isoleucine, leucine or threonine; residue corresponding to X100 is a basic, acidic, polar, aliphatic, non-polar residue or constrained residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, valine, leucine, or

isoleucine; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0106] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X7 is constrained or non-polar residue, particularly glycine or histidine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0107] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22,

1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0108] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X25 is a polar or acidic residue, particularly threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residues as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0109] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X27 is an aromatic residue, particularly tyrosine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue

differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0110] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X53 is a polar, non-polar, or acidic residue, particularly aspartic acid. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0111] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X64 is a non-polar or aliphatic residue, particularly valine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino

acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0112] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X80 is an aliphatic, non-polar, or polar residue, particularly valine or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0113] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the

preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0114] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly glycine or cysteine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0115] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly valine, leucine, isoleucine, threonine, or cysteine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0116] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X100 is a basic, acidic, polar, aliphatic, or non-polar residue, particularly lysine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0117] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X108 is a basic or constrained residue, particularly histidine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0118] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-

211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0119] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X151 is a constrained, non-polar or aliphatic residue, particularly alanine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0120] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at

least the following additional feature: residue corresponding to X165 is a polar, non-polar or aliphatic residue, particularly asparagine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0121] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X173 is an acidic, non-polar or aliphatic residue, particularly valine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0122] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly serine, glutamine, or leucine. In some embodiments, the

ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0123] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0124] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid or glutamine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as

compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0125] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X210 is a polar or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0126] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16,

18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0127] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X212 is polar, aliphatic, or non-polar residue, particularly valine or serine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0128] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X216 is a is constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino

acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0129] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X223 is a non-polar or aliphatic residue, particularly valine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0130] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional feature: residue corresponding to X226 is a non-polar or polar residue, particularly threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the

preceding features, with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0131] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; and the residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:48). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:48), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0132] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; and the residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:42, 44, 46, or

90). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:42, 44, 46, or 90), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0133] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; the residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and the residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:88, 94 or 102). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:88, 94 or 102), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0134] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-

polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, glutamine or serine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:98). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:98), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0135] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residues as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:84). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence

that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:84), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0136] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; the residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:64). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:64), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0137] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue,

particularly methionine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X64 is a polar, non-polar or aliphatic residue, particularly valine; residue corresponding to X80 is an aliphatic, non-polar, or polar residue, particularly threonine or valine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X100 is a basic, acidic, polar, or aliphatic, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:22 or 24). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:22 or 24), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0138] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X194 is a constrained, polar, or non-polar residue, particularly asparagine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid or asparagine; residue corresponding

to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:58). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:58), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0139] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X66 is an acidic residue, particularly glutamic acid; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly cysteine, threonine, valine, leucine, or isoleucine; residue corresponding to X147 is an aromatic or aliphatic residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; and residue corresponding to X211 is a basic, aliphatic, or non-polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:40). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:40), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0140] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X64 is a non-polar or aliphatic residue, particularly valine; residue corresponding to X80 is an aliphatic, non-polar or polar residue, particularly threonine or valine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X100 is a basic, acidic, polar, non-polar or aliphatic residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X194 is a constrained, polar, or non-polar residue, particularly asparagine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid or asparagine; residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:14 or 16). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:14 or 16), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0141] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X25 is a polar or acidic residue, particularly threonine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X53 is a polar, non-polar, or acidic residue, particularly aspartic acid; residue corresponding to X64 is a non-polar or aliphatic residue, particularly valine; residue corresponding to X80 is an aliphatic, non-polar or polar residue, particularly threonine or valine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X100 is a basic, acidic, polar, non-polar or aliphatic residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X194 is a constrained, polar, or non-polar residue, particularly asparagine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid or asparagine; residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:6). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:6), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0142] In some embodiments, an improved ketoreductase comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 111, 112, or 139, or a region thereof, such as residues 90-211, having the specified features at residues corresponding to X190 and X202 or the specified

features at residues corresponding to X190, X195 and X202 as described herein, further includes at least the following additional features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X25 is a polar or acidic residue, particularly threonine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X53 is a polar, non-polar, or acidic residue, particularly aspartic acid; residue corresponding to X64 is a non-polar or aliphatic residue, particularly valine; residue corresponding to X76 is an aliphatic, non-polar or polar residue, particularly alanine; residue corresponding to X80 is an aliphatic, non-polar or polar residue, particularly threonine or valine; residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X100 is a basic, acidic, polar, non-polar or aliphatic residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly phenylalanine or leucine; residue corresponding to X194 is a constrained, polar, or non-polar residue, particularly asparagine or leucine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid or asparagine; residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine; and residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-26, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:8). In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features (*e.g.*, SEQ ID NO:8), with the proviso that the ketoreductase has an amino acid sequence having at least the preceding features.

[0143] In some embodiments, the improved ketoreductases of the disclosure comprises an amino acid sequence that has a region or domain corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 in which the residue corresponding to X190 is a constrained residue, and the residue corresponding to X202 is an aromatic residue. In some embodiments, the domain or region corresponding to residues 90-211 comprises an amino acid sequence in which the residue

corresponding to X190 is proline, and the residue corresponding to X202 is a tryptophan. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residue positions in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with a domain or region that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features at residues corresponding to X190 and X202, with the proviso that the ketoreductase domain or region comprises an amino acid sequence having at least the preceding features.

[0144] In some embodiments, the improved ketoreductases of the disclosure comprises an amino acid sequence that has a region or domain corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 in which the residue corresponding to X190 is a constrained residue; residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and the residue corresponding to X202 is an aromatic residue. In some embodiments, the domain or region corresponding to residues 90-211 comprises an amino acid sequence in which the residue corresponding to X190 is proline; residue corresponding to X195 is proline, arginine, lysine, aspartic acid, or asparagine, particularly arginine; and the residue corresponding to X202 is tryptophan. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with a domain or region that is at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding features at residues corresponding to X190, X195 and X202, with the proviso that the ketoreductase domain or region comprises an amino acid sequence having at least the preceding features.

[0145] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202, or the specified features at residues corresponding to X190, X195, and X202, can further include in the region or domain one or more of the features selected from the following: residue corresponding to X93 is a polar, aliphatic, or non-polar residue; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue; residue corresponding to X95 is an aliphatic, non-polar, or acidic residue; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue; residue corresponding to X97 is a basic, constrained or polar residue; residue corresponding to X100 is a basic, acidic, polar, aliphatic, or non-polar residue; residue corresponding to X108 is a basic or constrained residue; residue corresponding to X111 is a non-polar or aliphatic residue; residue corresponding to X139 is a non-polar or aliphatic residue; residue corresponding to X145 is an acidic, aliphatic, or non-polar residue; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue; residue corresponding to X148 is a non-polar or aliphatic residue; residue corresponding to X151 is a constrained, non-polar or aliphatic residue; residue corresponding to X152 is a polar, aromatic, aliphatic, or non-polar residue; residue corresponding to X163 is a non-polar or aliphatic residue; residue corresponding to X165 is a polar, non-polar or aliphatic residue; residue corresponding to X173 is an acidic, non-polar or aliphatic residue; residue corresponding to X179 is an aromatic, basic, aliphatic, or non-polar residue; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue; residue corresponding to X196 is a non-polar or aliphatic residue; residue corresponding to X197 is an acidic residue; residue corresponding to X198 is an acidic or polar residue; residue corresponding to X210 is a polar or basic residue; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residues not specified by X above as compared to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations.

[0146] In some embodiments, the ketoreductases polypeptides having a domain or region with an amino acid sequence corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139, as described above, can have one or more conservative mutations in the domain or region as compared to the amino acid sequence of the corresponding domain of SEQ ID NO: 2, 4 or 114. Examples of such conservative mutations include amino acid replacements such as, but limited to: replacement of residue corresponding to X93 isoleucine (I) with another polar residue, *e.g.*, serine;

replacement of residue corresponding to X94 alanine (A) with another non-polar residue, *e.g.*, glycine; replacement of residue corresponding to X95 valine (V) with another non-polar or aliphatic residue, *e.g.*, leucine; and replacement of residue corresponding to X96 serine (S) with another polar residue, *e.g.*, threonine; replacement of residue corresponding to X148 valine (V) with another non-polar or aliphatic residue, *e.g.*, isoleucine; replacement of residue corresponding to X152 threonine with another polar residue, *e.g.*, serine; replacement of residue corresponding to X163 valine (V) with another non-polar or aliphatic residue, *e.g.*, isoleucine; replacement of residue corresponding to X179 tyrosine (Y) with another aromatic residue, *e.g.*, phenylalanine; and replacement of residue X196 valine (V) with another aliphatic residue, *e.g.*, leucine; replacement of residue X198 aspartic acid (D) with another acidic residue, *e.g.*, glutamic acid.

[0147] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202, or the specified features at residues corresponding to X190, X195, and X202, can further include in the region or domain one or more of the features selected from the following: residue corresponding to X93 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine or isoleucine, particularly isoleucine, serine, alanine, or glycine; residue corresponding to X94 is cysteine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly cysteine, glycine, or alanine; residue corresponding to X95 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine, leucine, or glutamic acid; residue corresponding to X96 is cysteine, serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly asparagine, serine, valine, leucine, isoleucine, or threonine; residue corresponding to X97 is lysine, arginine, histidine, proline, serine, threonine, glutamine, or asparagine, particularly lysine, histidine, or serine; residue corresponding to X100 is lysine, arginine, serine, threonine, glutamine, asparagine, glycine, alanine, valine, leucine, or isoleucine, particularly glutamic acid, lysine, glutamine, or alanine; residue corresponding to X108 is arginine, lysine, histidine or proline, particularly arginine or histidine; residue corresponding to X111 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly methionine; residue corresponding to X139 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly leucine; residue corresponding to X145 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glutamic acid or leucine; residue corresponding to X147 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly phenylalanine or leucine; residue corresponding to X151 is proline, histidine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine; residue corresponding to X152 is serine, threonine, glutamine, asparagine, tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or

isoleucine, particularly threonine, tryptophan, alanine or serine; residue corresponding to X163 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly isoleucine; residue corresponding to X165 is serine, threonine, glutamine asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly asparagine; residue corresponding to X173 is aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, isoleucine, particularly valine; residue corresponding to X179 is tyrosine, phenylalanine, tryptophan, arginine, lysine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly tyrosine, phenylalanine, lysine, or leucine; residue corresponding to X194 is proline, histidine, serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly proline, glutamine, serine, or leucine; residue corresponding to X196 is glycine, methionine, alanine, valine, leucine or isoleucine, particularly leucine; residue corresponding to X197 is aspartic acid or glutamic acid, particularly glutamic acid; residue corresponding to X198 is aspartic acid, glutamic acid, serine, threonine, glutamine, or asparagine, particularly aspartic acid, glutamic acid, or glutamine; residue corresponding to X210 is arginine, lysine, serine, threonine, glutamine, or asparagine, particularly threonine or arginine; and residue corresponding to X211 is lysine, arginine, aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, or asparagine, particularly valine, leucine, threonine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally from about 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions not specified by X above as compared to the corresponding domain of a reference sequence based on SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations.

[0148] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, threonine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO: 2, 4 or 114. In

some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0149] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, threonine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0150] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine,

leucine, or isoleucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly serine or glutamine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, threonine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residues as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0151] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine, cysteine, valine, leucine, or isoleucine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly leucine, serine or glutamine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine, leucine, isoleucine, or threonine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residues as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence

corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0152] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly threonine or leucine; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, isoleucine, leucine, or valine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0153] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine; residue corresponding to X94 is a cysteine, aliphatic, or non-polar residue, particularly cysteine or glycine; residue corresponding to X96 is a cysteine, polar, aliphatic or non-polar residue, particularly cysteine, threonine, valine, leucine, or isoleucine; residue corresponding to X100 is a basic, acidic, polar, aliphatic or non-polar residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic, or non-polar residue, particularly leucine; residue corresponding to X152 is a polar, aromatic, aliphatic, or non-polar residue, particularly serine; residue corresponding to X194 is a constrained, polar, aliphatic, or

non-polar residue, particularly serine or glutamine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; and residue corresponding and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly valine. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0154] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine or glycine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly isoleucine, leucine or threonine; residue corresponding to X147 is an aromatic, aliphatic or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly glutamine or serine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, valine, leucine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an

amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0155] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO: 111, 112, or 139 and having the specified features at residues corresponding to X190 and X202 or the specified features at residues corresponding to X190, X195 and X202 as described herein, can further include in the region or domain one or more or all of the features selected from the following: residue corresponding to X93 is a polar, aliphatic, or non-polar residue, particularly serine or glycine; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue, particularly cysteine; residue corresponding to X96 is a cysteine, polar, aliphatic, or non-polar residue, particularly isoleucine, leucine or threonine; residue corresponding to X100 is a basic, acidic, polar, aliphatic, non-polar residue or constrained residue, particularly lysine; residue corresponding to X147 is an aromatic, aliphatic or non-polar residue, particularly leucine; residue corresponding to X194 is a constrained, polar, aliphatic, or non-polar residue, particularly glutamine or serine; residue corresponding to X196 is a non-polar or aliphatic residue, particularly leucine; residue corresponding to X198 is an acidic or polar residue, particularly glutamic acid; and residue corresponding to X211 is a basic, aliphatic, non-polar, acidic, or polar residue, particularly threonine, valine, leucine, or isoleucine. In some embodiments, the region or domain corresponding to residues 90-211 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, or 1-20 residue differences at other amino acid residue positions as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0156] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more of the following features: residue corresponding to X7 is a constrained or non-polar residue; residue corresponding to X17 is a non-polar or aliphatic residue; residue corresponding to X25 is a polar or acidic residue; residue corresponding to X27 is an aromatic

residue; residue corresponding to X41 is a polar, aliphatic, or non-polar residue; residue corresponding to X53 is a polar, non-polar, or acidic residue; residue corresponding to X57 is a non-polar or aliphatic residue; residue corresponding to X64 is a polar, aliphatic, or non-polar residue; residue corresponding to X66 is an acidic residue; residue corresponding to X68 is a polar, acidic, aliphatic, or non-polar residue; residue corresponding to X72 is a basic residue; residue corresponding to X76 is an aliphatic, non-polar, or polar residue; residue corresponding to X80 is an aliphatic, non-polar, or polar residue. In some embodiments, the polypeptides comprising a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at residue positions not specified by X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, or 1-16 residue differences at other amino acid residue positions not defined by X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, or 16 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0157] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more of the following features: residue corresponding to X7 is histidine, proline, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glycine or histidine; residue corresponding to X17 is glycine, methionine, alanine, valine, leucine, isoleucine, particularly methionine; residue corresponding to X25 is glutamic acid, aspartic acid, serine, threonine, glutamine, or asparagine, particularly threonine or aspartic acid; residue corresponding to X27 is tyrosine, phenylalanine, tryptophan, particularly tyrosine; residue corresponding to X41 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly serine or alanine; residue corresponding to X53 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, isoleucine, aspartic acid, or glutamic acid, particularly threonine, glycine, or aspartic acid; residue corresponding to X57 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine; residue corresponding to X64 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly serine, alanine, or valine; residue corresponding to X66 is aspartic acid or glutamic acid; residue corresponding to X68 is serine, threonine, glutamine, asparagine, aspartic acid, glutamic acid, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly threonine, aspartic acid, alanine, valine, or glutamic acid; residue corresponding to X72 is lysine or arginine, particularly arginine; residue corresponding to X76 is serine, threonine, glutamine, asparagine, glycine, alanine, valine, leucine, or isoleucine, particularly alanine or threonine; and residue corresponding to X80 is

serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine or isoleucine, particularly alanine, threonine, or valine. In some embodiments, the polypeptides comprising a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at residue positions not specified by X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, or 1-16 residue differences at other amino acid residue positions not defined by X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, or 16 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0158] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have at least the following feature: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine. In some embodiments, the polypeptides comprising a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at other residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the region or domain corresponding to residues 1-89 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, or 1-16 residue differences at other amino acid residue positions as compared to the corresponding domain or region of a reference sequence based on SEQ ID NO: 2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, or about 16 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding feature, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 1-89 of a reference sequence based on SEQ ID NO: 2, 4 or 114 having the preceding feature.

[0159] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more or at least all of the following features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; and residue corresponding to X66 is an acidic residue, particularly glutamic acid. In some embodiments, the polypeptides comprising a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at other residue positions as compared to

the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the region or domain corresponding to residues 1-89 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, or 1-16 residue differences at other amino acid residue positions as compared to the corresponding domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, or about 16 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 1-89 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0160] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more or at least all of the following features: residue corresponding to X7 is a constrained or non-polar residue, particularly histidine; residue corresponding to X17 is a non-polar or aliphatic residue, particularly methionine; residue corresponding to X27 is an aromatic residue, particularly tyrosine; residue corresponding to X64 is a polar, aliphatic, or non-polar residue, particularly valine; and residue corresponding to X80 is an aliphatic, non-polar, or polar residue, particularly threonine or valine. In some embodiments, the polypeptides comprising a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at other residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the region or domain corresponding to residues 1-89 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, or 1-16 residue differences at other amino acid residue positions as compared to the corresponding domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, or about 16 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 1-89 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding features.

[0161] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139, where

the domain or region can have one or more of the following features: residue corresponding to X212 is a polar, aliphatic, or non-polar; residue corresponding to X216 is a constrained or basic residue; residue corresponding to X223 is a non-polar or aliphatic residue; residue corresponding to X226 is a non-polar or polar residue; residue corresponding to X233 is a polar or acidic; residue corresponding to X235 is a polar or aromatic residue; residue corresponding to X248 is a non-polar or aromatic residue; and residue corresponding to X249 is an aromatic residue. In some embodiments, the amino acid sequence can have at least two, three, four, five, six or more of the additional features defined by X above. In some embodiments, the polypeptides comprising an amino acid sequence that is based on the sequence formula of SEQ ID NO: 111, 112, or 139 (or region thereof) can have additionally one or more residue differences at residue positions not specified by an X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, or 1-10, residue differences at other amino acid residue positions not defined by X above. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, or about 10 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0162] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more of the following features: residue corresponding to X212 is serine, threonine, glutamine, asparagine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly threonine, serine, or valine; residue corresponding to X216 is proline, histidine, arginine or lysine, particularly histidine or arginine; residue corresponding to X223 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine; residue corresponding to X226 is glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, or asparagine, particularly threonine; residue corresponding to X233 is serine, threonine, glutamine, asparagine, aspartic acid, glutamic acid, particularly asparagine or aspartic acid; residue corresponding to X235 is serine, threonine, glutamine, asparagine, tyrosine, phenylalanine, tryptophan, particularly serine or tryptophan; residue corresponding to X248 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, or tryptophan, particularly glycine or tryptophan; and residue corresponding to X249 is tyrosine, phenylalanine, or tryptophan, particularly tryptophan. In some embodiments, the amino acid sequence can have at least two, three, four, five, six or more of the additional features defined by X above. In some embodiments, the polypeptides comprising an amino acid sequence that is based on the sequence formula of SEQ ID NO: 111, 112, or 139 (or region thereof) can have additionally one or more residue differences at residue positions not specified by an X above as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the differences can be 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, or 1-10, residue differences at other amino

acid residue positions not defined by X above. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, or about 10 residue differences at other amino acid residue positions. In some embodiments, the differences comprise conservative mutations.

[0163] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region has at least the following feature: residue corresponding to X216 is a constrained or basic residue, particularly arginine. In some embodiments, the polypeptide comprising a region or domain corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at other residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114 having the preceding feature. In some embodiments, the region or domain corresponding to residues 212-252 can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, or 1-10 residue differences at other amino acid residue positions as compared to the corresponding domain of the reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, or about 10 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 212-252 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding feature.

[0164] In some embodiments, the ketoreductase polypeptide can further comprise a domain or region corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139, where the domain or region can have one or more or at least all of the following features: residue corresponding to X212 is a polar, aliphatic, or non-polar residue, particularly threonine, serine, or valine; residue corresponding to X216 is a constrained or basic residue, particularly histidine or arginine; residue corresponding to X223 is a polar, aliphatic, or non-polar, particularly valine; residue corresponding to X233 is a polar or acidic residue, particularly asparagine or aspartic acid; residue corresponding to X235 is a polar or aromatic residue, particularly serine or tryptophan; residue corresponding to X248 is a non-polar or aromatic residue, particularly glycine or tryptophan; and residue corresponding to X249 is an aromatic residue, particularly tryptophan. In some embodiments, the polypeptide comprising a region or domain corresponding to residues 212-252 of the sequence formula of SEQ ID NO: 111, 112, or 139 can have additionally one or more residue differences at other residue positions as compared to the reference sequence of SEQ ID NO: 2, 4 or 114. In some embodiments, the region or domain corresponding to residues 212-252 can have additionally 1-2, 1-3,

1-4, 1-5, 1-6, 1-7, 1-8, 1-9, or 1-10 residue differences at other amino acid residue positions as compared to the corresponding domain of a reference sequence based on SEQ ID NO:2, 4 or 114. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, or about 10 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase region or domain comprises an amino acid sequence having at least the preceding features, and wherein the amino acid sequence has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity as compared to the amino acid sequence corresponding to residues 212-252 of a reference sequence based on SEQ ID NO:2, 4 or 114 having the preceding feature.

[0165] Table 2 below provides a list of specific SEQ ID NOs disclosed herein with associated activities. The sequences below are derived from the wild-type *L. kefir* ketoreductase sequences (SEQ ID NO: 3 and 4) unless otherwise specified. In Table 2 below, each row lists two SEQ ID NOs, where the odd number refers to the nucleotide sequence that codes for the amino acid sequence provided by the even number. The column listing the # of mutations is with respect to the number of amino acid substitutions as compared to the *L. kefir* KRED amino acid sequence of SEQ ID NO:4. In the activity column, one “+” corresponds to the ability of 10 g/L of the enzyme to convert 10-20% of 1 g/L of substrate in about 24 hours. Two plus signs “++” indicates that the polypeptide is about 1 to 50 times more active than SEQ ID NO:90. Three plus signs “+++” indicates that the polypeptide is about 50 to 250 times more active than SEQ ID NO:90. Four plus signs “++++” indicates that the polypeptide is about 250 to 1000 times more active than SEQ ID NO:90, and five plus signs “+++++” indicates that the polypeptide is greater than 1000 times more active than SEQ ID NO:90.

[0166] Table 2: List of Sequences and Corresponding Activity Improvement

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
89/90	G7H; S96T; F147L; Y190P; V196L; A202W	6	+
47/48	G7H; A94G; F147L; Y190P; V196L; A202W	6	++
45/46	G7H; S96L; F147L; Y190P; V196L; A202W	6	++
43/44	G7H; S96V; F147L; Y190P;	6	++

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
	V196L; A202W		
41/42	G7H; S96I; F147L; Y190P; V196L; A202W	6	++
99/100	G7H; S96T; E145L; F147L; Y190P; V196L; A202W	7	++
91/92	G7H; S96T; F147L; Y190P; V196L; A202W; Y249W	7	++
93/94	G7H; S96T; F147L; Y190P; V196L; A202W; K211V	7	++
101/102	G7H; S96T; F147L; Y190P; V196L; A202W; K211I	7	++
85/86	G7H; S96T; F147L; Y190P; L195R; V196L; A202W	7	++
95/96	G7H; S96T; F147L; Y190P; L195D; V196L; A202W	7	++
87/88	G7H; S96T; F147L; Y190P; L195R; V196L; A202W; K211I	8	++
97/98	G7H; S96T; F147L; Y190P; P194L; L195R; V196L; A202W	8	+++
69/70	G7H; D66E; A94G; S96V; F147L; Y190P; L195R; V196L; A202W; K211V	10	+++
83/84	G7H; I93S; A94C; S96L; F147L; Y190P; L195R; V196L; A202W; K211V	10	+++
75/76	G7H; D66E; A80V; A94C; S96L; F147L; Y190P; L195R;	11	+++

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
	V196L; A202W; K211L		
73/74	G7H; D66E; A80V; I93S; A94C; S96V; F147L; Y190P; L195R; V196L; A202W; K211T	12	+++
63/64	G7H; D66E; I93S; A94C; S96L; E145Q; F147L; Y190P; L195R; V196L; A202W; K211V	12	+++
103/104	G7H; A94C; S96I; F147L; Y190P; L195R; V196L; A202W;K211T	9	+++
67/68	G7H; D66E; A94G; S96I; F147L; Y190P; L195R; V196L; A202W; K211L	10	+++
105/106	G7H; A80V; S96C; F147L; Y190P; L195R; V196L; A202W; K211V	9	+++
71/72	G7H; D66E; A94G; S96V; F147L; T152S; Y190P; L195R; V196L; A202W; K211V; S235W	12	+++
65/66	G7H; D66E; A94G; V95L; S96V; F147L; Y190P; L195R; V196L; A202W; K211V	11	+++
23/24	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; L195R; V196L; A202W; K211V	15	++++
81/82	G7H; I93S; A94C; S96L; F147L; Y190P; P194Q; L195R; V196L; A202W; K211V	11	+++
79/80	G7H; I93S; A94C; S96L; F147L; Y190P; P194Q; L195R; V196L; A202W; K211V;J226T	12	+++
107/108	G7H; A68V; I93S; A94C; S96L; R108H; F147L; Y179F; Y190P; L195R; V196L; D198E; A202W; K211V	14	+++
49/50	G7H; A68V; I93S; A94C; S96L; R108H; F147L; I165N; Y190P; P194S; L195R; V196L; A202W; K211I	14	+++

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
77/78	G7H; I93S; A94C; S96L; R108H; F147L; I165N; Y190P; P194Q; L195R; V196L; A202W; K211V;	13	+++
9/10	G7H L17M; F27Y; A80T; I93S; A94C; S96L; F147L; Y190P; L195R; V196L; A202W; K211V; T212S	14	+++
33/34	G7H; L17M; I57V; I93S; A94C; S96L; F147L; V148I; D173V; Y190P; L195R; V196L; A202W; K211L	14	+++
35/36	G7H; L17M; I57V; I93S; A94C; S96L; F147L; Y190P; L195R; V196L; A202W; K211V	12	+++
57/58	G7H; D66E; I93S; A94C; S96I; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	14	++++
39/40	G7H; D66E; I93S; A94C; S96I; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V	13	++++
31/32	G7H; L17M; I57V; A80T; I93S; A94C; S96L; F147L; V163I; Y190P; L195R; V196L; A202W; K211V	14	+++
21/22	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; L195R; V196L; A202W; K211V	15	++++
37/38	G7H; D66E; I93S; A94C; S96I; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	14	++++
53/54	G7H; D66E; I93S; A94C; S96I; F147L; P151A; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	15	++++
11/12	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; L195R; V196L; A202W; T210R; K211V	16	++++
29/30	G7H; L17M; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; L195R; V196L; A202W; K211V; H216R	15	++++

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
27/28	G7H; L17M; F27Y; A64V; I93S; A94C; S96L; F147L; Y190P; P194Q; L195R; V196L; A202W; K211V; H216R	15	++++
15/16	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	18	+++++
109/110	G7H; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	16	++++
61/62	G7H; D66E; I93S; A94C; S96I; K97H; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	15	++++
59/60	G7H; D66E; I93S; A94C; S96I; F147L; T152S; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	15	++++
51/52	G7H; D66E; I93S; A94C; V95E; S96I; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	15	++++
55/56	G7H; D66E; I93S; A94C; S96I; F147L; Y190P; P194Q; L195R; V196L; D198Q; A202W; K211V; H216R	14	++++
25/26	G7H; L17M; F27Y; A64V; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	17	++++
13/14	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198Q; A202W; K211V; H216R	18	+++++
19/20	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; T152S; Y190P; P194Q; L195R; V196L; D198Q; A202W; K211V; H216R	19	+++++
5/6	G7H; L17M; D25T; F27Y; G53D; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	20	+++++

SEQ ID NO	Residue Changes Compared to SEQ ID NO:4	No. of mutations from <i>L. kefir</i> SEQ ID NO:4	Activity ^a
7/8	G7H; L17M; D25T; F27Y; G53D; A64V; T76A; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; H216R	21	+++++
17/18	G7H; L17M; F27Y; A64V; A80T; I93S; A94C; S96L; E100K; F147L; Y190P; P194Q; L195R; V196L; D198E; A202W; K211V; T212V; H216R; I223V	20	++++

[0167] In some embodiments, the polypeptide has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a polypeptide a reference sequence based on SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, or 110, with the proviso that the ketoreductase polypeptide amino acid sequence includes any one set of the substitution combinations listed in Table 2 as compared to SEQ ID NO:4. In some embodiments, the ketoreductase polypeptides can have additionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-25, 1-30, 1-35 or about 1-40 residue differences at other amino acid residue positions as compared to the reference sequence. In some embodiments, the number of differences can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 residue differences at other amino acid residues. In some embodiments, the differences comprise conservative mutations.

[0168] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinoliny) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110. Because the reference polypeptide having the amino acid sequence of SEQ ID NO:90 is capable of converting the substrate to the product at a rate (for example, 10-20% of 1 g/L substrate converted to product in 24 hours with about 10 g/L of the KRED) and with a

stereoselectivity (99% stereomeric excess) that is improved over wild-type (SEQ ID NO:4), the polypeptides herein that are improved over SEQ ID NO:90 are also improved over wild-type.

[0169] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 1-50 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 42, 44, 46, 48, 86, 88, 92, 94, 96, 100 and 102.

[0170] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 50-250 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 10, 32, 34, 36, 50, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 98, 104, 106 and 108.

[0171] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 250-1000 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 12, 18, 22, 24, 26, 28, 30, 38, 40, 52, 54, 56, 58, 60, 62, and 110.

[0172] In some embodiments, the ketoreductase polypeptides are capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate, with a percent stereomeric excess of at least about 99% and at a rate that is at least 1000 fold improved over a reference polypeptide having the amino acid sequence of SEQ ID NO: 90. Exemplary polypeptides with such properties include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

[0173] In some embodiments, the improved ketoreductase polypeptides can have an improved resistance to acetone as a competitive inhibitor to the conversion of the substrate to the product as

compared to the reference polypeptide having the amino acid sequence of SEQ ID NO: 90.

Exemplary polypeptides that have this improved resistance include, but are not limited to, polypeptides which comprise amino acid sequences corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 98, 104, 106, 108, and 110.

[0174] In some embodiments, the ketoreductase polypeptides are capable of converting at least about 95% of the substrate to the product in less than about 24 hours when carried out with greater than about 100 g/L of substrate and less than about 5 g/L of the polypeptide. Exemplary polypeptides that have this capability include, but are not limited to, polypeptides which comprises amino acid sequences corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

[0175] In some embodiments, the ketoreductase polypeptides of the disclosure are highly stereoselective such that it can reduce the substrate to the product in greater than about 99%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% stereomeric excess. Exemplary ketoreductase polypeptides with such high stereoselectivity include, but are not limited to, the polypeptides comprising the amino acid sequences corresponding to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110.

[0176] In some embodiments, the improved ketoreductase polypeptides can comprise an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:114, or a region or domain thereof, such as residues 90-211, with the proviso that the residues corresponding to residue 190 of SEQ ID NO:2, 4 or 114 is proline, the residue corresponding to residue 195 of SEQ ID NO:2, 4 or 114 is arginine, and the residue corresponding to residue 202 of SEQ ID NO:2, 4 or 114 is tryptophan, and additionally has one or more of the following substitutions such that the polypeptide is further improved (e.g., with respect to stereoselectivity, enzymatic activity, and/or thermostability) over the wild-type *kefir* ketoreductase or another engineered ketoreductase (such as SEQ ID NO:90): 7→H; 17→M; 25→T; 27→Y; 41→S; 53→D; 57→V; 64→V; 66→E; 68→V, E; 72→R; 76→A; 80→T, V; 93→S, A, G; 94→C, G; 95→L, E; 96→V, L, I, T; 97→H, S; 100→K, Q, A; 108→H; 111→M; 139→L; 145→L; 147→L; 152→W, A, S; 163→I; 179→F, K, L; 194→Q, S, L; 196→L; 197→E; 198→E, Q; 210→R; 211→V, L, R, T, D, I; 212→S, V; 216→R; 223→V; 233→N; 235→W; 248→W; and 249→W.

[0177] In some embodiments, the improved ketoreductase polypeptides can comprise an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:2, 4 or 114 (or a region or domain thereof, such as

residues 90-211) with the proviso that the residues corresponding to residue 190 of SEQ ID NO:2, 4 or 114 is a proline; the residue corresponding to residue 195 of SEQ ID NO:2, 4 or 114 is arginine; and the residue corresponding to residue 202 of SEQ ID NO:2, 4 or 114 is tryptophan, and additionally has at least one or more of the following substitutions such that the polypeptide is further improved (*e.g.*, with respect to stereoselectivity, enzymatic activity, and/or thermostability) over the wild-type *kefir* ketoreductase or another engineered ketoreductase (such as SEQ ID NO:90): 17→M; 27→Y; 64→V; 80→T; 93→S; 94→C; 96→L; 100→K; 147→L; 152→S; 194→Q; and 211→V.

[0178] As will be appreciated by those of skill in the art, some of the above-defined categories of amino acids, unless otherwise specified, are not mutually exclusive. Thus, amino acids having side chains exhibiting two or more physico-chemical properties can be included in multiple categories. The appropriate classification of any amino acid or residue will be apparent to those of skill in the art, especially in light of the detailed disclosure provided herein.

[0179] In some embodiments, the improved engineered ketoreductase enzymes comprise deletions of the naturally occurring ketoreductase polypeptides or deletions of other engineered ketoreductase polypeptides. In some embodiments, each of the improved engineered ketoreductase enzymes described herein can comprise deletions of the polypeptides described herein. Thus, for each and every embodiment of the ketoreductase polypeptides of the disclosure, the deletions can comprise one or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acids, 5 or more amino acids, 6 or more amino acids, 8 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, up to 10% of the total number of amino acids, up to 20% of the total number of amino acids, or up to 30% of the total number of amino acids of the ketoreductase polypeptides, as long as the functional activity of the ketoreductase activity is maintained. In some embodiments, the deletions can comprise, 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-11, 1-12, 1-14, 1-15, 1-16, 1-18, 1-20, 1-22, 1-24, 1-25, 1-30, 1-35 or about 1-40 amino acid residues. In some embodiments, the number of deletions can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 20, 22, 24, 26, 30, 35 or about 40 amino acids. In some embodiments, the deletions can comprise deletions of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, or 20 amino acid residues.

[0180] As described herein, the ketoreductase polypeptides of the disclosure can be in the form of fusion polypeptides in which the ketoreductase polypeptides are fused to other polypeptides, such as, by way of example and not limitation, antibody tags (*e.g.*, myc epitope), purifications sequences (*e.g.*, His tags), and cell localization signals (*e.g.*, secretion signals). Thus, the ketoreductase polypeptides can be used with or without fusions to other polypeptides.

[0181] The polypeptides described herein are not restricted to the genetically encoded amino acids. In addition to the genetically encoded amino acids, the polypeptides described herein may be comprised, either in whole or in part, of naturally-occurring and/or synthetic non-encoded amino acids. Certain commonly encountered non-encoded amino acids of which the polypeptides described herein may be comprised include, but are not limited to: the D-stereoisomers of the genetically-encoded amino acids; 2,3-diaminopropionic acid (Dpr); α -aminoisobutyric acid (Aib); ϵ -aminohexanoic acid (Aha); δ -aminovaleric acid (Ava); N-methylglycine or sarcosine (MeGly or Sar); ornithine (Orn); citrulline (Cit); t-butylalanine (Bua); t-butylglycine (Bug); N-methylisoleucine (MeIle); phenylglycine (Phg); cyclohexylalanine (Cha); norleucine (Nle); naphthylalanine (Nal); 2-chlorophenylalanine (Ocf); 3-chlorophenylalanine (Mcf); 4-chlorophenylalanine (Pcf); 2-fluorophenylalanine (Off); 3-fluorophenylalanine (Mff); 4-fluorophenylalanine (Pff); 2-bromophenylalanine (Obf); 3-bromophenylalanine (Mbf); 4-bromophenylalanine (Pbf); 2-methylphenylalanine (Omf); 3-methylphenylalanine (Mmf); 4-methylphenylalanine (Pmf); 2-nitrophenylalanine (Onf); 3-nitrophenylalanine (Mnf); 4-nitrophenylalanine (Pnf); 2-cyanophenylalanine (Ocf); 3-cyanophenylalanine (Mcf); 4-cyanophenylalanine (Pcf); 2-trifluoromethylphenylalanine (Otf); 3-trifluoromethylphenylalanine (Mtf); 4-trifluoromethylphenylalanine (Ptf); 4-aminophenylalanine (Paf); 4-iodophenylalanine (Pif); 4-aminomethylphenylalanine (Pamf); 2,4-dichlorophenylalanine (Opef); 3,4-dichlorophenylalanine (Mpcf); 2,4-difluorophenylalanine (Opff); 3,4-difluorophenylalanine (Mpff); pyrid-2-ylalanine (2pAla); pyrid-3-ylalanine (3pAla); pyrid-4-ylalanine (4pAla); naphth-1-ylalanine (1nAla); naphth-2-ylalanine (2nAla); thiazolylalanine (taAla); benzothienylalanine (bAla); thienylalanine (tAla); furylalanine (fAla); homophenylalanine (hPhe); homotyrosine (hTyr); homotryptophan (hTrp); pentafluorophenylalanine (5ff); styrylalanine (sAla); authrylalanine (aAla); 3,3-diphenylalanine (Dfa); 3-amino-5-phenylpentanoic acid (Afp); penicillamine (Pen); 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic); β -2-thienylalanine (Thi); methionine sulfoxide (Mso); N(w)-nitroarginine (nArg); homolysine (hLys); phosphonomethylphenylalanine (pmPhe); phosphoserine (pSer); phosphothreonine (pThr); homoaspartic acid (hAsp); homoglutamic acid (hGlu); 1-aminocyclopent-(2 or 3)-ene-4 carboxylic acid; pipecolic acid (PA), azetidine-3-carboxylic acid (ACA); 1-aminocyclopentane-3-carboxylic acid; allylglycine (aOly); propargylglycine (pgGly); homoalanine (hAla); norvaline (nVal); homoleucine (hLeu), homovaline (hVal); homoisoleucine (hIle); homoarginine (hArg); N-acetyl lysine (AcLys); 2,4-diaminobutyric acid (Dbu); 2,3-diaminobutyric acid (Dab); N-methylvaline (MeVal); homocysteine (hCys); homoserine (hSer); hydroxyproline (Hyp) and homoproline (hPro). Additional non-encoded amino acids of which the polypeptides described herein may be comprised will be apparent to those of skill in the art (see, e.g., the various amino acids provided in Fasman, 1989, *CRC Practical Handbook of Biochemistry and Molecular Biology*, CRC Press, Boca Raton, FL,

at pp. 3-70 and the references cited therein, all of which are incorporated by reference). These amino acids may be in either the L- or D-configuration.

[0182] Those of skill in the art will recognize that amino acids or residues bearing side chain protecting groups may also comprise the polypeptides described herein. Non-limiting examples of such protected amino acids, which in this case belong to the aromatic category, include (protecting groups listed in parentheses), but are not limited to: Arg(tos), Cys(methylbenzyl), Cys(nitropyridinesulfonyl), Glu(δ -benzylester), Gln(xanthyl), Asn(N- δ -xanthyl), His(bom), His(benzyl), His(tos), Lys(fmoc), Lys(tos), Ser(O-benzyl), Thr (O-benzyl) and Tyr(O-benzyl).

[0183] Non-encoding amino acids that are conformationally constrained of which the polypeptides described herein may be composed include, but are not limited to, N-methyl amino acids (L-configuration); 1-aminocyclopent-(2 or 3)-ene-4-carboxylic acid; pipecolic acid; azetidine-3-carboxylic acid; homoproline (hPro); and 1-aminocyclopentane-3-carboxylic acid.

[0184] As described above the various modifications introduced into the naturally occurring polypeptide to generate an engineered ketoreductase enzyme can be targeted to a specific property of the enzyme.

6.3 Polynucleotides Encoding Engineered Ketoreductases

[0185] In another aspect, the present disclosure provides polynucleotides encoding the engineered ketoreductase enzymes. The polynucleotides may be operatively linked to one or more heterologous regulatory sequences that control gene expression to create a recombinant polynucleotide capable of expressing the polypeptide. Expression constructs containing a heterologous polynucleotide encoding the engineered ketoreductase can be introduced into appropriate host cells to express the corresponding ketoreductase polypeptide.

[0186] Because of the knowledge of the codons corresponding to the various amino acids, availability of a protein sequence provides a description of all the polynucleotides capable of encoding the subject. The degeneracy of the genetic code, where the same amino acids are encoded by alternative or synonymous codons allows an extremely large number of nucleic acids to be made, all of which encode the improved ketoreductase enzymes disclosed herein. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the protein. In this regard, the present disclosure specifically contemplates each and every possible variation of polynucleotides that could be made by selecting combinations based on the possible codon choices, and all such variations are to be considered specifically disclosed for any polypeptide disclosed herein, including the amino acid sequences presented in Table

2. In some embodiments, the codons are preferably selected to fit the host cell in which the protein is being produced. For example, preferred codons used in bacteria are used to express the gene in bacteria; preferred codons used in yeast are used for expression in yeast; and preferred codons used in mammals are used for expression in mammalian cells. By way of example, the polynucleotide of SEQ ID NO: 3 has been codon optimized for expression in *E. coli*, but otherwise encodes the naturally occurring ketoreductase of *Lactobacillus kefir*.

[0187] In some embodiments, all codons need not be replaced to optimize the codon usage of the ketoreductases since the natural sequence will comprise preferred codons and because use of preferred codons may not be required for all amino acid residues. Consequently, codon optimized polynucleotides encoding the ketoreductase enzymes may contain preferred codons at about 40%, 50%, 60%, 70%, 80%, or greater than 90% of codon positions of the full length coding region.

[0188] In some embodiments, the polynucleotide comprises a nucleotide sequence encoding a ketoreductase polypeptide with an amino acid sequence that has at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more sequence identity to any of the reference engineered ketoreductase polypeptides described herein. Accordingly, in some embodiments, the polynucleotide encodes an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: the residue corresponding to position X190 is a constrained residue, particularly proline; and the residue corresponding to X202 is an aromatic residue, particularly tryptophan, with the proviso that the encoded ketoreductase polypeptide has an amino sequence in which the residue corresponding to X190 is a constrained residue, and the residue corresponding to X202 is an aromatic residue. In some embodiments, the polynucleotide encodes a ketoreductase that has an amino acid sequence in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan.

[0189] In some embodiments, the polynucleotide encodes a ketoreductase polypeptide comprising an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence based on SEQ ID NO: 2, 4 or 114 having the following features: the residue corresponding to position X190 is a constrained residue, particularly proline; the residue corresponding to X195 is a basic, acidic, non-polar or polar residue, particularly proline, arginine, lysine, aspartic acid, or asparagine; and the residue corresponding to X202 is an aromatic residue, particularly tryptophan, with the proviso that the encoded ketoreductase polypeptide comprises an amino acid sequence having at least the preceding features (*i.e.*, the residue corresponding to position X190 is a constrained residue; the residue corresponding to X195 is a basic, acidic, non-polar or polar residue; and the residue corresponding to

X202 is an aromatic residue. In some embodiments, the encoded ketoreductase has an amino acid sequence in which the residue corresponding to X190 is proline; the residue corresponding to X195 is proline, arginine, lysine, aspartic acid, or asparagine; and the residue corresponding to X202 is tryptophan. In some embodiments, the polynucleotide encodes an engineered ketoreductase polypeptide comprising an amino acid sequence selected from SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110.

[0190] In some embodiments, the polynucleotide encodes a ketoreductase polypeptide comprising an amino acid sequence that is at least about 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a reference sequence selected from SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 92, 94, 96, 98, 100, 102, 104, 106, 108, and 110, where the encoded polypeptide has the features specified herein for residues corresponding to X190 and X202, or has the features specified herein for residues X190, X195 and X202.

[0191] In some embodiments, the polynucleotides encoding the engineered ketoreductases are selected from SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, and 109. In some embodiments, the polynucleotides are capable of hybridizing under highly stringent conditions to a polynucleotide comprising SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, or 109, wherein the polynucleotide hybridizing under highly stringent conditions encodes a ketoreductase polypeptide capable of reducing or converting the substrate of formula (I) to the product of formula (II). In some embodiments, the polypeptide encoded by the stringently hybridizing polynucleotide is capable of reducing or converting the substrate of formula (III) to the product of formula (IV). In some embodiments, the polypeptide encoded by the stringently hybridizing polynucleotide will have the specified enzymatic activity, and the features specified for residues corresponding to X190 and X202 or the features specified for residues corresponding to X190, X195, and X202.

[0192] In some embodiments, the polynucleotides encode the polypeptides described herein but have about 80% or more sequence identity, about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more sequence identity at the nucleotide level to a reference polynucleotide encoding the engineered ketoreductase. In some embodiments, the reference polynucleotide is selected from SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,

37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, and 109.

[0193] An isolated polynucleotide encoding an improved ketoreductase polypeptide may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the isolated polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides and nucleic acid sequences utilizing recombinant DNA methods are well known in the art. Guidance is provided in Sambrook et al., 2001, *Molecular Cloning: A Laboratory Manual*, 3rd Ed., Cold Spring Harbor Laboratory Press; and *Current Protocols in Molecular Biology*, Ausubel, F. ed., Greene Pub. Associates, 1998, updates to 2006.

[0194] For bacterial host cells, suitable promoters for directing transcription of the nucleic acid constructs of the present disclosure, include the promoters obtained from the *E. coli* lac operon, *E. coli* trp operon, *Streptomyces coelicolor* agarase gene (dagA), *Bacillus subtilis* levansucrase gene (sacB), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus subtilis* xylA and xylB genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, *Proc. Natl Acad. Sci. USA* 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, *Proc. Natl Acad. Sci. USA* 80: 21-25).

[0195] For filamentous fungal host cells, suitable promoters for directing the transcription of the nucleic acid constructs of the present disclosure include promoters obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase, and *Fusarium oxysporum* trypsin-like protease (WO 96/00787), as well as the NA2-tpi promoter (a hybrid of the promoters from the genes for *Aspergillus niger* neutral alpha-amylase and *Aspergillus oryzae* triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof.

[0196] In a yeast host, useful promoters can be from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos et al., 1992, *Yeast* 8:423-488.

[0197] The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the

3' terminus of the nucleic acid sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

[0198] For example, exemplary transcription terminators for filamentous fungal host cells can be obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase, and *Fusarium oxysporum* trypsin-like protease.

[0199] Exemplary terminators for yeast host cells can be obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos et al., 1992, *supra*.

[0200] The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA that is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used. Exemplary leaders include M13 phage pIII leader sequence, *E. coli* maltose binding protein leader sequence, and *E. coli* pelB leader sequence. Leader sequences for filamentous fungal host cells can be obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase. Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

[0201] The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleic acid sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention. Exemplary polyadenylation sequences for filamentous fungal host cells can be from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease, and *Aspergillus niger* alpha-glucosidase. Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Mol Cell Bio* 15:5983-5990.

[0202] The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleic acid sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region that encodes the secreted polypeptide. Alternatively, the 5' end of the

coding sequence may contain a signal peptide coding region that is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region.

[0203] Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

[0204] Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiol Rev* 57: 109-137.

[0205] Effective signal peptide coding regions for filamentous fungal host cells can be the signal peptide coding regions obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Rhizomucor miehei* aspartic proteinase, *Humicola insolens* cellulase, and *Humicola lanuginosa* lipase.

[0206] Useful signal peptides for yeast host cells can be from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding regions are described by Romanos et al., 1992, *supra*.

[0207] The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* lactase (WO 95/33836).

[0208] Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

[0209] It may also be desirable to add regulatory sequences, which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or

physical stimulus, including the presence of a regulatory compound. In prokaryotic host cells, suitable regulatory sequences include the lac, tac, and trp operator systems. In yeast host cells, suitable regulatory systems include, as examples, the ADH2 system or GAL1 system. In filamentous fungi, suitable regulatory sequences include the TAKA alpha-amylase promoter, *Aspergillus niger* glucoamylase promoter, and *Aspergillus oryzae* glucoamylase promoter.

[0210] Other examples of regulatory sequences are those which allow for gene amplification. In eukaryotic systems, these include the dihydrofolate reductase gene, which is amplified in the presence of methotrexate, and the metallothionein genes, which are amplified with heavy metals. In these cases, the nucleic acid sequence encoding the KRED polypeptide of the present invention would be operably linked with the regulatory sequence.

[0211] Thus, in another embodiment, the present disclosure is also directed to a recombinant expression vector comprising a polynucleotide encoding an engineered ketoreductase polypeptide or a variant thereof, and one or more expression regulating regions such as a promoter and a terminator, a replication origin, etc., depending on the type of hosts into which they are to be introduced. The various nucleic acid and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleic acid sequence encoding the polypeptide at such sites. Alternatively, the nucleic acid sequence of the present disclosure may be expressed by inserting the nucleic acid sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0212] The recombinant expression vector may be any vector (*e.g.*, a plasmid or virus), which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the polynucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

[0213] The expression vector may be an autonomously replicating vector, *i.e.*, a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

[0214] The expression vector of the present invention preferably contains one or more selectable markers, which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers, which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol (Example 1) or tetracycline resistance. Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3.

[0215] Selectable markers for use in a filamentous fungal host cell include, but are not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hph* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), and *trpC* (anthranilate synthase), as well as equivalents thereof. Embodiments for use in an *Aspergillus* cell include the *amdS* and *pyrG* genes of *Aspergillus nidulans* or *Aspergillus oryzae* and the *bar* gene of *Streptomyces hygroscopicus*.

[0216] The expression vectors of the present invention preferably contain an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome. For integration into the host cell genome, the vector may rely on the nucleic acid sequence encoding the polypeptide or any other element of the vector for integration of the vector into the genome by homologous or nonhomologous recombination.

[0217] Alternatively, the expression vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, preferably 400 to 10,000 base pairs, and most preferably 800 to 10,000 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleic acid sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

[0218] For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are P15A ori (as shown in the plasmid of FIG. 5) or the origins of replication of plasmids pBR322, pUC19, pACYC177 (which plasmid has the P15A ori), or pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, or pAM β 1 permitting replication in *Bacillus*. Examples of

origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6. The origin of replication may be one having a mutation which makes it's functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, *Proc Natl Acad Sci. USA* 75:1433).

[0219] More than one copy of a nucleic acid sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleic acid sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleic acid sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleic acid sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

[0220] Many of the expression vectors for use in the present invention are commercially available. Suitable commercial expression vectors include p3xFLAGTM™ expression vectors from Sigma-Aldrich Chemicals, St. Louis MO., which includes a CMV promoter and hGH polyadenylation site for expression in mammalian host cells and a pBR322 origin of replication and ampicillin resistance markers for amplification in *E. coli*. Other suitable expression vectors are pBluescriptII SK(-) and pBK-CMV, which are commercially available from Stratagene, LaJolla CA, and plasmids which are derived from pBR322 (Gibco BRL), pUC (Gibco BRL), pREP4, pCEP4 (Invitrogen) or pPoly (Lathé et al., 1987, *Gene* 57:193-201).

6.4 Host Cells for Expression of Ketoreductase Polypeptides

[0221] In another aspect, the present disclosure provides a host cell comprising a polynucleotide encoding an improved ketoreductase polypeptide of the present disclosure, the polynucleotide being operatively linked to one or more control sequences for expression of the ketoreductase enzyme in the host cell. Host cells for use in expressing the KRED polypeptides encoded by the expression vectors of the present invention are well known in the art and include but are not limited to, bacterial cells, such as *E. coli*, *Lactobacillus kefir*, *Lactobacillus brevis*, *Lactobacillus minor*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, BHK, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and growth conditions for the above-described host cells are well known in the art.

[0222] Polynucleotides for expression of the ketoreductase may be introduced into cells by various methods known in the art. Techniques include among others, electroporation, biolistic particle

bombardment, liposome mediated transfection, calcium chloride transfection, and protoplast fusion. Various methods for introducing polynucleotides into cells will be apparent to the skilled artisan.

[0223] An exemplary host cell is *Escherichia coli* W3110. The expression vector was created by operatively linking a polynucleotide encoding an improved ketoreductase into the plasmid pCK110900 operatively linked to the *lac* promoter under control of the *lacI* repressor. The expression vector also contained the P15a origin of replication and the chloramphenicol resistance gene. Cells containing the subject polynucleotide in *Escherichia coli* W3110 were isolated by subjecting the cells to chloramphenicol selection.

6.5 Methods of Generating Engineered Ketoreductase Polypeptides.

[0224] In some embodiments, to make the improved KRED polynucleotides and polypeptides of the present disclosure, the naturally-occurring ketoreductase enzyme that catalyzes the reduction reaction is obtained (or derived) from *Lactobacillus kefir* or *Lactobacillus brevis* or *Lactobacillus minor*. In some embodiments, the parent polynucleotide sequence is codon optimized to enhance expression of the ketoreductase in a specified host cell. As an illustration, the parental polynucleotide sequence encoding the wild-type KRED polypeptide of *Lactobacillus kefir* was constructed from oligonucleotides prepared based upon the known polypeptide sequence of *Lactobacillus kefir* KRED sequence available in Genbank database (Genbank accession no. AAP94029 GI:33112056). The parental polynucleotide sequence, designated as SEQ ID NO: 1, was codon optimized for expression in *E. coli* and the codon-optimized polynucleotide cloned into an expression vector, placing the expression of the ketoreductase gene under the control of the *lac* promoter and *lacI* repressor gene. Clones expressing the active ketoreductase in *E. coli* were identified and the genes sequenced to confirm their identity. The sequence designated (SEQ ID NO: 1) was the parent sequence utilized as the starting point for most experiments and library construction of engineered ketoreductases evolved from the *Lactobacillus kefir* ketoreductase.

[0225] The engineered ketoreductases can be obtained by subjecting the polynucleotide encoding the naturally occurring ketoreductase to mutagenesis and/or directed evolution methods, as discussed above. An exemplary directed evolution technique is mutagenesis and/or DNA shuffling as described in Stemmer, 1994, *Proc Natl Acad Sci USA* 91:10747-10751; WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; WO 01/75767 and U.S. Pat. 6,537,746. Other directed evolution procedures that can be used include, among others, staggered extension process (StEP), in vitro recombination (Zhao et al., 1998, *Nat. Biotechnol.* 16:258-261), mutagenic PCR (Caldwell et al., 1994, *PCR Methods Appl.* 3:S136-S140), and cassette mutagenesis (Black et al., 1996, *Proc Natl Acad Sci USA* 93:3525-3529). Additional mutagenesis and directed evolution techniques useful for the purposes herein can be found in the following references: Ling, et al., 1997, "Approaches to DNA

mutagenesis: an overview," *Anal. Biochem.* 254(2):157-78; Dale et al., 1996, "Oligonucleotide-directed random mutagenesis using the phosphorothioate method," *Methods Mol. Biol.* 57:369-74; Smith, 1985, "In vitro mutagenesis," *Ann. Rev. Genet.* 19:423-462; Botstein et al., 1985, "Strategies and applications of in vitro mutagenesis," *Science* 229:1193-1201; Carter, 1986, "Site-directed mutagenesis," *Biochem. J.* 237:1-7; Kramer et al., 1984, "Point Mismatch Repair," *Cell*, 38:879-887; Wells et al., 1985, "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites," *Gene* 34:315-323; Minshull et al., 1999, "Protein evolution by molecular breeding," *Curr Opin Chem Biol* 3:284-290; Christians et al., 1999, "Directed evolution of thymidine kinase for AZT phosphorylation using DNA family shuffling," *Nature Biotech* 17:259-264; Crameri et al., 1998, "DNA shuffling of a family of genes from diverse species accelerates directed evolution," *Nature* 391:288-291; Crameri et al., 1997, "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," *Nature Biotech* 15:436-438; Zhang et al., 1997, "Directed evolution of an effective fructosidase from a galactosidase by DNA shuffling and screening," *Proc Natl Acad Sci USA* 94:45-4-4509; Crameri et al., 1996, "Improved green fluorescent protein by molecular evolution using DNA shuffling," *Nature Biotech* 14:315-319; and Stemmer, 1994, "Rapid evolution of a protein in vitro by DNA shuffling," *Nature* 370:389-391. All publications are incorporated herein by reference.

[0226] The clones obtained following mutagenesis treatment are screened for engineered ketoreductases having a desired improved enzyme property. Measuring enzyme activity from the expression libraries can be performed using the standard biochemistry technique of monitoring the rate of decrease (via a decrease in absorbance or fluorescence) of NADH or NADPH concentration, as it is converted into NAD^+ or NADP^+ . In this reaction, the NADH or NADPH is consumed (oxidized) by the ketoreductase as the ketoreductase reduces a ketone substrate to the corresponding hydroxyl group. The rate of decrease of NADH or NADPH concentration, as measured by the decrease in absorbance or fluorescence, per unit time indicates the relative (enzymatic) activity of the KRED polypeptide in a fixed amount of the lysate (or a lyophilized powder made therefrom). Where the improved enzyme property desired is thermal stability, enzyme activity may be measured after subjecting the enzyme preparations to a defined temperature and measuring the amount of enzyme activity remaining after heat treatments. Clones containing a polynucleotide encoding a ketoreductase are then isolated, sequenced to identify the nucleotide sequence changes (if any), and used to express the enzyme in a host cell.

[0227] Where the sequence of the engineered polypeptide is known, the polynucleotides encoding the enzyme can be prepared by standard solid-phase methods, according to known synthetic methods. In some embodiments, fragments of up to about 100 bases can be individually synthesized, then joined (e.g., by enzymatic or chemical ligation methods, or polymerase mediated methods) to form

any desired continuous sequence. For example, polynucleotides and oligonucleotides of the invention can be prepared by chemical synthesis using, *e.g.*, the classical phosphoramidite method described by Beaucage et al., 1981, *Tet Lett* 22:1859-69, or the method described by Matthes et al., 1984, *EMBO J.* 3:801-05, *e.g.*, as it is typically practiced in automated synthetic methods. According to the phosphoramidite method, oligonucleotides are synthesized, *e.g.*, in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors. In addition, essentially any nucleic acid can be obtained from any of a variety of commercial sources, such as The Midland Certified Reagent Company, Midland, TX, The Great American Gene Company, Ramona, CA, ExpressGen Inc. Chicago, IL, Operon Technologies Inc., Alameda, CA, and many others.

[0228] Engineered ketoreductase enzymes expressed in a host cell can be recovered from the cells and or the culture medium using any one or more of the well known techniques for protein purification, including, among others, lysozyme treatment, sonication, filtration, salting-out, ultra-centrifugation, and chromatography. Suitable solutions for lysing and the high efficiency extraction of proteins from bacteria, such as *E. coli*, are commercially available under the trade name CellLytic B™ from Sigma-Aldrich of St. Louis MO.

[0229] Chromatographic techniques for isolation of the ketoreductase polypeptide include, among others, reverse phase chromatography high performance liquid chromatography, ion exchange chromatography, gel electrophoresis, and affinity chromatography. Conditions for purifying a particular enzyme will depend, in part, on factors such as net charge, hydrophobicity, hydrophilicity, molecular weight, molecular shape, etc., and will be apparent to those having skill in the art.

[0230] In some embodiments, affinity techniques may be used to isolate the improved ketoreductase enzymes. For affinity chromatography purification, any antibody which specifically binds the ketoreductase polypeptide may be used. For the production of antibodies, various host animals, including but not limited to rabbits, mice, rats, etc., may be immunized by injection with the ketoreductase polypeptide. The polypeptide may be attached to a suitable carrier, such as BSA, by means of a side chain functional group or linkers attached to a side chain functional group. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacilli Calmette Guerin) and Corynebacterium parvum.

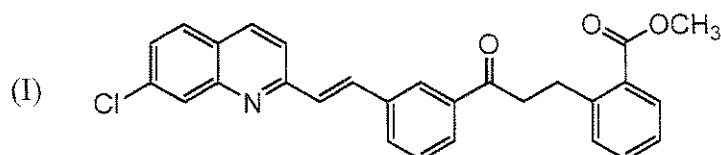
[0231] In some embodiments, the ketoreductases may be prepared and used in the form of cells expressing the enzymes, as crude extracts, or as isolated or purified preparations. The ketoreductases may be prepared as lyophilizates, in powder form (*e.g.*, acetone powders), or prepared as enzyme

solutions. In some embodiments, the ketoreductases can be in the form of substantially pure preparations.

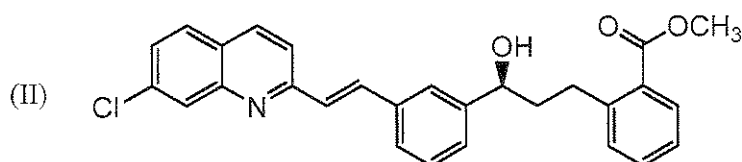
[0232] In some embodiments, the ketoreductase polypeptides can be attached to a solid substrate. The substrate can be a solid phase, surface, and/or membrane. A solid support can be composed of organic polymers such as polystyrene, polyethylene, polypropylene, polyfluoroethylene, polyethyleneoxy, and polyacrylamide, as well as co-polymers and grafts thereof. A solid support can also be inorganic, such as glass, silica, controlled pore glass (CPG), reverse phase silica or metal, such as gold or platinum. The configuration of the substrate can be in the form of beads, spheres, particles, granules, a gel, a membrane or a surface. Surfaces can be planar, substantially planar, or non-planar. Solid supports can be porous or non-porous, and can have swelling or non-swelling characteristics. A solid support can be configured in the form of a well, depression, or other container, vessel, feature, or location. A plurality of supports can be configured on an array at various locations, addressable for robotic delivery of reagents, or by detection methods and/or instruments.

6.6 Methods of Using the Engineered Ketoreductase Enzymes and Compounds Prepared Therewith

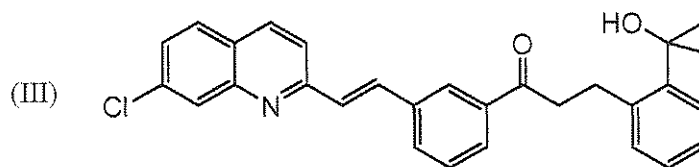
[0233] The ketoreductase enzymes described herein can catalyze the reduction of the substrate of structural formula (I), 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester:



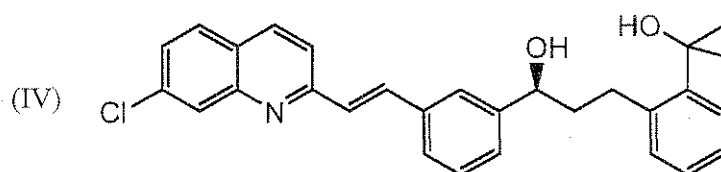
to the corresponding stereoisomeric product of structural formula (II), (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate ("the product"):



[0234] In another embodiment, the ketoreductase enzymes described herein are capable of catalyzing the reduction reaction of the compound of structural formula (III), 2-[2-[3-[3-[2-(7-chloro-2-quinoliny) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol (also a “substrate”),



to the corresponding stereoisomeric product of structural formula (IV, (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol (which can also be referred to as a “product” with respect to the substrate of formula (III)):



[0235] In some embodiments, the ketoreductases of the disclosure may be used in a method for reducing the substrate having the chemical formula (I) or (III) to the corresponding product, where the method comprises contacting or incubating the substrate with any one (or more) of the ketoreductase polypeptides described herein under reaction conditions suitable for reducing or converting the substrate to the product of formula (II) or formula (IV), respectively.

[0236] In some embodiments of the method for reducing the substrate to the product, the ketoreductase polypeptide, as compared to the wild-type *L. kefir* or *L. brevis* or *L. minor* KRED sequences of SEQ ID NO:4, 2 and 114, have at least the following features: (1) residue corresponding to X190 is a constrained residue and (2) residue corresponding to X202 is an aromatic residue. In some embodiments, the ketoreductase polypeptide, as compared to the wild-type *L. kefir* or *L. brevis* or *L. minor* KRED sequences of SEQ ID NO:4, 2 and 114, have at least the following features: (1) residue corresponding to X190 is a constrained residue; (2) residue corresponding to 195 is a basic, acidic, or polar residue; and (3) residue corresponding to X202 is an aromatic residue.

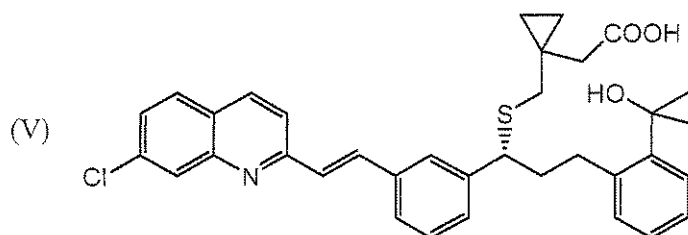
[0237] In some embodiments of the method for reducing the substrate to the product, the substrate is reduced to the product in greater than about 99% stereomeric excess, wherein the ketoreductase

polypeptide comprises a sequence that corresponds to SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 111, or 112.

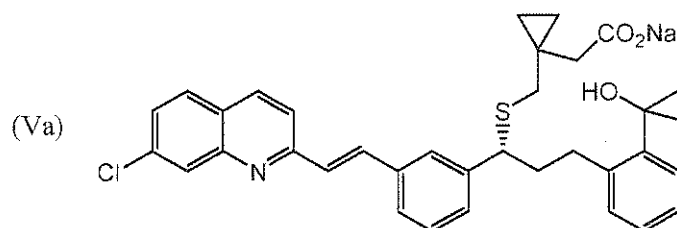
[0238] In some embodiments of the method for reducing the substrate to the product, at least about 95% of the substrate is converted to the product in less than about 24 hours when carried out with greater than about 100 g/L of substrate and less than about 5 g/L of the polypeptide, wherein the polypeptide comprises an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

[0239] In some embodiments of the method for reducing the substrate to the product, at least about 10-20% of 1 g/L substrate is converted to the product in less than about 24 hours with about 10 g/L of the polypeptide, wherein the polypeptide comprises an amino acid sequence corresponding to 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 111, or 112.

[0240] In some embodiments, the ketoreductase polypeptides provided herein can be used in the production of intermediates for the synthesis of the compound of the structural formula (V):

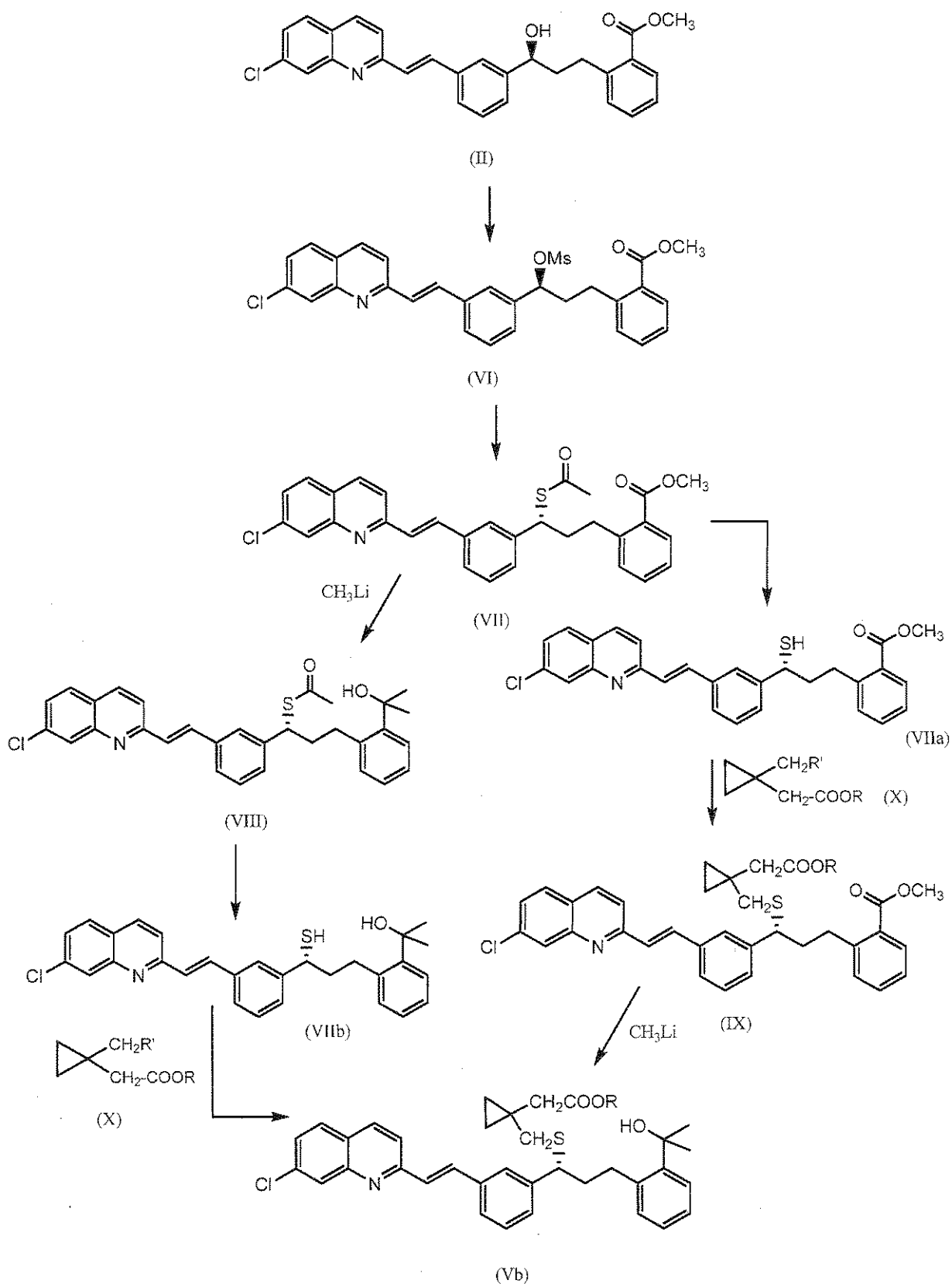


including solvates, hydrates, and pharmaceutically acceptable salts thereof. The compound of formula (V), 2-[1-[[[(1R)-1-[3-[(E)-2-(7-chloroquinolin-2-yl)ethenyl]phenyl]-3-[2-(2-hydroxypropan-2-yl)phenyl]propyl]sulfanylmethyl]cyclopropyl]acetic acid, also known as Montelukast, is available commercially in the sodium salt form shown in formula (Va) (*i.e.*, sodium (R,E)-2-(1-((1-(3-(2(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propylthio)methyl)cyclopropyl)acetate):



[0241] As described above, without being bound by theory, Montelukast is a leukotriene receptor antagonist (LTRA) and appears to block the action of leukotriene D4 on the cysteinyl leukotriene receptor CysLT1. It is prescribed for the treatment of allergies and in the maintenance treatment of asthma (see, *e.g.*, U.S. Patent No. 5,565,473). In some embodiments of the synthesis of Montelukast, an important intermediate is the compound of formula (II). Accordingly, in a method for the synthesis of the compound (V), a step in the method can comprise reacting or contacting the substrate of formula (I) with a ketoreductase polypeptide of the disclosure under conditions suitable for reducing or converting the substrate to the product of formula (II).

[0242] In some embodiments, the compound of formula (V) can be synthesized from the compound of formula (II) as illustrated in Scheme I and as described in US application publications 20070135480 and 20050245568.

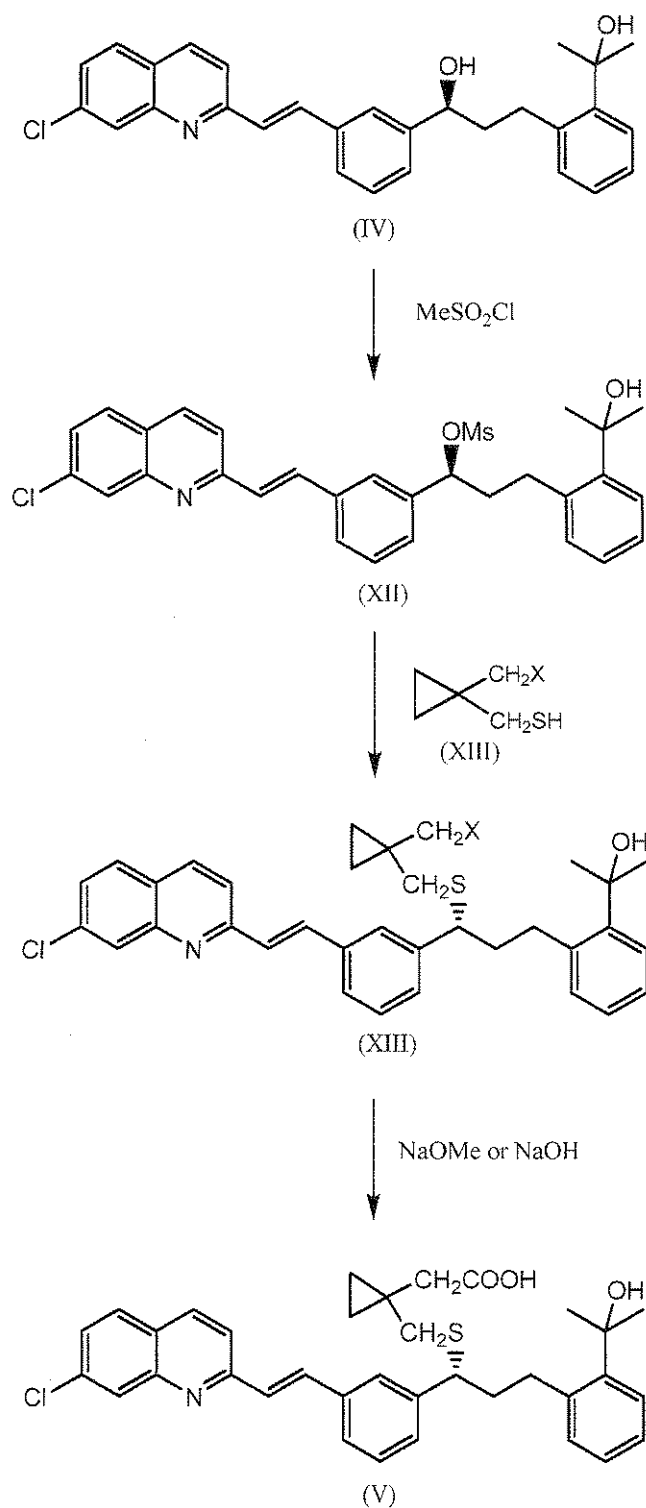


Scheme 1

[0243] Accordingly, in some embodiments, a method for synthesis of the compound (V) can comprise: (a) reducing or converting compound (I) to compound (II) with a ketoreductase of the disclosure; (b) reacting compound (II) with methylsulfonyl chloride to form compound of formula (VI); (c) converting compound (VI) to the thio compound of formula (VII) followed by conversion to the compound of formula (VIIa); (d) reacting the thio compound (VIIa) with the compound of formula (X) to form the compound of formula (IX), where R' is a leaving group and R is H or C1-C4 alkyl; and (e) converting compound (IX) to the compound of formula (Vb), or a salt thereof, *e.g.*, formula (Va). In some embodiments, other alkylsulfonyl halides or an arylsulfonyl halides can be used in place of methylsulfonyl chloride. The conversion of the compound of formula (IX) to the compound of formula (Vb) can use CH₃Li but the step can also be carried out using a Grignard reagent, *e.g.*, methylmagnesium halide (see US application publication 20070135480). In some embodiments, an alternative process following step (c) above can comprise: (d) converting the compound of formula (VII) to the compound of formula (VIII) followed by conversion to the compound of formula (VIIb), and (e) reacting the thio compound (X) with the compound (VIIb) to form the compound of formula (Vb), or a salt thereof. Details and conditions for each of the steps is described in US application publications 20070135480 and 20050245568.

[0244] In some embodiments, the synthesis of Montelukast can use the intermediate of formula (IV). Accordingly, in some embodiments, in a method for the synthesis of the compound of formula (V), a step in the method can comprise reducing or converting the substrate of formula (III) to the product of formula (IV) by contacting the substrate with the ketoreductases disclosed herein under reaction conditions suitable for reducing or converting the substrate to the product of formula (VI).

[0245] In some embodiments, the Montelukast compound can be synthesized from the product of formula (IV) as illustrated in Scheme II, and as described in US application publication No. 2005/0234241 and US Patent No. 7,189,853:

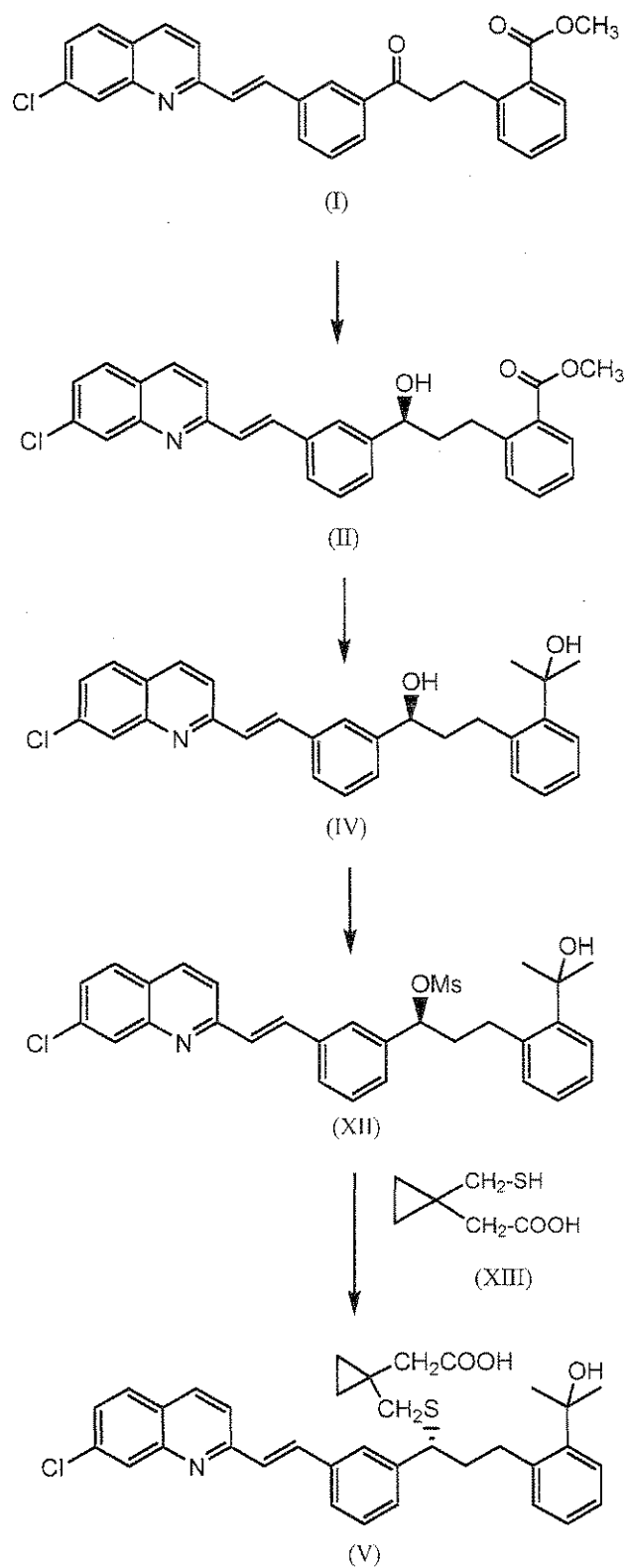


Scheme 2

[0246] Accordingly, in some embodiments, the method for synthesis of compound (V) can comprise:
(a) reducing or converting compound (I) to compound (II) with a ketoreductase of the disclosure; (b)

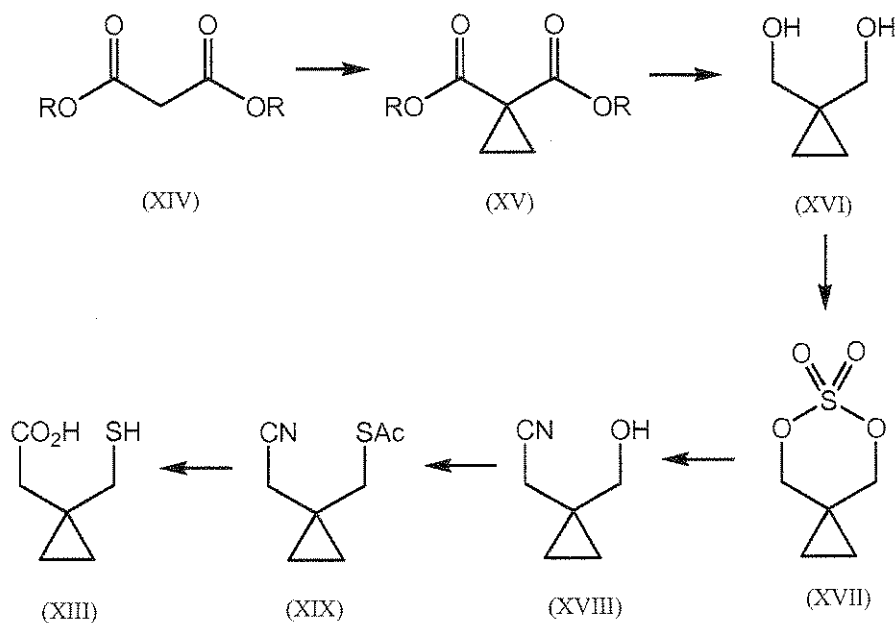
reacting the compound of formula (IV) with methylsulfonylchloride to form the compound of formula (VI); (c) coupling the thiol compound of formula (XIII) with the compound of formula (IV) to form the compound of formula (VII), where X is $-\text{CN}$ or CONH_2 ; and (d) converting the compound of formula (VII) to the compound of formula (V), or a salt thereof.

[0247] In some embodiments, the Montelukast compound can also be synthesized from the product of formula (II) as illustrated in Scheme III below, and as described in US Patent No. 5,614,632, the disclosure of which is incorporated herein by reference (see Examples 5-8 of US Patent 5,614,632). In Scheme III, the substrate of formula (I) is reduced to the product of formula (II) using the ketoreductases of the disclosure; and then converted to the compound of formula (IV), for example by use of a Grignard reagent (methyl magnesium chloride). Compound of formula (IV) is reacted with methylsulfonylchloride to form the mesylate compound (XIII), although other alkylsulfonyl halides or arylsulfonyl halides can be used. Reaction of compound (XIII) with the thiol compound of formula (XIII) results in compound (V), which can be converted to the sodium salt form.



Scheme 3

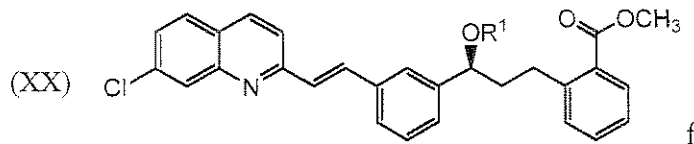
[0248] The thiol compound of formula (XIII) can be synthesized according to Scheme 4 (see, *e.g.*, US Patent No. 5,614,632):



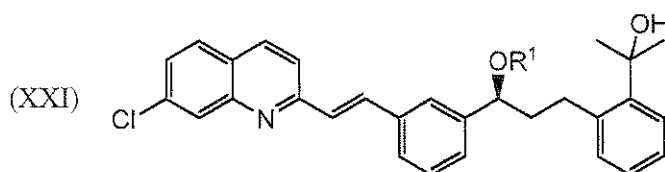
Scheme 4

[0249] The R group in Scheme 4 can be lower alkyl, preferably a C1-C4 alkyl. Variations in the synthesis of Montelukast from the compounds of formula (II) or formula (IV) are also described in US Patent No. 5,565,473; US publication 20050107612; US publication 20050245569; US publication 20060004204; and US publication 20060194839; all references incorporated herein by reference.

[0250] In view of the importance of the mesylate compounds of formula (VI) and formula (XII), the ketoreductases of the disclosure can be used in the synthesis of the compound of formula (XX):



or the compound of formula (XXI):



wherein R^1 is an alkylsulfonyl, (per)fluoroalkylsulfonyl, or an arylsulfonyl. In some embodiments, the alkyl is a lower alkyl, *e.g.*, C1-C4 alkyl, and the aryl is a benzyl. In some embodiments, R^1 is toluenesulfonyl or methylsulfonyl.

[0251] In some embodiments, a method for synthesis of compound (XX) can comprise: (a) contacting compound (I) with a ketoreductase described herein under reaction conditions suitable for reduction of compound (I) to compound (II); and (b) reacting compound (II) with an alkylsulfonyl, (per)fluoroalkylsulfonyl, arylsulfonyl halide or anhydride to form compound (XX). In some embodiments, the alkylsulfonyl halide used in (b) is methylsulfonyl chloride, such that R^1 in compound (XX) is methylsulfonyl.

[0252] In some embodiments, a method for synthesis of the compound of formula (XXI) can comprise: (a) contacting the compound (III) with a ketoreductase described herein under reaction conditions suitable for reduction of compound (III) to compound (IV); and (b) reacting compound (VI) with an alkylsulfonyl or arylsulfonyl halide or anhydride to form the compound (XXI). In some embodiments, the alkylsulfonyl halide used in (b) is methylsulfonyl chloride, such that R^1 in compound (XXI) is methylsulfonyl.

[0253] Alternatively, in some embodiments, a method for the synthesis of compound (XXI) can use the process illustrated in Scheme 3, where the method comprises: (a) contacting compound (I) with a ketoreductase described herein under reaction conditions suitable for reduction of compound (I) to compound (II); (b) converting compound (II) to compound (IV); and (c) reacting compound (IV) with an alkylsulfonyl, (per)fluoroalkylsulfonyl, arylsulfonyl halide to form compound (XXI). As noted above, the conversion of compound (II) to compound (IV) in (b) can use a Grignard reagent or CH_3Li .

[0254] In some embodiments, the ketoreductases of the disclosure can be present as compositions, for example reaction compositions, with the substrates acted on by the ketoreductases, and/or with the products produced by the ketoreductase reaction. Accordingly, in some embodiments, a composition can comprise a ketoreductase of the present disclosure, and a substrate of structural formula (I) or the substrate of structural formula (III). In some embodiments, a composition can comprise a ketoreductase of the present disclosure, and a product of structural formula (II) or a product of

structural formula (IV). In some embodiments, the composition can comprise a ketoreductase of the disclosure, the substrate of formula (I) and the product of formula (II). In some embodiments, the compositions can comprise a ketoreductase of the disclosure, a substrate of formula (III), and a product of formula (IV).

[0255] Because the ketoreductase reactions can be carried in the presence of a co-factor (NADH or NADPH) regenerating system., the reaction conditions can further include elements of a co-factor regenerating system, which are described in further detail below. Accordingly, in some embodiments, the foregoing compositions of ketoreductases can further include a cofactor regenerating system comprising glucose dehydrogenase and glucose; formate dehydrogenase and formate; or isopropanol and a secondary alcohol dehydrogenase. In some embodiments, the secondary alcohol dehydrogenase is an engineered ketoreductase. Other enzymes and substrates that can be used for co-factor recycling will be well known to the skilled artisan.

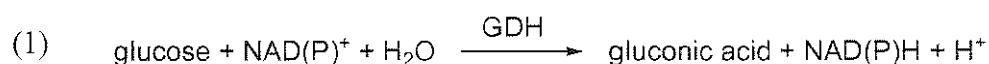
[0256] As is known by those of skill in the art, ketoreductase-catalyzed reduction reactions typically require a cofactor. Reduction reactions catalyzed by the engineered ketoreductase enzymes described herein also typically require a cofactor, although many embodiments of the engineered ketoreductases require far less cofactor than reactions catalyzed with wild-type ketoreductase enzymes. As used herein, the term “cofactor” refers to a non-protein compound that operates in combination with a ketoreductase enzyme. Cofactors suitable for use with the engineered ketoreductase enzymes described herein include, but are not limited to, NADP^+ (nicotinamide adenine dinucleotide phosphate), NADPH (the reduced form of NADP^+), NAD^+ (nicotinamide adenine dinucleotide) and NADH (the reduced form of NAD^+). Generally, the reduced form of the cofactor is added to the reaction mixture. The reduced NAD(P)H form can be optionally regenerated from the oxidized NAD(P)^+ form using a cofactor regeneration system.

[0257] The term “cofactor regeneration system” refers to a set of reactants that participate in a reaction that reduces the oxidized form of the cofactor (e.g., NADP^+ to NADPH). Cofactors oxidized by the ketoreductase-catalyzed reduction of the keto substrate are regenerated in reduced form by the cofactor regeneration system. Cofactor regeneration systems comprise a stoichiometric reductant that is a source of reducing hydrogen equivalents and is capable of reducing the oxidized form of the cofactor. The cofactor regeneration system may further comprise a catalyst, for example an enzyme catalyst, that catalyzes the reduction of the oxidized form of the cofactor by the reductant. Cofactor regeneration systems to regenerate NADH or NADPH from NAD^+ or NADP^+ , respectively, are known in the art and may be used in the methods described herein.

[0258] Suitable exemplary cofactor regeneration systems that may be employed include, but are not limited to, glucose and glucose dehydrogenase, formate and formate dehydrogenase, glucose-6-

phosphate and glucose-6-phosphate dehydrogenase, a secondary (e.g., isopropanol) alcohol and secondary alcohol dehydrogenase, phosphite and phosphite dehydrogenase, molecular hydrogen and hydrogenase, and the like. These systems may be used in combination with either NADP⁺/NADPH or NAD⁺/NADH as the cofactor. Electrochemical regeneration using hydrogenase may also be used as a cofactor regeneration system. See, e.g., U.S. Pat. Nos. 5,538,867 and 6,495,023, both of which are incorporated herein by reference. Chemical cofactor regeneration systems comprising a metal catalyst and a reducing agent (for example, molecular hydrogen or formate) are also suitable. See, e.g., PCT publication WO 2000/053731, which is incorporated herein by reference.

[0259] The terms “glucose dehydrogenase” and “GDH” are used interchangeably herein to refer to an NAD⁺ or NADP⁺-dependent enzyme that catalyzes the conversion of D-glucose and NAD⁺ or NADP⁺ to gluconic acid and NADH or NADPH, respectively. Equation (1), below, describes the glucose dehydrogenase-catalyzed reduction of NAD⁺ or NADP⁺ by glucose.



[0260] Glucose dehydrogenases that are suitable for use in the practice of the methods described herein include both naturally occurring glucose dehydrogenases, as well as non-naturally occurring glucose dehydrogenases. Naturally occurring glucose dehydrogenase encoding genes have been reported in the literature. For example, the *Bacillus subtilis* 61297 GDH gene was expressed in *E. coli* and was reported to exhibit the same physicochemical properties as the enzyme produced in its native host (Vasantha et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:785). The gene sequence of the *B. subtilis* GDH gene, which corresponds to Genbank Acc. No. M12276, was reported by Lampel et al., 1986, *J. Bacteriol.* 166:238-243, and in corrected form by Yamane et al., 1996, *Microbiology* 142:3047-3056 as Genbank Acc. No. D50453. Naturally occurring GDH genes also include those that encode the GDH from *B. cereus* ATCC 14579 (*Nature*, 2003, 423:87-91; Genbank Acc. No. AE017013) and *B. megaterium* (*Eur. J. Biochem.*, 1988, 174:485-490, Genbank Acc. No. X12370; *J. Ferment. Bioeng.*, 1990, 70:363-369, Genbank Acc. No. GI216270). Glucose dehydrogenases from *Bacillus sp.* are provided in PCT publication WO 2005/018579 as SEQ ID NOS: 10 and 12 (encoded by polynucleotide sequences corresponding to SEQ ID NOS: 9 and 11, respectively, of the PCT publication), the disclosure of which is incorporated herein by reference.

[0261] Non-naturally occurring glucose dehydrogenases may be generated using known methods, such as, for example, mutagenesis, directed evolution, and the like. GDH enzymes having suitable activity, whether naturally occurring or non-naturally occurring, may be readily identified using the assay described in Example 4 of PCT publication WO 2005/018579, the disclosure of which is incorporated herein by reference. Exemplary non-naturally occurring glucose dehydrogenases are

provided in PCT publication WO 2005/018579 as SEQ ID NOS: 62, 64, 66, 68, 122, 124, and 126. The polynucleotide sequences that encode them are provided in PCT publication WO 2005/018579 as SEQ ID NOS: 61, 63, 65, 67, 121, 123, and 125, respectively. All of these sequences are incorporated herein by reference. Additional non-naturally occurring glucose dehydrogenases that are suitable for use in the ketoreductase-catalyzed reduction reactions disclosed herein are provided in U.S. application publication Nos. 2005/0095619 and 2005/0153417, the disclosures of which are incorporated herein by reference.

[0262] Glucose dehydrogenases employed in the ketoreductase-catalyzed reduction reactions described herein may exhibit an activity of at least about 10 $\mu\text{mol}/\text{min}/\text{mg}$ and sometimes at least about 10^2 $\mu\text{mol}/\text{min}/\text{mg}$ or about 10^3 $\mu\text{mol}/\text{min}/\text{mg}$, up to about 10^4 $\mu\text{mol}/\text{min}/\text{mg}$ or higher in the assay described in Example 4 of PCT publication WO 2005/018579.

[0263] The ketoreductase-catalyzed reduction reactions described herein are generally carried out in a solvent. Suitable solvents include water, organic solvents (*e.g.*, ethyl acetate, butyl acetate, 1-octanol, heptane, octane, methyl t-butyl ether (MTBE), toluene, and the like), ionic liquids (*e.g.*, 1-ethyl 4-methylimidazolium tetrafluoroborate, 1-butyl-3-methylimidazolium tetrafluoroborate, 1-butyl-3-methylimidazolium hexafluorophosphate, and the like). In some embodiments, aqueous solvents, including water and aqueous co-solvent systems, are used.

[0264] Exemplary aqueous co-solvent systems have water and one or more organic solvent. In general, an organic solvent component of an aqueous co-solvent system is selected such that it does not completely inactivate the ketoreductase enzyme. Appropriate co-solvent systems can be readily identified by measuring the enzymatic activity of the specified engineered ketoreductase enzyme with a defined substrate of interest in the candidate solvent system, utilizing an enzyme activity assay, such as those described herein.

[0265] The organic solvent component of an aqueous co-solvent system may be miscible with the aqueous component, providing a single liquid phase, or may be partly miscible or immiscible with the aqueous component, providing two liquid phases. Generally, when an aqueous co-solvent system is employed, it is selected to be biphasic, with water dispersed in an organic solvent, or vice-versa. Generally, when an aqueous co-solvent system is utilized, it is desirable to select an organic solvent that can be readily separated from the aqueous phase. In general, the ratio of water to organic solvent in the co-solvent system is typically in the range of from about 90:10 to about 10:90 (v/v) organic solvent to water, and between 80:20 and 20:80 (v/v) organic solvent to water. The co-solvent system may be pre-formed prior to addition to the reaction mixture, or it may be formed *in situ* in the reaction vessel.

[0266] The aqueous solvent (water or aqueous co-solvent system) may be pH-buffered or unbuffered. Generally, the reduction can be carried out at a pH of about 10 or below, usually in the range of from about 5 to about 10. In some embodiments, the reduction is carried out at a pH of about 9 or below, usually in the range of from about 5 to about 9. In some embodiments, the reduction is carried out at a pH of about 8 or below, often in the range of from about 5 to about 8, and usually in the range of from about 6 to about 8. The reduction may also be carried out at a pH of about 7.8 or below, or 7.5 or below. Alternatively, the reduction may be carried out at a neutral pH, *i.e.*, about 7.

[0267] During the course of the reduction reactions, the pH of the reaction mixture may change. The pH of the reaction mixture may be maintained at a desired pH or within a desired pH range by the addition of an acid or a base during the course of the reaction. Alternatively, the pH may be controlled by using an aqueous solvent that comprises a buffer. Suitable buffers to maintain desired pH ranges are known in the art and include, for example, phosphate buffer, triethanolamine buffer, and the like. Combinations of buffering and acid or base addition may also be used.

[0268] When the glucose/glucose dehydrogenase cofactor regeneration system is employed, the co-production of gluconic acid ($pK_a=3.6$), as represented in equation (1) causes the pH of the reaction mixture to drop if the resulting aqueous gluconic acid is not otherwise neutralized. The pH of the reaction mixture may be maintained at the desired level by standard buffering techniques, wherein the buffer neutralizes the gluconic acid up to the buffering capacity provided, or by the addition of a base concurrent with the course of the conversion. Combinations of buffering and base addition may also be used. Suitable buffers to maintain desired pH ranges are described above. Suitable bases for neutralization of gluconic acid are organic bases, for example amines, alkoxides and the like, and inorganic bases, for example, hydroxide salts (*e.g.*, NaOH), carbonate salts (*e.g.*, NaHCO_3), bicarbonate salts (*e.g.*, K_2CO_3), basic phosphate salts (*e.g.*, K_2HPO_4 , Na_3PO_4), and the like. The addition of a base concurrent with the course of the conversion may be done manually while monitoring the reaction mixture pH or, more conveniently, by using an automatic titrator as a pH stat. A combination of partial buffering capacity and base addition can also be used for process control.

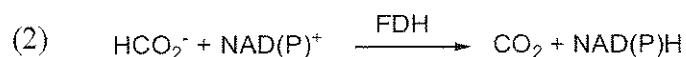
[0269] When base addition is employed to neutralize gluconic acid released during a ketoreductase-catalyzed reduction reaction, the progress of the conversion may be monitored by the amount of base added to maintain the pH. Typically, bases added to unbuffered or partially buffered reaction mixtures over the course of the reduction are added in aqueous solutions.

[0270] In some embodiments, the co-factor regenerating system can comprise a formate dehydrogenase. The terms "formate dehydrogenase" and "FDH" are used interchangeably herein to refer to an NAD^+ or NADP^+ -dependent enzyme that catalyzes the conversion of formate and NAD^+ or NADP^+ to carbon dioxide and NADH or NADPH, respectively. Formate dehydrogenases that are

suitable for use as cofactor regenerating systems in the ketoreductase-catalyzed reduction reactions described herein include both naturally occurring formate dehydrogenases, as well as non-naturally occurring formate dehydrogenases. Formate dehydrogenases include those corresponding to SEQ ID NOS: 70 (*Pseudomonas sp.*) and 72 (*Candida boidinii*) of PCT publication WO 2005/018579, which are encoded by polynucleotide sequences corresponding to SEQ ID NOS: 69 and 71, respectively, of PCT publication 2005/018579, the disclosures of which are incorporated herein by reference. Formate dehydrogenases employed in the methods described herein, whether naturally occurring or non-naturally occurring, may exhibit an activity of at least about 1 $\mu\text{mol}/\text{min}/\text{mg}$, sometimes at least about 10 $\mu\text{mol}/\text{min}/\text{mg}$, or at least about 10^2 $\mu\text{mol}/\text{min}/\text{mg}$, up to about 10^3 $\mu\text{mol}/\text{min}/\text{mg}$ or higher, and can be readily screened for activity in the assay described in Example 4 of PCT publication WO 2005/018579.

[0271] As used herein, the term “formate” refers to formate anion (HCO_2^-), formic acid (HCO_2H), and mixtures thereof. Formate may be provided in the form of a salt, typically an alkali or ammonium salt (for example, HCO_2Na , KHCO_2NH_4 , and the like), in the form of formic acid, typically aqueous formic acid, or mixtures thereof. Formic acid is a moderate acid. In aqueous solutions within several pH units of its pKa (pKa=3.7 in water) formate is present as both HCO_2^- and HCO_2H in equilibrium concentrations. At pH values above about pH 4, formate is predominantly present as HCO_2^- . When formate is provided as formic acid, the reaction mixture is typically buffered or made less acidic by adding a base to provide the desired pH, typically of about pH 5 or above. Suitable bases for neutralization of formic acid include, but are not limited to, organic bases, for example amines, alkoxides and the like, and inorganic bases, for example, hydroxide salts (e.g., NaOH), carbonate salts (e.g., NaHCO_3), bicarbonate salts (e.g., K_2CO_3), basic phosphate salts (e.g., K_2HPO_4 , Na_3PO_4), and the like.

[0272] For pH values above about pH 5, at which formate is predominantly present as HCO_2^- , Equation (2) below, describes the formate dehydrogenase-catalyzed reduction of NAD^+ or NADP^+ by formate.

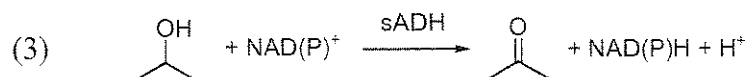


[0273] When formate and formate dehydrogenase are employed as the cofactor regeneration system, the pH of the reaction mixture may be maintained at the desired level by standard buffering techniques, wherein the buffer releases protons up to the buffering capacity provided, or by the addition of an acid concurrent with the course of the conversion. Suitable acids to add during the course of the reaction to maintain the pH include organic acids, for example carboxylic acids, sulfonic acids, phosphonic acids, and the like, mineral acids, for example hydrohalic acids (such as

hydrochloric acid), sulfuric acid, phosphoric acid, and the like, acidic salts, for example dihydrogenphosphate salts (*e.g.*, KH_2PO_4), bisulfate salts (*e.g.*, NaHSO_4) and the like. Some embodiments utilize formic acid, whereby both the formate concentration and the pH of the solution are maintained.

[0274] When acid addition is employed to maintain the pH during a reduction reaction using the formate/formate dehydrogenase cofactor regeneration system, the progress of the conversion may be monitored by the amount of acid added to maintain the pH. Typically, acids added to unbuffered or partially buffered reaction mixtures over the course of conversion are added in aqueous solutions.

[0275] The terms “secondary alcohol dehydrogenase” and “sADH” are used interchangeably herein to refer to an NAD^+ or NADP^+ -dependent enzyme that catalyzes the conversion of a secondary alcohol and NAD^+ or NADP^+ to a ketone and NADH or NADPH , respectively. Equation (3), below, describes the reduction of NAD^+ or NADP^+ by a secondary alcohol, illustrated by isopropanol.



[0276] Secondary alcohol dehydrogenases that are suitable for use as cofactor regenerating systems in the ketoreductase-catalyzed reduction reactions described herein include both naturally occurring secondary alcohol dehydrogenases, as well as non-naturally occurring secondary alcohol dehydrogenases. Naturally occurring secondary alcohol dehydrogenases include known alcohol dehydrogenases from, *Thermoanaerobium brockii*, *Rhodococcus erythropolis*, *Lactobacillus kefir*, *Lactobacillus minor* and *Lactobacillus brevis*, and non-naturally occurring secondary alcohol dehydrogenases include engineered alcohol dehydrogenases derived therefrom. Secondary alcohol dehydrogenases employed in the methods described herein, whether naturally occurring or non-naturally occurring, may exhibit an activity of at least about $1 \mu\text{mol}/\text{min}/\text{mg}$, sometimes at least about $10 \mu\text{mol}/\text{min}/\text{mg}$, or at least about $10^2 \mu\text{mol}/\text{min}/\text{mg}$, up to about $10^3 \mu\text{mol}/\text{min}/\text{mg}$ or higher.

[0277] Suitable secondary alcohols include lower secondary alkanols and aryl-alkyl carbinols. Examples of lower secondary alcohols include isopropanol, 2-butanol, 3-methyl-2-butanol, 2-pentanol, 3-pentanol, 3,3-dimethyl-2-butanol, and the like. In one embodiment the secondary alcohol is isopropanol. Suitable aryl-alkyl carbinols include unsubstituted and substituted 1-arylethanol.

[0278] When a secondary alcohol and secondary alcohol dehydrogenase are employed as the cofactor regeneration system, the resulting NAD^+ or NADP^+ is reduced by the coupled oxidation of the secondary alcohol to the ketone by the secondary alcohol dehydrogenase. Some engineered ketoreductases also have activity to dehydrogenate a secondary alcohol reductant. In some

embodiments using secondary alcohol as reductant, the engineered ketoreductase and the secondary alcohol dehydrogenase are the same enzyme.

[0279] In carrying out embodiments of the ketoreductase-catalyzed reduction reactions described herein employing a cofactor regeneration system, either the oxidized or reduced form of the cofactor may be provided initially. As described above, the cofactor regeneration system converts oxidized cofactor to its reduced form, which is then utilized in the reduction of the ketoreductase substrate.

[0280] In some embodiments, cofactor regeneration systems are not used. For reduction reactions carried out without the use of a cofactor regenerating systems, the cofactor is added to the reaction mixture in reduced form.

[0281] In some embodiments, when the process is carried out using whole cells of the host organism, the whole cell may natively provide the cofactor. Alternatively or in combination, the cell may natively or recombinantly provide the glucose dehydrogenase.

[0282] In carrying out the stereoselective reduction reactions described herein, the engineered ketoreductase enzyme, and any enzymes comprising the optional cofactor regeneration system, may be added to the reaction mixture in the form of the purified enzymes, whole cells transformed with gene(s) encoding the enzymes, and/or cell extracts and/or lysates of such cells. The gene(s) encoding the engineered ketoreductase enzyme and the optional cofactor regeneration enzymes can be transformed into host cells separately or together into the same host cell. For example, in some embodiments one set of host cells can be transformed with gene(s) encoding the engineered ketoreductase enzyme and another set can be transformed with gene(s) encoding the cofactor regeneration enzymes. Both sets of transformed cells can be utilized together in the reaction mixture in the form of whole cells, or in the form of lysates or extracts derived therefrom. In other embodiments, a host cell can be transformed with gene(s) encoding both the engineered ketoreductase enzyme and the cofactor regeneration enzymes.

[0283] Whole cells transformed with gene(s) encoding the engineered ketoreductase enzyme and/or the optional cofactor regeneration enzymes, or cell extracts and/or lysates thereof, may be employed in a variety of different forms, including solid (*e.g.*, lyophilized, spray-dried, and the like) or semisolid (*e.g.*, a crude paste).

[0284] The cell extracts or cell lysates may be partially purified by precipitation (ammonium sulfate, polyethyleneimine, heat treatment or the like, followed by a desalting procedure prior to lyophilization (*e.g.*, ultrafiltration, dialysis, and the like). Any of the cell preparations may be stabilized by cross-linking using known cross-linking agents, such as, for example, glutaraldehyde or immobilization to a solid phase (*e.g.*, Eupergit C, and the like).

[0285] The solid reactants (*e.g.*, enzyme, salts, etc.) may be provided to the reaction in a variety of different forms, including powder (*e.g.*, lyophilized, spray dried, and the like), solution, emulsion, suspension, and the like. The reactants can be readily lyophilized or spray dried using methods and equipment that are known to those having ordinary skill in the art. For example, the protein solution can be frozen at -80°C in small aliquots, then added to a prechilled lyophilization chamber, followed by the application of a vacuum. After the removal of water from the samples, the temperature is typically raised to 4°C for two hours before release of the vacuum and retrieval of the lyophilized samples.

[0286] The quantities of reactants used in the reduction reaction will generally vary depending on the quantities of product desired, and concomitantly the amount of ketoreductase substrate employed. The following guidelines can be used to determine the amounts of ketoreductase, cofactor, and optional cofactor regeneration system to use. Generally, keto substrates can be employed at a concentration of about 20 to 300 grams/liter using from about 50 mg to about 5 g of ketoreductase and about 10 mg to about 150 mg of cofactor. Those having ordinary skill in the art will readily understand how to vary these quantities to tailor them to the desired level of productivity and scale of production. Appropriate quantities of optional cofactor regeneration system may be readily determined by routine experimentation based on the amount of cofactor and/or ketoreductase utilized. In general, the reductant (*e.g.*, glucose, formate, isopropanol) is utilized at levels above the equimolar level of ketoreductase substrate to achieve essentially complete or near complete conversion of the ketoreductase substrate.

[0287] The order of addition of reactants is not critical. The reactants may be added together at the same time to a solvent (*e.g.*, monophasic solvent, biphasic aqueous co-solvent system, and the like), or alternatively, some of the reactants may be added separately, and some together at different time points. For example, the cofactor regeneration system, cofactor, ketoreductase, and ketoreductase substrate may be added first to the solvent.

[0288] For improved mixing efficiency when an aqueous co-solvent system is used, the cofactor regeneration system, ketoreductase, and cofactor may be added and mixed into the aqueous phase first. The organic phase may then be added and mixed in, followed by addition of the ketoreductase substrate. Alternatively, the ketoreductase substrate may be premixed in the organic phase, prior to addition to the aqueous phase.

[0289] Suitable conditions for carrying out the ketoreductase-catalyzed reduction reactions described herein include a wide variety of conditions which can be readily optimized by routine experimentation that includes, but is not limited to, contacting the engineered ketoreductase enzyme and substrate at an

experimental pH and temperature and detecting product, for example, using the methods described in the Examples provided herein.

[0290] The ketoreductase catalyzed reduction is typically carried out at a temperature in the range of from about 15°C to about 75°C. For some embodiments, the reaction is carried out at a temperature in the range of from about 20°C to about 55°C. In still other embodiments, it is carried out at a temperature in the range of from about 20°C to about 45°C. The reaction may also be carried out under ambient conditions.

[0291] The reduction reaction is generally allowed to proceed until essentially complete, or near complete, reduction of substrate is obtained. Reduction of substrate to product can be monitored using known methods by detecting substrate and/or product. Suitable methods include gas chromatography, HPLC, and the like. Conversion yields of the alcohol reduction product generated in the reaction mixture are generally greater than about 50%, may also be greater than about 60%, may also be greater than about 70%, may also be greater than about 80%, may also be greater than 90%, and are often greater than about 97%.

7. Examples

[0292] Various features and embodiments of the disclosure are illustrated in the following representative examples, which are intended to be illustrative, and not limiting.

[0293] In the following descriptions, wherever glucose dehydrogenase (GDH) is used, it is GDH CDX901, obtainable from Jülich Chiral Solutions, Jülich, Germany.

Example 1: Wild-type Ketoreductase Gene Acquisition and Construction of Expression Vectors.

[0294] Ketoreductase (KRED) encoding genes were designed for expression in *E. coli* based on the reported amino acid sequence of the ketoreductase and a codon optimization algorithm as described in Example 1 of US provisional application Serial No. 60/848,950, incorporated herein by reference. Genes were synthesized using oligonucleotides composed of 42 nucleotides and cloned into expression vector pCK110900 (depicted as FIG. 3 in United States Patent Application Publication 20060195947) under the control of a *lac* promoter. The expression vector also contained the P15a origin of replication and the chloramphenicol resistance gene. Resulting plasmids were transformed into *E. coli* W3110 using standard methods. Codon optimized genes and the encoding polypeptides as well are listed in Table 3. The activity of the wild-type ketoreductases was confirmed as described in US provisional application Serial No. 60/848,950.

[0295] Table 3

Table 3: Abbreviations, source and references for Ketoreductases used

KRED	Microorganism from which enzyme was originally identified	Genbank Acc. No.	GI number	Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO or source
ADH-CM	<i>Candida magnoliae</i>	AB036927.1	12657576	SEQ ID No 1 in US Patent Appln Publn 20060195947	SEQ ID No 2 in US Patent Appln Publn 20060195947
YDL	<i>Saccharomyces cerevisiae</i>	NP_010159.1	6320079	SEQ ID NO:121	SEQ ID NO:122
ADH-LB	<i>Lactobacillus brevis</i>	INXQ_A	30749782	SEQ ID NO:1	SEQ ID N:2
ADH-RE	<i>Rhodococcus erythropolis</i>	AAN73270.1	34776951	SEQ ID NO:123	SEQ ID NO:124
YGL	<i>Saccharomyces cerevisiae</i>	NP_011476	6321399	SEQ ID NO:125	SEQ ID NO:126
YPR	<i>Saccharomyces cerevisiae</i>	NP_010656.1	6320576	SEQ ID NO:127	SEQ ID NO:128
GRE	<i>Saccharomyces cerevisiae</i>	NP_014490.1	6324421	SEQ ID NO:129	SEQ ID NO:130
ADH-LK	<i>Lactobacillus kefir</i>	AAP94029.1	33112056	SEQ ID NO:3	SEQ ID NO:4
ADH-SB	<i>Sporobolomyces salmonicolor</i>	Q9UUN9	30315955	SEQ ID NO:131	SEQ ID NO:132
ADH-SC	<i>Streptomyces coelicolor</i>	NP_631415.1	21225636	SEQ ID NO:133	SEQ ID NO:134
ADH-TB	<i>Thermoanaerobium brockii</i>	X64841.1	1771790	SEQ ID NO:135	SEQ ID NO:136
ADH-CP	<i>Candida parapsilosis</i>	BAA24528	2815409		Julich Chiral Solutions Cat. No. 03.11
DR-LB	<i>Lactobacillus brevis</i> diacetyl reductase	ABJ63353.1	116098204		Julich Chiral Solutions Cat. No. 8.1
ADH-HE	Horse liver	DEHOAL	625197	SEQ ID NO:137	SEQ ID NO:138
ADH-CB	<i>Candida boidinii</i>	CAD66648	28400789		Julich Chiral Solutions Cat.

					No. 02.10
LDH-LL	<i>Lactobacillus leichmannii</i>				Fluka Cat. No. 61306
ADH-AF	<i>Aspergillus flavus</i>	P41747	1168346	SEQ ID NO 115	SEQ ID NO 116
ADH-OO1	<i>Oenococcus oeni</i>	ZP_00318704.1	48864831	SEQ ID NO 117	SEQ ID NO 118
ADH-RU	<i>Ralstonia eutropha</i>	ZP_00202558.1	46131317	SEQ ID NO 119	SEQ ID NO 120

[0296] Polynucleotides encoding engineered ketoreductases of the present invention were likewise cloned into vector pCK110900 for expression in *E. coli* W3110.

Example 2: Production of Ketoreductase Powders; Shake Flask Procedure.

[0297] A single microbial colony of *E. coli* containing a plasmid with the ketoreductase gene of interest was inoculated into 50 ml Terrific Broth containing 30 µg/ml chloramphenicol and 1% glucose. Cells were grown overnight (at least 16 hrs) in an incubator at 30°C with shaking at 250 rpm. The culture was diluted into 250 ml Terrific Broth (12 g/L bacto-tryptone, 24g/L yeast extract, 4 ml/L glycerol, 65mM potassium phosphate, pH 7.0, 1mM MgSO₄, 30 µg/ml chloramphenicol) in 1 liter flask to an optical density at 600 nm (OD₆₀₀) of 0.2 and allowed to grow at 30°C. Expression of the ketoreductase gene was induced with 1mM IPTG when the OD₆₀₀ of the culture is 0.6 to 0.8 and incubated overnight (at least 16 hrs). Cells were harvested by centrifugation (5000rpm, 15 min, 4°C) and the supernatant discarded. The cell pellet was resuspended with an equal volume of cold (4°C) 100mM triethanolamine (chloride) buffer, pH 7.0 (including 2 mM MgSO₄ in the case of ADH-LK and ADH-LB and engineered ketoreductases derived therefrom), and harvested by centrifugation as above. The washed cells were resuspended in two volumes of the cold triethanolamine (chloride) buffer and passed through a French Press twice at 12000psi while maintained at 4°C. Cell debris was removed by centrifugation (9000 rpm, 45 min., 4°C). The clear lysate supernatant was collected and stored at -20°C. Lyophilization of frozen clear lysate provided a dry powder of crude ketoreductase enzyme.

Example 3: Production of Ketoreductases; Fermentation Procedure.

[0298] In an aerated agitated 15L fermenter, 6.0L of growth medium containing 0.88 g/L ammonium sulfate, 0.98 g/L of sodium citrate; 12.5 g/L of dipotassium hydrogen phosphate trihydrate, 6.25g/L of potassium dihydrogen phosphate, 6.2 g/L of Tastone-154 yeast extract, 0.083 g/L ferric ammonium citrate, and 8.3 ml/L of a trace element solution containing 2 g/L of calcium chloride dihydrate, 2.2

g/L of zinc sulfate septahydrate, 0.5 g/L manganese sulfate monohydrate, 1 g/L cuprous sulfate heptahydrate, 0.1 g/L ammonium molybdate tetrahydrate and 0.02 g/L sodium tetraborate decahydrate was brought to a temperature of 30°C. The fermenter was inoculated with a late exponential culture of *E. coli* W3110, containing a plasmid with the ketoreductase gene of interest, grown in a shake flask as described in Example 3 to a starting OD600 of 0.5 to 2.0. The fermenter was agitated at 500-1500 rpm and air was supplied to the fermentation vessel at 1.0-15.0 L/min to maintain dissolved oxygen level of 30% saturation or greater. The pH of the culture was controlled at 7.0 by addition of 20% v/v ammonium hydroxide. Growth of the culture was maintained by the addition of a feed solution containing 500g/L cerelose, 12 g/L ammonium chloride and 10.4 g/L magnesium sulfate heptahydrate. After the culture reached an OD600 of 50, the expression of ketoreductase was induced by the addition of isopropyl-b-D-thiogalactoside (IPTG) to a final concentration of 1mM. The culture was grown for another 14 hours. The culture was then chilled to 4°C and maintained at 4°C until harvested. Cells were harvested by centrifugation at 5000G for 40 minutes in a Sorval RC12BP centrifuge at 4°C. Harvested cells were used directly in the following downstream recovery process or were stored at 4°C until such use.

[0299] The cell pellet was resuspended in 2 volumes of 100 mM triethanolamine (chloride) buffer, pH 6.8, at 4°C to each volume of wet cell paste. The intracellular ketoreductase was released from the cells by passing the suspension through a homogenizer fitted with a two-stage homogenizing valve assembly using a pressure of 12000 psig. The cell homogenate was cooled to 4°C immediately after disruption. A solution of 10% w/v polyethyleneimine, pH 7.2, was added to the lysate to a final concentration of 0.5% w/v and stirred for 30 minutes. The resulting suspension was clarified by centrifugation at 5000G in a standard laboratory centrifuge for 30 minutes. The clear supernatant was decanted and concentrated ten fold using a cellulose ultrafiltration membrane with a molecular weight cut off of 30Kd. The final concentrate was dispensed into shallow containers, frozen at -20°C and lyophilized to powder. The ketoreductase powder was stored at -80°C.

Example 4: Analytical methods for the conversion of 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester to (S)-2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester.

[0300] Reduction of 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester and chiral purity of the alcohol product was determined by reverse phase HPLC (2.1 x 50 mm Zorbax XDB column with guard cartridge; 90:10 ACN/0.25% AcOH in H₂O at 0.6 mL/min at 30°C; detection at 287 nm with the following retention times: enantiomeric alcohols 0.55 min; ketone 0.72 min) or normal phase, chiral HPLC (2.1 x 150 mm ChiralPak AS-H column with guard cartridge,

10:90 isopropylalcohol/heptane at 0.5 mL/min at 40°C; detection at 287 nm with the following retention times: (S)-alcohol 7.1 min.; (R)-alcohol 5.7 min; ketone 4.5 min).

Example 5: Analytical methods for the conversion of 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]-phenyl]-1-methyl-1-ethanol to (S)-2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-hydroxypropyl]-phenyl]-1-methyl-1-ethanol.

[0301] Reduction of 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]-phenyl]-1-methyl-1-ethanol (prepared by oxidation of the corresponding alcohol) and purity of the alcohol product was determined by HPLC (4.6 x 50 mm Phenomix Gemini C18, 110A column with the following elution profile: 40% to 80% in water/0.1%TFA gradient for 4 min, 1.5 min hold, return to 40% acetonitrile/0.1% TFA in 1 min with a flow rate of 0.5 mL/min; ambient temperature; detection at 254 nm with the following retention times: alcohol 4.4 min, ketone 5.7 min).

[0302] Chiral purity was assessed by HPLC (2.1 x 150 mm ChiralPak AD-H column; solvent: 40:60 isopropyl alcohol:heptane; flow rate = 0.5 mL/min at 40°C; detection at 280 nm with the following retention times: (S)-alcohol 12.0 min.; (R)-alcohol 11.2 min; ketone 10.3 min).

Example 6: Evaluation of Wild-Type Ketoreductases for Reduction of 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester

[0303] KREDs described in Table 3 of Example 1 were screened using NADH and NADPH as co-factors and glucose dehydrogenase/glucose or isopropylalcohol as co-factor regeneration system. To wells in a 96 deep-well plate was added 250 µL of 100 mM triethanolamine(chloride) buffer pH7.0 containing 1.0 g/L NAD(P), 30-50 g/L of KRED variant, 200 µL of IPA and 50 µL of 10-20 g/L of the ketone substrate in THF. Alternatively, each well in a 96 deep-well plate was pre-loaded with 10-20 mg of CaCO₃, 250 µL of 100 mM triethanolamine(chloride) buffer pH7.0 containing 1.0 g/L NAD(P), 30-50 g/L of KRED, 10-20 g/L of GDH and 10% glucose). The plates were sealed with aluminum/polypropylene laminate heat seal tape (Velocity 11 (Menlo Park, CA), Cat# 06643-001), and shaken at room temperature overnight. The reactions were quenched by the addition of 1000 µL of EtOAc. After centrifuge (4000 rpm for 10 min. at 22°C), the organic phase was assayed for conversion using the normal phase HPLC method in Example 4. None of these enzymes showed any activity under any of the conditions tested (detection limit ~0.5% conversion).

[0304] This example demonstrates that wild-type ketoreductases have very little if any activity on 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester.

Example 7: Example 7: Evaluation of ADH-LK Variants for Reduction of 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester

[0305] Several ADH-LK variants that had been generated were evaluated and it was found that an ADH-LK variant with SEQ ID NO:90 converted the substrate to the chiral (S)-2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester when evaluated under the conditions described in Example 6 and as listed in Table 4.

[0306] Table 4

Table 4: Activity of an ADH-LK variant		
SEQ ID NO	# of mutations from ADH-LK	Activity
ADH-LK	0	0
90	6	<0.03 g/L.g _{enzyme} .day

[0307] This example shows that an ADH-LK variant containing G7H, S96T, F147L, Y190P, V196L, A202W mutations converts 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester to (S)-2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester with high stereoselectivity (>99% stereomeric excess).

Example 8: High Throughput HPLC Assay for Ketoreductase Activity on 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester using isopropylalcohol for co-factor recycling.

[0308] Plasmid libraries obtained by directed evolution and containing evolved ketoreductase genes were transformed into *E. coli* and plated on Luria-Bertani (LB) broth containing 1% glucose and 30 µg/mL chloramphenicol (CAM). After incubation for at least 16 hrs at 30°C, colonies were picked using a Q-bot® robotic colony picker (Genetix USA, Inc., Beaverton, OR) into 96-well shallow well microtiter plates containing 180 µL Terrific broth (TB), 1% glucose, 30 µg/mL chloramphenicol (CAM), and 2 mM MgSO₄. Cells were grown overnight at 30°C with shaking at 200 rpm. 20 µL of this culture was then transferred into 96-deep well plates containing 350 µL Terrific broth (TB), 2 mM MgSO₄ and 30 µg/mL CAM. After incubation of deep-well plates at 30°C with shaking at 250 rpm for 2.5 to 3 hours (OD₆₀₀ 0.6-0.8), recombinant gene expression by the cell cultures was induced by isopropyl thiogalactoside (IPTG) to a final concentration of 1 mM. The plates were then incubated at 30°C with shaking at 250 rpm for 15-23 hrs.

[0309] To wells of a 96-well microtiter plate was added 100 µL 100mM triethanolamine(chloride) buffer pH7.0 containing 0.2 mM Na-NADP, and 2 mM MgSO₄, and a sufficient volume of cell culture such that the best known enzyme at any point in time (e.g. SEQ ID:90 in the first round of evolution) would give 10-20% conversion of ketone to (S)-alcohol. IPA and a solution containing 1.67 to 16.7 g/L 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester in THF was added to the wells to give a final composition of 100mM triethanolamine(chloride)

buffer pH7.0, THF and IPA in a 4:1:5 ratio by volume (final substrate concentration of 1 to 10 g/L). Acetone was added to a final concentration of 0 to 2% as desired (typically as a solution in IPA or THF). The plates were heat sealed as described in Example 6 and incubated at room temperature or 40°C for 4 or 24 hours with shaking. At the end of the reaction, substrate and product were quenched with 1000 μ L 1:4 THF:Acetonitrile. Following centrifugation at room temperature, the supernatant was analyzed for conversion using the reverse phase HPLC methods described in Example 4. For reactions to be assayed for enantioselectivity, the reactions were quenched with 1 mL of EtOAc, centrifuged and the organic phase was subjected to chiral analysis via the normal phase HPLC method described in Example 4.

[0310] This example describes the method that was used to identify KRED variants improved for 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester reduction.

Example 9: Reduction of 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester by Engineered Ketoreductases Derived from ADH-LK.

[0311] To an amber vial under air with stir bar was added, in order, 50-500 mg of substrate, 1.5 mL 100 mM triethanolamine(chloride) buffer pH 7.0 or 8.0, containing 0.33 g/L NADP-Na and 10.0-33.3 g/L of KRED variant, 2 mM of MgSO₄, 2.5 mL IPA and 0.5 mL of co-solvent (THF or toluene). The vials were closed and immersed in an oil bath controlled at the desired temperature. Two 50 μ L aliquots were taken at 1, 2, 4 and 8hr and four 50 μ L aliquots were taken at t=24h. The aliquots were diluted with 1000 μ L THF and centrifuged (4000 rpm for 10 minutes at 22°C) to remove debris. The supernatant was diluted 9x with acetonitrile and conversion determined as described in Example 4. Chiral analysis was performed on the 24 hr samples: 0.5 volume of brine and 2 volumes of THF were added to achieve a clean phase break and the organic phase was dried with MgSO₄. The organic phase was diluted 10x with EtOAc and analyzed as described in Example 4. Table 5 gives the SEQ ID NO. corresponding to the ketoreductase, the number of amino acid mutations from the wild-type ADH-LK and the conversion of 2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester to (S)-2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester. All variants tested gave (S)-2-[3-[3-[2-(7-chloro-2-quinoliny)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester of >99.2% stereomeric excess (reference standard was 99.2% ee; the undesired stereomer was undetectable).

Table 5: Activity of ADH-LK Variants at the Indicated Temperature			
SEQ ID NO	# of mutations ADH-LK	Activity	Temperature (°C)
90	6	+	rt

48	6	++	rt
46	6	++	rt
44	6	++	rt
42	6	++	rt
100	7	++	rt
92	7	++	rt
94	7	++	rt
102	7	++	rt
86	7	++	rt
96	7	++	rt
88	8	++	rt
98	8	+++	rt
70	10	+++	rt
84	10	+++	rt
76	11	+++	rt
74	12	+++	rt
64	12	+++	rt
104	9	+++	rt
68	10	+++	rt
106	9	+++	rt
72	12	+++	rt
66	11	+++	rt
24	15	++++	rt
82	11	+++	35
80	12	+++	rt
108	14	+++	rt

50	14	+++	rt
78	13	+++	35
10	14	+++	rt
34	14	+++	rt
36	12	+++	rt
58	14	++++	35
40	13	++++	40
32	14	+++	35
22	15	++++	40
38	14	++++	40
54	15	++++	40
12	16	++++	40
30	15	++++	40
28	15	++++	40
16	18	+++++	45
110	16	++++	40
62	15	++++	40
60	15	++++	40
52	15	++++	40
56	14	++++	40
26	17	++++	40
14	18	+++++	40
20	19	+++++	45
6	20	+++++	40
8	21	+++++	45

18	20	++++	40
----	----	------	----

+: <0.03 g product per liter/g enzyme/day; ++: 0.03 to 1 g product per liter/g enzyme/day; +++: 1 to 5 g product per liter/g enzyme/day; ++++: 5 to 20 g product per liter/g enzyme/day; +++++ >20 g product per liter/g enzyme/day.

Example 10: Reduction of 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol by an Engineered Ketoreductase Derived from ADH-LK.

[0312] To an amber vial under air with stir bar was added, in order, 500 mg 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol, 1.5 mL 100 mM triethanolamine(chloride) buffer pH7.0, containing 0.89 g/L NADP-Na and 13.3 g/L of KRED variant SEQ ID NO:20, 2 mM MgSO₄, 2.5 mL IPA and 0.5 mL of co-solvent (THF or toluene). The vials were closed and immersed in an oil bath controlled at 40°C. Samples were taken (30 µL) at 6, 24, and 29h and diluted with 1500 µL of THF; 30 µL of the diluted sample was concentrated to dryness, dissolved in 1000 µL acetonitrile prior to HPLC analysis for chemical conversion as described in Example 5.

[0313] Chiral analysis was performed after working up the entire reaction mixture at 29h as follows: the sample was diluted with 2 mL brine and 6 mL THF affording a clean phase break. The aqueous phase was extracted with ethyl acetate (3x10 mL) and the combined organic layers were dried over MgSO₄. The organic solution was filtered through a bed of Celite and concentrated to dryness. The analytical sample was prepared by dissolving 1 mg of the residue in 1 mL acetonitrile and analyzed as described in Example 5. (S)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol was obtained with >99% stereomeric excess. Conversion was greater than about 67%.

Example 11: Preparative scale production of (S)-2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-hydroxypropyl]benzoic acid methyl ester.

[0314] To a jacketed 2-L 3-neck flask under nitrogen with jacket temperature set at 51°C via an external heat exchanger and equipped with internal thermometer and mechanical stirrer at 250 rpm was added 300 mL 100 mM pH 8.0 triethanolamine*HCl, 0.6 mL 1 M MgSO₄, 3.0 g of SEQ ID NO:20 catalyst as prepared in Example 3, 0.1 g NADP-Na₂, to give a pale yellow solution. After stirring for 10 minutes, 100 g 2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl]phenyl]-3-ketopropyl]benzoic acid methyl ester was added portion-wise over ~5 minutes. To the slurry was added 500 mL (390 g) of IPA and 100 mL (85 g) toluene. The progress of the reaction was monitored by achiral HPLC as

described in Example 4 and 6. The procedure as described in Example 9 was used for sampling and sample prep.

[0315] After stirring at 45°C for 24 hours, the reaction was complete according achiral HPLC analysis. The reaction mixture was filtered through three layers of 150mm diameter Whatman#2 filter paper via an air-driven vacuum pump. Approximately 10 minutes was required to complete the filtration to give a tan paste. The tan paste was washed with 2 x 500 mL water. The tan pasted was air-dried over-night to give 104 g of a tan solid of (*S*)-2-[3-2[-(7-chloro-2-quinolinyl)ethenyl] phenyl]-3-hydroxypropyl] benzoic acid methyl ester monohydrate (100%yield; product is a mono-hydrate) with a chemical purity of 98.5 HPLC area percent (the major impurity being 0.3-0.4 HPLC area percent of the starting material). The (*R*)-stereoisomer was undetectable.

[0316] All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

CLAIMS:

1. A ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline; residue corresponding to X195 is arginine; and the residue correspond X202 is a tryptophan,

in which the residue in the ketoreductase polypeptide corresponding to X190 is proline, the residue corresponding to X195 is arginine, and the residue corresponding to X202 is tryptophan.

2. The polypeptide of claim 1, which is capable of converting the substrate to the product with a percent stereomeric excess of:

- i) at least 95%; or
- ii) at least 99%.

3. The polypeptide of claim 1, in which the ketoreductase amino acid sequence has additionally one or more of the following features:

- residue corresponding to X7 is histidine;
- residue corresponding to X17 is methionine;
- residue corresponding to X25 is aspartic acid;
- residue corresponding to X27 is tyrosine;
- residue corresponding to X41 is serine or alanine;
- residue corresponding to X53 is aspartic acid;
- residue corresponding to X57 is valine;
- residue corresponding to X64 is valine;
- residue corresponding to X66 is glutamic acid;
- residue corresponding to X68 is valine;
- residue corresponding to X72 is arginine;
- residue corresponding to X76 is alanine;

residue corresponding to X80 is threonine or valine;
residue corresponding to X93 is serine;
residue corresponding to X94 is cysteine or glycine;
residue corresponding to X95 is leucine or glutamic acid;
residue corresponding to X96 is cysteine, asparagine, valine, leucine, isoleucine,
or threonine;

residue corresponding to X97 histidine or serine;
residue corresponding to X100 is lysine;
residue corresponding to X108 is histidine;
residue corresponding to X111 is methionine;
residue corresponding to X139 is leucine;
residue corresponding to X145 is glutamine or leucine;
residue corresponding to X147 is leucine;
residue corresponding to X148 is valine;
residue corresponding to X151 is alanine;
residue corresponding to X152 is serine;
residue corresponding to X163 is isoleucine;
residue corresponding to X165 is asparagine;
residue corresponding to X173 is valine;
residue corresponding to X179 is phenylalanine, lysine, or leucine;
residue corresponding to X194 is glutamine, serine, or leucine;
residue corresponding to X196 is leucine;
residue corresponding to X197 is glutamic acid;
residue corresponding to X198 is glutamic acid or glutamine;
residue corresponding to X210 is arginine;
residue corresponding to X211 is valine, leucine, threonine, or isoleucine;
residue corresponding to X212 is serine or valine;
residue corresponding to X216 is arginine;
residue corresponding to X223 is valine;
residue corresponding to X226 is threonine;
residue corresponding to X233 is asparagine or aspartic acid;
residue corresponding to X235 is tryptophan;
residue corresponding to X248 is glycine or tryptophan;

residue corresponding to X249 is tryptophan; and

wherein optionally the amino acid sequence has one or more residue differences at other amino acid residue positions as compared to the reference sequence.

4. The polypeptide of claim 1, in which the ketoreductase:

i) comprises an amino acid sequence selected from SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 96, 98, 104, 106, 108, and 110; or

ii) is capable of converting the substrate to the product at a rate that is at least 1-50 times greater than the reference polypeptide, and wherein the ketoreductase optionally comprises an amino acid sequence corresponding to SEQ ID NO: 86, 88 or 96; or

iii) is capable of converting the substrate to the product at a rate that is at least 50-250 times greater than the reference polypeptide, and wherein the ketoreductase optionally comprises an amino acid sequence corresponding to SEQ ID NO: 10, 32, 34, 36, 50, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 98, 104, 106, and 108.

5. The polypeptide of claim 1, which is capable of:

i) converting the substrate to the product at a rate that is at least 250-1000 times greater than the reference polypeptide, and wherein the ketoreductase optionally comprises an amino acid sequence corresponding to SEQ ID NO: 12, 18, 22, 24, 26, 28, 30, 38, 40, 52, 54, 56, 58, 60, 62, and 110; or

ii) converting the substrate to the product at a rate that is at least 1000 times greater than the reference polypeptide, and wherein the ketoreductase optionally comprises an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, and 20; or

iii) converting at least 95% of the substrate to the product in less than 24 hours when carried out with greater than 100 g/L of substrate and less than 5 g/L of the polypeptide, and wherein the ketoreductase optionally comprises an amino acid sequence corresponding to SEQ ID NO: 6, 8, 14, 16, and 20.

6. The polypeptide of claim 1, which has an improved resistance to acetone as a competitive inhibitor to the conversion of the substrate to the product as compared to the reference polypeptide, and wherein the ketoreductase optionally comprises an amino

acid sequence selected from SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 98, 104, 106, 108, and 110.

7. A polynucleotide encoding a polypeptide according to any one of claims 1-6, and which optionally comprises a sequence selected from SEQ ID NO: 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 95, 97, 103, 105, 107, and 109.

8. An expression vector comprising the polynucleotide of claim 7 operably linked to control sequences suitable for directing expression in a host cell.

9. A host cell comprising the expression vector of claim 8.

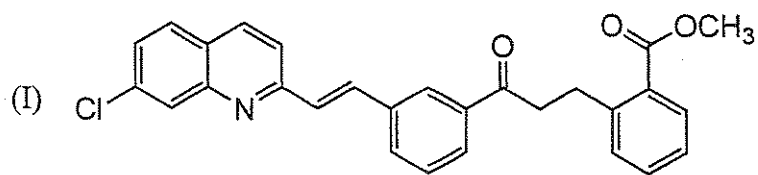
10. A composition comprising:

a) a ketoreductase of:

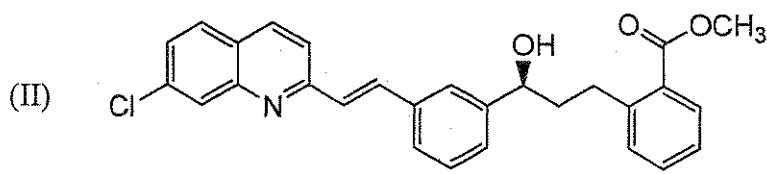
i) any one of claims 1-6; or

ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan; and

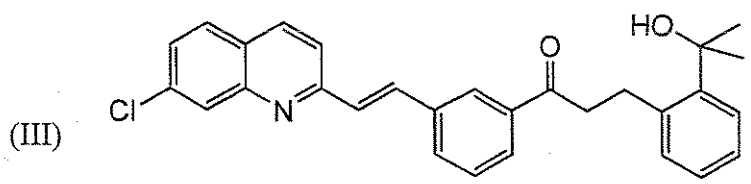
b) a substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester of structural formula (I)



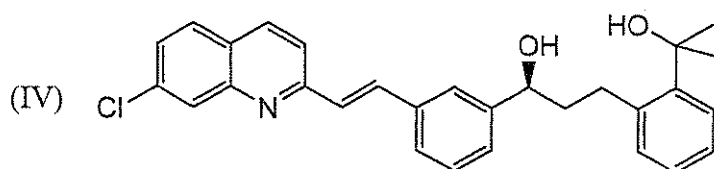
a product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate of structural formula (II)



a substrate 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol of structural formula (III)



or a product (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol of structural formula (IV)

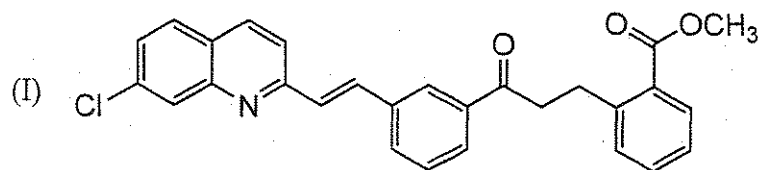


11. The composition of claim 10 in which the substrate is:

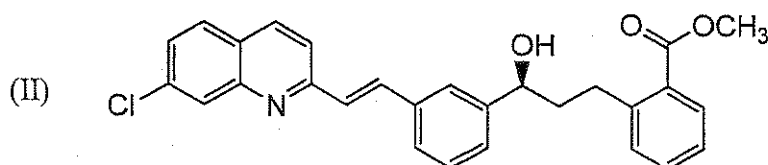
i) the substrate of structural formula (I) and the composition further includes the product of structural formula (II); or

ii) the substrate of structural formula (II) and the composition further includes the product of structural formula (IV).

12. A method for reducing the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester of formula (I)



to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate of formula (II)



which comprises contacting the substrate of formula (I) with the ketoreductase polypeptide of:

- i) any one of claims 1-6; or
- ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

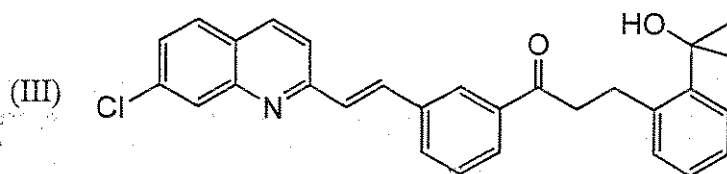
under reaction conditions suitable for reducing or converting the substrate to the product of formula (II).

13. The method of claim 12 in which:

- i) the product is present at an stereomeric excess greater than about 99%; or
- ii) at least 95% of the substrate is reduced to the product in less than 24 hours, wherein the concentration of the substrate is at least 100 g/L and the concentration of

the polypeptide is less than 5 g/L, and wherein the polypeptide comprises an amino acid sequence that corresponds to SEQ ID NO: 6, 8, 14, 16, and 20.

14. A method for reducing the substrate 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl)ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol of formula (III)

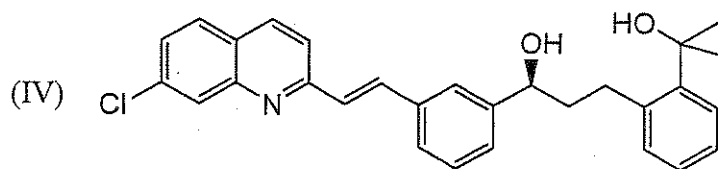


to the product (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol, which comprises contacting the substrate of formula (III) with the ketoreductase polypeptide of:

i) any one of claims 1-6; or

ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

under reaction conditions suitable for reducing the substrate to the product of formula (IV)

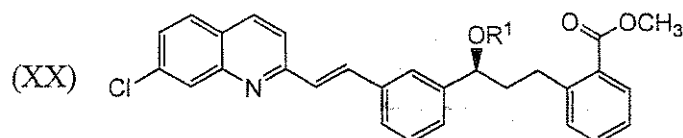


15. The method of claim 14, wherein:

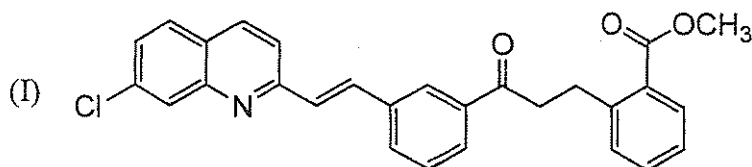
i) the product is present at an stereomeric excess greater than about 99%; or

ii) at least 95% of the substrate is reduced to the product in less than 24 hours, wherein the concentration of the substrate is at least 100 g/L and the concentration of the polypeptide is less than 5 g/L, and wherein the polypeptide comprises an amino acid sequence that corresponds to SEQ ID NO: 6, 8, 14, 16, and 20.

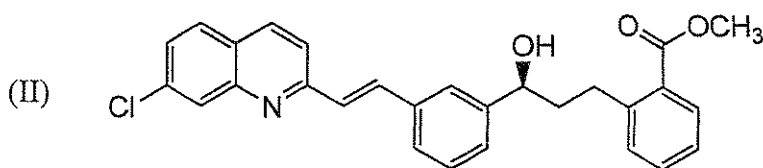
16. A method for the synthesis of the compound of formula (XX):



wherein R1 is an alkylsulfonyl or arylsulfonyl, the method comprising: (a) reducing the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester of formula (I)



to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate of formula (II)



by contacting the substrate of formula (I) with the ketoreductase polypeptide of:

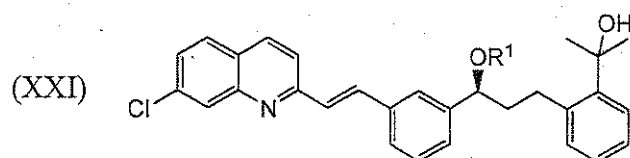
i) any one of claims 1-6: or

ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features:

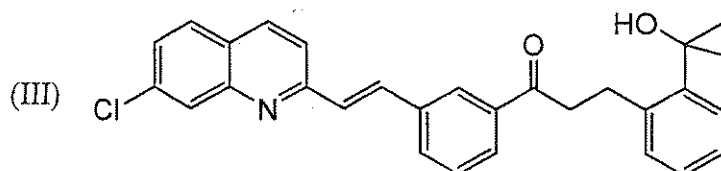
residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

under reaction conditions suitable for reducing or converting the substrate to the product of formula (II); and (b) reacting the compound of formula (II) with an alkylsulfonyl halide or an arylsulfonyl halide under conditions suitable for formation of compound (XX), and wherein optionally the alkylsulfonyl halide is methylsulfonyl chloride.

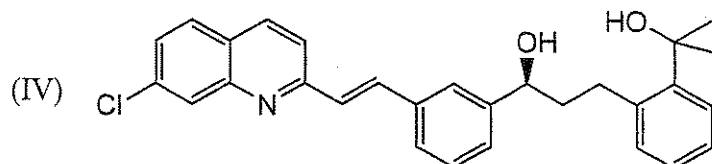
17. A method for the synthesis of the compound of formula (XXI):



wherein R1 is an alkylsulfonyl or arylsulfonyl, the method comprising: (a) reducing the substrate 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol of formula (III)



to the product (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol of formula (IV)



by contacting the substrate of formula (III) with the ketoreductase polypeptide of:

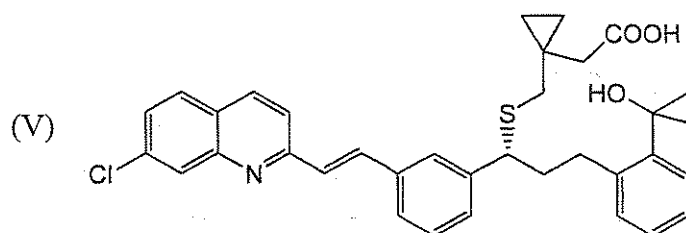
i) any one of claims 1-6; or

ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the

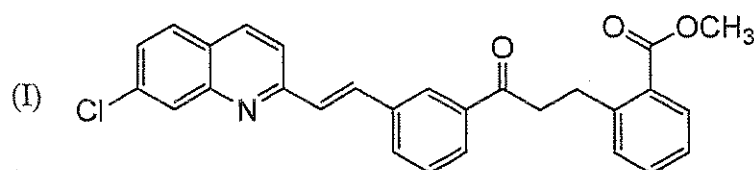
product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

under reaction conditions suitable for reducing or converting the substrate to the product of formula (IV) and (b) reacting the compound of formula (IV) with an alkylsulfonyl halide or an arylsulfonyl halide under conditions suitable for formation of compound (XXI), and wherein optionally the alkylsulfonyl halide is methylsulfonyl chloride.

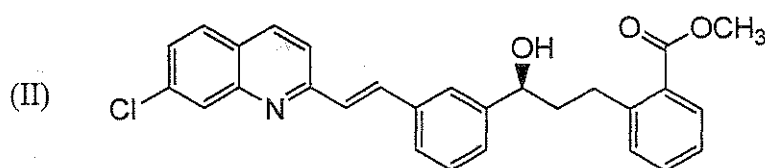
18. A method for the synthesis of compound (V)



or salts, hydrates or solvates thereof, wherein a step in the method comprises reducing the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester of formula (I)



to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate of formula (II)



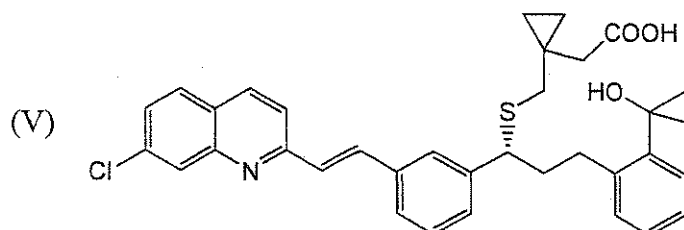
by contacting the substrate of formula (I) with the ketoreductase polypeptide of:

i) any one of claims 1-6; or

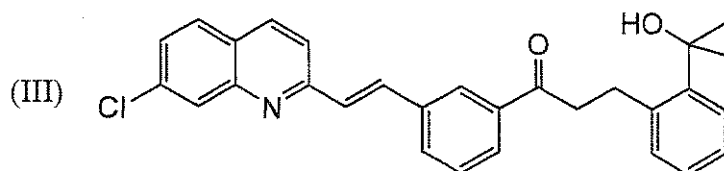
ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

under reaction conditions suitable for reducing or converting the substrate to the product of formula (II).

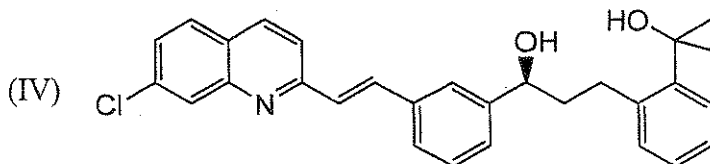
19. A method for the synthesis of compound (V)



or salts, hydrates or solvates thereof, wherein a step in the method comprises reducing substrate 2-[2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl]phenyl]-2-propanol of formula (III)



to the product (S,E)-1-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-(2-(2-hydroxypropan-2-yl)phenyl)propan-1-ol of formula (IV)



by contacting the substrate of formula (III) with the ketoreductase polypeptide of:

i) any one of claims 1-6; or

ii) a ketoreductase polypeptide capable of converting the substrate 2-[3-[3-[2-(7-chloro-2-quinolinyl) ethenyl] phenyl]-3-oxopropyl] benzoic acid methyl ester to the product (S,E)-methyl 2-(3-(3-(2-(7-chloroquinolin-2-yl)vinyl)phenyl)-3-hydroxypropyl)benzoate at a rate that is at least 1.5 times the rate of the polypeptide of SEQ ID NO:4, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 114 having the following features: residue corresponding to X190 is proline, and residue corresponding to X202 is tryptophan; in which the residue corresponding to X190 is proline, and the residue corresponding to X202 is tryptophan,

under reaction conditions suitable for reducing the substrate to the product of formula (IV).

376247-018
SEQUENCE LISTING

<110> LIANG, Jack
BORUP, Birthe
MITCHELL, Vesna
MUNDORFF, Emily
LALONDE, James
HUISMAN, Gjal't

<120> KETOREDUCTASE POLYPEPTIDES AND USES THEREOF

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atgtcctaacc gtctggatgg caaagtagcc atcattaccg gcgggactct gggatatcgg 60
ttggcaatcg ccacgaaatt tgtagaggag ggtgcgaaag taatgattac tggtcgtcac 120
tccgatgtag gtgaaaaggc cgccaaatca gtaggcactc cggatcagat tcagtttttt 180
cagcacgatt catccgatga agatggctgg acgaaactgt tcgacgccac cgagaaagca 240
ttcggcccgg ttagcacctt agtgaacaat gcagggattg cagttaacaa aagcgttgaa 300
gaaactacca cggccgaatg gcgtaaactg ctggccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgagcctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggctat atcaagacct cgctggtcga tgatctgccg 600
ggtgctgagg aagcgatgtc acagcgtagc aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catatatctg tgtgtacctg gcattcaatg aatcgaaatt tgcgacgggt 720
tccgaatttg tggtcgacgg cgggtatacc gcacagtaat ga 762
```

<210> 2

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Translation of Codon Optimized L. Brevis Sequence

<400> 2

```
Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Ile Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
50     55     60
Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
65     70     75     80
Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
85     90     95
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Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
100 105 110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130 135 140
Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
145 150 155 160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165 170 175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
180 185 190
Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
195 200 205
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210 215 220
Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
225 230 235 240
Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245 250

```

<210> 3
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon Optimized L. Kefir Sequence

```

<400> 3
atgaccgatc gtctgaaggg caaagtagcc atcgtaacgg gcgggactct gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgcca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccggtta atctggatgg tgtttttttc 360
ggcaccgcgc tgggcattca gcgcattgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgagggggt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggctat atcaagaccc cgctgggtcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 4
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Translation of Codon Optimized L. kefir Sequence

```

<400> 4
Met Thr Asp Arg Leu Lys Gly Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20 25 30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50 55 60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65 70 75 80

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Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Phe Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
 180 185 190
 Thr Pro Leu Val Asp Asp Leu Glu Gly Ala Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 5
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 5
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcggt 60
 ttggcaatcg ccaccaaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcgaca ctgatgttat tcgctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttcggccccg ttacgaccgt cgtgaacaat gcaggagatt gcgttttgaa aagcgtaaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
 gggttgggagg aaatgatgtc acagcgtagc gtaaccccta tgggcccgcg tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 6
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 6
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Thr Lys Tyr Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Asp Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
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65 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 70 75 80
 85 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 115 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 120 125
 130 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 135 140
 145 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 150 155 160
 165 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 170 175
 180 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 185 190
 195 Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 200 205
 210 Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
 215 220
 225 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 230 235 240
 245 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 250

<210> 7
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 7
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccc gcgggacaat gggatcgggt 60
 ttggcaatcg ccaccaaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcgaca ctgatgttat tgcctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacgccac cgaggagacc 240
 ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcggtaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgcc tgggcattca gcgcattgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtaaccccta tgggccgcat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 8
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 8
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Thr Lys Tyr Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Asp Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60

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Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Glu Thr
65 70 75 80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85 90 95
Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100 105 110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130 135 140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145 150 155 160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165 170 175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180 185 190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195 200 205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210 215 220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225 230 235 240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245 250

<210> 9
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 9
atgaccgatc gtctgaagca taaagtagcc atcgtaaccc gcggggacaat gggatatcggg 60
ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcgtttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtcttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt ggttggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtatctccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 10
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 10
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
20 25 30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
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```

      50              55              60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
65 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
      85              90              95
Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
      100             105             110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
      115             120             125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
      130             135             140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
      165             170             175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
      180             185             190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
      195             200             205
Arg Thr Val Ser Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
      210             215             220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
      245             250

```

<210> 11
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 11
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcggggacaat gggatatcggg 60
ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctagtggtat tgcgtttgtc 180
cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggaggtt gcgttttgaa aagcggtaaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg cgtttttttc 360
ggcaccctgc tgggcattca ggcgatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagacct cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagg gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcactctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 12
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 12
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
20 25 30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45

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Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Arg Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 13
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 13
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcggt 60
 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttcgcccggt ttacgaccgt cgtgaacaat gcaggaggtt gcgttttgaa aagcggttaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tcagctggaa 600
 gggttggagg aaatgatgtc acagcgtagc gtaaccccta tgggccgcat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 14
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 14
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala

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35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Gln Arg Leu Asp Gln Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 15
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 15
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcgg 60
 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggctcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttat tcgctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttccggcccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgtaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgtggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccggggccc atcaagacc agcggctcga tgagctggaa 600
 ggttgggagg aaatgatgtc acagcgtacg gtaacccta tgggccgcat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 16
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 16
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
 20 25 30

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Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 17
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 17
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcgggt 60
 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggctcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcgagg ctgatgttat tcgctttgtc 180
 cagcagcatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttccggcccg ttacgaccgt cgtgaacaat gcaggagggt gcgttttgaa aagcgtaaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtag gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtagtgctta tgggccgcat tggcgaaccg 660
 aatgacgtcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 18
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 18
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
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20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Val Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Val Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 19
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 19
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 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttccggcccg ttacgaccgt cgtgaacaat gcaggagatt gcgttttgaa aagcggtaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgtccctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tcagctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtaacccta tgggccgcat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 20
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 20
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15

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Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Gln Arg Leu Asp Gln Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 21
 <211> 759
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Variant of L. kefir

<400> 21
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 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttcgggcccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcggttaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgta atctggatgg tgttttttc 360
 ggcacccgtc tgggcataca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgtgca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 22
 <211> 252
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variant of L. kefir

<400> 22
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
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1	Met	Gly	Ile	Gly	5	Leu	Ala	Ile	Ala	Asp	10	Lys	Tyr	Val	Glu	Glu	15	Gly	Ala
				20						25						30			
	Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala			
			35					40							45				
	Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Val			
		50					55					60							
	Ser	Asp	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Thr			
65					70					75							80		
	Phe	Gly	Pro	Val	Thr	Thr	Val	Val	Asn	Asn	Ala	Gly	Ser	Cys	Val	Leu			
				85					90						95				
	Lys	Ser	Val	Lys	Asp	Thr	Thr	Thr	Glu	Trp	Arg	Lys	Leu	Leu	Ser				
			100						105					110					
	Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg			
		115					120						125						
	Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile			
		130				135						140							
	Glu	Gly	Leu	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys			
145					150					155						160			
	Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu			
				165						170					175				
	Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys			
			180						185					190					
	Thr	Pro	Arg	Leu	Asp	Asp	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln			
		195					200						205						
	Arg	Thr	Val	Thr	Pro	Met	Gly	His	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala			
		210				215						220							
	Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly			
225					230					235					240				
	Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln							
			245						250										

<210> 23
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 23
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 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcctttgtc 180
 cagcagcatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
 ttccggcccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgtgtc acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtaacccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 24
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 24

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 25
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 25
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 ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgctcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcgagg ctgatgttat tcgctttgtc 180
 cagcagcatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcggcccgg ttacgaccgt cgtgaacaat gcaggaggtt gcgttttgaa aagcgttaaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
 gggtgggagg aaatgatgtc acagcgtagc gtaacccta tgggccgcat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

<210> 26
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

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<400> 26

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
50      55      60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65      70      75      80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85      90      95
Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 27

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 27

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ttggcaatcg ccgataaata cgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgagg ctgatgttat tgcgtttgtc 180
cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggaggat gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttcc 360
ggcaccgcgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcgggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcaactgaa ggactacgat 540
gtgctgtgtc acacagtaca tccgggcccc atcaagaccc agcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccgcat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 28

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> variant of L. kefir

<400> 28

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Tyr Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Gln Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 29

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 29

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcctttgtc 180
cagcagcatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttaaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagaccc cgcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaacccta tgggccgcat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

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<210> 30

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 30

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 31

<211> 759

<212> DNA

<213> Artificial sequence

<220>

<223> Variant of L. kefir

<400> 31

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacaat gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgcca ctgatgttgt gcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcgattc gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgta acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaattcg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 32

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> Variant of L. kefir

<400> 32

```

Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Val Arg Phe Val Gln His Asp Ala
50      55      60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
65      70      75      80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85      90      95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Ile Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 33

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 33

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atgaccgatac gtctgaagca taaagtagcc atcgtaaccg gcggggacaat gggatatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttgt gcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggagatt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt gattggcgat ccgacgctgg gggcgtaaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctgggtt gcgcactgaa ggactacgat 540
gtgctgtgca acacagtaca tccggggccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg ttaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcactctgacg aatcgaaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 34

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 34

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Val Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Ile Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Val Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Leu Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

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<210> 35

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 35

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atgaccgatc gtctgaagca taaagtagcc atcgtaacccg gcggggacaat ggggtatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgggca ctgatgttgt gcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggggagt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt ggttggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 36

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 36

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Met Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Val Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 37

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 37

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcggt 60
ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttatcac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggagatt gcgttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaacta ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgccg tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgta acacagtaca tccgggcccc atcaagacct agcggctcga tgagctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaaccctta tgggccgcac tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcactctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

```

<210> 38

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 38

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50      55      60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65      70      75      80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Ile
85      90      95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

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<210> 39

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 39

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgtcat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca cgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggtccc atcaagaccc agcggctcga tgagctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcaacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 40

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 40

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Ile
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 41

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 41

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atgaccgatc gtctgaagca taaagtagcc atcgtaacgc gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgagg ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgcgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc aaaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgc cgggtatacc gcacagtga 759

```

<210> 42

<211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 42

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ile
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

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<210> 43
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 43

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggattg cagttgtgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccgcgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtttgggagg aaatgatgtc acagcgtagc aaaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 44
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 44
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Val
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 45
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 45
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 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttccggcccg ttacgaccgt cgtgaacaat gcagggattg cagttttaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccggggccc atcaagaccc cgctgtctga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc aaaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcactctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 46
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of *L. kefir*

<400> 46
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Leu
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 47
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of *L. kefir*

<400> 47
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcggt 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcgcccggg ttacgaccgt cgtgaacaat gcagggattg gagtttccaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 48
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 48
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Gly Val Ser
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 49
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 49
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgggt 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg catccgatga agtgggctgg acgaaaactgt tcgacaccac cgaggaggca 240
 ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttgaa 300
 gacactacca cggaggaatg gcataaactg ctgtccgta atctggatgg tgttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtaacatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagacct ctcggtcga tgatctggaa 600
 gggtgggagg aaatgatgtc acagcgtacg atcaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720

gcagaattcg tggctgcacgg cgggtataacc gcacagtga

759

<210> 50
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 50
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Val Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp His Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Asn Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Ser Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Ile Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 51
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 51
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact ggggtatcgg 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaa tagttattac tggctcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cgcacgatg cgtccgaaga agcaggctgg acgaaaactgt tcgacaccac cgaggaggca 240
 ttccggcccg ttacgaccgt cgtgaacaat gcaggggagt gcgagattaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccgcat tggcgaaccg 660

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aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggctgcagg tgggtataacc gcacagtga 759

<210> 52
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 52
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20 25 30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50 55 60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65 70 75 80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Glu Ile
85 90 95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100 105 110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130 135 140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145 150 155 160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165 170 175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180 185 190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195 200 205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210 215 220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225 230 235 240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245 250

<210> 53
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 53
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggctcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctatccgtta atctggatgg tgtttttttc 360
ggcaccgccg tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat gcgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600

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ggttgggagg aaatgatgtc acagcgtacg gtaacccta tgggccgcat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtataacc gcacagtga 759

<210> 54
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 54
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1 5 10 15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20 25 30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35 40 45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50 55 60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65 70 75 80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Ile
85 90 95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100 105 110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130 135 140
Glu Gly Leu Val Gly Asp Ala Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145 150 155 160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165 170 175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180 185 190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195 200 205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210 215 220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225 230 235 240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245 250

<210> 55
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 55
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcggggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggaggtt gcgttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccgcc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540

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gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tcagctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccccta tgggccgcat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

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<210> 56
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 56

Met	Thr	Asp	Arg	Leu	Lys	His	Lys	Val	Ala	Ile	Val	Thr	Gly	Gly	Thr
1				5					10					15	
Leu	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Asp	Lys	Phe	Val	Glu	Glu	Gly	Ala
			20					25					30		
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala
			35				40					45			
Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Ala
	50					55					60				
Ser	Glu	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Ala
65					70				75					80	
Phe	Gly	Pro	Val	Thr	Thr	Val	Val	Asn	Asn	Ala	Gly	Ser	Cys	Val	Ile
				85				90					95		
Lys	Ser	Val	Glu	Asp	Thr	Thr	Thr	Glu	Glu	Trp	Arg	Lys	Leu	Leu	Ser
			100					105					110		
Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg
			115				120					125			
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile
			130				135				140				
Glu	Gly	Leu	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys
145					150					155					160
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu
				165					170					175	
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys
			180					185					190		
Thr	Gln	Arg	Leu	Asp	Gln	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln
			195				200					205			
Arg	Thr	Val	Thr	Pro	Met	Gly	Arg	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala
			210			215					220				
Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly
225					230					235					240
Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln				
				245					250						

<210> 57
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 57

atgaccgatc	gtctgaagca	taaagtagcc	atcgtaaccg	gcgggacact	gggtatcggt	60
ttggcaatcg	ccgataaatt	tgtagaggag	ggtgcgaaag	tagttattac	tggtcgtcac	120
gcggatgtag	gtgaaaaggc	cgccaaatca	atcggcggca	ctgatgttat	tcgctttgtc	180
cagcacgatg	cgtccgaaga	agcaggctgg	acgaaactgt	tcgacaccac	cgaggaggca	240
ttcggccccg	ttacgaccgt	cgtgaacaat	gcagggagtt	gcgttattaa	aagcgttgaa	300
gacactacca	cggaggaatg	gcgtaaactg	ctgtccgtta	atctggatgg	tggttttttc	360
ggcaccgcc	tgggcattca	gcgcatgaaa	aataaaggct	tgggcgctag	catcatcaat	420
atgagcagta	ttgaggggct	cgtaggcgat	ccgacgctgg	gggcatacaa	cgcttccaag	480

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ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
ggttggggagg aaatgatgtc acagcgtacg gtaaccctta tgggccgcat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

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<210> 58
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 58

Met	Thr	Asp	Arg	Leu	Lys	His	Lys	Val	Ala	Ile	Val	Thr	Gly	Gly	Thr
1				5					10					15	
Leu	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Asp	Lys	Phe	Val	Glu	Glu	Gly	Ala
			20					25					30		
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala
		35				40						45			
Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Ala
	50					55				60					
Ser	Glu	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Ala
65					70				75					80	
Phe	Gly	Pro	Val	Thr	Thr	Val	Val	Asn	Asn	Ala	Gly	Ser	Cys	Val	Ile
			85					90					95		
Lys	Ser	Val	Glu	Asp	Thr	Thr	Thr	Glu	Glu	Trp	Arg	Lys	Leu	Leu	Ser
		100						105					110		
Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg
		115					120					125			
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile
	130					135					140				
Glu	Gly	Leu	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys
145					150				155						160
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu
			165						170					175	
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys
		180						185					190		
Thr	Gln	Arg	Leu	Asp	Glu	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln
	195						200					205			
Arg	Thr	Val	Thr	Pro	Met	Gly	Arg	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala
	210					215					220				
Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly
225					230					235					240
Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln				
			245					250							

<210> 59
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 59

atgaccgatc	gtctgaagca	taaagtagcc	atcgtaaccg	gcgggacact	gggtatcggt	60
ttggcaatcg	ccgataaatt	tgtagaggag	ggtgcgaaaag	tagttattac	tggtcgtcac	120
gcggatgtag	gtgaaaaggc	cgccaaatca	atcggcgggca	ctgatgttat	tcgctttgtc	180
cagcagcatg	cgtccgaaga	agcaggctgg	acgaaactgt	tcgacaccac	cgaggaggca	240
ttcggccccg	ttacgaccgt	cgtgaacaat	gcaggggagtt	gcgttattaa	aagcgttgaa	300
gacactacca	cggaggaatg	gcgtaaactg	ctgtccgtta	atctggatgg	tgtttttttc	360
ggcaccgcc	tgggcattca	gcgcatgaaa	aataaaggct	tgggcgctag	catcatcaat	420

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atgagcagta ttgaggggct cgtagggcgt ccgtctctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggcccgat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

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<210> 60
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

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<400> 60
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50      55      60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65      70      75      80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Ile
85      90      95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 61
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

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<400> 61
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggcttg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttattca tagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360

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ggcaccgcc tgggcattca ggcgatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggggat cgcacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt ggcgactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgagctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaaccctta tgggcccgcg tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg tgggtatacc gcacagtga 759

```

<210> 62
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 62
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50      55      60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65      70      75      80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ser Cys Val Ile
85      90      95
His Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Val Thr Pro Met Gly Arg Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 63
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

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<400> 63
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaaag tagttattac tggtcgtcac 120
cgggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggagggt gcgttttgaa aagcgttgaa 300

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gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcataaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttacaggggt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcactctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 64
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 64

```

Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Gln Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 65
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 65

```

atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240

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ttcggccccg ttacgaccgt cgtgaacaat gcagggattg ggcttgtgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag tatcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtc acacagtaca tccgggcccc atcaagacct cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 66
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 66
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Gly Leu Val
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 67
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 67
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180

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cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg gggttattaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccggtt atctggatgg tgttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtc acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc ttaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 68
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 68
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Gly Val Ile
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Leu Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 69
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 69
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120

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gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg gggttgtgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggctgacgg cgggtatacc gcacagtga 759

```

<210> 70
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

```

<400> 70
Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10     15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Gly Val Val
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 71
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 71
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60

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ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcgcccggt ttacgaccgt cgtgaacaat gcagggattg gggttgtgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgtcgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgactgaa ggactacgat 540
gtgctgtgca acacagtaca tccgggcccc atcaagaccc cgcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatggaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtataacc gcacagtga 759

```

<210> 72
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 72

Met	Thr	Asp	Arg	Leu	Lys	His	Lys	Val	Ala	Ile	Val	Thr	Gly	Gly	Thr	1	5	10	15
Leu	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Asp	Lys	Phe	Val	Glu	Glu	Gly	Ala	20	25	30	
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala	35	40	45	
Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Ala	50	55	60	
Ser	Glu	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Ala	65	70	75	80
Phe	Gly	Pro	Val	Thr	Val	Val	Asn	Asn	Ala	Gly	Ile	Gly	Val	Val		85	90	95	
Lys	Ser	Val	Glu	Asp	Thr	Thr	Thr	Glu	Trp	Arg	Lys	Leu	Leu	Ser		100	105	110	
Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg	115	120	125	
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile	130	135	140	
Glu	Gly	Leu	Val	Gly	Asp	Pro	Ser	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys	145	150	155	160
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu	165	170	175	
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys	180	185	190	
Thr	Pro	Arg	Leu	Asp	Asp	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln	195	200	205	
Arg	Thr	Val	Thr	Pro	Met	Gly	His	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala	210	215	220	
Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Trp	Lys	Phe	Ala	Thr	Gly	225	230	235	240
Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln					245	250		

<210> 73
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 73

376247-018

```

atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatcgggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcggtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcgtttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggagggt 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggaggtt gcgttgtgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc acaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 74
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 74

Met	Thr	Asp	Arg	Leu	Lys	His	Lys	Val	Ala	Ile	Val	Thr	Gly	Gly	Thr
1				5					10					15	
Leu	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Asp	Lys	Phe	Val	Glu	Glu	Gly	Ala
			20					25					30		
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala
		35					40					45			
Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Ala
	50					55					60				
Ser	Glu	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Val
65					70					75				80	
Phe	Gly	Pro	Val	Thr	Val	Val	Asn	Asn	Ala	Gly	Ser	Cys	Val	Val	
			85				90					95			
Lys	Ser	Val	Glu	Asp	Thr	Thr	Thr	Glu	Glu	Trp	Arg	Lys	Leu	Leu	Ser
		100					105						110		
Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg
		115					120					125			
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile
	130					135					140				
Glu	Gly	Leu	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys
145					150					155				160	
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu
			165						170					175	
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys
		180						185					190		
Thr	Pro	Arg	Leu	Asp	Asp	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln
		195					200					205			
Arg	Thr	Thr	Thr	Pro	Met	Gly	His	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala
	210					215					220				
Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly
225					230					235				240	
Ala	Glu	Phe	Val	Val	Asp	Gly	Gly	Tyr	Thr	Ala	Gln				
			245						250						

<210> 75
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 75

```

atgaccgatac gctctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgaaga agcaggctgg acgaaactgt tcgacaccac cgaggagggt 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggattt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagacct cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg ttaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcactctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggctgacgg cgggtatacc gcacagtga 759

```

<210> 76

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 76

```

Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50      55      60
Ser Glu Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Val
65      70      75      80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Cys Val Leu
85      90      95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Leu Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 77

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 77

```

atgaccgatc gtctgaagca taaagtagcc atcgtaaccc gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggctcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcaggagatt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcataaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtaacatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagacct agcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc gcagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 78

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 78

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp His Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Asn Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Gln Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 79

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 79

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atgaccgatc gtctgaagca taaagtagcc atcgtaacgc gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggagatt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgita atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtca acacagtaca tccgggcccc atcaagaccc agcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggacctg tgtgtacctg gcattctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 80

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 80

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Gln Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Thr Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 81

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 81

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact ggggtatcggg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcaggagggt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagacct agcggctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgac aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 82

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 82

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Gln Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 83

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 83

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggagtt gcgttttgaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgca acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc gtaaccctta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 84

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 84

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 85

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 85

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcggtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccgcgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgtgtc acacagtaca tccgggcccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtagc aaaacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 86

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 86

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35      40      45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50      55      60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65      70      75      80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
85      90      95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100     105     110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115     120     125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130     135     140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145     150     155     160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165     170     175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180     185     190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195     200     205
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210     215     220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225     230     235     240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245     250

```

<210> 87

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 87

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atgaccgatac gtctgaagca taaagtagcc atcgtaacgg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcaccgcgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccggggccc atcaagaccc cgcggtcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg ataacccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 88

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 88

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Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Ile Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

```

<210> 89

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 89

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atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttat tgcctttgtc 180
cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggccccg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcaccctgc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgctgttca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

```

<210> 90

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 90

```

Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
1      5      10      15
Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
20     25     30
Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
35     40     45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
50     55     60
Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
65     70     75     80
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
85     90     95
Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
100    105    110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
115    120    125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
130    135    140
Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
145    150    155    160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
165    170    175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
180    185    190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
195    200    205
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
210    215    220
Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
225    230    235    240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245    250

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<210> 91

<211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 91
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 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcggtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgttca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc aaaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcattctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtggacc gcacagtga 759

<210> 92
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 92
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Trp Thr Ala Gln
 245 250

<210> 93
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 93
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcggccccg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtag gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgtgta acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
 gggtgggagg aaatgatgtc acagcgtacg gttaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 94
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 94
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 95
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 95
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcggtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcggccccg ttacgaccgt cgtgaacaat gcaggggattg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgtc tgggcattca gcgcataaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgttca acacagtaca tccgggcccc atcaagaccc cgcatctcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtagc aaaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 96
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 96
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Asp Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 97
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of *L. kefir*

<400> 97
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcggt 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttccggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcgggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc tgcggctcga tgatctggaa 600
 ggtttgggagg aaatgatgtc acagcgtagc aaaaccctta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 98
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of *L. kefir*

<400> 98
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Leu Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln

<210> 99
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 99
 atgaccgatc gtctgaagca taaagtagcc atcgtaacccg gcgggacact gggatcgggt 60
 ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcagcatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttccggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttttggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcgggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
 gggttgggagg aaatgatgtc acagcgtagc aaaaccccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 100
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 100
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Leu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240

Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250 376247-018

<210> 101
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 101
 atgaccgatac gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
 ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttccggcccg ttacgaccgt cgtgaacaat gcagggttg cagttacaaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggtgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgactgaa ggactacgat 540
 gtgctgttca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
 ggttgggagg aaatgatgtc acagcgtacg attacccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 102
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 102
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Thr
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Leu Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Ile Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly

225 230 235 240
Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
245 250

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<210> 103
<211> 759
<212> DNA
<213> Artificial Sequence
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<220>
<223> variant of L. kefir

<400>	103						
atgaccgatc	gtctgaagca	taaagtagcc	atcgtaac	cg	gggacact	gggtatcggt	60
ttggcaatcg	ccgataaatt	tgtagaggag	ggtgcgaaag	tagttattac	tggtcgtcac		120
gcggatgtag	gtgaaaaggc	cgccaaatca	atcggcggca	ctgatgttat	tcgctttgtc		180
cagcacgatg	cgtccgatga	agcaggcttg	acgaaactgt	tcgacaccac	cgaggaggca		240
ttcggccggg	ttacgacccg	cgtgaacaat	gcagggaatt	gcgttattaa	aagcgttgaa		300
gacactacca	cggaggaaatg	gcgtaaactg	ctgtccgtta	atctggatgg	tgtttttttc		360
ggcaccgcgc	tgggcattca	gcgcatgaaa	aataaaggct	tgggcgctag	catcatcaat		420
atgagcagta	ttgaggggct	cgtaggcgat	ccgacgctgg	gggcatacaa	cgcttccaag		480
ggggcggtag	gtatcatgtc	gaaaagcgca	gcgctggatt	gcgcactgaa	ggactacgat		540
gtgctgttca	acacagtaca	tccgggcccc	atcaagacc	cgcggtctga	tgatctggaa		600
ggttgggagg	aatgatgtc	acagcgtacg	acaaccctta	tgggccacat	tggcgaaccg		660
aatgacatcg	catgtactctg	tgtgtacctg	gcattctgacg	aatcgaaatt	tgcgacgggt		720
qcagaatttg	tggctcgacgg	cgggtatacc	gcacagtga				759

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<210> 104
<211> 252
<212> PRT
<213> Artificial sequence
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<220>
<223> Variant of L. kefir

<400>	104															
Met	Thr	Asp	Arg	Leu	Lys	His	Lys	Val	Ala	Ile	Val	Thr	Gly	Gly	Thr	
1				5					10					15		
Leu	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Asp	Lys	Phe	Val	Glu	Glu	Gly	Ala	
			20					25					30			
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Ala	Asp	Val	Gly	Glu	Lys	Ala	Ala	
		35					40					45				
Lys	Ser	Ile	Gly	Gly	Thr	Asp	Val	Ile	Arg	Phe	Val	Gln	His	Asp	Ala	
	50					55					60					
Ser	Asp	Glu	Ala	Gly	Trp	Thr	Lys	Leu	Phe	Asp	Thr	Thr	Glu	Glu	Ala	
65					70					75					80	
Phe	Gly	Pro	Val	Thr	Val	Val	Val	Asn	Asn	Ala	Gly	Ile	Cys	Val	Ile	
				85				90						95		
Lys	Ser	Val	Glu	Asp	Thr	Thr	Thr	Glu	Glu	Trp	Arg	Lys	Leu	Leu	Ser	
			100					105					110			
Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg	
		115					120					125				
Met	Lys	Asn	Lys	Gly	Leu	Gly	Ala	Ser	Ile	Ile	Asn	Met	Ser	Ser	Ile	
	130					135					140					
Glu	Gly	Leu	Val	Gly	Asp	Pro	Thr	Leu	Gly	Ala	Tyr	Asn	Ala	Ser	Lys	
145					150					155				160		
Gly	Ala	Val	Arg	Ile	Met	Ser	Lys	Ser	Ala	Ala	Leu	Asp	Cys	Ala	Leu	
				165					170					175		
Lys	Asp	Tyr	Asp	Val	Arg	Val	Asn	Thr	Val	His	Pro	Gly	Pro	Ile	Lys	
			180					185					190			
Thr	Pro	Arg	Leu	Asp	Asp	Leu	Glu	Gly	Trp	Glu	Glu	Met	Met	Ser	Gln	
		195					200					205				
Arg	Thr	Thr	Thr	Pro	Met	Gly	His	Ile	Gly	Glu	Pro	Asn	Asp	Ile	Ala	
	210					215					220					

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Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 105
 <211> 759
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Variant of L. kefir

<400> 105
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcggt 60
 ttggcaatcg ccgataaatt ttagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tgcgtttgtc 180
 cagcagcatg cgtccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggtt 240
 ttccggcccgg ttacgaccgt cgtgaacaat gcagggattg cgggtgtgtaa aagcgttgaa 300
 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgcgctctga tgatctggaa 600
 gggttgggagg aaatgatgtc acagcgtagc gtaaccccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 106
 <211> 252
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Variant of L. kefir

<400> 106
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Val
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Cys
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Arg Leu Asp Asp Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala

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210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
 245 250

<210> 107
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 107
 atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggatatcgg 60
 ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
 gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
 cagcacgatg cgtccgatga agtgggctgg acgaaactgt tcgacaccac cgaggaggca 240
 ttcgccccgg ttacgaccgt cgtgaacaat gcagggagtt gcgttttaaa aagcgttgaa 300
 gacactacca cggaggaatg gcataaactg ctgtccgtta atctggatgg tgtttttttc 360
 ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
 atgagcagta ttgaggggct tgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactttgat 540
 gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgcggtctga tgagctggaa 600
 gggtgggagg aaatgatgtc acagcgtagc gtaaccccta tgggccacat tggcgaaccg 660
 aatgacatcg catggatctg tgtgtacctg gcactctgac aatcgaaatt tgcgacgggt 720
 gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 108
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of L. kefir

<400> 108
 Met Thr Asp Arg Leu Lys His Lys Val Ala Ile Val Thr Gly Gly Thr
 1 5 10 15
 Leu Gly Ile Gly Leu Ala Ile Ala Asp Lys Phe Val Glu Glu Gly Ala
 20 25 30
 Lys Val Val Ile Thr Gly Arg His Ala Asp Val Gly Glu Lys Ala Ala
 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Val Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Trp His Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Phe Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Pro Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln
 195 200 205

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Arg Thr Val Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
 210 215 220
 Trp Ile Cys Val Tyr Leu Ala Ser Asp Glu Ser Lys Phe Ala Thr Gly
 225 230 235 240
 Ala Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
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 gcggatgtag gtgaaaaggc cgccaaatca atcggcgga ctgatgttat tcgctttgtc 180
 cagcacgatg tctccgatga agcaggctgg acgaaactgt tcgacaccac cgaggagacc 240
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 gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
 ggcaccgctc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
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 ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
 gtgctgttca acacagtaca tccggggccc atcaagaccc agcggctcga tgagctggaa 600
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 aatgacatcg catggatctg tgtgtacctg gcacttgacg aatcgaaatt tgcgacgggt 720
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 35 40 45
 Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Val
 50 55 60
 Ser Asp Glu Ala Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Thr
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ser Cys Val Leu
 85 90 95
 Lys Ser Val Lys Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Leu Val Gly Asp Pro Thr Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Pro Ile Lys
 180 185 190
 Thr Gln Arg Leu Asp Glu Leu Glu Gly Trp Glu Glu Met Met Ser Gln

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Arg	Thr	195	Val	Thr	Pro	Met	Gly	200	Arg	Ile	Gly	Glu	Pro	205	Asn	Asp	Ile	Ala
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Trp	Ile	Cys	Val	Tyr	Leu	Ala	Ser	Asp	Glu	Ser	Lys	Phe	Ala	Thr	Gly			
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Lys	Val	Met	Ile	Thr	Gly	Arg	His	Xaa	Asp	Val	Gly	Glu	Lys	Ala	Ala
		35				40					45				
Lys	Ser	Val	Gly	Xaa	Pro	Asp	Gln	Xaa	Gln	Phe	Phe	Gln	His	Asp	Xaa
		50				55				60					
Ser	Xaa	Glu	Xaa	Gly	Trp	Thr	Xaa	Leu	Phe	Asp	Xaa	Thr	Glu	Lys	Xaa
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Phe	Gly	Pro	Val	Ser	Thr	Leu	Val	Asn	Asn	Ala	Gly	Xaa	Xaa	Xaa	Xaa
			85					90					95		
Xaa	Ser	Val	Xaa	Glu	Thr	Thr	Thr	Ala	Glu	Trp	Xaa	Lys	Leu	Xaa	Ala
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Val	Asn	Leu	Asp	Gly	Val	Phe	Phe	Gly	Thr	Arg	Leu	Gly	Ile	Gln	Arg
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145      150      155      160
Gly Ala Xaa Arg Xaa Met Ser Lys Ser Ala Ala Leu Xaa Cys Ala Leu
      165      170      175
Lys Asp Xaa Asp Val Arg Val Asn Thr Val His Pro Gly Xaa Ile Lys
      180      185      190
Thr Xaa Xaa Xaa Asp Xaa Leu Pro Gly Xaa Glu Glu Ala Met Ser Gln
      195      200      205
Arg Xaa Xaa Xaa Pro Met Gly Xaa Ile Gly Glu Pro Asn Asp Xaa Ala
      210      215      220
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Ser Glu Phe Val Val Asp Gly Xaa Xaa Thr Ala Gln
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		20						25				30			
Lys	Val	Val	Ile	Thr	Gly	Arg	His	Xaa	Asp	Val	Gly	Glu	Lys	Ala	Ala

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Lys Ser 35 Ile Gly Xaa Thr Asp 40 Val Xaa Arg Phe Val 45 Gln His Asp Xaa
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 Ser Xaa Glu Xaa Gly Trp Thr Xaa Leu Phe Asp Xaa Thr Glu Glu Xaa
 65 70 75 80
 Phe Gly Pro Val Thr Val Val Asn Asn Ala Gly Xaa Xaa Xaa Xaa
 85 90 95
 Xaa Ser Val Xaa Asp Thr Thr Thr Glu Glu Trp Xaa Lys Leu Xaa Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Xaa Asn Met Ser Ser Ile
 130 135 140
 Xaa Gly Xaa Xaa Gly Asp Xaa Xaa Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Xaa Arg Xaa Met Ser Lys Ser Ala Ala Leu Xaa Cys Ala Leu
 165 170 175
 Lys Asp Xaa Asp Val Arg Val Asn Thr Val His Pro Gly Xaa Ile Lys
 180 185 190
 Thr Xaa Xaa Xaa Xaa Xaa Leu Glu Gly Xaa Glu Glu Met Met Ser Gln
 195 200 205
 Arg Xaa Xaa Xaa Pro Met Gly Xaa Ile Gly Glu Pro Asn Asp Xaa Ala
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 35 40 45
 Arg Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Val Gln His Asp Ala
 50 55 60
 Ser Asp Glu Thr Gly Trp Thr Lys Leu Phe Asp Thr Thr Glu Glu Ala
 65 70 75 80
 Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser

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85 90 95
 Lys Ser Val Glu Asp Thr Thr Thr Glu Glu Trp Arg Lys Leu Leu Ser
 100 105 110
 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
 115 120 125
 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
 130 135 140
 Glu Gly Phe Val Gly Asp Pro Ala Leu Gly Ala Tyr Asn Ala Ser Lys
 145 150 155 160
 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
 165 170 175
 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
 180 185 190
 Thr Pro Leu Val Asp Asp Leu Glu Gly Ala Glu Glu Met Met Ser Gln
 195 200 205
 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
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 20 25 30
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 35 40 45

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His Ala Leu Lys Gly Asp Trp Pro Leu Pro Val Lys Met Pro Leu Val
 50 55 60
 Gly Gly His Glu Gly Ala Gly Val Val Val Ala Arg Gly Asp Leu Val
 65 70 75 80
 Thr Glu Phe Glu Ile Gly Asp His Ala Gly Leu Lys Trp Leu Asn Gly
 85 90 95
 Ser Cys Leu Ala Cys Glu Phe Cys Lys Gln Ala Asp Glu Pro Leu Cys
 100 105 110
 Pro Asn Ala Ser Leu Ser Gly Tyr Thr Val Asp Gly Thr Phe Gln Gln
 115 120 125
 Tyr Ala Ile Gly Lys Ala Thr His Ala Ser Lys Leu Pro Lys Asn Val
 130 135 140
 Pro Leu Asp Ala Val Ala Pro Val Leu Cys Ala Gly Ile Thr Val Tyr
 145 150 155 160
 Lys Gly Leu Lys Glu Ser Gly Val Arg Pro Gly Gln Thr Val Ala Ile
 165 170 175
 Val Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Leu Gln Tyr Ala Lys
 180 185 190
 Ala Met Gly Ile Arg Val Val Ala Ile Asp Gly Gly Glu Lys Gln
 195 200 205
 Ala Met Cys Glu Gln Leu Gly Ala Glu Ala Tyr Val Asp Phe Thr Lys
 210 215 220
 Thr Gln Asp Leu Val Ala Asp Val Lys Ala Ala Thr Pro Glu Gly Leu
 225 230 235 240
 Gly Ala His Ala Val Ile Leu Leu Ala Val Ala Glu Lys Pro Phe Gln
 245 250 255
 Gln Ala Ala Glu Tyr Val Ser Arg Gly Thr Val Val Ala Ile Gly Leu
 260 265 270
 Pro Ala Gly Ala Phe Leu Arg Ala Pro Val Phe Asn Thr Val Val Arg
 275 280 285
 Met Ile Asn Ile Lys Gly Ser Tyr Val Gly Asn Arg Gln Asp Gly Val
 290 295 300
 Glu Ala Val Asp Phe Phe Ala Arg Gly Leu Ile Lys Ala Pro Phe Lys
 305 310 315 320
 Thr Ala Pro Leu Gln Asp Leu Pro Lys Ile Phe Glu Leu Met Glu Gln
 325 330 335
 Gly Lys Ile Ala Gly Arg Tyr Val Leu Glu Ile Pro Glu
 340 345

<210> 117

<211> 729

<212> DNA

<213> Artificial sequence

<220>

<223> Codon optimized version of the adh gene from *Oenococcus oeni*

<400> 117

atgtttgatc gcctgaaggg taagggtggcg atcgtcaccg gcggtaatag cgggtattggt 60
 aaggcaatcg cggcagactt catcgccgag ggcgcgaaag tagtgattac cggtcgcaac 120
 caagagaagg gtcgccagac tgcgctggaa atcgccgggtg acattctgtt cattcagcag 180
 gacgtgagcc aggaggcgga ctggcagaaa gttatctcca aaaccatcga gaagttcggg 240
 aagtttgata ttctggttaa caacgctggc gtcggcgggc tgggtaagcc actggcagaa 300
 atgtccctgt ctgaattcaa ttggacccaa tccattaatc tgtccggtaa cttcctgggt 360
 attcacttcg cgctgaacaa aatgaccgaa cctggtagca ttattgacgt aagcagcgcg 420
 gctggcctgc gtggttttcc gggcgagcc gattatagcg ctcccaaagg tggtagcgcg 480
 ctgctgacgc gcgccgcggc gctggaagcg ctgcaaatgg gtaaaaagat ccgtgtaaac 540
 tctattcacc caggttggat tgataccgat atcgtaacaa aagatatgct tgagcaggtt 600
 atcgcatgga cccctatgca tcacctgggc caaccgaaag atattgcaa gctggcgacg 660
 tatctggcat ctgacgagtc cgagtatact acgggctccg aactggcagc cgacggcggt 720
 ctgatggca 729

<210> 118

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> The adh from *Oenococcus oeni*

<400> 118

```

Met Phe Asp Arg Leu Lys Gly Lys Val Ala Ile Val Thr Gly Gly Asn
1      5      10      15
Ser Gly Ile Gly Lys Ala Ile Ala Asp Phe Ile Ala Glu Gly Ala
20      25      30
Lys Val Val Ile Thr Gly Arg Asn Gln Glu Lys Gly Arg Gln Thr Ala
35      40      45
Leu Glu Ile Ala Gly Asp Ile Leu Phe Ile Gln Gln Asp Val Ser Gln
50      55      60
Glu Ala Asp Trp Gln Lys Val Ile Ser Lys Thr Ile Glu Lys Phe Gly
65      70      75      80
Lys Phe Asp Ile Leu Val Asn Asn Ala Gly Val Gly Gly Val Gly Lys
85      90      95
Pro Leu Ala Glu Met Ser Leu Ser Glu Phe Asn Trp Thr Gln Ser Ile
100     105     110
Asn Leu Ser Gly Asn Phe Leu Gly Ile His Phe Ala Leu Asn Lys Met
115     120     125
Thr Glu Pro Gly Ser Ile Ile Asp Val Ser Ser Ala Ala Gly Leu Arg
130     135     140
Gly Phe Pro Gly Ala Ala Asp Tyr Ser Ala Ser Lys Gly Gly Thr Arg
145     150     155     160
Leu Leu Thr Arg Ala Ala Ala Leu Glu Ala Leu Gln Met Gly Lys Lys
165     170     175
Ile Arg Val Asn Ser Ile His Pro Gly Trp Ile Asp Thr Asp Ile Val
180     185     190
Pro Lys Asp Met Arg Glu Gln Val Ile Ala Met Thr Pro Met His His
195     200     205
Leu Gly Gln Pro Lys Asp Ile Ala Lys Leu Ala Thr Tyr Leu Ala Ser
210     215     220
Asp Glu Ser Glu Tyr Thr Thr Gly Ser Glu Leu Ala Ala Asp Gly Gly
225     230     235     240
Leu Met Ala

```

<210> 119

<211> 768

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized version of the adh gene from *Ralstonia eutropha*

<400> 119

```

atgcagggca aaattgcact ggttacgggc ggtgcgtctg gtatgggtct ggccttcacc 60
cgtcgcctgg cccaagaagg cgcacgtggt tacttcaccg acattaacgg cgccgcgggt 120
cacgcgacgg aaagcgagct gcagggtgct ggtctggcgg tcgtattcct gcgtcatgac 180
gtgacccagg aaaacgactg gctgcgcgtc ctggaacata ttggcgtgtg tgacggtcgc 240
ctggatgtac tggatgaataa tgccggcatt gcgatttctc acaacattga gacttgtact 300
actgaggatt ttgatcgcac gctgaatggt aacctgaagt ccgtgtttct gggctgcaaa 360
cacggtctgg ctctgatgaa acagaagggt ggcagcatca ttaacgtag ctctatcacc 420
gcgatttgcg gcgaacctgt ggcgctggcg tatagcgcta gcaaagccgg cgtccgtttt 480
ctgagcaagt ctgttgccct gcattgtgcg gagaagggtc acgccatccg tggttaacagc 540
ctgcaccggg gttacattga taccgcgtg ctggcaggca gcaacgcggg tggctccctg 600
accgctgacg aggtaacgcg gagccgtgta cgtattggcg gtgaaattcc gctgaaacgt 660
cgcggcaccc cggacgaagt tgcaggcgcg gttctgtacc tggctagcga tgaatccacc 720
tatgttactg gtactgagct ggtaattgat ggcggctacg catgtcat 768

```

<210> 120

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

<223> The adh from *Ralstonia eutropha*

<400> 120

```

Met Gln Gly Lys Ile Ala Leu Val Thr Gly Gly Ala Ser Gly Met Gly
1      5      10      15
Leu Ala Phe Thr Arg Arg Leu Ala Gln Glu Gly Ala Arg Val Tyr Phe
20      25      30
Thr Asp Ile Asn Gly Ala Ala Gly His Ala Thr Glu Ser Glu Leu Gln
35      40      45
Gly Ala Gly Leu Ala Val Val Phe Leu Arg His Asp Val Thr Gln Glu
50      55      60
Asn Asp Trp Leu Arg Val Leu Glu His Ile Gly Ala Val Asp Gly Arg
65      70      75      80
Leu Asp Val Leu Val Asn Asn Ala Gly Ile Ala Ile Ser His Asn Ile
85      90      95
Glu Thr Cys Thr Thr Glu Asp Phe Asp Arg Thr Leu Asn Val Asn Leu
100     105     110
Lys Ser Val Phe Leu Gly Cys Lys His Gly Leu Ala Leu Met Lys Gln
115     120     125
Lys Gly Gly Ser Ile Ile Asn Val Ser Ser Ile Thr Ala Ile Cys Gly
130     135     140
Glu Pro Val Ala Leu Ala Tyr Ser Ala Ser Lys Ala Gly Val Arg Phe
145     150     155     160
Leu Ser Lys Ser Val Ala Leu His Cys Ala Glu Lys Gly Tyr Ala Ile
165     170     175
Arg Val Asn Ser Leu His Pro Gly Tyr Ile Asp Thr Pro Leu Leu Ala
180     185     190
Gly Ser Asn Ala Gly Gly Ser Leu Thr Ala Asp Glu Val Thr Ala Ser
195     200     205
Arg Val Arg Ile Gly Gly Glu Ile Pro Leu Lys Arg Arg Gly Thr Pro
210     215     220
Asp Glu Val Ala Gly Ala Val Leu Tyr Leu Ala Ser Asp Glu Ser Thr
225     230     235     240
Tyr Val Thr Gly Thr Glu Leu Val Ile Asp Gly Gly Tyr Ala Cys His
245     250     255

```

<210> 121

<211> 939

<212> DNA

<213> Artificial Sequence

<220>

<223> YDL ADH from *Saccharomyces cerevisiae*

<400> 121

```

atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcgggc ctggtacacg ttggtataaa aatgaagaaa ctgacgcgac cttctccaat 120
agtctggttg aacaaatcgt gtatgcgttg aaactgccgg ggattatcca catcgacgcc 180
gcggagattt atcgcaccta cccggaagtg ggtaaagcac tgtccctgac cgaaaagcct 240
cgtaacgcga tttttctgac ggataaatat tctccgcaga ttaaaatgag tgactcccct 300
gcggacggtc tggatttagc attgaagaaa atgggtacag attatgttga tttatatctg 360
ttacattccc cgtttgtttc gaaggaagtg aatggcttaa gcttagaaga ggcttggaag 420
gatattggagc agttatacaa aagtggtaaa gctaaaaaca tcgggggttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaaacata ttctccgctg ggcccgcctg agaagaaaac cgcgaggat 660
gacagccaac cattttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggctctgaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgttaa 939

```

<210> 122
 <211> 312
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YDL ADH from *Saccharomyces cerevisiae*

<400> 122
 Met Ser Phe His Gln Gln Phe Phe Thr Leu Asn Asn Gly Asn Lys Ile
 1 5 10 15
 Pro Ala Ile Ala Ile Ile Gly Thr Gly Thr Arg Trp Tyr Lys Asn Glu
 20 25 30
 Glu Thr Asp Ala Thr Phe Ser Asn Ser Leu Val Glu Gln Ile Val Tyr
 35 40 45
 Ala Leu Lys Leu Pro Gly Ile Ile His Ile Asp Ala Ala Glu Ile Tyr
 50 55 60
 Arg Thr Tyr Pro Glu Val Gly Lys Ala Leu Ser Leu Thr Glu Lys Pro
 65 70 75 80
 Arg Asn Ala Ile Phe Leu Thr Asp Lys Tyr Ser Pro Gln Ile Lys Met
 85 90 95
 Ser Asp Ser Pro Ala Asp Gly Leu Asp Leu Ala Leu Lys Lys Met Gly
 100 105 110
 Thr Asp Tyr Val Asp Leu Tyr Leu Leu His Ser Pro Phe Val Ser Lys
 115 120 125
 Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140
 Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
 145 150 155 160
 Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175
 Val Asn Gln Ile Glu Phe Ser Pro Phe Leu Gln Asn Gln Thr Pro Gly
 180 185 190
 Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205
 Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220
 Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
 225 230 235 240
 Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255
 Thr Thr Ser Ser Lys Pro Gln Arg Ile Ser Asp Ala Gln Asn Leu Phe
 260 265 270
 Ser Phe Asp Leu Thr Ala Glu Glu Val Asp Lys Ile Thr Glu Leu Gly
 275 280 285
 Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300
 Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 123
 <211> 1047
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ADH from *Rhodococcus erythropolis*

<400> 123
 atgaaagcca ttccagtagac tcgtatcggg gcggaaccag aactgactga aatcccgaag 60
 ccggaaccgg gcccgggcga agtactgctg gaagtcacgg cagctggcgt gtgccattcc 120
 gatgatttca ttatgtctct gccggaagaa cagtacacct acggcctgcc gctgaccctg 180
 ggtcatgaag gtgctggtaa agttgccgca gttggcgaag gtgttgaagg gttggatatt 240
 ggcaccaatg tggttgtgta cggcccatgg ggttgtggca actgttggca ttgcagtcag 300
 ggccctggaga actattgctc ccgtgcgcag gaactgggta ttaaccgcc tggctctggg 360
 gctccggggg ctttggcaga atttatgatt gtcgactcac cacgtcattt ggtcccgaat 420

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ggcgatttag accctgttaa aactgttccg ttgactgatg cgggcctgac cccataccat 480
gcaatcaaac gctccctgcc gaaactgcgc ggcggtctct atgcagtagt gatcggtacg 540
ggtggcctgg gccacgtggc tatccaactg ctgcgtcatt tatctgctgc aacgggtgatc 600
gccttgacg tttctgccga taaactggaa ctggctacca aagtcggcgc acatgaagta 660
gtcctgtctg ataaagatgc agcggagaat gtgcgtaaaa ttactggtag ccaaggtgca 720
gctttggtgt tggattttgt gggctatcag cctaccattg acaccgccat ggcaagtggc 780
ggcgtgggct ctgacgtcac cattgtttgt atcgggtgat gccaggcaca tgcgaaagt 840
ggtttcttcc agagtcctta tgaggcatcg gttacggtac cttattgggg cgctcgaat 900
gaactgatcg aattgatcga tctggcgcat gctggtatct tcgacattgc cgttgagacc 960
ttctctttgg ataatggtgc agaggcctat cgtcgcctgg ctgcgggcac actgtcaggc 1020
cgtgcggtag tcgtcccggg cctgtaa 1047

```

<210> 124

<211> 348

<212> PRT

<213> Artificial Sequence

<220>

<223> ADH from Rhodococcus erythropolis

<400> 124

```

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1      5      10      15
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
      20      25      30
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
      35      40      45
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
      50      55      60
Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
      65      70      75      80
Gly Thr Asn Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
      85      90      95
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
      100      105      110
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
      115      120      125
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
      130      135      140
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
      145      150      155      160
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
      165      170      175
Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
      180      185      190
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
      195      200      205
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
      210      215      220
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
      225      230      235      240
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
      245      250      255
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
      260      265      270
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
      275      280      285
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
      290      295      300
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ala Val Glu Thr
      305      310      315      320
Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
      325      330      335
Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu
      340      345

```

<210> 125
 <211> 1047
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> YGL ADH from *Saccharomyces cerevisiae*

<400> 125
 atgaccacgg aaaaaaccgt agtggttcgtg tcaggcgcgga ccggttttat tgctctgcac 60
 gtggttagatg acctgctgaa aactgggttac aaagtaattg gttccgggtcg ttctcaggaa 120
 aaaaatgacg gtttgctgaa gaagttcaag tccaaccgga atctgagcat ggaaattgtg 180
 gaagatattg cggcaccaaa cgcccttcgat aaagtattcc agaaacatgg taaagaaatt 240
 aaagtgggtcc tgcataatcgc gtccccgggtc catttcaaca ctaccgattt cgaaaaaagac 300
 ttactgatcc cggcgggtaaa cgggtaccaa tctatttttg aagcaattaa gaactatgcc 360
 gcagacaccg tggaaaaagt ggttattact tcatctgttg ccgctgtggc ctctccgggt 420
 gatatgaaag ataccagctt cgtgggttaac gaagaatcct ggaataaaga cacctgggaa 480
 tcgtgtcagg cgaatgctgt gtccgcttat tgcggttcta aaaaattcgc agagaaaacg 540
 gcgtgggact tcttgaaga aaaccagagc agcattaaat ttactctgtc cacgattaac 600
 ccaggcttcg tttttgggtcc gcagctgttc gccgactcct tgcgcaatgg tattaactct 660
 agcagtgcga ttattgcgaa cctgggtgtcg tataaattag gggataactt ctacaattat 720
 agcggccccgt ttatcgacgt ccgtgacgtt tccaaagctc atctgctggc atttgagaaa 780
 cctgaatgcg ccggtcagcg cctgtttctg tgcgaggata tgttctgttc ccaggaagcc 840
 ctggacattc tgaacgaaga atttccacag ctgaagggca agatcgcaac gggcgaacct 900
 ggcagcggct cgaccttcct gactaaaaat tgttgcaaat gcgacaatcg taaaactaaa 960
 aacttgcttg gcttccagtt caacaaattc cgcgactgca ttgtcgatac tgcgtcccg 1020
 ttgttggaag tgcaaagcaa aagctaa 1047

<210> 126
 <211> 348
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YGL ADH from *Saccharomyces cerevisiae*

<400> 126
 Met Thr Thr Glu Lys Thr Val Val Phe Val Ser Gly Ala Thr Gly Phe
 1 5 10 15
 Ile Ala Leu His Val Val Asp Asp Leu Leu Lys Thr Gly Tyr Lys Val
 20 25 30
 Ile Gly Ser Gly Arg Ser Gln Glu Lys Asn Asp Gly Leu Leu Lys Lys
 35 40 45
 Phe Lys Ser Asn Pro Asn Leu Ser Met Glu Ile Val Glu Asp Ile Ala
 50 55 60
 Ala Pro Asn Ala Phe Asp Lys Val Phe Gln Lys His Gly Lys Glu Ile
 65 70 75 80
 Lys Val Val Leu His Ile Ala Ser Pro Val His Phe Asn Thr Thr Asp
 85 90 95
 Phe Glu Lys Asp Leu Leu Ile Pro Ala Val Asn Gly Thr Lys Ser Ile
 100 105 110
 Leu Glu Ala Ile Lys Asn Tyr Ala Ala Asp Thr Val Glu Lys Val Val
 115 120 125
 Ile Thr Ser Ser Val Ala Ala Leu Ala Ser Pro Gly Asp Met Lys Asp
 130 135 140
 Thr Ser Phe Val Val Asn Glu Glu Ser Trp Asn Lys Asp Thr Trp Glu
 145 150 155 160
 Ser Cys Gln Ala Asn Ala Val Ser Ala Tyr Cys Gly Ser Lys Lys Phe
 165 170 175
 Ala Glu Lys Thr Ala Trp Asp Phe Leu Glu Glu Asn Gln Ser Ser Ile
 180 185 190
 Lys Phe Thr Leu Ser Thr Ile Asn Pro Gly Phe Val Phe Gly Pro Gln
 195 200 205
 Leu Phe Ala Asp Ser Leu Arg Asn Gly Ile Asn Ser Ser Ser Ala Ile
 210 215 220
 Ile Ala Asn Leu Val Ser Tyr Lys Leu Gly Asp Asn Phe Tyr Asn Tyr
 225 230 235 240

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Ser Gly Pro Phe Ile Asp Val Arg Asp Val Ser Lys Ala His Leu Leu
 245 250 255
 Ala Phe Glu Lys Pro Glu Cys Ala Gly Gln Arg Leu Phe Leu Cys Glu
 260 265 270
 Asp Met Phe Cys Ser Gln Glu Ala Leu Asp Ile Leu Asn Glu Glu Phe
 275 280 285
 Pro Gln Leu Lys Gly Lys Ile Ala Thr Gly Glu Pro Gly Ser Gly Ser
 290 295 300
 Thr Phe Leu Thr Lys Asn Cys Cys Lys Cys Asp Asn Arg Lys Thr Lys
 305 310 315 320
 Asn Leu Leu Gly Phe Gln Phe Asn Lys Phe Arg Asp Cys Ile Val Asp
 325 330 335
 Thr Ala Ser Gln Leu Leu Glu Val Gln Ser Lys Ser
 340 345

<210> 127

<211> 939

<212> DNA

<213> Artificial Sequence

<220>

<223> YPR ADH from *Saccharomyces cerevisiae*

<400> 127

atgccggcaa cggttaaaaaa cagcagtgct accttaaaat taaacacagg tgcgagcatt 60
 cctgtcctgg gggttcggcac ctggcgctct gtcgataaca acggctatca tagtgtaatt 120
 gcggcgctga aagcggggta ccgtcatatc gatgctgcgg ccatctatct gaatgaagaa 180
 gaagtcggcc gtgcgatcaa ggactccggt gtccctcgtg aagaaatttt tattaccacc 240
 aaactgtggg gcaccgaaca acgcgatcca gaagcagccc tgaacaaatc tctgaaacgt 300
 ctgggtctgg actatgtgga cctgtatctg atgcactggc cggcccctct gaaaacagac 360
 cgtgtaactg acggtaacgt cctgtgcatc ccgacctgg aagatggcac cgtggacatc 420
 gataccaaag agtgggaattt tattaaaacc tgggaactga tgcaggaatt gccgaaaact 480
 ggtaagacca aagccgtcgg tgtgtccaat ttttccatca acaatatcaa agaactgctg 540
 gaatcgccaa ataacaaggc cgttccagca accaatcaga tcgagattca tccgttgctg 600
 ccgcaggatg aattaatcgc cttttgtaaa gaaaaaggca ttgtggtcga agcatatagc 660
 ccattcggct ccgctaacgc ccgcgtgctg aaagaacagg cgattatcga tatggccaaa 720
 aagcacggcg tcgaaccggc gcaactgatt atcagctggc cgattcagcg cggttatgtg 780
 gtattggcca agtccgtaaa tccggagcgt atcgtgtcga actttaagat ttttaccctg 840
 ccagaggatg atttcaaac catctctaac ctgagcaaag tgcacggtac caaacgtgtc 900
 gttgacatga aatggggctc atttccgatt tttcaataa 939

<210> 128

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> YPR ADH from *Saccharomyces cerevisiae*

<400> 128

Met Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn Thr
 1 5 10 15
 Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val Asp
 20 25 30
 Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr Arg
 35 40 45
 His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Val Gly Arg
 50 55 60
 Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr Thr
 65 70 75 80
 Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn Lys
 85 90 95
 Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met His
 100 105 110
 Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val Leu
 115 120 125

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Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys Glu
 130 135 140
 Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys Thr
 145 150 155 160
 Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn Ile
 165 170 175
 Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr Asn
 180 185 190
 Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala Phe
 195 200 205
 Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly Ser
 210 215 220
 Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala Lys
 225 230 235 240
 Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile Gln
 245 250 255
 Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile Val
 260 265 270
 Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr Ile
 275 280 285
 Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met Lys
 290 295 300
 Trp Gly Ser Phe Pro Ile Phe Gln
 305 310

<210> 129
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GRE ADH from *Saccharomyces cerevisiae*

<400> 129
 atgtctgtgt tcgtgtcagg cgcgaaatggt ttatttgctc agcacatcgt agatctgctg 60
 ctgaaagaag attacaaagt aattgggttcc gcacgttctc aggaaaaagc tgaaaatttg 120
 accgaagcct tcggtaacaa cccgaaatgt agcatggaag tgggtgcctga tattagcaaa 180
 ctggatgcct tcgatcatgt attccagaaa catggtaaaag atattaaaat cgtcctgcat 240
 accgcgtccc cgttttgttt cgatattacc gattccgaac gtgacttact gatcccggtg 300
 gtaaacggtg tcaaaggtat ttgacacagt attaagaaat atgccgcaga cagcgtggaa 360
 cgcggtggtt tgacttcac tttacgccgcg gtatttgata tggcgaagga aaacgataag 420
 agcctgacct tcaacgaaga atcctggaat ccggcgacct ggggaatcgtg tcagagtgtg 480
 ccggtgaacg cttattgctg ttctaaaaaa ttcgcagaga aagcagcgtg ggaattcttg 540
 gaagaaaacc gtgatagcgt gaaatttgag ctgacagcgg tcaaccaggt ttacgttttt 600
 ggtccgcaga tgttcgataa agatgttaaa aaacacttga acaccagctg cgaactggtg 660
 aactctctga tgcattctgag ccctgaagat aaaattccgg aactgttttg cggttacatc 720
 gacgtccgtg acgttgcgaa agctcatctg gttgcatttc agaaacgtga aacaatcggg 780
 cagcgcctga tcgtgtcgga ggcacgtttc acgatgcagg acgttctgga cattctgaac 840
 gaagactttc cagtactgaa gggcaatatt ccggtcgga agcctggcag cggcgccacc 900
 cataatactc tgggcgccac cctggacaat aaaaaagca aaaaattgct gggcttcaaa 960
 ttccgtaatc tgaaagagac tattgacgat actgcgtccc agatcctgaa attcgaaggt 1020
 cgcatttaa 1029

<210> 130
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GRE ADH from *Saccharomyces cerevisiae*

<400> 130
 Met Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His Ile
 1 5 10 15
 Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala Arg
 20 25 30

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Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn Pro
 35 40 45
 Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala Phe
 50 55 60
 Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu His
 65 70 75 80
 Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp Leu
 85 90 95
 Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile Lys
 100 105 110
 Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser Tyr
 115 120 125
 Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr Phe
 130 135 140
 Asn Glu Glu Ser Trp Asn Pro Ala Thr Trp Glu Ser Cys Gln Ser Asp
 145 150 155 160
 Pro Val Asn Ala Tyr Cys Gly Ser Lys Lys Phe Ala Glu Lys Ala Ala
 165 170 175
 Trp Glu Phe Leu Glu Glu Asn Arg Asp Ser Val Lys Phe Glu Leu Thr
 180 185 190
 Ala Val Asn Pro Val Tyr Val Phe Gly Pro Gln Met Phe Asp Lys Asp
 195 200 205
 Val Lys Lys His Leu Asn Thr Ser Cys Glu Leu Val Asn Ser Leu Met
 210 215 220
 His Leu Ser Pro Glu Asp Lys Ile Pro Glu Leu Phe Gly Gly Tyr Ile
 225 230 235 240
 Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln Lys Arg
 245 250 255
 Glu Thr Ile Gly Gln Arg Leu Ile Val Ser Glu Ala Arg Phe Thr Met
 260 265 270
 Gln Asp Val Leu Asp Ile Leu Asn Glu Asp Phe Pro Val Leu Lys Gly
 275 280 285
 Asn Ile Pro Val Gly Lys Pro Gly Ser Gly Ala Thr His Asn Thr Leu
 290 295 300
 Gly Ala Thr Leu Asp Asn Lys Lys Ser Lys Lys Leu Leu Gly Phe Lys
 305 310 315 320
 Phe Arg Asn Leu Lys Glu Thr Ile Asp Asp Thr Ala Ser Gln Ile Leu
 325 330 335
 Lys Phe Glu Gly Arg Ile
 340

<210> 131
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon optimized ADH from *S. salmonicolor*

<400> 131
 atggcaaaga tcgacaacgc agttctgccc gaggggttctc tgggtgctggt caccggcgcg 60
 aacggctttg tcgctagcca tgtgggtcgaa caactgctgg aacacggcta taagggtgagc 120
 ggcactgctc gctctgcctc caaactggcg aacctgcaga aacgttggga cgccaaatac 180
 cctgggtcgtt tcgagactgc cgttggttgaa gacatgctga agcaggggtg atatgatgaa 240
 gttattaaag gcgcggcagg tgtcgcctac atcgcgtccg tggctcagctt ttctaacaaa 300
 tatgatgagg tggtaactcc tgcgatcggg ggcacgctga atgccctgag tgccgcagct 360
 gctacgcctt ccgtgaaacg ttttgtgctg accagcagca ctgtttctgc actgattcca 420
 aaacctaacg tcgaaggtat ttatctggat gagaagagct ggaacctgga aagcattgat 480
 aaggctaaaa ccctgcctga atctgatccg cagaaaagcc tgtgggtcta cgccgcaagc 540
 aaaacggaag cggaactggc tgcctggaaa ttcattggacg aaaacaaacc gcactttact 600
 ctgaatgccg ttctgccaaa ctacactatc ggtaccattt ttgaccacga aacccaatcc 660
 ggttccactt ccggctggat gatgtctctg ttcaatggcg aagtatctcc ggcactggcg 720
 ctgatgccgc cgcagtacta tgtctctgca gttgatatac gtctgctgca cctgggttgt 780
 ctggttctgc cgcaaactga acgccgtcgt gtttacggca ccgcaggcac ctttgattgg 840
 aacaccgttc tggcgacctt ccgtaaactt tatccgtcca agacgttccc ggctgacttt 900
 ccggatcagg gccaggatct gtccaaattt gataccgccc cgagcctgga gattctgaaa 960
 tccctgggccc gccctggctg gcgtagcatc gaggaatcta tcaaagatct ggtgggttcc 1020

gagaccgcct aa

<210> 132
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ADH from *S. salmonicolor*

<400> 132
 Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15
 Val Thr Gly Ala Asn Gly Phe Val Ala Ser His Val Val Glu Gln Leu
 20 25 30
 Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45
 Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60
 Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
 65 70 75 80
 Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
 85 90 95
 Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
 100 105 110
 Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
 115 120 125
 Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
 130 135 140
 Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
 145 150 155 160
 Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
 165 170 175
 Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
 180 185 190
 Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
 195 200 205
 Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
 210 215 220
 Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
 225 230 235 240
 Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
 245 250 255
 His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
 260 265 270
 Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
 275 280 285
 Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
 290 295 300
 Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
 305 310 315 320
 Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
 325 330 335
 Leu Val Gly Ser Glu Thr Ala
 340

<210> 133
 <211> 1041
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon optimized ADH from *S. coelicolor*

<400> 133
 atgaaggcac tgcagtaccg caccatcggc gccccgcccc aggtcgtcac cgtcccgac 60

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ccggagccgg gccccggcca ggtgctgttg aaggtgaccg cggccggagt ctgccactcc 120
gacatcgagg tgatgagctg gcccgcgag ggcttcccgt acgagctgcc gctcaccctc 180
ggccacgagg gcgtcgccac cgtggccgag ctccggcgccg ggggtgacggg gctcgccgag 240
ggcgacgcgg tcgccgtgta cgggccctgg ggctgcggca cctgcgcca gtgcgcggag 300
ggcaaggaga actactgcct gcgcgcccgc gagctgggca tccgtccgcc ggggctcggg 360
cgtccggggg ccatggccga gtacctgctg atcgacgacc cccggcacct ggtcccgcgtg 420
gacgggctcg acccggtcgc ggcgggtgccc ctaccgacg ccggactgac gccgtaccac 480
gcgatcaagc ggtcgctgcc caagctggtc cccggctcca ccgcggtggg catcggcacc 540
ggtgggtctc gccacgtcgc catccagctg ctgcgcgccc tgacgtccgc ccgggtgggtc 600
gccctggacg tcagcgagga gaagctgcgc ctgcgccgtg cgggtgggcgc gcacgaggcg 660
gtgctgtcgg acgcgaaggc cgcggacgcg gtgcgcgaga tcaccggcgg tctcgggtgcc 720
gaggccgtgt tcgacttcgt cggcgtggcg cccaccgtgc agaccgccgg agccgtcgcg 780
gccgtcgagg gcgatgtcac cctggctcggc atcggcggcg gatcgctgcc cgtcggcttc 840
ggcatgctgc cgttcgaggt gtcgggtcaac gccccctact ggggcagccg cagcgagctg 900
accgaggtgc tgaacctggc ccgctccggt gccgtgtcgg tgcacaccga gacgtactcc 960
ctggacgacg ccccgctcgc ctacgagcgg ctgcacgagg gcagggtcaa cggccgcgcg 1020
gtgatcctgc cccacggctg a 1041

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<210> 134

<211> 346

<212> PRT

<213> Artificial Sequence

<220>

<223> ADH from *S. coelicolor*

<400> 134

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Met Lys Ala Leu Gln Tyr Arg Thr Ile Gly Ala Pro Pro Glu Val Val
1      5      10      15
Thr Val Pro Asp Pro Glu Pro Gly Pro Gly Gln Val Leu Leu Lys Val
20     25     30
Thr Ala Ala Gly Val Cys His Ser Asp Ile Ala Val Met Ser Trp Pro
35     40     45
Ala Glu Gly Phe Pro Tyr Glu Leu Pro Leu Thr Leu Gly His Glu Gly
50     55     60
Val Gly Thr Val Ala Ala Leu Gly Ala Gly Val Thr Gly Leu Ala Glu
65     70     75     80
Gly Asp Ala Val Ala Val Tyr Gly Pro Trp Gly Cys Gly Thr Cys Ala
85     90     95
Lys Cys Ala Glu Gly Lys Glu Asn Tyr Cys Leu Arg Ala Asp Glu Leu
100    105    110
Gly Ile Arg Pro Pro Gly Leu Gly Arg Pro Gly Ser Met Ala Glu Tyr
115    120    125
Leu Leu Ile Asp Asp Pro Arg His Leu Val Pro Leu Asp Gly Leu Asp
130    135    140
Pro Val Ala Ala Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145    150    155    160
Ala Ile Lys Arg Ser Leu Pro Lys Leu Val Pro Gly Ser Thr Ala Val
165    170    175
Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180    185    190
Ala Leu Thr Ser Ala Arg Val Val Ala Leu Asp Val Ser Glu Glu Lys
195    200    205
Leu Arg Leu Ala Arg Ala Val Gly Ala His Glu Ala Val Leu Ser Asp
210    215    220
Ala Lys Ala Ala Asp Ala Val Arg Glu Ile Thr Gly Gly Leu Gly Ala
225    230    235    240
Glu Ala Val Phe Asp Phe Val Gly Val Ala Pro Thr Val Gln Thr Ala
245    250    255
Gly Ala Val Ala Val Glu Gly Asp Val Thr Leu Val Gly Ile Gly
260    265    270
Gly Gly Ser Leu Pro Val Gly Phe Gly Met Leu Pro Phe Glu Val Ser
275    280    285
Val Asn Ala Pro Tyr Trp Gly Ser Arg Ser Glu Leu Thr Glu Val Leu
290    295    300
Asn Leu Ala Arg Ser Gly Ala Val Ser Val His Thr Glu Thr Tyr Ser
305    310    315    320

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Leu Asp Asp Ala Pro Leu Ala Tyr Glu Arg Leu His Glu Gly Arg Val
325 330 335
Asn Gly Arg Ala Val Ile Leu Pro His Gly
340 345

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<210> 135
<211> 1056
<212> DNA
<213> Artificial Sequence
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<400> 135						
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gcgccaggcc	cgttcgatgc	aattgtgcgc	cctctggcag	tagcgcctgt	taccagcgat	120
attcatactg	tgtttgaagg	tgccattggc	gagcgtcaca	atatgattct	gggccatgaa	180
gccgcttggt	aagttggtga	ggttggcagc	gcagtgaaag	atttcaaac	gggcgatcgc	240
gttgtcgttc	cagcgaattc	cccggaattg	cgaccagcg	aagttccagc	cggctaccat	300
cagcactctg	cgggcatgtc	ggcggcttgg	aaattcagca	atgtaaaagg	tgggtgtgtc	360
ggtgaatttt	ttcacgttaa	cgacgcagac	atgaatctgg	cgcacctgcc	gaaagaaatc	420
ccgctggaag	cagcggttat	gattccggat	atgatgacca	cgggttttca	cggcgcagag	480
ctggcggaca	ttgaactggg	cgctacggta	gccgtactgg	gcacggctc	ggtgggcctg	540
atggcagttg	cagggcgtaa	gctgcgcggc	gcaggctcga	ttattgccgt	tggttctcgc	600
ccggtgtgtg	tggacgcgcg	taagtattat	ggtgcaacgg	acattgtcaa	ttacaaggac	660
ggcccaattg	aatctcagat	catgaacctg	acggaaggta	aaggcgttga	cgccgcgatt	720
atcgttggcg	gcaacgccga	catcatggcg	accgcagtta	aaatcgtcaa	gccaggtggt	780
actattgcta	acgtcaacta	cttcggcgaa	ggtgaggtcc	tgctgtccc	acgtctggaa	840
tggggtttgc	gtattggcaca	taaaaccatt	aaaggttgcc	tgtgcccagg	cggccgtctg	900
cgtatggaac	gctgtatcga	tctggtcttc	tacaaacgcg	tggtatcctag	caaactgggtg	960
actcacgttt	tccgcggctt	tgataaacatc	gaaaagcgtt	ttatgctgat	gaaagataaa	1020
ccgaaaatc	tgattaaacc	ggttgtcatc	ctggct			1056

<210> 136
<211> 352
<212> PRT
<213> Artificial sequence

Met	Lys	Gly	Phe	Ala	Met	Leu	Ser	Ile	Gly	Lys	Val	Gly	Trp	Ile	Glu
1				5					10				15		
Lys	Glu	Lys	Pro	Ala	Pro	Gly	Pro	Phe	Asp	Ala	Ile	Val	Arg	Pro	Leu
			20					25					30		
Ala	Val	Ala	Pro	Cys	Thr	Ser	Asp	Ile	His	Thr	Val	Phe	Glu	Gly	Ala
		35					40					45			
Ile	Gly	Glu	Arg	His	Asn	Met	Ile	Leu	Gly	His	Glu	Ala	Val	Gly	Glu
	50				55						60				
Val	Val	Glu	Val	Gly	Ser	Glu	Val	Lys	Asp	Phe	Lys	Pro	Gly	Asp	Arg
65				70						75					80
Val	Val	Val	Pro	Ala	Ile	Thr	Pro	Asp	Trp	Arg	Thr	Ser	Glu	Val	Gln
			85						90					95	
Arg	Gly	Tyr	His	Gln	His	Ser	Gly	Gly	Met	Leu	Ala	Gly	Trp	Lys	Phe
			100					105					110		
Ser	Asn	Val	Lys	Asp	Gly	Val	Phe	Gly	Glu	Phe	Phe	His	Val	Asn	Asp
		115					120					125			
Ala	Asp	Met	Asn	Leu	Ala	His	Leu	Pro	Lys	Glu	Ile	Pro	Leu	Glu	Ala
	130					135					140				
Ala	Val	Met	Ile	Pro	Asp	Met	Met	Thr	Thr	Gly	Phe	His	Gly	Ala	Glu
145					150					155					160
Leu	Ala	Asp	Ile	Glu	Leu	Gly	Ala	Thr	Val	Ala	Val	Leu	Gly	Ile	Gly
			165						170					175	
Pro	Val	Gly	Leu	Met	Ala	Val	Ala	Gly	Ala	Lys	Leu	Arg	Gly	Ala	Gly
			180					185					190		

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Arg Ile Ile Ala Val Gly Ser Arg Pro Val Cys Val Asp Ala Ala Lys
    195    200    205
Tyr Tyr Gly Ala Thr Asp Ile Val Asn Tyr Lys Asp Gly Pro Ile Glu
    210    215    220
Ser Gln Ile Met Asn Leu Thr Glu Gly Lys Gly Val Asp Ala Ala Ile
    225    230    235    240
Ile Ala Gly Gly Asn Ala Asp Ile Met Ala Thr Ala Val Lys Ile Val
    245    250    255
Lys Pro Gly Gly Thr Ile Ala Asn Val Asn Tyr Phe Gly Glu Gly Glu
    260    265    270
Val Leu Pro Val Pro Arg Leu Glu Trp Gly Cys Gly Met Ala His Lys
    275    280    285
Thr Ile Lys Gly Gly Leu Cys Pro Gly Gly Arg Leu Arg Met Glu Arg
    290    295    300
Leu Ile Asp Leu Val Phe Tyr Lys Arg Val Asp Pro Ser Lys Leu Val
    305    310    315    320
Thr His Val Phe Arg Gly Phe Asp Asn Ile Glu Lys Ala Phe Met Leu
    325    330    335
Met Lys Asp Lys Pro Lys Asp Leu Ile Lys Pro Val Val Ile Leu Ala
    340    345    350

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<210> 137

<211> 1125

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized ADH from Horse Liver, E form

<400> 137

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atgagcacag cagggaaagt aattaaatgc aaagcagctg tgctgtggga ggaaaagaaa 60
ccattttcca ttgaggaggt ggaggtcgca cctccgaagg cccatgaagt ccgtattaag 120
atggtggcca cagggatctg tcgctcagat gaccacgtgg ttagtgggac cctggtcaca 180
cctctgcctg tgatcgcagg ccatgaggca gctggcattg tggagagcat cggggaaggc 240
gtcactacag tacgtccagg tgataaagtc atcccactgt ttactcctca gtgtgggaaa 300
tgccgtgttt gtaaacaccc tgaaggcaac ttctgtttga aaaatgatct gagcatgcct 360
cgtgggacca tgcaggatgg taccagccgt ttcacctgcc gtgggaagcc tatccaccac 420
ttcctgggca ccagcacctt ctcccagtac accgtgggtg acgagatctc agtggccaag 480
atcgatgcgg cctcacccgt ggagaaagtc tgtctgattg gctgtgggtt ttctactggt 540
tatgggtctg cagtcaaggt tgccaaggct acccagggct ccacctgtgc cgtgtttggc 600
ctgggggggg tgggcctgtc tgttatcatg ggctgtaaag cagccggggc ggcccgtatc 660
attggggtgg acatcaacaa agacaagtgt gcaaaggcca aagaagtggg tgccactgag 720
tgtgtcaacc ctccaggacta caagaaacct atccaggagg tgctgacaga aatgagcaat 780
gggggcgtgg atttttcatt tgaagtcatt ggtcgtctgg acaccatggt gactgccttg 840
tcatgtctgc aagaagcata tgggtgtgag gtcacgttag gggtagctcc tgattcccaa 900
aatctgtcta tgaatcctat gttgtctgtg agtgggcgta cctggaaaag ggctattttt 960
ggtgggttta agagtaaaga ttctgtccct aaactgggtg ccgattttat ggctaaaaag 1020
tttgcaactg atcctttaat ccccatgtt ttaccttttg aaaaaattaa tgaagggttt 1080
gacctgctgc gctctgggga gagtatccgt accatcctga cgttt 1125

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<210> 138

<211> 375

<212> PRT

<213> Artificial Sequence

<220>

<223> ADH from Horse Liver, E form

<400> 138

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Met Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp
1      5      10      15
Glu Glu Lys Lys Pro Phe Ser Ile Glu Val Glu Val Ala Pro Pro
    20      25      30
Lys Ala His Glu Val Arg Ile Lys Met Val Ala Thr Gly Ile Cys Arg
    35      40      45
Ser Asp Asp His Val Val Ser Gly Thr Leu Val Thr Pro Leu Pro Val

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50 55 60
 Ile Ala Gly His Glu Ala Ala Gly Ile Val Glu Ser Ile Gly Glu Gly
 65 70 75 80
 Val Thr Thr Val Arg Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro
 85 90 95
 Gln Cys Gly Lys Cys Arg Val Cys Lys His Pro Glu Gly Asn Phe Cys
 100 105 110
 Leu Lys Asn Asp Leu Ser Met Pro Arg Gly Thr Met Gln Asp Gly Thr
 115 120 125
 Ser Arg Phe Thr Cys Arg Gly Lys Pro Ile His His Phe Leu Gly Thr
 130 135 140
 Ser Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Ile Ser Val Ala Lys
 145 150 155 160
 Ile Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly
 165 170 175
 Phe Ser Thr Gly Tyr Gly Ser Ala Val Lys Val Ala Lys Val Thr Gln
 180 185 190
 Gly Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val
 195 200 205
 Ile Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Gly Val Asp
 210 215 220
 Ile Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Val Gly Ala Thr Glu
 225 230 235 240
 Cys Val Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Thr
 245 250 255
 Glu Met Ser Asn Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg
 260 265 270
 Leu Asp Thr Met Val Thr Ala Leu Ser Cys Cys Gln Glu Ala Tyr Gly
 275 280 285
 Val Ser Val Ile Val Gly Val Pro Pro Asp Ser Gln Asn Leu Ser Met
 290 295 300
 Asn Pro Met Leu Leu Leu Ser Gly Arg Thr Trp Lys Gly Ala Ile Phe
 305 310 315 320
 Gly Gly Phe Lys Ser Lys Asp Ser Val Pro Lys Leu Val Ala Asp Phe
 325 330 335
 Met Ala Lys Lys Phe Ala Leu Asp Pro Leu Ile Thr His Val Leu Pro
 340 345 350
 Phe Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu Arg Ser Gly Glu Ser
 355 360 365
 Ile Arg Thr Ile Leu Thr Phe
 370 375

<210> 139

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> Engineered Ketoreductase Sequence Formula with L. minor backbone

<223> Synthetic Construct

<220>

<221> MISC_FEATURE

<222>(7)..(7)

<223> Xaa is a constrained or non-polar residue

<220>

<221> MISC_FEATURE

<222>(17)..(17)

<223> Xaa is a non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(25)..(25)

<223> Xaa is a polar or acidic residue

<220>
<221> MISC_FEATURE
<222>(27)..(27)
<223> Xaa is an aromatic residue

<220>
<221> MISC_FEATURE
<222>(41)..(41)
<223> Xaa is a polar, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(53)..(53)
<223> Xaa is a polar, non-polar, or acidic residue

<220>
<221> MISC_FEATURE
<222>(57)..(57)
<223> Xaa is a non-polar or aliphatic residue

<220>
<221> MISC_FEATURE
<222>(64)..(64)
<223> Xaa is a polar, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(66)..(66)
<223> Xaa is an acidic residue

<220>
<221> MISC_FEATURE
<222>(68)..(68)
<223> Xaa is a polar, acidic, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(72)..(72)
<223> Xaa is a basic residue

<220>
<221> MISC_FEATURE
<222>(76)..(76)
<223> Xaa is an aliphatic, non-polar, or polar residue

<220>
<221> MISC_FEATURE
<222>(80)..(80)
<223> Xaa is an aliphatic, non-polar, or polar residue

<220>
<221> MISC_FEATURE
<222>(93)..(93)
<223> Xaa is is a polar, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(94)..(94)
<223> Xaa is a cysteine, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222>(95)..(95)
<223> Xaa is an aliphatic, non-polar, or acidic residue

<220>
<221> MISC_FEATURE
<222>(96)..(96)

<223> Xaa is is a cyteine, polar, aliphatic, or non-polar residue

<220>

<221> MISC_FEATURE

<222>(97)..(97)

<223> Xaa is a constrained or polar residue

<220>

<221> MISC_FEATURE

<222>(100)..(100)

<223> Xaa is a basic, acidic, polar, aliphatic, or non-polar residue

<220>

<221> MISC_FEATURE

<222>(108)..(108)

<223> Xaa is a basic or constrained residue

<220>

<221> MISC_FEATURE

<222>(111)..(111)

<223> Xaa is a non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(139)..(139)

<223> Xaa is a non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(145)..(145)

<223> Xaa is an acidic, aliphatic, or non-polar residue

<220>

<221> MISC_FEATURE

<222>(147)..(147)

<223> Xaa is an aromatic, aliphatic, or non-polar residue

<220>

<221> MISC_FEATURE

<222>(151)..(151)

<223> Xaa is a constrained, non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(152)..(152)

<223> Xaa is a polar, aromatic, aliphatic, or non-polar residue

<220>

<221> MISC_FEATURE

<222>(163)..(163)

<223> Xaa is a non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(165)..(165)

<223> Xaa is a polar, non-polar or aliphatic residue

<220>

<221> MISC_FEATURE

<222>(173)..(173)

<223> Xaa is an acidic, non-polar or aliphatic residue

<220>

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 Ser Asp Glu Xaa Gly Trp Thr Lys Leu Phe Asp Xaa Thr Glu Glu Xaa
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 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
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 Lys Asp Xaa Asp Val Arg Val Asn Thr Val His Pro Gly Xaa Ile Lys
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 Trp Ile Cys Val Tyr Leu Ala Ser Xaa Glu Xaa Lys Phe Ala Thr Gly
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