KETOREDUCTASE POLYPEPTIDES FOR THE REDUCTION OF ACETOPHENONES

1.

[0001] This application claims benefit under 35 U.S.C. § 119(e) of application Serial No. 60/972,058, filed September 13, 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 376247-017.txt is herein incorporated by reference. The electronic copy of the Sequence Listing was created on September 13, 2008, with a file size of 213Kbytes.

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 and by stereospecific reduction of corresponding racemic aldehyde substrates. KREDs typically convert ketone and aldehyde substrates 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), but not both.

[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., 2000, *Biotransformations in organic chemistry*, 4th Ed. Springer, Berlin Heidelberg New York; 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 and aldehyde reductions, or by use of 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; U.S. Patent Nos. 5,559,030; U.S. Patent No. 5,700,670 and U.S. Patent No. 5,891,685), reduction of dioxocarboxylic acids (*e.g.*, U.S. Patent No. 6,399,339), reduction of tert-butyl (*S*) chloro-5-hydroxy-3-oxohexanoate (*e.g.*, U.S. Patent No. 6,645,746 and WO 01/40450), reduction pyrrolotriazine-based compounds (*e.g.*, U.S. application No. 2006/0286646); reduction of substituted acetophenones (*e.g.*, U.S. 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 substrates to its corresponding chiral alcohol products.

4. SUMMARY

[0007] The present disclosure provides engineered ketoreductase ("KRED") enzymes that are capable of stereoselectively reducing a defined keto substrate to its corresponding alcohol product 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:98) or when compared with other engineered ketoreductase enzymes.

[0007a] In one aspect, there is provided a ketoreductase polypeptide derived from a wild-type Lactobacillus ketoreductase of SEQ ID NO: 2, 4, or 98 capable of stereoselectively reducing acetophenone to (S)-1-phenethanol, wherein the polypeptide has a proline residue at the residue corresponding to X190 of SEQ ID NO:2, 4 or 98.

[0007b] It is shown in the present disclosure

that naturally occurring ketoreductases from *Lactobacillus* species reduce the compound acetophenone to (*R*)-1-phenethanol. Since the wild-type enzymes are generally selective for reducing the acetophenone to their corresponding (*R*)-alcohols, these naturally occurring enzymes are (*R*)-selective ketoreductases, or (*R*)-ketoreductases. For substituted acetophenones, such as 2',6'-dichloro-3'-fluoroacetophenone, these wild-type *L. kefir* or *L. brevis or L. minor* ketoreductase enzymes display insignificant, if any, activity towards the substituted acetophenone substrate. However, the engineered ketoreductase enzymes of the present disclosure, which are derived from a wild-type *Lactobacillus* species ketoreductase, are capable of reducing acetophenone to (*S*)-1-

phenethanol. Hence, the ketoreductases described herein are characterized by reversed enantioselectivity as compared to the wild-type *L. kefir* or *L. brevis* or *L. minor* ketoreductases for the reduction of acetophenone. These polypeptides of the disclosure are consequently referred to as (*S*)-selective ketoreductases, or (*S*)-ketoreductases. The reversed enantioselectivity is based on mutating the residue at position 190 (*i.e.*, X190) of the wild type ketoreductase enzyme to a residue which is not tyrosine, preferably to a non-aromatic residue, and particularly to a proline residue.

[0008] Moreover, the engineered enzymes described herein can have one or more improved properties in addition to the altered stereoselectivity. For example, the engineered ketoreductase polypeptide can have increased enzymatic activity as compared to the wild-type ketoreductase enzyme for reducing the substrate to the product and/or further increases stereoselectivity for the (*S*) enantiomer. Improvements in enzyme properties can also include, among others, increases in thermostability, solvent stability, or reduced product inhibition. As further disclosed herein, while the wildtype ketoreductases show insignificant activity in reducing substituted acetophenones, the disclosure provides ketoreductases of capable of reducing or converting a substituted acetophenone, 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol.

[0009] Accordingly, in some embodiments, the present disclosure relates to ketoreductase polypeptides having at the residue corresponding to X190 of SEQ ID NO:2, 4 or 98 a residue which is not a tyrosine. In some embodiments, this residue is a non-aromatic residue, such as, for example, an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, this residue is proline.

[0010] In addition to the features at the residue corresponding to X190, 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 98. In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical as compared to a reference sequence based on SEQ ID NO: 2, 4 or 98 having at the residue corresponding to X190 a non-aromatic residue, including an aliphatic, constrained, non-polar, or cysteine residue, particularly alanine, isoleucine, cysteine, or proline, with the proviso that the ketoreductase polypeptide has at the residue corresponding to X190 a residue which is other than a tyrosine, particularly a non-aromatic residue. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is alanine, isoleucine, cysteine, or proline, particularly proline. In some embodiments, these residue differences results in an improved property, such as increased enzymatic activity for the substrate. The improved properties can be in reference to the wildtype ketoreductase enzyme or in reference to an engineered

ketoreductase enzyme. For example, in some embodiments, improvements in the ketoreductase enzymes are compared to the properties of the engineered enzyme having the amino acid sequence corresponding to SEQ ID NO:6, which is capable of converting the substrate to the product with a stereomeric excess greater than 99% with measurable activity, and therefore improved as compared to the wild-type *L. kefir* or *L. brevis or L. minor* ketoreductases. 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:95, 96 and 119 (or a region thereof, such as residues 90-211).

[0011] In some embodiments, the ketoreductase polypeptide of the disclosure are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric excess greater than 99% and at a rate that is improved over the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides that are improved over SEQ ID NO:6 with respect to enzymatic activity, include but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 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, and 94.

[0012] In some embodiments, the ketoreductase polypeptides are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric excess greater than 99% and at a rate that is improved over the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has improved thermostability as compared to the polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides having such improvements include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 16, 18, 20, 22, 26, 28, 30, 32, 34, 38, 40, 42, 44, 46, 54, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0013] In some embodiments, the ketoreductase polypeptides are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides capable of such an improvement include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 10, 14, 16, 18, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0014] In some embodiments, the ketoreductase polypeptides are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric

excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has an improved thermostability as compared to the polypeptide of SEQ ID NO:6. Exemplary polypeptides having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 16, 18, 22, 26, 28, 30, 32, 34, 38, 40, 42, 44, 46, 54, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0015] In some embodiments, the ketoreductase polypeptides are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric excess greater than 99% and at a rate that is at least about 1500% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides capable of such an improvement include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0016] In some embodiments, the ketoreductase polypeptide are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with a stereomeric excess greater than 99% and at a rate that is at least about 1500% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has an improved thermostability as compared to the polypeptide of SEQ ID NO:6. Exemplary polypeptides having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0017] In some embodiments, the ketoreductase polypeptide are capable of converting in less than about 24 hours at least about 95% of the 2', 6'-dichloro-3'-fluoroacetophenone substrate to (*S*)-1-(2,6-dichloro-3-fluorophenyl) ethanol, in at least about 99% stereomeric excess, when carried out with the polypeptide at an amount of less than about 1% by weight with respect to the amount of the 2', 6'-dichloro-3'-fluoroacetophenone substrate. Exemplary polypeptides that have this capability include, but are not limited to, polypeptides comprising amino acid sequences corresponding to 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0018] In some embodiments, the ketoreductase polypeptides are capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide is also capable, after a heat treatment of 50°C for 2 hours, of converting the substrate to the product at a rate that is at least

about 400% greater than the polypeptide having the sequence of SEQ ID NO:16 (where the polypeptide of SEQ ID NO:16 was also treated with the same heat treatment). Exemplary polypeptides having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0019] In some embodiments, the improved ketoreductase polypeptides capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol comprise a region or domain having 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 a region or domain corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 98 having at the residue corresponding to X190 a non-aromatic residue, including an aliphatic, constrained, non-polar, or cysteine residue, particularly alanine, isoleucine, cysteine, or proline, with the proviso that the ketoreductase polypeptide region or domain has at the residue corresponding to X190 a residue other than a tyrosine. In some embodiments, the ketoreductase polypeptide has a region or domain corresponding to residues 90-211 of the reference sequence in which the residue corresponding to X190 is a non-aromatic residue. In some embodiments, this residue corresponding to X190 can be an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, the residue corresponding to X190 can be alanine, isoleucine, cysteine, or proline, particularly proline. In some embodiments, the ketoreductase polypeptides can have one or more residue differences in the domain or region as compared to the reference sequence. Various residue positions that can differ from the reference sequence are provided in the detailed description.

[0020] The present disclosure also 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 encoding the engineered ketoreductases include, but are not limited to, polynucleotides comprising sequences corresponding 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, and 93.

In one aspect, there is provided a polynucleotide encoding a polypeptide as defined herein, wherein the polynucleotide is optionally selected from the group consisting of SEQ ID NO: 9, 13, 17, 19, 21, 23, 27, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 55, 57, 59, 61, 63, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, and 93. In another aspect, there is provided an expression vector comprising the polynucleotide as defined herein, operably linked to at least one control sequence suitable for directing expression in a host cell.

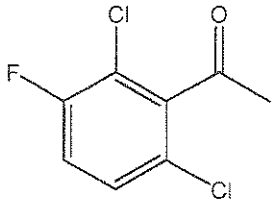
[0021] The present disclosure also provides host cells comprising the polynucleotides and/or expression vectors described herein. In one aspect, there is provided a host cell comprising the expression vector as defined herein. The host cells may be *L. kefir* or *L. brevis*, or they may be a different 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 substituted acetophenone substrates of formula (I) or (III) to the corresponding (*S*)-alcohol product of formula (II) or (IV), respectively.

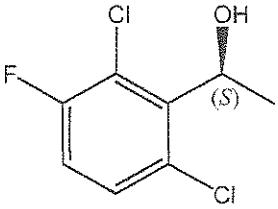
[0022] Whether carrying out the method with whole cells, cell extracts or purified ketoreductase enzymes, a single ketoreductase enzyme may be used or, alternatively, mixtures of two or more ketoreductase enzymes may be used.

[0023] As noted above, the ketoreductase enzymes described herein are capable of catalyzing the reduction reaction of a 2',6'-substituted acetophenone, which can be optionally substituted at one or more of the 3', 4', and 5' positions, to the corresponding (*S*)-alcohol product.

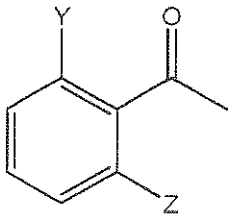
[0024] In some embodiments, the ketoreductase enzymes are capable of reducing or converting the ketone of structural formula (I), 2',6'-dichloro-3'-fluoroacetophenone:

(I) 

to the corresponding chiral alcohol product of structural formula (II), (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol:

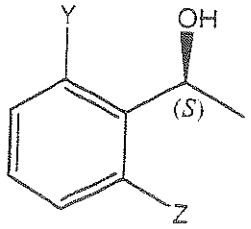
(II) 

[0025] In some embodiments, the ketoreductase enzymes described herein are capable of catalyzing the reduction of 2',6'-substituted acetophenone compounds of structural formula (III):

(III) 

optionally substituted at one or more of the 3', 4', and 5' positions, wherein Y and Z are independently selected from CH_3, CF_3, NH_2, OH, OCH_3, Cl, and Br, to the corresponding chiral alcohol product of structural formula (IV):

(IV)



[0026] Accordingly, in some embodiments, the disclosure provides a method for reducing a 2',6' substituted acetophenone substrate, optionally substituted at one or more of the 3', 4' and 5' positions, to the corresponding substituted (*S*)-phenethanol, where the method comprises contacting the substrate with the ketoreductases described herein under reaction conditions suitable for reducing or converting the substrate to the corresponding substituted (*S*)-phenethanol.

[0026a] In one aspect, there is provided a method for stereoselectively reducing a 2',6'-substituted acetophenone substrate, optionally substituted at one or more of 3', 4' and 5' positions, to the corresponding substituted (S)-1-phenethanol, which comprises contacting the substrate with the ketoreductase polypeptide as defined herein under reaction conditions suitable for stereoselectively reducing or converting the substrate to the corresponding (S)-alcohol product.

[0026b] In some embodiments of this method, the substrate is reduced to the product in greater than about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% stereomeric excess.

[0027] In some embodiments, the disclosure provides a method for reducing a 2',6' substituted acetophenone of formula (III) to the corresponding substituted (*S*)-phenethanol of formula (IV), where the method comprises contacting the substrate with the ketoreductases described herein under reaction conditions suitable for reducing or converting the substrate of formula (III) to the corresponding substituted (*S*)-phenethanol product of formula (IV). In some embodiments of this method, the substrate is reduced to the product in greater than about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% stereomeric excess.

[0028] In some embodiments, the disclosure provides a method for reducing a 2',6'-dichloro-3'-fluoroacetophenone substrate of formula (I) to its corresponding (*S*)-alcohol product of formula (II), (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol, where the method comprises contacting or incubating the 2', 6'-dichloro-3'-fluoroacetophenone with the ketoreductases described herein under reaction conditions suitable for reducing or converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-

dichloro-3-fluorophenyl]-ethanol. In some embodiments of this method, the substrate is reduced to the product in greater than about 85%, 90%, 95%, 99%, or 99.9% stereomeric excess. In some embodiments, the substrate is reduced to the product in greater than about 85% stereomeric excess, wherein the ketoreductase polypeptide comprises an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119. In some embodiments, the substrate is reduced to the product in greater than about 99% stereomeric excess, wherein the ketoreductase polypeptides used in the

method 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, 90, 92, and 94.

[0029] In some embodiment of this method, at least about 95% of the substrate is reduced to the product in greater than about 99% stereomeric excess in less than 24 hours when the method is carried out with the ketoreductase polypeptide at an amount of less than about 1% by weight with respect to the amount of the 2', 6'-dichloro-3'-fluoroacetophenone substrate, wherein the ketoreductase polypeptides comprise amino acid sequences that corresponds to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

In one aspect, there is provided a composition comprising a 2',6'-substituted acetophenone, optionally substituted at one or more of 3', 4' and 5' positions, and/or the corresponding substituted (S)-1-phenethanol, and a ketoreductase as defined herein, and wherein the substrate is optionally 2',6'-dichloro-3'-fluoroacetophenone of formula (I), and the corresponding substituted (S)-1-phenethanol is (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol of formula (II).

[0030] In some embodiments, the disclosure provides compositions of a ketoreductases described herein and a 2,6 substituted acetophenone, optionally substituted at one or more of 3', 4' or 5' positions, and/or the corresponding substituted (*S*)-phenethanol. In some embodiments, the compositions comprise a ketoreductase described herein and the compound of formula (I) and/or the compound of formula (II). In some embodiments, the compositions comprise a ketoreductase described herein and the compound of formula (III), and/or the compound of formula (IV). In some embodiments, the compositions comprise a ketoreductase described herein, and the compound of formula (V) and/or the compound of formula (VI). In some embodiments, the compositions can further comprise a cofactor regenerating system.

[0031] In some embodiments, the disclosure relates to use of the engineered ketoreductases in the synthesis of protein kinase inhibitors described in WO06021886, WO06021884, WO06021881, and WO04076412.

[0031a] In one aspect, there is provided a method for producing the protein tyrosine kinase inhibitor compound of structural formula (VII), including salts, hydrates and solvates thereof, which comprises a step of reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase polypeptide as defined herein under suitable reaction conditions.

[0031b] In one aspect, there is provided a method for producing the protein tyrosine kinase inhibitor compound of structural formula (VIII), including salts, hydrates and solvates thereof, which comprises a step of reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase

polypeptide as defined herein under suitable reaction conditions.

[0031c] In some embodiments, in a method for synthesis of these protein kinase inhibitors, a step in the method can comprise reducing or converting the substrate 2',6'-dichloro-3'-fluoroacetophenone of formula (I) to its corresponding (*S*)-alcohol product of formula (II), (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with the ketoreductases of the disclosure.

5. BRIEF DESCRIPTION OF THE FIGURES

[0032] FIG.1 illustrates the role of ketoreductases (KRED) in the conversion of the substrate compound of formula (I), 2',6'-dichloro-3-fluoroacetophenone, to the corresponding chiral alcohol product of formula (II), (*S*)-1-[2,6,-dichloro-3-fluorophenyl]-ethanol. In this reaction, the substrate is reduced biocatalytically to the corresponding (*S*)-alcohol. This reduction uses a KRED described herein and a co-factor such as NADPH. A glucose dehydrogenase (GDH) is used to covert/recycle $NADP^+$ to NADPH. Glucose is converted to gluconic acid, which in turn is converted to its sodium salt (sodium gluconate) with the addition of sodium hydroxide.

6. DETAILED DESCRIPTION

6.1 Definitions

[0033] As used herein, the following terms are intended to have the following meanings.

[0034] "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.

[0035] "Coding sequence" refers to that portion of a nucleic acid (*e.g.*, a gene) that encodes an amino acid sequence of a protein.

[0036] "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.

[0037] "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.

[0038] "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.

[0039] "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.

[0040] 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.

[0041] "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.

[0042] "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.

[0043] "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.

[0044] "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 [major enantiomer − minor enantiomer]/[major enantiomer + minor enantiomer]. This can also be referred to as stereomeric excess (s.e). 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.

[0045] "Highly stereoselective" refers to a ketoreductase polypeptide that is capable of converting or reducing 2',6'-dichloro-3'-fluoroacetophenone (formula (I)) to the corresponding (*S*)-alcohol product (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol (formula (II)) with at least about 85% stereomeric excess.

[0046] "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, pH activity profile, cofactor requirements, refractoriness to inhibitors (*e.g.*, product inhibition), stereospecificity, and stereoselectivity (including stereoselectivity).

[0047] "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 (see Example 5) 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.

[0048] "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.

[0049] "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.

[0050] "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 (isopropyl alcohol, 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.

[0051] "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.

[0052] "Thermo- and solvent stable" refers to a ketoreductase polypeptide that are both thermostable and solvent stable.

[0053] "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: 38 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.

[0054] "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).

[0055] "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).

[0056] "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).

[0057] "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).

[0058] "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).

[0059] "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).

[0060] "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.

[0061] "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).

[0062] "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).

[0063] "Cysteine" The amino acid 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.

[0064] "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).

[0065] "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).

[0066] "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. In some embodiments, conservative mutations as used herein 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.

[0067] 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

[0068] "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.

[0069] "Deletion" refers to modification to the polypeptide by removal of one or more amino acids from the reference polypeptide. Deletions in an amino acid sequence can comprise removal of 1 or more amino acids, 2 or more amino acids, 3 or more amino acids, 4 or more amino acid, 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 15% of the total number of amino acids, or up to 20% of the total number of amino acids making up the reference enzyme 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.

[0070] "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.

[0071] "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.

[0072] "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.

[0073] "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.

[0074] "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.

[0075] "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.

[0076] "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.

[0077] "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.

[0078] "Preferred, optimal, 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 multivariat 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).

[0079] "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 a polynucleotide of interest, *e.g.*, the coding region of the nucleic acid sequence encoding a polypeptide.

[0080] "Operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to a polynucleotide sequence (*i.e.*, in a functional relationship) such that the control sequence directs the expression of the polynucleotide and/or a polypeptide encoded by the polynucleotide.

[0081] "Promoter sequence" is a nucleic acid sequence that is recognized by a host cell for expression of a polynucleotide. The control sequence may comprise an appropriate promoter sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polynucleotide. 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

[0082] The present disclosure provides engineered ketoreductase ("KRED") enzymes that are capable of stereoselectively reducing a defined keto substrate to its corresponding alcohol product and having an improved property when compared with the naturally-occurring, wild-type KRED enzyme obtained from *L. kefir* (SEQ ID NO:2) or *L. brevis* (SEQ ID NO:4) or *L. minor* (SEQ ID NO:98) or when compared with other engineered ketoreductase enzymes. As shown in the present disclosure, the wild-type *L. kefir* or *L. brevis or L. minor* ketoreductase enzymes have very little activity, if any for the reduction of 2',6'-dichloro-3'-fluoroacetophenone (*See* the Examples). With less substituted acetophenone substrates for which the wild-type enzymes have greater activity, the wild-type enzymes are generally selective for reducing the acetophenones to their corresponding (*R*)-alcohols. Wild-type *Lactobacillus* species ketoreductases reduce the prototypical reference compound acetophenone to (*R*)-1-phenethanol and are consequently referred to as (*R*)-selective ketoreductases, or (*R*)-ketoreductases. However, the engineered ketoreductase enzymes of the disclosure, derived from a wild-type *Lactobacillus* species ketoreductase enzyme, reduce acetophenone to (*S*)-1-phenethanol, and are consequently referred to as (*S*)-selective ketoreductases, or (*S*)-ketoreductases. Hence, the improved ketoreductase polypeptides of the disclosure are capable of a reversed enantioselectivity for the reduction of acetophenones as compared to the wild-type *L. kefir* or *L. brevis* or *L. minor* ketoredutases. This reversed enantioselectivity is based on mutating the residue at position 190 of the wild type enzyme, preferably to a non-aromatic residue, particularly to a proline residue. Without being bound by theory, the wild-type tyrosine residue at position 190 appears to clash with the substrate in the pro-*S* conformation. Thus, in some embodiments, the ketoreductase polypeptides of the disclosure have at the residue corresponding to position 190 of SEQ ID NO:2 or 4 or 98 a residue which is not a tyrosine. Preferably, this residue is a non-aromatic residue, such as, for example, an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, this residue is proline.

[0083] In some embodiments, as noted above, the engineered ketoreductase with improved enzyme properties are describe in reference to *Lactobacillus kefir* ketoreductase of SEQ ID NO:4 or

Lactobacillus brevis ketoreductase of SEQ ID NO:2 or *Lactobacillus minor* ketoreductase of SEQ ID NO:98. 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". A substitution mutation, which is a replacement of an amino acid residue in a reference sequence, for example the wildtype ketoreductases of SEQ ID NO:2 and SEQ ID NO:4 and SEQ ID NO:98, 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 16 of SEQ ID NO:2 can be mutated "to a" polar 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 16 of SEQ ID NO:2 is a polar residue, threonine, but it can be mutated to a different polar residue, for example, the mutation can be a "T16S" (16→S) mutation.

[0084] The naturally occurring polynucleotide encoding 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 isolated 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:97 for Lactobacillus minor).

[0085] In some embodiments, the improved property (as compared to wild-type or another engineered polypeptide) of the ketoreductase polypeptide is with respect to an increase of its stereoselectivity for reducing or converting a substituted acetophenone substrate of formula (III) to its corresponding (S)-alcohol product of formula (IV). In some embodiments, the improved property of the ketoreductase property is with respect to an increase in stereoselectivity in reducing 2'6'-dichloro-3-fluoroacetophenone to (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol. In some embodiments, the improved property of the ketoreductase polypeptide is with respect to an increase in its rate of conversion of the substrate to 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.

[0086] 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) to result in the 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.

[0087] 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.

[0088] In some embodiments, the ketoreductase polypeptides herein comprise an amino acid sequence that is at least about 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 98 having at the residue corresponding to X190 a non-aromatic residue (*e.g.*, an aliphatic, constrained, non-polar,

or cysteine residue), preferably alanine, isoleucine, cysteine, or proline, particularly a proline, with the proviso that the ketoreductase polypeptide has at the residue corresponding to X190 a residue which is other than a tyrosine, particularly a non-aromatic residue. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, the ketoreductase has an amino acid sequence in which the residue corresponding to X190 is alanine, isoleucine, cysteine, or proline, particularly proline. 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 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 or about 1-40 residue differences at other amino acid residues 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 or about 40 residue differences at other amino acid residues as compared to the reference sequence.

[0089] In some embodiments, these stereoselective or highly stereoselective (herein, capable of reducing the substrate to the product with an e.e. that is at least about 85%) ketoreductase polypeptides comprise an amino acid sequence that corresponds to the sequence formulas as laid out in SEQ ID NO: 95, 96 and 119 (or a region or domain thereof, such as residues 90-211). SEQ ID NO:95 is based on the wild-type amino acid sequence of the Lactobacillus brevis ketoreductase (SEQ ID NO:2); SEQ ID NO:96 is based on the wild-type amino acid sequence of the Lactobacillus kefir ketoreductase (SEQ ID NO:4); and SEQ ID NO:119 is based on the wild-type amino acid sequence of the Lactobacillus minor ketoreductase (SEQ ID NO:98). The ketoreductase based on the sequence formula of SEQ ID NO: 95, 96, or 119 specify that the residue corresponding to X190 is a non-aromatic residue. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is alanine, isoleucine, cysteine, or proline. In some embodiments, the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X190 is proline.

[0090] In some embodiments, the ketoreductase polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, having the specified features for residue X190 as described herein, can further include one or more of the features selected from the following: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, acidic or basic residue; residue corresponding to X16 is a polar residue;

residue corresponding to X43 is a nonpolar or polar residue; residue corresponding to X60 is an aromatic, non-polar, or aliphatic residue; residue corresponding to X94 is a cysteine, non-polar or aliphatic residue; residue corresponding to X95 is a non-polar or aliphatic residue; residue corresponding to X96 is a polar or acidic residue; residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue; residue corresponding to X120 is an aromatic, non-polar or aliphatic residue; residue corresponding to X125 is a polar or non-polar residue; residue corresponding to X142 is a polar residue; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue; residue corresponding to X149 is a non-polar or aromatic residue; residue corresponding to X150 is a constrained or acidic residue; residue corresponding to X152 is a non-polar or polar residue; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue; residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue; residue corresponding to X205 is a basic, nonpolar or aliphatic residue; and residue corresponding to X206 is a non-polar or aromatic residue. In some embodiments, the amino acid sequence can have two, three, four, five, six or more of the features. In some embodiments, the polypeptides comprising an amino acid sequence that corresponds to the sequence formula provided in SEQ ID NO: 95, 96, or 119 (or region thereof) can have additionally one or more of the residues not specified by an X to be mutated as compared to the reference sequence of SEQ ID NO: 2, 4 or 98. In some embodiments, the mutations can be 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 mutations at other amino acid residues not defined by X above. In some embodiments, the number of mutations 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 other amino acid residues. In some embodiments, the mutations comprise conservative mutations.

[0091] In some embodiments, the polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, 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 98. Exemplary conservative mutations include amino acid replacements such as, but not limited to: replacement of residue corresponding to X16 threonine (T) with another polar residue, *e.g.*, asparagine, glutamine, or serine; replacement of residue corresponding to X43 valine with another non-polar or aliphatic residue, *e.g.*, isoleucine; replacement of residue corresponding to X60 with an aliphatic or aromatic residue, *e.g.*, alanine; replacement of residue corresponding to X94 alanine (A) with another non-polar or aliphatic residue, *e.g.*, valine, leucine, or isoleucine; replacement of residue corresponding to X95 valine (V) with another non-polar or aliphatic residue, *e.g.*, alanine, leucine, or isoleucine; replacement of residue corresponding to X96 serine (S) with another polar residue, *e.g.*, asparagine, glutamine, or threonine; replacement of residue corresponding to X142 serine (S) with

another polar residue, *e.g.*, serine or asparagine; replacement of residue corresponding to X196 valine (V) with another non-polar or aliphatic residue, *e.g.*, alanine, leucine, or isoleucine; and replacement of residue corresponding to X205 alanine (A) with another non-polar or aliphatic residue, *e.g.*, valine, leucine, or isoleucine.

[0092] In some embodiments, the ketoreductase polypeptides comprising an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, having the specified features for residue X190 as described herein, can further include one or more features selected from the following: residue corresponding to X7 is tryptophan, tyrosine, phenylalanine, proline, histidine, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, asparagine, arginine, or lysine, particularly glycine, histidine, threonine, proline, tryptophan, arginine, histidine, or asparagine; residue corresponding to X16 is serine, threonine, asparagine, or glutamine, particularly serine; residue corresponding to X43 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly isoleucine; residue corresponding to X60 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine; residue corresponding to X94 is cysteine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine, valine or cysteine; residue corresponding to X95 is glycine, methionine, alanine, valine, leucine, isoleucine, particularly isoleucine or leucine; residue corresponding to X96 is aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine, particularly serine, asparagine, threonine or glutamic acid; residue corresponding to X97 is serine, threonine, asparagine, glutamine, glycine, methionine, alanine, valine, leucine, isoleucine, lysine or arginine, particularly lysine, threonine, valine, arginine, methionine, or isoleucine; residue corresponding to X120 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly phenylalanine or valine; residue corresponding to X125 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glycine or serine; residue corresponding to X142 is a serine, threonine, asparagine, or glutamine residue, particularly asparagine; residue corresponding to X147 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, asparagine, or glutamine, particularly phenylalanine, leucine, isoleucine, valine, or glutamine; residue corresponding to X149 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, or tryptophan, particularly glycine or phenylalanine; residue corresponding to X150 is proline, histidine, aspartic acid, or glutamic acid, particularly aspartic acid or histidine; residue corresponding to X152 is glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, asparagine, or glutamine, particularly serine, threonine, or methionine; residue corresponding to X196 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly

valine, isoleucine, methionine, phenylalanine, or isoleucine; residue corresponding to X202 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine, tryptophan, tyrosine, or methionine; residue corresponding to X205 is lysine, arginine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly arginine; and residue corresponding to X206 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, tryptophan, particularly methionine or tyrosine. In some embodiments, the amino acid sequence can have two, three, four, five, six or more of the features. In some embodiments, the polypeptides comprising an amino acid sequence that corresponds to the sequence formulas provided in SEQ ID NO: 95, 96, or 119 (or region thereof) can have additionally one or more of the residues not specified by an X to be mutated as compared to the reference sequence of SEQ ID NO: 2, 4 or 98. In some embodiments, the mutations can be 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 mutations at other amino acid residues not defined by X above. In some embodiments, the number of mutations 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 other amino acid residues. In some embodiments, the mutations comprise conservative mutations.

[0093] In some embodiments, a stereoselective ketoreductase polypeptide comprising an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine, and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0094] In some embodiments, a stereoselective ketoreductase polypeptide comprising an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have

additionally one or more or at least all of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or arginine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0095] In some embodiments, a stereoselective ketoreductase polypeptide comprising an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or arginine; residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue, particularly methionine, valine, isoleucine, threonine, or arginine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0096] In some embodiments, a stereoselective ketoreductase polypeptide comprising an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X94 is a cysteine, non-polar or an aliphatic residue, particularly cysteine or valine; residue corresponding to X96 is a polar or acidic residue, particularly threonine; and residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0097] In some embodiments, a stereoselective ketoreductase polypeptide comprising an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or arginine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly valine, isoleucine, methionine, phenylalanine, or isoleucine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0098] In some embodiments, a stereoselective ketoreductase polypeptide comprises an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly valine, isoleucine, methionine, phenylalanine, or isoleucine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue. 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 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0099] In some embodiments, a stereoselective ketoreductase polypeptide comprises an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119, or a region thereof, such as residues 90-211, having the features at residue corresponding to X190 as described herein, can have additionally one or more or at least all of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or arginine; residue corresponding to X96 is a polar or acidic residue, particularly threonine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly valine, isoleucine, methionine, phenylalanine, or isoleucine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0100] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0101] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X16 is a 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0102] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X43 is a non-polar or aliphatic residue, particularly 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0103] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X60 is an aromatic, 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0104] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue

corresponding to X94 is a cysteine, non-polar or an aliphatic residue, particularly cysteine 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0105] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X95 is a non-polar or aliphatic residue, particularly 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0106] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X96 is a polar or acidic residue, particularly threonine or glutamic 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or

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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0107] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue, particularly methionine, valine, isoleucine, threonine, or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0108] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X120 is an aromatic, 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0109] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X125 is a polar 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0110] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X142 is a polar 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0111] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0112] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X149 is a non-polar or aromatic residue, particularly phenylalanine. 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 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0113] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue

corresponding to X150 is a constrained or acidic 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0114] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X152 is a non-polar or polar 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0115] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0116] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0117] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X205 is a basic, nonpolar or aliphatic residue, particularly arginine 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0118] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and the residue corresponding to X206 is non-polar or 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 residues as compared to the reference sequence of SEQ ID NO:2, 4 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0119] In some embodiments, an improved ketoreductase polypeptide of the disclosure comprises an amino acid sequence that has any one of the set of mutations listed in Table 2 below. 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 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, 90, 92, and 94, wherein the ketoreductase polypeptide amino acid sequence includes any one set of the substitution combinations listed in Table 2. 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 residues 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.

[0120] In some embodiments, the improved ketoreductase polypeptide 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,

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, and 94.

[0121] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline, and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:8, 10, 14, 16, 24, 26 or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:8, 10, 14, 16, 24, 26 or 48)

[0122] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X125 is a polar or non-polar residue, particularly serine; and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:52. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:52).

[0123] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X95 is a non-polar or aliphatic residue, particularly leucine or isoleucine; and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:20, 62, or 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:20, 62, or 64).

[0124] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X206 is a non-polar or 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, 1-25, 1-30, 1-35 or about 1-40 residue differences at other residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:36. 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 with 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 to a

reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:36).

[0125] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, tryptophan, proline, threonine, or arginine; and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:54 or 56. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:54 or 56).

[0126] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:22, 66, 68, or 72. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:22, 66, 68, or 72).

[0127] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:28, 30, or 32. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:28, 30, or 32).

[0128] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X152 is a non-polar or polar residue, particularly methionine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X205 is a basic, nonpolar or aliphatic residue, particularly arginine 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, 1-25, 1-30, 1-35 or about 1-40 residue differences at other residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:20. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:20).

[0129] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X43 is a non-polar or aliphatic residue, particularly isoleucine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:70. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:70).

[0130] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X94 is a cysteine, non-polar or an aliphatic residue, particularly cysteine or valine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X205 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, 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, 1-25, 1-30, 1-35 or about 1-40 residue differences at other residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the

preceding features, such as SEQ ID NO:34. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:34).

[0131] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue, particularly arginine, valine, methionine, threonine, or isoleucine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; and residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:74. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:74).

[0132] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or

phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:40, 76, 78, 80, or 82. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:40, 76, 78, 80, or 82).

[0133] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X94 is a cysteine, non-polar or an aliphatic residue, particularly cysteine or valine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:42. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:42).

[0134] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X94 is a cysteine, non-polar or an aliphatic residue, particularly cysteine or valine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X149 is a non-polar or aromatic residue, particularly phenylalanine; residue corresponding to X150 is a constrained or acidic residue, particularly histidine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as 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 differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:84).

[0135] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X96 is a polar or acidic residue, particularly threonine or glutamic acid; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:44 or 46. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:44 or 46).

[0136] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211, in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X96 is a polar or acidic residue, particularly threonine or glutamic acid; residue corresponding to X120 is an aromatic, non-polar or aliphatic residue, particularly valine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:86. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:86).

[0137] In some embodiments, an improved ketoreductase comprises an amino acid sequence based on the sequence formula of SEQ ID NO: 95, 96, or 119, or a region thereof, such as residues 90-211,

in which the amino acid sequence has at least the following features: residue corresponding to X190 is an non-aromatic residue, particularly alanine, isoleucine, cysteine, or proline; residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly histidine, threonine, proline, tryptophan or arginine; residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue, particularly valine, methionine, threonine, or isoleucine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, leucine, or isoleucine; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue, particularly methionine, isoleucine, leucine, or phenylalanine; and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly methionine, tyrosine, or tryptophan. 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 residue positions as compared to a reference sequence of SEQ ID NO:2, 4 or 98 with the preceding features, such as SEQ ID NO:88, 90, 92 or 94. 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 with 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 to a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features (*e.g.*, SEQ ID NO:88, 90, 92 or 94).

[0138] 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: 95, 96, or 119 in which the residue corresponding to X190 is not tyrosine. 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 a non-aromatic residue, such as an aliphatic, constrained, non-polar, or cysteine 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 alanine, isoleucine, cysteine, or proline, particularly proline. 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 corresponding domain of a reference sequence based on SEQ ID NO: 2, 4, or 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, 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 corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96, or 119 in which the residue corresponding to X190 has at least the preceding features, and wherein the amino acid sequence of the domain or region has at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence corresponding to residues 90-211 of a reference sequence based on SEQ ID NO:2, 4 or 98 with the preceding features.

[0139] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96 or 119 and having the specified features at residue corresponding to X190 as described herein, can further include in the region or domain one or more of the features selected from the following: residue corresponding to X94 is a cysteine, non-polar or an aliphatic residue; residue corresponding to X95 is a non-polar or aliphatic residue; residue corresponding to X96 is a polar or acidic residue; residue corresponding to X97 is a polar, non-polar, aliphatic, or basic residue; residue corresponding to X120 is an aromatic, non-polar or aliphatic residue; residue corresponding to X125 is a polar or non-polar residue; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue; residue corresponding to X149 is a non-polar or aromatic residue; residue corresponding to X150 is a constrained or acidic residue; residue corresponding to X152 is a non-polar or polar residue; residue corresponding to X196 is an aliphatic, non-polar, or aromatic residue; residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue; residue corresponding to X205 is a basic, nonpolar or aliphatic residue; and residue corresponding to X206 is non-polar or aromatic 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 as compared to the corresponding domain of a reference sequence based on SEQ ID NO:2, 4 or 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, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations.

[0140] 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: 95, 96 or 119, 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 98. Examples of such conservative mutations include amino acid replacements such as, but limited to: replacement of residue corresponding to X94 alanine (A) with another non-polar or aliphatic residue, *e.g.*, valine, leucine, or isoleucine; replacement of residue corresponding to X95 valine (V) with another non-polar or aliphatic residue, *e.g.*, alanine, leucine, or isoleucine; replacement of residue

corresponding to X96 serine (S) with another polar residue, *e.g.*, asparagine, glutamine, or threonine; replacement of residue corresponding to X196 valine (V) with another non-polar or aliphatic residue, *e.g.*, alanine, leucine, or isoleucine; and replacement of residue corresponding to X205 alanine (A) with another non-polar or aliphatic residue, *e.g.*, valine, leucine, or isoleucine.

[0141] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96 or 119 and having the specified features at residue corresponding to X190 as described herein, can further include in the region or domain one or more of the features selected from the following: residue corresponding to X94 is cysteine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine, valine or cysteine; residue corresponding to X95 is glycine, methionine, alanine, valine, leucine, isoleucine, particularly isoleucine or leucine; residue corresponding to X96 is aspartic acid, glutamic acid, serine, threonine, asparagine, or glutamine, particularly serine, asparagine, threonine or glutamic acid; residue corresponding to X97 is serine, threonine, asparagine, glutamine, glycine, methionine, alanine, valine, leucine, isoleucine, lysine or arginine, particularly lysine, threonine, valine, arginine, methionine, or isoleucine; residue corresponding to X120 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly phenylalanine or valine; residue corresponding to X125 is glycine, methionine, alanine, valine, leucine, or isoleucine, particularly glycine or serine; residue corresponding to X142 is a serine, threonine, asparagine, or glutamine residue, particularly asparagine; residue corresponding to X147 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, asparagine, or glutamine, particularly phenylalanine, leucine, isoleucine, valine, or glutamine; residue corresponding to X149 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, or tryptophan, particularly glycine or phenylalanine; residue corresponding to X150 is proline, histidine, aspartic acid, or glutamic acid, particularly aspartic acid or histidine; residue corresponding to X152 is glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, asparagine, or glutamine, particularly serine, threonine, or methionine; residue corresponding to X196 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly valine, isoleucine, methionine, phenylalanine, or isoleucine; residue corresponding to X202 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine, tryptophan, tyrosine, or methionine; residue corresponding to X205 is lysine, arginine, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly arginine; and residue corresponding to X206 is glycine, methionine, alanine, valine, leucine, isoleucine, tyrosine, phenylalanine, tryptophan, particularly methionine or tyrosine. 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 as compared to the corresponding domain of a reference sequence based on SEQ ID NO:2, 4 or 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, or about 20 residue differences at other amino acid residues in the domain. In some embodiments, the differences comprise conservative mutations.

[0142] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96 or 119 and having the specified features at residue corresponding to X190 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 X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine, and residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or tyrosine. 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 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, 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 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 98 with the preceding features.

[0143] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96 or 119 and having the specified features at residue corresponding to X190 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 X97 is a polar, non-polar, aliphatic, or basic residue, particularly methionine, valine, isoleucine, threonine, or arginine; residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine; residue corresponding to X202 is an aliphatic, aromatic, or a non-polar residue, particularly tryptophan, methionine, or tyrosine. 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 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, 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 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 98 with the preceding features.

[0144] In some embodiments, the ketoreductase polypeptide with a domain or region corresponding to residues 90-211 of the sequence formula of SEQ ID NO:95, 96 or 119 and having the specified features at residue corresponding to X190 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, non-polar or an aliphatic residue, particularly cysteine or valine; residue corresponding to X96 is a polar or acidic residue, particularly threonine; and residue corresponding to X147 is an aromatic, polar, non-polar, or aliphatic residue, particularly glutamine, isoleucine, or leucine. 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 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, 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 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 98 with the preceding features.

[0145] In some embodiments, the ketoreductase polypeptide can further include a region or domain corresponding to residues 1-89 of the sequence formula of SEQ ID NO:95, 96, or 119. In some embodiments, the region or domain corresponding to residues 1-89 can have one or more of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue; residue corresponding to X16 is a polar residue; residue corresponding to X43 is a nonpolar or polar residue; and residue corresponding to X60 is an aromatic or non-polar, or aliphatic residue.

[0146] In some embodiments, the domain or region corresponding to residues 1-89 can have at least 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence corresponding to residues 1-89 of a reference sequence based on SEQ ID NO:2, 4, or 98 having at the residue corresponding to X7 an aromatic, non-polar, polar, constrained,

or basic residue, particularly a histidine, with the proviso that the region or domain of the ketoreductase polypeptide has an amino acid sequence in which the residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue, particularly a histidine. 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 residues as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 98. 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 polypeptide comprises an amino acid sequence with 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 98 with the preceding features.

[0147] In some embodiments, the region or domain corresponding to residues 1-89 can have one or more or at least all of the following features: residue corresponding to X7 is an aromatic, non-polar, polar, constrained, or basic residue; residue corresponding to X16 is a polar residue; residue corresponding to X43 is a nonpolar or polar residue; and residue corresponding to X60 is an aromatic or non-polar, or aliphatic residue. 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 residues as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 98. 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 residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 98 with the preceding features.

[0148] In some embodiments, the region or domain corresponding to residues 1-89 can have one or more or at least all of the following features: residue corresponding to X7 is tryptophan, tyrosine, phenylalanine, proline, histidine, glycine, methionine, alanine, valine, leucine, isoleucine, serine, threonine, glutamine, asparagine, arginine, or lysine, particularly glycine, histidine, threonine, proline, tryptophan, arginine, histidine, or asparagine; residue corresponding to X16 is serine, threonine, asparagine, or glutamine, particularly serine; residue corresponding to X43 is glycine, methionine,

alanine, valine, leucine, or isoleucine, particularly isoleucine; and residue corresponding to X60 is tyrosine, phenylalanine, tryptophan, glycine, methionine, alanine, valine, leucine, or isoleucine, particularly alanine. 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 residues as compared to the domain of a reference sequence based on SEQ ID NO:2, 4 or 98. 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 residues in the domain. In some embodiments, the differences comprise conservative mutations. In some embodiments, the ketoreductase polypeptide comprises an amino acid sequence with 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 98 with the preceding features.

[0149] Table 2 below provides a list of some of the SEQ ID NOs disclosed herein with associated activity levels with respect to reduction of substituted acetophenones. All sequences below are derived from the wild-type *L. kefir* ketoreductase sequences (SEQ ID NO: 3 and 4) unless otherwise specified.

[0150] Table 2: List of Sequences

Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO.	Polypeptide Residue Substitutions as Compared to SEQ ID NO: 4	Activity	Stability
3	4	None. (Wild-type *L. kefir* sequence)	-	-
5	6	Y190C	+	-
7	8	Y190A; V196I;	++	+
9	10	Y190P; V196I;	++	
11	12	K97R; Y190C;	+	
13	14	Y190P; V196L	++	
15	16	Y190A; V196L	++	+
47	48	Y190P; V196M;	+	
49	50	Y190P; V196F;	+	
51	52	G125S; Y190P; V196L;	+	
19	20	V95I; Y190P; V196I;	+	+
17	18	T152M; Y190P; V196I; M205R;	+++	+
23	24	Y190P; V196L; (as compared to SEQ ID NO:2)	++	

Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO.	Polypeptide Residue Substitutions as Compared to SEQ ID NO: 4	Activity	Stability
25	26	Y190A; V196L; (as compared to SEQ ID NO:2)	++	+
35	36	Y190P; V196L; M206Y;	+++	
53	54	G7N; Y190A; V196L;	++	+
55	56	G7H; Y190P; V196L;	++	
61	62	V95L; Y190P; V196L;	++	
63	64	V95I; Y190P; V196L;	++	
57	58	T16S; Y190P; V196L;	++	
59	60	Y190P; V196L	++	
21	22	F147L; Y190P; V196L;	++	++
65	66	F147Q; Y190A; V196L;	++	+
67	68	F147I; Y190P; V196L;	++	++
69	70	V43I; F147L; Y190P; V196L;	++	++
71	72	F147L; Y190A; V196L;	++	++
31	32	Y190P; V196L; A202W;	+++	+
27	28	Y190P; V196L; A202M;	++	+
29	30	Y190A; V196L; A202Y;	++	+
33	34	A94V; Y190A; V196L; M205V;	+++	+
73	74	K97R; F147I; Y190P; V196L;	+++	+
37	38	F147L; Y190P; V196L; A202W;	+++	++
39	40	G7H; F147L; Y190P; V196L; A202W;	+++	++
75	76	G7T; F147L; Y190P; V196L; A202W;	+++	++
77	78	G7P; F147L; Y190P; V196L; A202W;	+++	++
79	80	G7W; F147L; Y190P; V196L; A202W;	+++	++
81	82	G7R; F147L; Y190P; V196L; A202W;	+++	++
83	84	G7H; A94C; F147L; G149F; D150H; Y190P; V196L; A202W;	+++	++
41	42	G7H; A94V; F147L; Y190P; V196L; A202W;	+++	++
43	44	G7H; S96E; F147L; Y190P; V196L; A202W;	+++	++
85	86	G7H; S96T; F120V; F147L; Y190P; V196L; A202W;	+++	++
45	46	G7H; S96T; F147L; Y190P; V196L; A202W;	+++	++
87	88	G7H; K97V; F147L; Y190P; V196L; A202W;	+++	++

Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO.	Polypeptide Residue Substitutions as Compared to SEQ ID NO: 4	Activity	Stability
89	90	G7H; K97M; F147L; Y190P; V196L; A202W;	+++	++
91	92	G7H; K97T; F147L; Y190P; V196L; A202W;	+++	++
93	94	G7H; K97I; F147L; Y190P; V196L; A202W;	+++	++

[0151] In Table 2 above, in the activity column, a single plus "+" indicates an activity improvement of 100-450% of the activity of SEQ ID NO:6, two pluses "++" indicates an activity improvement of 450-1500% of SEQ ID NO:6, and three pluses "+++" indicates an activity improvement of greater than 1500% of SEQ ID NO:6. In the stability column, a single plus "+" indicates that the polypeptide exhibits measurable activity after heat treatment of 2 hours at 50°C, two pluses "++" indicates that the polypeptide has greater than 400% improvement in activity as compared to SEQ ID NO:16 when comparing activity for both proteins after heat treatment of 2 hours at 50°C.

[0152] In some embodiments, the ketoreductase polypeptides of the disclosure are improved as compared to an engineered KRED enzyme having (*S*) selectivity, *e.g.*, SEQ ID NO:6, with respect to their rate of enzymatic activity, for example, their rate of converting the substrate to the product. The polypeptide having the sequence of SEQ ID NO:6 is used herein as a reference polypeptide because the wild-type *L. kefir* or *L. brevis* KRED do not exhibit appreciable activity for converting 2', 6'-dichloro-3'-fluoroacetophenone to (S)-1-[2,6-dichloro-3-fluorophenyl]-ethanol. 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, or 300-fold over the rate of SEQ ID NO:6. In some embodiments, the ketoreductase polypeptides are capable of converting the substrate to the product at a rate that is at least 100%, 150%, 200%, 250%, 300%, 400%, 450%, 500%, 750%, 1000%, 1250%, or 1500% of the rate of SEQ ID NO:6.

[0153] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is improved over the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides that are improved over SEQ ID NO:6 with respect to enzymatic activity, include but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 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, and 94.

[0154] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with

an stereomeric excess greater than 99% and at a rate that is improved over the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has improved thermostability as compared to the polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides having such improvements include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 16, 18, 20, 22, 26, 28, 30, 32, 34, 38, 40, 42, 44, 46, 54, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0155] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides capable of such an improvement include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 10, 14, 16, 18, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0156] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has an improved thermostability as compared to the polypeptide of SEQ ID NO:6. Exemplary polypeptides having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 8, 16, 18, 22, 26, 28, 30, 32, 34, 38, 40, 42, 44, 46, 54, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0157] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 1500% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6. Exemplary polypeptides capable of such an improvement include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0158] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2', 6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 1500% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide also has an improved thermostability as compared to the polypeptide of SEQ ID NO:6. Exemplary polypeptides

having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0159] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting in less than about 24 hours at least about 95% of the 2',6'-dichloro-3'-fluoroacetophenone substrate to (*S*)-1-(2,6-dichloro-3-fluorophenyl) ethanol, in at least about 99% stereomeric excess, when carried out with the polypeptide at an amount of less than about 1% by weight with respect to the amount of the 2',6'-dichloro-3'-fluoroacetophenone substrate. Exemplary polypeptides that have this capability include, but are not limited to, polypeptides comprising amino acid sequences corresponding to 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0160] In some embodiments, the ketoreductase polypeptide of the disclosure is capable of converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol with an stereomeric excess greater than 99% and at a rate that is at least about 450% greater than the ketoreductase polypeptide having the sequence of SEQ ID NO:6, wherein the polypeptide is also capable, after a heat treatment of 50°C for 2 hours, of converting the substrate to the product at a rate that is at least about 400% greater than the polypeptide having the sequence of SEQ ID NO:16 (where the polypeptide of SEQ ID NO:16 was also treated with the same heat treatment). Exemplary polypeptides having such properties include, but are not limited to, polypeptides comprising amino acid sequences corresponding to SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0161] In some embodiments, the ketoreductase polypeptide is capable of stereoselectively reducing the substrate to the product with a percent e.e. that is at least about 99%, where the polypeptide comprises an 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, or 94.

[0162] In some embodiments, the ketoreductase polypeptide is capable of stereoselectivity reducing a 2',6'-dichloro-3-fluoroacetophenone to (*S*)-1-(2,6-dichloro-3-fluorophenyl) ethanol with a percent stereomeric excess of at least about 25%, 50%, 75%, 80%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9%, or 99.99%.

[0163] In some embodiments, the 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 98, or a region or domain thereof, such as residues 90-211, with the proviso that the residue corresponding to residue X190 is not tyrosine, particularly a non-

aromatic residue, and where the polypeptide is capable of reducing the substrate to the product with at least about 85% e.e. In some embodiments, the residue corresponding to X190 is an aliphatic, constrained, non-polar, or cysteine residue. In some embodiments, the residue corresponding to X190 is proline, and additionally has one or more of the following substitutions such that the polypeptide is further improved (with respect to stereoselectivity, enzymatic activity, and/or thermostability) over the wild-type *L. kefir* ketoreductase or another engineered ketoreductase: 7→H,T,P,W,R,N (*i.e.*, the residue corresponding to residue 7 of SEQ ID NO:2, 4, or 98 is substituted to histidine, threonine, proline, tryptophan, arginine, or asparagine); 16→S; 43→I; 60→A; 94→C,V; 95→I,L; 96→E,T; 97→R,V,M,T,I; 120→V; 125→S; 142→N; 147→L,Q,I,V; 149→F; 150→H; 152→H; 196→I,L,M,F; 202→W,M,F; and 206→Y. In some embodiments, the residue corresponding to X190 is proline, and additionally has one or more of the following substitutions such that the polypeptide is further improved over the wild-type kefir ketoreductase or another engineered ketoreductase: 7→H; 94→V; 96→T; 147→L; 196→L; and 202→W.

[0164] As will be appreciated by those of skill in the art, some of the above-defined categories, 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.

[0165] 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.

[0166] As described herein, the ketoreductase polypeptides of the disclosure can be in the form of fusion polypeptides in which the ketoreductases polypeptides are fused to other polypeptides, such as antibody tags (*e.g.*, myc epitope) or purifications sequences (*e.g.*, His tags). Thus, the ketoreductase polypeptides can be used with or without fusions to other polypeptides.

[0167] In some embodiments, 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-stereomers 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); styrylkalanine (sAla); authrylalanine (aAla); 3,3-diphenylalanine (Dfa); 3-amino-5-phenypentanoic 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); homoglutanic 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); homoisolencine (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.

[0168] 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 (nitropyridinesulfenyl), 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).

[0169] 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.

[0170] 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

[0171] 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.

[0172] 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 various 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*.

[0173] In some embodiments, the polynucleotide comprises a nucleotide sequence encoding a ketoreductase polypeptide with an amino acid sequence that has at least about 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, where the encoded ketoreductase polypeptide comprises an amino acid sequence in which the residue corresponding to X190 of SEQ ID NO:2, 4 or 98 is not a tyrosine. In some embodiments, the polynucleotide encodes a ketoreductase polypeptide comprising an amino acid sequence in which the residue corresponding to X190 is a non-aromatic residue. In some embodiments, the polynucleotide encodes a ketoreductase polypeptide comprising an amino acid sequence in which the residue corresponding to X190 is alanine, isoleucine, cysteine, or proline, particularly proline. 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, 90, 92, and 94.

[0174] 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, and 93. 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, and 93, wherein the polynucleotide hybridizing under highly stringent conditions has (*S*)-selectivity for a substituted acetophenone substrate, *e.g.*, capable for reducing or converting the substrate of structural formula (I) to the product of structural formula (II). In some embodiments, the

polynucleotides hybridizing under highly stringent conditions are capable of reducing or converting the substrate of structural formula (III) to the product of structural formula (IV).

[0175] 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 a polynucleotide sequence corresponding 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, and 93.

[0176] 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.

[0177] 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, *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). Further promoters are described in Sambrook et al., *supra*.

[0178] 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.

[0179] 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.

[0180] 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.

[0181] 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.

[0182] 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*.

[0183] 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 for filamentous fungal host cells are 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).

[0184] 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.

[0185] 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.

[0186] 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.

[0187] 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.

[0188] 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.

[0189] 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*.

[0190] 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).

[0191] 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.

[0192] 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.

[0193] 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.

[0194] Thus, in some embodiments, 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.

[0195] 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.

[0196] 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.

[0197] The expression vector of the present invention preferably contains one or more selectable markers, which permit easy selection of transformed cells. A selectable marker can be 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.

[0198] 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 adenyltransferase), 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*.

[0199] The expression vectors of the present invention can 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.

[0200] 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.

[0201] 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 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 pAMβ1 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).

[0202] 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.

[0203] Many of the expression vectors for use in the present disclosure 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 (Lathe et al., 1987, *Gene* 57:193-201).

6.4 Host Cells for Expression of Ketoreductase Polypeptides

[0204] 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.

[0205] 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.

[0206] 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 can be isolated by subjecting the cells to chloramphenicol selection.

6.5 Methods of Generating Engineered Ketoreductase Polypeptides.

[0207] 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: 3, 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: 3) was the parent sequence utilized as

the starting point for most experiments and library construction of engineered ketoreductases evolved from the *Lactobacillus kefir* ketoreductase.

[0208] 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.

[0209] 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 $NADP^+$. (For example, see Example 7.) 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). The stereochemistry of the products can be ascertained by various known techniques, and as provided in the Examples. 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.

[0210] 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 litigation 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.

[0211] 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 CelLytic B™ from Sigma-Aldrich of St. Louis MO.

[0212] 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.

[0213] 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. The ketoreductase 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.

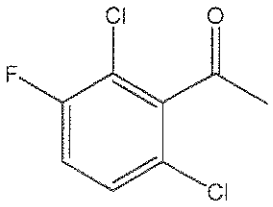
[0214] The ketoreductases may be prepared and used in the form of cells expressing the enzymes, as crude extracts, or as isolated or purified preparations. The ketoreductases may be prepared as lyophilizates, in powder form (*e.g.*, acetone powders), or prepared as enzyme solutions. In some embodiments, the ketoreductases can be in the form of substantially pure preparations.

[0215] 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.

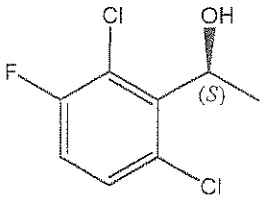
6.6 Methods of Using the Engineered Ketoreductase Enzymes and Compounds Prepared Therewith

[0216] The ketoreductase enzymes described herein are capable of catalyzing the reduction reaction of the keto group in a 2',6' substituted acetophenone substrate, optionally substituted at one or more of 3', 4' or 5' positions, to the corresponding substituted (*S*)-phenethanol.

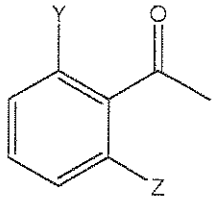
[0217] In some embodiments, the ketoreductases are capable of reducing or converting the substrate compound of structural formula (I), (2',6'-dichloro-3'-fluoroacetophenone):

(I) 

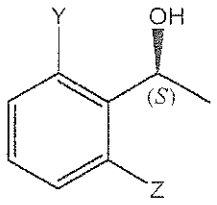
to the corresponding chiral alcohol product of structural formula (II), (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol:

(II) 

[0218] In some embodiments, the ketoreductases described herein are capable of reducing or converting 2',6'-substituted acetophenone compounds of structural formula (III):

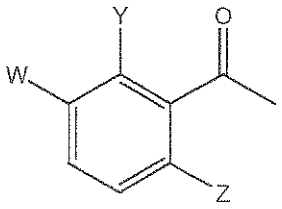
(III) 

wherein Y and Z are independently selected from CH_3, CF_3, NH_2, OH, OCH_3, Cl, and Br, to the corresponding chiral alcohol product of structural formula (IV):

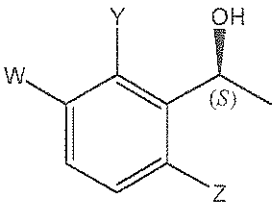
(IV) 

[0219] In some embodiments, a ketoreductase enzyme described herein is capable of catalyzing the reduction reaction of 2',6'-substituted acetophenone compounds of structural formula (III), which can be similarly substituted at one or more of the 3', 4', and 5' positions, to the corresponding (*S*)-alcohol product. The capability of the ketoreductases described herein to catalyze the reduction reaction of a specific further substituted 2',6'-substituted acetophenone compound, in addition to acetophenone, can be determined by routine experimentation, for example by methods such as described in the

Examples. The compound, 2',6'-dichloro-3'-fluoroacetophenone, of structural formula (I) is an example of a further substituted 2',6'-substituted acetophenone compound. As such, in some embodiments, the ketoreductase enzymes disclosed herein are capable of catalyzing the reduction reaction of the compound of structural formula (V):

(V) 

wherein Y and Z are independently selected from CH_3, CF_3, NH_2, OH, OCH_3, Cl, and Br, and W is selected from H or F, Cl, or Br. to the corresponding (*S*) alcohol product of the structural formula (VI):

(VI) 

[0220] Thus, in some embodiments, the ketoreductases described herein can be used in a method for reducing a 2',6'-substituted acetophenone substrate, optionally substituted at one or more of 3', 4' or 5' positions, to the corresponding substituted (*S*)-phenethanol, where the method comprises contacting the substituted acetophenone substrate with the ketoreductases described herein under reaction conditions suitable for reducing or converting the substituted acetophenone to the corresponding substituted (*S*)-phenethanol. In some embodiments of this method, the substrate is reduced to the product in greater than about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% stereomeric excess.

[0221] In some embodiments, the ketoreductases described herein can be used in a method for reducing the 2',6'-substituted acetophenone substrate of formula (III) to corresponding substituted (*S*)-phenethanol compound of formula (IV), where the method comprises contacting or incubating the compound of formula (III) with a ketoreductase polypeptide described herein under reaction conditions suitable for reducing or converting the compound of formula (III) to the corresponding substituted (*S*)-phenethanol compound of formula (IV). In some embodiments of this method, the substrate is reduced to the product in greater than about 25%, 50%, 75%, 80%, 85%, 90%, 95%, 99%, or 99.9% stereomeric excess.

[0222] In some embodiments, the ketoreductases described herein can be used in a method for reducing a 2',6'-dichloro-3'-fluoroacetophenone substrate of formula (I) to its corresponding (*S*)-alcohol product, (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol, of formula (II), where the method comprises contacting or incubating 2',6'-dichloro-3'-fluoroacetophenone with a ketoreductase polypeptide described herein under reaction conditions suitable for reducing or converting 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2,6-dichloro-3-fluorophenyl]-ethanol. In some embodiments of this method, the substrate is reduced to the product in greater than about 85%, 90%, 95%, 99%, or 99.9% stereomeric excess. In some embodiments, the substrate is reduced to the product in greater than about 85% stereomeric excess, wherein the ketoreductase polypeptide comprises an amino acid sequence based on the sequence formula of SEQ ID NO:95, 96 or 119.

[0223] In some embodiments, an engineered (*S*)-selective ketoreductase enzyme derived from a wild-type *Lactobacillus* species ketoreductase enzyme can be used in a method to reduce acetophenone to (*S*)-1-phenethanol in greater than about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.9% or more stereomeric excess.

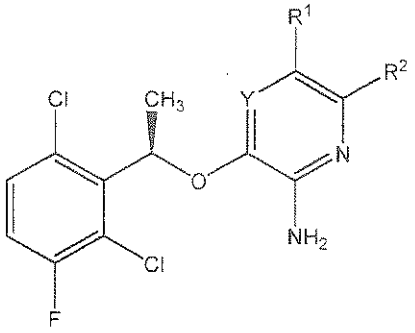
[0224] In some embodiments, the substrate is reduced to the product in greater than about 99% stereomeric excess, wherein the ketoreductase polypeptide used in the method comprises an amino acid sequence selected from SEQ ID NO: 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 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, and 94. In some embodiments of this method, at least about 95% of the substrate is reduced to the product in greater than about 99% stereomeric excess in less than 24 hours when the method is carried out with the ketoreductase polypeptide at an amount of less than about 1% by weight with respect to the amount of the 2',6'-dichloro-3'-fluoroacetophenone substrate.

[0225] In some embodiments of the method, at least about 95% of the substrate is reduced to the product in at least about 99% stereomeric excess in less than 24 hours, when the method is conducted with at least about 200 g/L of substrate and less than about 1 g/L of the ketoreductase polypeptide, wherein the ketoreductase polypeptide used in the method comprises an amino acid sequence selected from SEQ ID NO: 18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

[0226] In some embodiments, the ketoreductases polypeptides and the methods of the present disclosure can be used for synthesis of protein tyrosine kinase inhibitor compounds described in WO2006021886 (aminoheteroaryl compounds), WO2006021884 (enantiomerically substantially pure aminoheteroaryl compounds), WO2006021881 (pyrazole-substituted aminoheteroaryl compounds),

and WO2004076412 (aminoheteroaryl compounds)), whose synthesis relies on the compound of formula (II) as an intermediate. All references are incorporated herein by reference in their entirety.

[0227] Accordingly, in some embodiments, the ketoreductase polypeptides and the methods described herein can be used in producing the protein tyrosine kinase inhibitor compound of structural formula (VII),

(VII) 

including salts, hydrates, and solvates thereof, as described in references WO04076412 and WO06021884, wherein R^1, R^2, Y and N are described therein. In some embodiments, for the compound of formula (VII),

Y is N or CR^{12};

R^1 is selected from hydrogen, halogen, C_{6-12} aryl, 5-12 membered heteroaryl, C_{3-12} cycloalkyl, 3-12 membered heteroalicyclic, $-O(CR^6R^7)_nR^4$, $-C(O)R^4$, $-C(O)OR^4$, -CN, $-NO_2$, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-C(O)NR^4R^5$, $-NR^4C(O)R^5$, $-C(=NR^6)NR^4R^5$, C_{1-8} alkyl, C_{2-8} alkenyl, and C_{2-8} alkynyl; and each hydrogen in R^1 is optionally substituted by one or more R^3 groups;

R^2 is hydrogen, halogen, C_{1-2} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR_6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$ or $-C(O)NR^4R^5$, and each hydrogen in R^2 is optionally substituted by R^8;

each R^3 is independently halogen, C_{1-2} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO^2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nOR^4$, $-(CR^6R^7)_nC(O)NR^4R^5$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)PR^5$ or $-C(O)NR^4R^5$, each hydrogen in R^3 is optionally substituted by R^8, and R^3 groups on adjacent atoms may combine to form a C_{6-12} aryl, 5-12 membered heteroaryl, C_{3-12} cycloalkyl or 3-12 membered heteroalicyclic group;

each R^4, R^5, R^6 and R^7 is independently hydrogen, halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl; or any two of R^4, R^5, R^6 and R^7 bound to the same nitrogen atom may, together with the nitrogen to which they are bound, be combined to form a 3 to 12 membered heteroalicyclic or 5-12 membered heteroaryl group optionally containing 1 to 3 additional heteroatoms selected from N, O, and S; or any two of R^4, R^5, R^6 and R^7 bound to the same carbon atom may be combined to form a C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic or 5-12 membered heteroaryl group; and each hydrogen in R^4, R^5, R^6 and R^7 is optionally substituted by R^8;

each R^8 is independently halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C6-12 aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-NH_2$, -CN, -OH, -O-C_{1-12} alkyl, -O-$(CH_2)_nC_{3-12}$ cycloalkyl, -O-$(CH_2)_nC_{6-12}$ aryl, -O-$(CH_2)_n$(3-12 membered heteroalicyclic) or -O-$(CH_2)_n$(5-12 membered heteroaryl); and each hydrogen in R^8 is optionally substituted by R^{11};

each R^9 and R^{10} is independently hydrogen, halogen, C_{1-12} alkyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nNCR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$ or $-C(O)NR^4R^5$; R^9 or R^{10} may combine with a ring atom of A or a substituent of A to form a C_{3-12} cycloalkyl, 3-12 membered heteroalicyclic, C_{6-12} aryl or 5-12 membered heteroaryl ring fused to A; and each hydrogen in R^9 and R^{10} is optionally substituted by R^3;

each R^{11} is independently halogen, C_{1-12} alkyl, C_{1-12} alkoxy, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, -O-C_{1-12} alkyl, -O-$(CH_2)_nC_{3-12}$ cycloalkyl, -O-$(CH_2)_nC_{6-12}$ aryl, -O-$(CH_2)_n$(3-12 membered heteroalicyclic), -O-$(CH_2)_n$(5-12 membered heteroaryl) or -CN, and each hydrogen in R^{11} is optionally substituted by halogen, -OH, -CN, $-C^{1-12}$ alkyl which may be partially or fully halogenated, -O-C_{1-12} alkyl which may be partially or fully halogenated, -CO, -SO or $-SO_2$;

R^{12} is hydrogen, halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$ or $-C(O)NR^4R^5$, and each hydrogen in R^{12} is optionally substituted by R^3;

each R^{13} is independently halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nOR^4$, $-(CR^6R^7)_nC(O)NR^4R^5$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$, $-C(O)NR^4R^5$, $-(CR^6R^7)_n$(3-12 membered heteroalicyclic), -

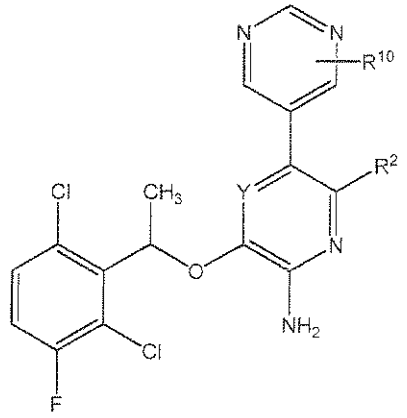
$(CR^6R^7)_n(C_{3-12}$ cycloalkyl), $-(CR^6R^7)_n(C_{6-12}$ aryl), $-(CR^6R^7)_n$(5-12 membered heteroaryl), $-(CR^6R^7)_nC(O)NR^4R^5$, or $-(CR^6R^7)_nC(O)R^4$, R^{13} groups on adjacent atoms may combine to form a C_{6-12} aryl, 5-12 membered heteroaryl, C_{3-12} cycloalkyl or 3-12 membered heteroalicyclic group, and each hydrogen in R^{13} is optionally substituted by R^3;

wherein, each m is independently 0, 1 or 2; each n is independently 0, 1 , 2, 3 or 4; and each p is independently 1 or 2. Descriptions of the various substituents as well as specific compounds encompassed by formula (VII) are described in WO04076412 and WO06021884.

[0228] Accordingly, in a method for producing an enantiomerically pure compound of structural formula (VII), a step in the method can comprise reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase polypeptides described herein under reaction conditions suitable for reducing or converting the substrate compound of formula (I) to the product compound of formula (II). Synthesis of the compounds of formula (VII) from the compound of formula (II) are described in the cited references.

[0229] In some embodiments, the ketoreductase polypeptides and the methods described herein can be used in producing the protein tyrosine kinase inhibitor compound of structural formula (VIII),

(VIII)



including salts, hydrates and solvates thereof, as described in WO06021886, where R^{10}, R^2, Y, and N are described therein. In some embodiments, for the compound of formula (VIII),

Y is N or CR^1;

R^1 is hydrogen, halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_pR^5$ or $-C(O)NR^4R^5$, and each hydrogen in R^1 is optionally substituted by R^3;

R^2 is hydrogen, halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$ or $-C(O)NR^4R^5$, and each hydrogen in R^2 is optionally substituted by R^8;

each R^3 is independently halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-O(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nOR^4$, $-(CR^6R^7)_nC(O)NR^4R^5$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)pR^5$ or $-C(O)NR^4R^5$, each hydrogen in R^3 is optionally substituted by R^8, and R^3 groups on adjacent atoms may combine to form a C_{6-12} aryl, 5-12 membered heteroaryl, C_{3-12} cycloalkyl or 3-12 membered heteroalicyclic group;

each R^4, R^5, R^6 and R^7 is independently hydrogen, halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl; or any two of R^4, R^5, R6 and R^7 bound to the same nitrogen atom may, together with the nitrogen to which they are bound, be combined to form a 3 to 12 membered heteroalicyclic or 5-12 membered heteroaryl group optionally containing 1 to 3 additional heteroatoms selected from N, O, and S; or any two of R^4, R^5, R^6 and R^7 bound to the same carbon atom may be combined to form a C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic or 5-12 membered heteroaryl group; and each hydrogen in R^4, R^5, R^6 and R^7 is optionally substituted by R^8;

each R^8 is independently halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-NH_2$, -CN, -OH, $-O-C_{1-12}$ alkyl, $-O-(CH_2)_nC_{3-12}$ cycloalkyl, $-O-(CH_2)_nC_{6-12}$ aryl, $-O-(CH_2)_n$(3-12 membered heteroalicyclic) or $-O-(CH_2)_n$(5-12 membered heteroaryl); and each hydrogen in R^8 is optionally substituted by R^9;

each R^9 is independently halogen, C_{1-12} alkyl, C_{1-12} alkoxy, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-O-C_{1-12}$ alkyl, $-O-(CH_2)_nC_{3-12}$ cycloalkyl, $-O-(CH_2)_nC_{6-12}$ aryl, $-O-(CH_2)_n$(3-12 membered heteroalicyclic), $-O-(CH_2)_n$(5-12 membered heteroaryl) or -CN, and each hydrogen in R^9 is optionally substituted by halogen, -OH, -CN, $-C_{1-12}$ alkyl which may be partially or fully halogenated, $-O-C_{1-12}$ alkyl which may be partially or fully halogenated, -CO, -SO or $-SO_2$;

R^{10} represents one, two or three optional substituents independently halogen, C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl, C_{3-12} cycloalkyl, C_{6-12} aryl, 3-12 membered heteroalicyclic, 5-12 membered heteroaryl, $-S(O)_mR^4$, $-SO_2NR^4R^5$, $-S(O)_2OR^4$, $-NO_2$, $-NR^4R^5$, $-(CR^6R^7)_nOR^4$, -CN, $-C(O)R^4$, $-OC(O)R^4$, $-0(CR^6R^7)_nR^4$, $-NR^4C(O)R^5$, $-(CR^6R^7)_nC(O)OR^4$, $-(CR^6R^7)_nOR^4$, $-(CR^6R^7)_nC(O)NR^4R^5$, $-(CR^6R^7)_nNCR^4R^5$, $-C(=NR^6)NR^4R^5$, $-NR^4C(O)NR^5R^6$, $-NR^4S(O)_PR^5$, $-C(O)NR^4R^5$, $-(CR^6R^7)_n$(3-12

membered heteroalicyclic), -$(CR^6R^7)_n(C_{3-12}$ cycloalkyl), -$(CR^6R^7)_n(C_{6-12}$ aryl), -$(CR^6R^7)_n$(5-12 membered heteroaryl), or -$(CR^6R^7)_nC(O)NR^4R^5$, and each hydrogen in R^{10} is optionally substituted by R^3;

wherein each m is independently 0, 1 or 2; each n is independently 0, 1 , 2, 3 or 4; and each p is independently 1 or 2. Descriptions of the various substituents as well as specific compounds encompassed by formula (VIII) are described in WO2006021886.

[0230] Accordingly, in a method for producing the compound of structural formula (VIII), a step in the method can comprise reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase polypeptides described herein under reaction conditions suitable for reducing or converting the substrate compound of formula (I) to the product compound of formula (II). Synthesis of the compounds of formula (VIII) from the compound of formula (II) are described in the cited reference.

[0231] 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.

[0232] 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.

[0233] 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.

[0234] 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.

$$(1) \qquad \text{glucose} + \text{NAD(P)}^+ + H_2O \xrightarrow{\text{GDH}} \text{gluconic acid} + \text{NAD(P)H} + H^+$$

[0235] 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.

[0236] 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.

[0237] Glucose dehydrogenases employed in the ketoreductase-catalyzed reduction reactions described herein may exhibit an activity of at least about 10 μmol/min/mg and sometimes at least about 10^2 μmol/min/mg or about 10^3 μmol/min/mg, up to about 10^4 μmol/min/mg or higher in the assay described in Example 4 of PCT publication WO 2005/018579.

[0238] 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.

[0239] 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.

[0240] 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.

[0241] 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 a neutral pH, *i.e.*, about 7.

[0242] 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.

[0243] When the glucose/glucose dehydrogenase cofactor regeneration system is employed, the co-production of gluconic acid (pKa=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.

[0244] 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.

[0245] In some embodiments, the co-factor regenerating system can comprises 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 μmol/min/mg, sometimes at least about 10 μmol/min/mg, or at least about 10^2 μmol/min/mg, up to about 10^3 μmol/min/mg or higher, and can be readily screened for activity in the assay described in Example 4 of PCT publication WO 2005/018579.

[0246] 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.

[0247] 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.

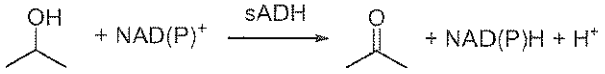
$$(2) \qquad HCO_2^- + NAD(P)^+ \xrightarrow{FDH} CO_2 + NAD(P)H$$

[0248] 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.

[0249] 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.

[0250] 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.

(3) 

[0251] 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, *Thermoanerobium brockii*, *Rhodococcus etythropolis*, *Lactobacillus kefir*, 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 μmol/min/mg, sometimes at least about 10 μmol/min/mg, or at least about 10^2 μmol/min/mg, up to about 10^3 μmol/min/mg or higher.

[0252] 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-akyl carbinols include unsubstituted and substituted 1-arylethanols.

[0253] 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.

[0254] 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.

[0255] 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.

[0256] 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.

[0257] 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.

[0258] 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).

[0259] 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 crosslinking using known crosslinking agents, such as, for example, glutaraldehyde or immobilization to a solid phase (*e.g.*, Eupergit C, and the like).

[0260] 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.

[0261] 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.

[0262] 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.

[0263] 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

[0264] 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.

[0265] 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.

[0266] 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

[0267] Various features and embodiments of the disclosure are illustrated in the following representative examples, which are intended to be illustrative, and not limiting,

[0268] In the following descriptions, wherever glucose dehydrogenase (GDH) is used, it is GDH CDX901, obtainable from Julich Chiral Solutions, Jülich, Germany.

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

[0269] 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 and WO2008042876, 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.

[0270]

Table 3: Abbreviations, source and references for Ketoreductases used

Keto-reductase abbreviation	Microorganism from which enzyme was originally identified	Genbank Acc. No.	GI no.	Polynucleotide SEQ ID NO.	Polypeptide SEQ ID NO, or Source
ADH-CM	*Candida magnoliae*	AB036927.1	12657576	SEQ ID No 1 in US Application Publication 20060195947	SEQ ID No 2 in US Application Publication 20060195947
YDL	*Saccharomyces cerevisiae*	NP_010159.1	6320079	SEQ ID NO:109	SEQ ID NO:110
ADH-LB	*Lactobacillus brevis*	1NXQ_A	30749782	SEQ ID NO:1	SEQ ID NO:2
ADH-RE	*Rhodococcus erythropolis*	AAN73270.1	34776951	SEQ ID NO:111	SEQ ID NO112
YGL	*Saccharomyces cerevisiae*	NP_011476	6321399	SEQ ID NO:113	SEQ ID NO:114
YPR	*Saccharomyces cerevisiae*	NP_010656.1	6320576	SEQ ID NO:115	SEQ ID NO:116
GRE	*Saccharomyces cerevisiae*	NP_014490.1	6324421	SEQ ID NO:117	SEQ ID NO:118
ADH-LK	*Lactobacillus kefir*	AAP94029.1	33112056	SEQ ID N:3	SEQ ID NO:4
ADH-SB	*Sporobolomyces salmonicolor*	Q9UUN9	30315955	SEQ ID No 103	SEQ ID No 104
ADH-SC	*Streptomyces coelicolor*	NP_631415.1	21225636	SEQ ID No 101	SEQ ID No 102
ADH-TB	*Thermoanaerobium brockii*	X64841.1	1771790	SEQ ID No 107	SEQ ID No 108
ADH-HE	*Horse liver*	DEHOAL	625197	SEQ ID No 105	SEQ ID NO 106
ADH-CP	*Candida parapsilosis*	BAA24528	2815409		Julich Chiral Solutions Cat. No. 03.11
DR-LB	*Lactobacillus brevis* *diacetyl reductase*	ABJ63353.1	116098204		Julich Chiral Solutions Cat. No. 8.1

ADH-CB	*Candida boidinii*	CAD66648	28400789		Julich Chiral Solutions Cat. No. 02.10
LDH-LL	*Lactobacillus leichmannii*				Fluka Cat. No. 61306

[0271] Polynucleotides encoding engineered ketoreductases of the present disclosure were likewise cloned into vector pCK110900 for expression in *E. coli* W3110.

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

[0272] A single microbial colony of *E. coli* containing a plasmid with the ketoreductase gene of interest was inoculated into 50 ml Luria Bertani 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 $MgSO_4$, 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 $MgSO_4$ 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.

7.3 Example 3: Production of Ketoreductases; Fermentation Procedure.

[0273] 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.

[0274] 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.

7.4 Example 4: Analytical methods to determine conversion and enantiomeric excess of 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol.

[0275] Reduction of 2',6'-dichloro-3'-fluoroacetophenone and chiral purity of the alcohol product was determined by Reverse Phase Chiral HPLC (4.6 x 150 mm Chiralpak AD-RH column (no guard cartridge); 50:50 ACN/H_2O at 0.8 mL/min; 25°C; detection at 254 nm with the following retention times: (*S*)-alcohol 5.77 min.; (*R*)-alcohol 6.19 min; ketone 7.49 min) or Normal Phase Chiral HPLC (4.6 x 250 mm Chiralpak AD column (no guard cartridge); 2:98 IPA/Hexane at 2.5 mL/min at room temperature (not regulated); detection at 220 nm with the following retention times: (*S*)-alcohol 4.72 min.; (*R*)-alcohol 5.30 min; ketone 2.03 min).

[0276] Alternatively, the following gas chromatographic analytical methods were used: an achiral method using an HP-5 column (30m x 0.25mm) with a temperature program of 100 °C (1 min) to 200 °C (4 min) at 50 °C/min (retention times were 4.33 min for the ketone and 4.70 min for the alcohol)

and a chiral method using a Beta Cyclodextrin (DM) column (30 m x 0.25 mm) at 165 °C isothermal (retention times were 3.42 min for the ketone, 5.92 min for the R-isomer and 6.25 min for the S-isomer).

7.5 Example 5: Evaluation of Wild-Type Ketoreductases for Reduction of 2',6'-dichloro-3'-fluoroacetophenone

[0277] KREDs described in Table 3 of Example 1 were screened using stoichiometric NADH or NADPH as co-factors. To each well of a 96-deep-well plate was added 5-10 mg of KRED, 20 mg of NAD(P)H in 500 μL of 100 mM pH 7.0 triethanolamine(chloride) buffer and 15 μL of the substrate (~40 g/L of substrate; conversion limited to ~25 by the co-factor). The plate was sealed and shaken for 6 hours. The reactions were quenched by the addition of 1 mL of EtOAc. The conversion and stereopurity of the product were assayed as described in Example 4.

[0278] Under these conditions, YDL, YGL, GRE, ADH-RE, ADH-SB, ADH-SC, ADH-HL, LDH-LL, ADH-CP, ADH-CB, and DR-LB gave no detectable conversion with either NADPH or NADH, whereas ADH-LB, and YPR gave <0.5% conversion. ADH-LK converted <1% of the substrate to the chiral alcohol

[0279] This example demonstrates that wild-type ketoreductases have very little if any activity on 2',6'-dichloro-3'-fluoroacetophenone.

7.6 Example 6: Evaluation of ADH-LK Variants for Reduction of 2',6'-dichloro-3'-fluoroacetophenone

[0280] Several ADH-LK variants that had been generated as described in U.S. application Serial No. 60/957,974, filed August 24, 2007 and US application Serial No. 12/197,286, filed August 24, 2008 converted >0.5% of the substrate to the chiral alcohol when evaluated under the conditions described in Example 5 and as listed in Table 4.

Table 4

SEQ ID NO.[c]	Conversion[a]	Enantiomeric excess[b]
4	0	0
115	+	+
117	+	++
111	+	++
119	++	++

121	++	++
113	++	++
6	++	++

[a] 0: 0.5-1% conversion: +: 1-20% conversion; ++ >20% conversion

[b] 0: <90% e.e. (*S*-enantiomer); +: 90-99% e.e. (*S*-enantiomer); ++ >99% e.e. (*S*-enantiomer).

[C] refers to SEQ ID NOs in US application Serial No. 60/957,974 and 12/197,286.

[0281] This example illustrates that ADH-LK variants in which the tyrosine residue at position 190 is altered to phenylalanine, proline, cysteine or alanine reduced 2',6'-dichloro-3'-fluoroacetophenone to the corresponding S-alcohol.

7.7 Example 7: High Throughput NADPH fluorescence prescreen to identify enzymes that reduce 2',6'-dichloro-3'-fluoroacetophenone.

[0282] Plasmid libraries obtained by directed evolution and containing evolved ketoreductase genes were transformed into *E. coli* W3110 and plated on Luria-Bertani (LB) agar medium 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 and 30 μg/mL chloramphenicol (CAM). Cells were grown overnight at 30°C with shaking at 200 rpm. 5 μL of this culture was then transferred into 96-deep well plates containing 380 μL Terrific broth (TB), 1 mM $MgSO_4$ 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 (OD_{600} 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 15-17 hrs.

[0283] Cells were pelleted via centrifugation, resuspended in 300 μL lysis buffer and lysed by shaking at room temperature for at least 1 hour. The lysis buffer contained 100 mM triethanolamine (chloride) buffer, pH 7.0-7.2, 1 mg/mL lysozyme and 750 μg/mL polymixin B sulfate. The plates are then spun in the centrifuge at 4000RPM for 20 minutes at 4°C, and the clear supernatant (lysate) analyzed in the fluorescent assay.

[0284] In 96-well black microtiter plates 20 μl of each lysate (pretreated for 0-24 hrs at 40-50°C ,diluted in 100 mM triethanolamine(chloride) buffer, pH 7.0, 1 mM $MgSO_4$ if necessary) was added to 180 μl of an assay mixture consisting of 100 mM triethanolamine(chloride) buffer, pH 7.0, 1mM $MgSO_4$, 0.2 g/L NADPH, 100-600 mM glucose, 600-900 mM sodium gluconate and 0.2 g/L 2',6'-

dichloro-3'-fluoroacetophenone and reaction progress measured by following the decrease in fluorescence of NADPH at 445 nm after excitation at 330 nm in a Flexstation (Molecular Devices, USA).

[0285] This example describes the method that was used to identify KRED variants improved for the rate of 2',6'-dichloro-3'-fluoroacetophenone reduction.

7.8 Example 8: Reduction of 2',6'-dichloro-3'-fluoroacetophenone by Engineered Ketoreductases Derived from ADH-LK.

[0286] Improved ADH-LK variants for the reduction of 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol were analyzed in small scale chemical reactions. To a 100 mL three-neck vessel equipped with a PTFE-coated magnetic stirring bar and a pH electrode connected to an automatic titrator for pH-controlled addition of base on-demand via a feeding tube into the vessel, was charged 30 ml 100 mM triethanolamine(chloride) buffer (pH 7), 2 mM $MgSO_4$), 200 mg KRED with SEQ ID NO. as described in the table below, 50 mg GDH, 15 mg NADP-Na, 3.13 g glucose, 6 g 2',6'-dichloro-3'-fluoroacetophenone (200 g/L) at 25°C. The automatic titrator maintained the pH at 7 by the addition of 4N NaOH, which was continuously recorded. Reaction progress was monitored by the rate and cumulative addition of the base and periodic sampling of the reaction mixture for extraction with ethylacetate and analysis by the method of Example 4.

[0287] 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',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol. The stereopurity of the S-alcohol was always >99.9%.

[0288] Table 5:

Table 5: Activity and stability of ADH-LK Variants

SEQ ID NO.	No. of mutations from ADH-LK	activity	stability
4	0	-	
6	1	+	
8	2	++	+
10	2	++	
12	2	+	
14	2	++	
16	2	++	+
48	2	+	

50	2	+	
52	3	+	
20	3	+	+
18	4	+++	+
36	3	+++	
54	3	++	+
56	3	++	
62	3	++	
64	3	++	
58	3	++	
60	2	++	
22	3	++	++
66	3	++	+
68	3	++	++
70	4	++	++
72	3	++	++
32	3	+++	+
28	3	++	+
30	3	++	+
34	4	+++	+
74	4	+++	+
38	4	+++	++
40	5	+++	++
76	5	+++	++
78	5	+++	++
80	5	+++	++
82	5	+++	++
84	8	+++	++
42	6	+++	++
44	6	+++	++
86	7	+++	++
46	6	+++	++
88	6	+++	++
90	6	+++	++

92	6	+++	++
94	6	+++	++

a. -: no activity; +: 100-450% the activity of SEQ ID No. 6; ++: 450-1500% the activity of SEQ ID No. 6; +++: >1500% the activity of SEQ ID No. 6.

b. +: measurable activity after 2 hrs at 50°C; ++: >400% the activity of SEQ ID No. 16 after 2 hrs at 50°C.

[0289] This Example illustrates that engineered ketoreductases derived from the wild-type ketoreductase ADH-LK provide improved activity compared to ketoreductase ADH-LK.

7.9 Example 9: Reduction of 2',6'-dichloro-3'-fluoroacetophenone by Engineered Ketoreductases Derived from ADH-LB.

[0290] Improved ADH-LB variants for the reduction of 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol were analyzed in small scale chemical reactions as described for ADH-LK variants in Example 8. Table 6 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',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol. The stereopurity of the S-alcohol was always >99.9%.

[0291] Table 6:

Table 6: Activity and stability of ADH-LK Variants

SEQ ID NO.	No. of mutations from ADH-LK	activity	stability
4	0	-	
6	1	+	
8	2	++	+
10	2	++	
12	2	+	
14	2	++	
16	2	++	+
48	2	+	
50	2	+	
52	3	+	

20	3	+	+
18	4	+++	+

a. -: no activity; +: 100-450% the activity of SEQ ID No. 6; ++: 450-1500% the activity of SEQ ID No. 6; +++: >1500% the activity of SEQ ID No. 6.

b. +: measurable activity after 2 hrs at 50°C; ++: after 2 hrs at 50°C, >400% the activity SEQ ID No. 16 after 2 hrs at 50°C.

[0292] This Example illustrates that engineered ketoreductases derived from the wild-type ketoreductase ADH-LB also provide improved activity compared to ketoreductase ADH-LB.

7.10 Example 10: Preparative scale production of (S)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol.

[0293] To a 500 mL jacketed three neck round bottom flask equipped with an Ace Glass mechanical stirrer (75 mm diameter teflon stirrer blade), and a pH electrode connected to an automatic titrator for pH-controlled addition of base on-demand via a delivery tube into the vessel, was added water (120 mL), triethanolamine (1.8 g) and then hydrochloric acid to adjust the pH to 7.0. Magnesium sulfate was added as a 1M solution (120 μL, 0.12 mmoles, 14.4 mg of $MgSO_4$). The solution was heated to 30°C with heating fluid circulating through the flask's jacket. Glucose (20 g) was added followed by Na-NADP (120 mg), GDH (0.50 g) and KRED having SEQ ID No. 38 (0.50 g). The pH stat was set to maintain the pH at 7.0±0.1 by the addition of 4N NaOH through the delivery tube. 2',6'-dichloro-3'-fluoroacetophenone (50 g) was added to start the reaction. The electrode required periodic rinsing to remove enzyme derived material. Additional glucose was added in portions as the reaction proceeded: 10 g at 104 min (after 17.5 mL of 4 N NaOH had been added), 5 g at 275 min (after 35.2 mL of 4 N NaOH had been added), 5 g at 379 min (after 42 mL of 4 N NaOH had been added), and 8 g at 488 min (after 47 mL of 4 N NaOH had been added). The reaction was stopped after 24 hr. Heptane (150 mL) was then added and the mixture was heated to 40°C for 45 min. After cooling to 30°C the resulting mixture was poured into a separatory funnel and the majority of the bottom aqueous layer was drained. The top layer, a heptane emulsion, was filtered (350 mL, 85 mm diameter coarse filter) through a celite pad under vacuum. The filter was washed with heptane (150 mL) and the filtrate was transferred to a separatory funnel and the two phases were separated. The heptane phase was concentrated on a rotary vacuum evaporator (~50°C, ~150 mmHg increasing to 40 mmHg) to yield (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol as an oil (47.8 g, 94%) which crystallized upon standing.

7.11 Example 11: Reduction of 2',6'-substituted acetophenones by Engineered Ketoreductases Derived from ADH-LK.

[0294] Wild-type ADH-LK and an ADH-LK variant improved for the reduction of 2',6'-dichloro-3'-fluoroacetophenone to (*S*)-1-[2',6'-dichloro-3'-fluorophenyl]-ethanol were tested for activity on two other 2',6'-substituted acetophenones. A solution was prepared of 5 mL 100 mM triethanolamine(chloride) buffer (pH 7, 2 mM $MgSO_4$), 33 mg KRED having SEQ ID No. 10, 8 mg GDH, 3 mg NADP-Na, and 330 mg glucose. 1 ml of this solution was treated with 0.3 ml 1M (sodium)phosphate buffer pH 7 and 20 mg of the 2',6'-substituted acetophenone at 25°C. Reaction samples (24hr) were analyzed by the methods of Example 5.

[0295] Table 7 gives the conversion of the two 2',6'-substituted acetophenones and the enantiomeric purity of the resulting chiral alcohol by ADH-LK and the ADH-K variant with SEQ ID NO 10.

[0296] Table 7:

Table 7: Activities of ADH-LK and an ADH-LK variant on two 2',6'-substituted acetophenones.

2',6'-substituted acetophenone	Wild-type ADH-LK (SEQ ID NO. 4)		Engineered KRED SEQ ID NO. 10	
	Conversion (%)	Stereopurity (%)	Conversion (%)	Stereopurity (%)
2',6'-dichloroacetophenone	0	-	88	>99 S
2',6'-dimethoxyacetophenone	0	-	72	>99 S

[0297] This example shows that an ADH-LK variant containing the Y190P mutation provides improved activity for 2'6'-substituted acetophenones, and provides the corresponding 2'6'-substituted (*S*)-1-phenethanol.

7.12 Example 12: Reduction of unsubstituted acetophenone by ADH-LK and Engineered Ketoreductases Derived from ADH-LK containing a mutation of Y190.

[0298] To each well of a 96-well plates containing 100 µL cell lysate per well, prepared as in Example 7, was added: 50 µL 7 mM Na-$NADP^+$ in 100 mM triethanolamine(chloride) buffer pH 7.0, 300 µL isopropanol, and 50 µL 100 mg/ml acetophenone in THF. The plates were sealed and agitated on an orbital shaker at 850 rpm, room temperature, for 24 h. 1 mL of methyl t-butyl ether (MTBE) was added to each well and the plates were sealed and then shaken at 850 rpm for 10 min at room temperature. The plates were centrifuged at 4,000 rpm (3220 x g) for 2 min to separate the phases and

50 μL of the organic phase from each well transferred to a well of a shallow well plate containing 150 μL MTBE. The plates were sealed and analyzed by normal-phase HPLC (Daicel Chiralcel OD-H column (4.6x 250 mm) equipped with OD-H guard column; 2.5 μL injection; Mobile Phase: 95:5 v/v Heptane – IPA; Flow-rate: 1.5 mL min-1; Column Temperature: 40°C; Wavelength: 215 nm). Retention times: acetophenone: 3.5 min; (R)-1-phenylethanol: 5.3 min; (S)-1-phenylethanol: 5.8 min.

[0299] Table 8 shows the conversion of the acetophenone and the stereomeric purity of the resulting chiral alcohol by ADH-LK and the ADH-LK variants.

[0300] Table 8:

Table 8: Activity and Stereoselectivity of ADH-LK Variants on Acetophenone

SEQ ID NO.	Conversion (%)	Enantiomeric excess (%)	R or S
4 (wild-type)	94	100	R
14	79	46	S
22	80	35	S
28	80	48	S
32	77	50	S
36	89	86	S
42	90	57	S
44	90	41	S

[0301] This example demonstrates that the wild-type Lactobacillus ketoreductase is R-selective on acetophenone and the engineered ketoreductases of the invention, derived therefrom are S-selective on acetophenone.

[0302] While various specific embodiments have been illustrated and described, it will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s).

[0303] All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entireties 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 derived from a wild-type Lactobacillus ketoreductase of SEQ ID NO: 2, 4, or 98 capable of stereoselectively reducing acetophenone to (S)-1-phenethanol, wherein the polypeptide has a proline residue at the residue corresponding to X190 of SEQ ID NO:2, 4 or 98.

2. The polypeptide of claim 1 wherein the polypeptide is capable of stereoselectively reducing acetophenone to (S)-1-phenethanol with a percent stereomeric excess of:

i) at least 90% or

ii) at least 99%.

3. The polypeptide of claim 1, which is a polypeptide capable of stereoselectively reducing 2',6'-dichloro-3'-fluoroacetophenone substrate to the product (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol with a percent stereomeric excess of at least 85%, which comprises an amino acid sequence that is at least 85% identical to a reference sequence based on SEQ ID NO:2, 4 or 98 having at the residue corresponding to X190 a proline, and which has at the residue corresponding to X190 a proline.

4. The polypeptide of claim 3, which comprises an amino acid sequence having additionally one or more of the following features:

residue corresponding to X7 is threonine, proline, tryptophan, arginine, histidine, or asparagine;

residue corresponding to X16 is serine;

residue corresponding to X43 is isoleucine;

residue corresponding to X60 is alanine;

residue corresponding to X94 is alanine, valine or cysteine;

residue corresponding to X95 is isoleucine or leucine;

residue corresponding to X96 is serine, asparagine, threonine or glutamic acid;

residue corresponding to X97 is lysine, threonine, valine, arginine, methionine, or isoleucine;

residue corresponding to X120 is phenylalanine or valine;

residue corresponding to X125 is glycine or serine;

residue corresponding to X142 is asparagine;

residue corresponding to X147 is phenylalanine, leucine, isoleucine, valine, or glutamine;

residue corresponding to X149 is glycine or phenylalanine;

residue corresponding to X150 is aspartic acid or histidine;

residue corresponding to X152 is serine, threonine, or methionine;

residue corresponding to X196 is valine, leucine, methionine, phenylalanine, or isoleucine;

residue corresponding to X202 is alanine, tryptophan, tyrosine, or methionine;

residue corresponding to X205 is arginine;

residue corresponding to X206 is methionine or tyrosine: and

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

5. The polypeptide of claim 3, wherein the percent stereomeric excess is:

i) at least 90%; or

ii) at least 99%, and wherein the polypeptide optionally comprises an amino acid sequence selected from SEQ ID NO: 10, 14, 18, 20, 22, 24, 28, 32, 36, 38, 40, 42, 44, 46, 48, 50, 52, 56, 58, 60, 62, 64, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

6. The polypeptide of claim 3, wherein the polypeptide is further capable of reducing the substrate to the product at a rate greater than the rate of reducing the substrate to the product by the ketoreductase polypeptide having the sequence of SEQ ID NO:6, and wherein the polypeptide optionally comprises an amino acid sequence selected from SEQ ID NO: 10, 14, 18, 20, 22, 24, 28, 32, 36, 38, 40, 42, 44, 46, 48, 50, 52, 56, 58, 60, 62, 64, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

7. The polypeptide of claim 6, wherein the polypeptide is further capable of reducing the substrate to the product at a rate that is at least 450% greater than the rate of reducing the substrate to the product by the ketoreductase polypeptide having the sequence of SEQ ID NO:6, and wherein the polypeptide optionally comprises an amino acid sequence selected from SEQ ID NO: 10, 14, 18, 22, 24, 28, 32, 36, 38, 40, 42, 44, 46, 56, 58, 60, 62, 64, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

8. The polypeptide of claim 6, wherein the polypeptide is further capable of reducing the substrate to the product at a rate that is at least 1500% greater than the rate of reducing the substrate to the product by the ketoreductase polypeptide having the sequence of SEQ ID NO:6, and wherein the polypeptide optionally comprises an amino acid sequence selected from SEQ ID NO: 18, 32, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

9. The polypeptide of claim 6, which is capable of converting in less than 24 hours at least 95% of the 2',6'-dichloro-3'-fluoroacetophenone substrate to (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol when carried out with the polypeptide at an amount of less than 1% by weight with respect to the amount of the 2',6'-dichloro-3'-fluoroacetophenone substrate, and wherein the polypeptide optionally comprises an amino acid sequence selected from SEQ ID NO:18, 32, 34, 36, 38, 40, 42, 44, 46, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94.

10. A polynucleotide encoding a polypeptide according to any one of claims 1 to 9, wherein the polynucleotide is optionally selected from the group consisting of SEQ ID NO: 9, 13, 17, 19, 21, 23, 27, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 55, 57, 59, 61, 63, 67, 69, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, and 93.

11. An expression vector comprising the polynucleotide of claim 10, operably linked to at least one control sequence suitable for directing expression in a host cell.

12. A host cell comprising the expression vector of claim 11.

13. A method for stereoselectively reducing a 2',6'-substituted acetophenone substrate, optionally substituted at one or more of 3', 4' and 5' positions, to the corresponding substituted (S)-1-phenethanol, which comprises contacting the substrate with the ketoreductase polypeptide of any one of claims 1-9 under reaction conditions suitable for stereoselectively reducing or converting the substrate to the corresponding (S)-alcohol product.

14. The method of claim 13, wherein:

(i) the substrate is 2',6'-dichloro-3'-fluoroacetophenone and the corresponding (S)-alcohol product is (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol,

and wherein optionally the (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol is formed in greater than 99% stereomeric excess;

(ii) the ketoreductase polypeptide comprises an amino acid sequence selected from SEQ ID NO: 10, 14, 18, 20, 22, 24, 28, 32, 36, 38, 40, 42, 44, 46, 48, 50, 52, 56, 58, 60, 62, 64, 68, 70, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, and 94; or

(iii) at least 95% of the substrate is reduced to the product in less than 24 hours when the method is conducted with at least 200 g/L of substrate and with less than 2 g/L of the polypeptide.

15. A method for producing the protein tyrosine kinase inhibitor compound of structural formula (VII), including salts, hydrates and solvates thereof, which comprises a step of reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase polypeptide of any one of claims 1-9 under suitable reaction conditions.

16. A method for producing the protein tyrosine kinase inhibitor compound of structural formula (VIII), including salts, hydrates and solvates thereof, which comprises a step of reducing or converting a compound of formula (I) to the compound of formula (II) using the ketoreductase polypeptide of any one of claims 1-9 under suitable reaction conditions.

17. A composition comprising a 2',6'-substituted acetophenone, optionally substituted at one or more of 3', 4' and 5' positions, and/or the corresponding substituted (S)-1-phenethanol, and a ketoreductase of any of claims 1-9, and wherein the substrate is optionally 2',6'-dichloro-3'-fluoroacetophenone of formula (I), and the corresponding substituted (S)-1-phenethanol is (S)-1-(2,6-dichloro-3-fluorophenyl) ethanol of formula (II).

SEQUENCE LISTING

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JENNE, Stephan
MUNDORFF, Emily
CHING, Charlene
GRUBER, John
KREBBER, Anke
HUISMAN, Gjalt

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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 gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggctgc atcaagaccc cgctggtcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Cys 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> 7
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 7
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcg atcaagaccc cgctgatcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Ala Ile Lys
180 185 190
Thr Pro Leu Ile 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> 9
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 9
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300

gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccg atcaagaccc cgctgatcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta 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 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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Ile 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> 11
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 11
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccag aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggctgt atcaagaccc cgctggtcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser
85 90 95
Arg 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 Cys 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> 13
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 13
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 15
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 15
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu 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> 17
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 17
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgatgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccg atcaagaccc cgctgatcga tgatctggaa 600
ggtgctgagg aaaggatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Met 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 Ile Asp Asp Leu Glu Gly Ala Glu Glu Arg 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> 19
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 19
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg caatttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccg atcaagaccc cgctgatcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Ile 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 Pro Ile Lys
180 185 190
Thr Pro Leu Ile 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> 21
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 21
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct ggtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta 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 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
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 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 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> 23

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

<220>
<223> Variant of L. brevis

<400> 23
atgtctaacc gtctggatgg caaagtagcc atcattaccg gcgggactct gggtatcggt 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
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgagcctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccg atcaagaccc cgctgctgga tgatctgccg 600
ggtgctgagg aagcgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catatatctg tgtgtacctg gcatctaatg aatcgaaatt tgcgacgggt 720
tccgaatttg tggtcgacgg cgggtatacc gcacagtaa 759

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

<220>
<223> Variant of L. brevis

<400> 24
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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 25
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. brevis

<400> 25
atgtctaacc gtctggatgg caaagtagcc atcattaccg gcgggactct gggtatcggt 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
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgagcctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcg atcaagaccc cgctgctgga tgatctgccg 600
ggtgctgagg aagcgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catatatctg tgtgtacctg gcatctaatg aatcgaaatt tgcgacgggt 720
tccgaatttg tggtcgacgg cgggtatacc gcacagtaa 759

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

<220>
<223> Variant of L. brevis

<400> 26
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
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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu 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> 27
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 27
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600

ggtatggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggc 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 28
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 28
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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Met 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> 29
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 29
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctcga tgatctggaa 600
ggttacgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 30
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 30
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
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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Tyr 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> 31
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 31
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt 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 aatcgaaatt tgcgacgggt 720
gcagaatttg 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 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
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 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> 33
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 33
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg tagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aagtgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 34
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 34
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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Val 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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Ala Glu Glu Val 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> 35
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 35
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgtattc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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
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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu Asp Asp Leu Glu Gly Ala Glu Glu Met Tyr 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> 37
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 37
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 38
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 38
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
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 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> 39
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 39
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 40
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 40
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 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> 41
<211> 759
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of L. kefir

<400> 41
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg tagtttccaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<210> 42
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 42
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 Val 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> 43
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 43
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttgaaaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 Glu
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
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 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
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 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

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

<220>
<223> Variant of L. kefir

<400> 47
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggccca atcaagaccc cgctgatgga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt 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 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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Met 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> 49
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 49
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccg atcaagaccc cgctgttcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Phe 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> 51
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 51
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgagcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggccca atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaacccctа tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 Ser 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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 53
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 53
atgaccgatc gtctgaagaa caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 Asn 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 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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu 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> 55
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 55
atgaccgatc gtctgaagca caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

<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 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 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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 57
<211> 759

<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 57
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggagtct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

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

<220>
<223> Variant of L. kefir

<400> 58
Met Thr Asp Arg Leu Lys Gly Lys Val Ala Ile Val Thr Gly Gly Ser
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 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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 59
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 59
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120

gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc gcacagtga 759

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

<220>
<223> Variant of L. kefir

<400> 60
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
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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 61
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 61
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cactgtccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660

aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Leu 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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 63
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 63
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg caatttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt cgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Ile 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 Pro Ile Lys
180 185 190
Thr Pro Leu Leu 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> 65
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 65
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggca ggtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta 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 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
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 Gln 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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu 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> 67
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 67
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggat agtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 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
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 Ile 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 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> 69
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 69
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatatag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggtt ggtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg 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 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 Ile 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 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 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> 71
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 71
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa aagcgtcgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct tgtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcgcc atcaagaccc cgctgctaga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 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
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 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 Ala Ile Lys
180 185 190
Thr Pro Leu Leu 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> 73
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 73
atgaccgatc gtctgaaggg caaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccag aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggat agtaggcgat ccgacgctgg gggcatacaa cgcttccaag 480
ggggcggtac gtatcatgtc gaaaagcgca gcgctggatt gcgcactgaa ggactacgat 540
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggtgctgagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 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
Phe Gly Pro Val Thr Thr Val Val Asn Asn Ala Gly Ile Ala Val Ser
85 90 95
Arg 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 Ile 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 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> 75
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 75
atgaccgatc gtctgaagac caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg 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 Thr 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 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> 77
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 77
atgaccgatc gtctgaagcc caaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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
Met Thr Asp Arg Leu Lys Pro 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 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> 79
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 79
atgaccgatc gtctgaagtg gaaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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
Met Thr Asp Arg Leu Lys Trp 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 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> 81
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 81
atgaccgatc gtctgaagcg taaagtagcc atcgtaaccg gcgggactct gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccaa 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
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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
Met Thr Asp Arg Leu Lys Arg 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 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> 83
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 83
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattt gcgtttccaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttttc 360
ggcacccgtc tgggcattca gcgcatgaaa aataaaggct tgggcgctag catcatcaat 420
atgagcagta ttgaggggct cgtattccat 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 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
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 Cys 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 Phe His 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> 85
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 85
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagttactaa aagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgtttttgtc 360
ggcacccgtc 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 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
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 Val 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> 87
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 87
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccgt gagcgttgaa 300
gacactacca cggaggaatg gcgtaaactg ctgtccgtta atctggatgg tgttttcttc 360
ggcacccgtc 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 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
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 Ser
85 90 95
Val 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> 89
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 89
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccat gagcgttgaa 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 tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg 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 Ser
85 90 95
Met 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> 91
<211> 759
<212> DNA

<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 91
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180
cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccac gagcgttgaa 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
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta tgggccacat tggcgaaccg 660
aatgacatcg catggatctg tgtgtacctg gcatctgacg aatcgaaatt tgcgacgggt 720
gcagaatttg tggtcgacgg cgggtatacc 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 Ser
85 90 95
Thr 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> 93
<211> 759
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of L. kefir

<400> 93
atgaccgatc gtctgaagca taaagtagcc atcgtaaccg gcgggacact gggtatcggt 60
ttggcaatcg ccgataaatt tgtagaggag ggtgcgaaag tagttattac tggtcgtcac 120
gcggatgtag gtgaaaaggc cgccaaatca atcggcggca ctgatgttat tcgctttgtc 180

cagcacgatg catccgatga agcaggctgg acgaaactgt tcgacaccac cgaggaggca 240
ttcggcccgg ttacgaccgt cgtgaacaat gcagggattg cagtttccat cagcgttgaa 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
gtgcgtgtca acacagtaca tccgggcccc atcaagaccc cgctgctcga tgatctggaa 600
ggttgggagg aaatgatgtc acagcgtacg aaaaccccta 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 Ser
85 90 95
Ile 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> 95
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Engineered Ketoreductase Sequence Formula with L. brevis backbone
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is a polar, non-polar, acidic, aromatic, constrained, or basic residue

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE

<222> (43)..(43)
<223> Xaa is a nonpolar or polar residue

<220>
<221> MISC_FEATURE
<222> (60)..(60)
<223> Xaa is an aromatic, non-polar, or aliphatic residue

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

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

<220>
<221> MISC_FEATURE
<222> (96)..(96)
<223> Xaa is an acidic or polar residue

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa is an basic, aliphatic, non-polar, or polar residue

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa is aromatic, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222> (125)..(125)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (142)..(142)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE
<222> (147)..(147)
<223> Xaa is an aromatic, aliphatic, polar, or non-polar residue

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa is a non-polar or aromatic residue

<220>
<221> MISC_FEATURE
<222> (150)..(150)
<223> Xaa is an acidic or constrained residue

<220>
<221> MISC_FEATURE
<222> (152)..(152)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (190)..(190)
<223> Xaa is a non-aromatic residue

<220>
<221> MISC_FEATURE
<222> (196)..(196)
<223> Xaa is an aliphatic, non-polar, or aromatic residue

<220>
<221> MISC_FEATURE
<222> (202)..(202)

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

<220>
<221> MISC_FEATURE
<222> (205)..(205)
<223> Xaa is a basic, nonpolar or aliphatic residue

<220>
<221> MISC_FEATURE
<222> (206)..(206)
<223> Xaa is an aromatic or non-polar residue

<400> 95
Met Ser Asn Arg Leu Asp Xaa Lys Val Ala Ile Ile Thr Gly Gly Xaa
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 Xaa Gly Glu Lys Ala Ala
35 40 45
Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Xaa 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 Xaa Xaa Xaa
85 90 95
Xaa 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 Xaa Gly Thr Arg Leu Xaa Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Xaa Ser Ile
130 135 140
Glu Gly Xaa Val Xaa Xaa Pro Xaa 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 Xaa Ile Lys
180 185 190
Thr Pro Leu Xaa Asp Asp Leu Pro Gly Xaa Glu Glu Xaa Xaa 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 Ter
245 250

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

<220>
<223> Engineered Ketoreductase Sequence Formula with L. kefir backbone
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is a polar, non-polar, acidic, aromatic, constrained, or basic residue

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE
<222> (43)..(43)
<223> Xaa is a nonpolar or polar residue

<220>
<221> MISC_FEATURE
<222> (60)..(60)
<223> Xaa is an aromatic, non-polar, or aliphatic residue

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

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

<220>
<221> MISC_FEATURE
<222> (96)..(96)
<223> Xaa is an acidic or polar residue

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa is an basic, aliphatic, non-polar, or polar residue

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa is aromatic, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE
<222> (125)..(125)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (142)..(142)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE
<222> (147)..(147)
<223> Xaa is an aromatic, aliphatic, polar, or non-polar residue

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa is a non-polar or aromatic residue

<220>
<221> MISC_FEATURE
<222> (150)..(150)
<223> Xaa is an acidic or constrained residue

<220>
<221> MISC_FEATURE
<222> (152)..(152)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (190)..(190)
<223> Xaa is a non-aromatic residue

<220>
<221> MISC_FEATURE
<222> (196)..(196)
<223> Xaa is an aliphatic, non-polar, or aromatic residue

<220>
<221> MISC_FEATURE
<222> (202)..(202)
<223> Xaa is an aromatic, non-polar, or aliphatic residue

<220>
<221> MISC_FEATURE
<222> (205)..(205)
<223> Xaa is a basic, nonpolar or aliphatic residue

<220>
<221> MISC_FEATURE
<222> (206)..(206)
<223> Xaa is an aromatic or non-polar residue

<400> 96
Met Thr Asp Arg Leu Lys Xaa Lys Val Ala Ile Val Thr Gly Gly Xaa
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 Xaa Gly Glu Lys Ala Ala
35 40 45
Lys Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Xaa 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 Xaa Xaa Xaa
85 90 95
Xaa 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 Xaa Gly Thr Arg Leu Xaa Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Xaa Ser Ile
130 135 140
Glu Gly Xaa Val Xaa Xaa Pro Xaa 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 Xaa Ile Lys
180 185 190
Thr Pro Leu Xaa Asp Asp Leu Glu Gly Xaa Glu Glu Xaa Xaa 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> Lactobacillus Minor

<400> 97
atgaccgatc ggttgaaggg gaaagtagca attgtaactg gcggtacctt gggaattggc 60
ttggcaatcg ctgataagtt tgttgaagaa ggcgcaaagg ttgttattac cggccgtcac 120
gctgatgtag gtgaaaaagc tgccagatca atcggcggca cagacgttat ccgttttgtc 180
caacacgatg cttctgatga aaccggctgg actaagttgt ttgatacgac tgaagaagca 240
tttggcccag ttaccacggt tgtcaacaat gccggaattg cggtcagcaa gagtgttgaa 300
gataccacaa ctgaagaatg gcgcaagctg ctctcagtta acttggatgg tgtcttcttc 360
ggtacccgtc ttggaatcca acgtatgaag aataaaggac tcggagcatc aatcatcaat 420
atgtcatcta tcgaaggttt tgttggtgat ccagctctgg gtgcatacaa cgcttcaaaa 480
ggtgctgtca gaattatgtc taaatcagct gccttggatt gcgctttgaa ggactacgat 540
gttcgggtta acactgttca tccaggttat atcaagacac cattggttga cgatcttgaa 600
ggggcagaag aaatgatgtc acagcggacc aagacaccaa tgggtcatat cggtgaacct 660
aacgatatcg cttggatctg tgtttacctg gcatctgacg aatctaaatt tgccactggt 720
gcagaattcg ttgtcgacgg agggtacacc gcccaatag 759

<210> 98
<211> 252
<212> PRT
<213> Lactobacillus Minor

<400> 98
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
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
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
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> 99
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> SADH from C. parapsilosis

<400> 99
atgtcaattc catcaagcca gtacggattc gtattcaata agcaatcagg acttaatttg 60
agaaatgatt tgcctgtcca caagcccaaa gcgggtcaat tgttgttgaa agttgatgct 120
gttggattgt gtcattctga tttacatgtc atttacgaag ggttggattg tggtgataat 180
tatgtcatgg gacatgaaat tgctggaact gttgctgctg tgggtgatga tgtcattaac 240
tacaaggttg gtgatcgtgt tgcctgtgtc ggacccaatg gatgtggtgg gtgcaagtat 300
tgtcgtggtg ccattgacaa tgtatgtaaa aacgcatttg gtgattggtt cggattgggg 360
tacgatggtg ggtatcaaca gtacttgttg gttactagac cacgtaactt gtctcgtatc 420
ccagataacg tatctgcaga cgtggctgcg gcttcaactg atgctgtatt gacaccatat 480
cacgcaatca agatggctca agtgtcacca acttcgaata tcttgcttat tggtgctggt 540
ggattgggtg gaaatgcaat tcaagttgcc aaggcatttg gtgcgaaagt tactgttttg 600
gacaaaaaaa aggaggctcg tgaccaagca aagaagttgg gtgctgatgc agtttatgaa 660
acattgccag aatccatttc tcctggctct ttttcagcat gttttgattt tgtttcagtg 720
caagctacat ttgatgtatg tcaaaagtat gttgaaccaa agggtgtaat tatgcccgtg 780
ggactcggtg ctcctaattt atcgtttaat ttgggagatt tggcattgag agaaattcga 840
atcttgggta gtttttgggg aactactaat gatttggatg atgttttgaa attggttagt 900
gaaggtaaag ttaaacccgt tgtgagaagt gccaaattga aggaattgcc agagtatatt 960
gaaaaattga gaaacaatgc ttatgaaggt agagttgttt ttaatccata g 1011

<210> 100
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> SADH from C. parapsilosis

<400> 100
Met Ser Ile Pro Ser Ser Gln Tyr Gly Phe Val Phe Asn Lys Gln Ser
1 5 10 15
Gly Leu Asn Leu Arg Asn Asp Leu Pro Val His Lys Pro Lys Ala Gly
20 25 30
Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35 40 45
His Val Ile Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
50 55 60
His Glu Ile Ala Gly Thr Val Ala Ala Val Gly Asp Asp Val Ile Asn
65 70 75 80
Tyr Lys Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85 90 95
Gly Cys Lys Tyr Cys Arg Gly Ala Ile Asp Asn Val Cys Lys Asn Ala
100 105 110

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

<210> 101
<211> 1041
<212> DNA
<213> Artificial Sequence

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

<400> 101
atgaaggcac tgcagtaccg caccatcggc gccccgcccg aggtcgtcac cgtcccggac 60
ccggagccgg gccccggcca ggtgctgttg aaggtgaccg cggccggagt ctgccactcc 120
gacatcgcgg tgatgagctg gcccgccgag ggcttcccgt acgagctgcc gctcaccctc 180
ggccacgagg gcgtcggcac cgtggccgcg ctcggcgccg gggtgacggg gctcgccgag 240
ggcgacgcgg tcgccgtgta cgggccctgg ggctgcggca cctgcgccaa gtgcgcggag 300
ggcaaggaga actactgcct gcgcgccgac gagctgggca tccgtccgcc ggggctcggg 360
cgtccggggt ccatggccga gtacctgctg atcgacgacc cccggcacct ggtcccgctg 420
gacgggctcg acccggtcgc ggcggtgccg ctcaccgacg ccggactgac gccgtaccac 480
gcgatcaagc ggtcgctgcc caagctggtc cccggctcca ccgcggtggt catcggcacc 540
ggtggtctcg gccacgtcgc catccagctg ctgcgcgccc tgacgtccgc ccgggtggtc 600
gccctggacg tcagcgagga gaagctgcgc ctcgcccgtg cggtgggcgc gcacgaggcg 660
gtgctgtcgg acgcgaaggc cgcggacgcg gtgcgcgaga tcaccggcgg tctcggtgcc 720
gaggccgtgt tcgacttcgt cggcgtggcg cccaccgtgc agaccgccgg agccgtcgcg 780
gccgtcgagg gcgatgtcac cctggtcggc atcggcggcg gatcgctgcc cgtcggcttc 840
ggcatgctgc cgttcgaggt gtcggtcaac gccccctact ggggcagccg cagcgagctg 900
accgaggtgc tgaacctggc ccgctccggt gccgtgtcgg tgcacaccga gacgtactcc 960
ctggacgacg cccgctcgc ctacgagcgg ctgcacgagg gcagggtcaa cggccgcgcg 1020
gtgatcctgc cccacggctg a 1041

<210> 102
<211> 346
<212> PRT
<213> Artificial Sequence

<220>
<223> ADH from S. coelicolor

<400> 102
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 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
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

<210> 103
<211> 1032
<212> DNA
<213> Artificial Sequence

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

<400> 103
atggcaaaga tcgacaacgc agttctgccg gagggttctc tggtgctggt caccggcgcg 60
aacggctttg tcgctagcca tgtggtcgaa caactgctgg aacacggcta taaggtgcgc 120
ggcactgctc gctctgcctc caaactggcg aacctgcaga aacgttggga cgccaaatac 180
cctggtcgtt tcgagactgc cgttgttgaa gacatgctga agcagggtgc atatgatgaa 240
gttattaaag gcgcggcagg tgtcgcccac atcgcgtccg tggtcagctt ttctaacaaa 300
tatgatgagg tggtaactcc tgcgatcggt ggcacgctga atgccctgcg 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 ttcatggacg aaaacaaacc gcactttact 600
ctgaatgccg ttctgccaaa ctacactatc ggtaccattt ttgacccaga aacccaatcc 660
ggttccactt ccggctggat gatgtctctg ttcaatggcg aagtatctcc ggcactggcg 720
ctgatgccgc cgcagtacta tgtctctgca gttgatatcg gtctgctgca cctgggttgt 780
ctggttctgc cgcaaatcga acgccgtcgt gtttacggca ccgcaggcac ctttgattgg 840
aacaccgttc tggcgacctt ccgtaaactg tatccgtcca agacgttccc ggctgacttt 900
ccggatcagg gccaggatct gtccaaattt gataccgccc cgagcctgga gattctgaaa 960
tccctgggcc gccctggctg gcgtagcatc gaggaatcta tcaaagatct ggtgggttcc 1020
gagaccgcct aa 1032

<210> 104
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> ADH from S. salmonicolor

<400> 104

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 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> 105
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized ADH from Horse Liver, E form

<400> 105
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 ttctgcttga aaaatgatct gagcatgcct 360
cgtgggacca tgcaggatgg taccagccgt ttcacctgcc gtgggaagcc tatccaccac 420
ttcctgggca ccagcacctt ctcccagtac accgtggtgg acgagatctc agtggccaag 480
atcgatgcgg cctcaccgct ggagaaagtc tgtctgattg gctgtgggtt ttctactggt 540
tatgggtctg cagtcaaggt tgccaaggtc acccagggct ccacctgtgc cgtgtttggc 600
ctgggggggg tgggcctgtc tgttatcatg ggctgtaaag cagccggggc ggcccgtatc 660
attggggtgg acatcaacaa agacaagttt gcaaaggcca aagaagtggg tgccactgag 720
tgtgtcaacc ctcaggacta caagaaacct atccaggagg tgctgacaga aatgagcaat 780
gggggcgtgg atttttcatt tgaagtcatt ggtcgtctgg acaccatggt gactgccttg 840
tcatgctgtc aagaagcata tggtgtgagc gtcatcgtag gggtacctcc tgattcccaa 900
aatctgtcta tgaatcctat gttgctgctg agtgggcgta cctggaaagg ggctattttt 960
ggtggtttta agagtaaaga ttctgtccct aaactggtgg ccgattttat ggctaaaaag 1020
tttgcactgg atcctttaat cacccatgtt ttacctttg aaaaaattaa tgaagggttt 1080
gacctgctgc gctctgggga gagtatccgt accatcctga cgttt 1125

<210> 106
<211> 375
<212> PRT
<213> Artificial Sequence

<220>
<223> ADH from Horse Liver, E form

<400> 106
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 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
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> 107
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon optimized ADH-TB from T brockii

<400> 107
atgaaaggct tcgccatgct gagcatcggc aaagtgggtt ggattgaaaa agaaaaaccg 60
gcgccaggcc cgttcgatgc aattgtgcgc cctctggcag tagcgccgtg taccagcgat 120
attcatactg tgtttgaagg tgccattggc gagcgtcaca atatgattct gggccatgaa 180
gccgttggtg aagttgttga ggttggcagc gaagtgaagg atttcaaacc gggcgatcgc 240
gttgtcgttc cagcgattac cccggattgg cgcaccagcg aagtccagcg cggctaccat 300
cagcactctg gcggcatgct ggccggctgg aaattcagca atgtaaagga tggtgtgttc 360
ggtgaatttt ttcacgttaa cgacgcagac atgaatctgg cgcacctgcc gaaagaaatc 420
ccgctggaag cagcggttat gattccggat atgatgacca cgggttttca cggcgcagag 480

ctggcggaca ttgaactggg cgctacggta gccgtactgg gcatcggtcc ggtgggcctg 540
atggcagttg caggcgctaa gctgcgcggc gcaggtcgta ttattgccgt tggttctcgc 600
ccggtgtgtg tggacgccgc taagtattat ggtgcaacgg acattgtcaa ttacaaggac 660
ggcccaattg aatctcagat catgaacctg acggaaggta aaggcgttga cgccgcgatt 720
atcgctggcg gcaacgccga catcatggcg accgcagtta aaatcgtcaa gccaggtggt 780
actattgcta acgtcaacta cttcggcgaa ggtgaggtcc tgcctgtccc acgtctggaa 840
tggggttgcg gtatggcaca taaaaccatt aaaggtggcc tgtgcccagg cggccgtctg 900
cgtatggaac gcctgatcga tctggtcttc tacaaacgcg tggatcctag caaactggtg 960
actcacgttt tccgcggctt tgataacatc gaaaaagctt ttatgctgat gaaagataaa 1020
ccgaaagatc tgattaaacc ggttgtcatc ctggct 1056

<210> 108
<211> 352
<212> PRT
<213> Artificial Sequence

<220>
<223> ADH-TB from T brockii

<400> 108
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
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

<210> 109
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> YDL ADH from Saccharomyces cervisiae

<400> 109
atgtcttttc accaacagtt tttcacgctg aacaacggca ataaaatccc ggcgattgcc 60
atcatcggca 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 ggcttggaaa 420
gatatggagc agttatacaa aagtggtaaa gctaaaaaca tcggggtttc caatttcgca 480
gtggaagacc tgcaacgtat cctgaaagtc gctgaagtta aacctcaggt caaccagatt 540
gagttctctc cgttcctgca aaaccaaaca ccaggcattt ataaattctg tcaggagcac 600
gatatcctgg tggaagcata ttctccgctg ggcccgctgc agaagaaaac cgcgcaggat 660
gacagccaac catttttga gtacgtcaaa gaattgagcg aaaaatacat caaatccgag 720
gcccagatca tcctgcgctg ggtcactaaa cgcggtgtgc tgccagttac cacctcttca 780
aagcctcagc gcattagcga tgctcagaac ctgttttcct tcgacctgac agcggaagag 840
gttgataaaa tcacggagct gggtctggaa catgaaccgc tgcgcctgta ctggaataaa 900
ttgtatggca aatataacta cgccgcccag aaagtgtaa 939

<210> 110
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> YDL ADH from Saccharomyces cervisiae

<400> 110
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> 111
<211> 1047
<212> DNA
<213> Artificial Sequence

<220>

<223> ADH from Rhodococcus erythropolis

<400> 111
atgaaagcca ttcagtacac tcgtatcggt 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
ggcctggaga actattgctc ccgtgcgcag gaactgggta ttaacccgcc tggtctgggt 360
gctccggggg ctttggcaga atttatgatt gtcgactcac cacgtcattt ggtcccgatt 420
ggcgatttag accctgttaa aactgttccg ttgactgatg cgggcctgac cccataccat 480
gcaatcaaac gctccctgcc gaaactgcgc ggcggctctt atgcagtagt gatcggtacg 540
ggtggcctgg gccacgtggc tatccaactg ctgcgtcatt tatctgctgc aacggtgatc 600
gccttggacg tttctgccga taaactggaa ctggctacca aagtcggcgc acatgaagta 660
gtcctgtctg ataaagatgc agcggagaat gtgcgtaaaa ttactggtag ccaaggtgca 720
gctttggtgt tggatttttgt gggctatcag cctaccattg acaccgccat ggcagtggcg 780
ggcgtgggct ctgacgtcac cattgttggt atcggtgatg gccaggcaca tgcgaaagtt 840
ggtttcttcc agagtcctta tgaggcatcg gttacggtac cttattgggg cgctcgtaat 900
gaactgatcg aattgatcga tctggcgcat gctggtattt tcgacattgc cgttgagacc 960
ttctctttgg ataatggtgc agaggcctat cgtcgcctgg ctgcgggcac actgtcaggc 1020
cgtgcggtag tcgtcccggg cctgtaa 1047

<210> 112
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> ADH from Rhodococcus erythropolis

<400> 112
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 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> 113
<211> 1047
<212> DNA
<213> Artificial Sequence

<220>
<223> YGL ADH from Saccharomyces cervisiae

<400> 113
atgaccacgg aaaaaaccgt agtgttcgtg tcaggcgcga ccggttttat tgctctgcac 60
gtggtagatg acctgctgaa aactggttac aaagtaattg gttccggtcg ttctcaggaa 120
aaaaatgacg gtttgctgaa gaagttcaag tccaacccga atctgagcat ggaaattgtg 180
gaagatattg cggcaccaaa cgccttcgat aaagtattcc agaaacatgg taaagaaatt 240
aaagtggtcc tgcatatcgc gtccccggtc catttcaaca ctaccgattt cgaaaaagac 300
ttactgatcc cggcggtaaa cggtaccaaa tctattttgg aagcaattaa gaactatgcc 360
gcagacaccg tggaaaaagt ggttattact tcatctgttg ccgcgttggc ctctccgggt 420
gatatgaaag ataccagctt cgtggttaac gaagaatcct ggaataaaga cacctgggaa 480
tcgtgtcagg cgaatgctgt gtccgcttat tgcggttcta aaaaattcgc agagaaaacg 540
gcgtgggact tcttggaaga aaaccagagc agcattaaat ttactctgtc cacgattaac 600
ccaggcttcg tttttggtcc gcagctgttc gccgactcct tgcgcaatgg tattaactct 660
agcagtgcga ttattgcgaa cctggtgtcg tataaattag gggataactt ctacaattat 720
agcggcccgt 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
aacttgctgg gcttccagtt caacaaattc cgcgactgca ttgtcgatac tgcgtcccag 1020
ttgctggaag tgcaaagcaa aagctaa 1047

<210> 114
<211> 348
<212> PRT
<213> Artificial Sequence

<220>
<223> YGL ADH from Saccharomyces cervisiae

<400> 114
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
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> 115
<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> YPR ADH from Saccharomyces cervisiae

<400> 115
atgccggcaa cgttaaaaaa cagcagtgct accttaaaat taaacacagg tgcgagcatt 60
cctgtcctgg ggttcggcac ctggcgctct gtcgataaca acggctatca tagtgtaatt 120
gcggcgctga aagcggggta ccgtcatatc gatgctgcgg ccatctatct gaatgaagaa 180
gaagtcggcc gtgcgatcaa ggactccggt gttcctcgtg aagaaatttt tattaccacc 240
aaactgtggg gcaccgaaca acgcgatcca gaagcagccc tgaacaaatc tctgaaacgt 300
ctgggtctgg actatgtgga cctgtatctg atgcactggc cggtccctct gaaaacagac 360
cgtgtaactg acggtaacgt cctgtgcatc ccgaccctgg aagatggcac cgtggacatc 420
gataccaaag agtggaattt tattaaaacc tgggaactga tgcaggaatt gccgaaaact 480
ggtaagacca aagccgtcgg tgtgtccaat ttttccatca acaatatcaa agaactgctg 540
gaatcgccaa ataacaaggt cgttccagca accaatcaga tcgagattca tccgttgctg 600
ccgcaggatg aattaatcgc cttttgtaaa gaaaaaggca ttgtggtcga agcatatagc 660
ccattcggct ccgctaacgc cccgctgctg aaagaacagg cgattatcga tatggccaaa 720
aagcacggcg tcgaaccggc gcaactgatt atcagctggt cgattcagcg cggttatgtg 780
gtattggcca agtccgtaaa tccggagcgt atcgtgtcga actttaagat ttttaccctg 840
ccagaggatg atttcaaaac catctctaac ctgagcaaag tgcacggtac caaacgtgtc 900
gttgacatga aatggggctc atttccgatt tttcaataa 939

<210> 116
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> YPR ADH from Saccharomyces cervisiae

<400> 116
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 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
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> 117
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> GRE ADH from Saccharomyces cervisiae

<400> 117
atgtctgtgt tcgtgtcagg cgcgaatggt tttattgctc agcacatcgt agatctgctg 60
ctgaaagaag attacaaagt aattggttcc gcacgttctc aggaaaaagc tgaaaatttg 120
accgaagcct tcggtaacaa cccgaaattt agcatggaag tggtgcctga tattagcaaa 180
ctggatgcct tcgatcatgt attccagaaa catggtaaag atattaaaat cgtcctgcat 240
accgcgtccc cgttttgttt cgatattacc gattccgaac gtgacttact gatcccggcg 300
gtaaacggtg tcaaaggtat tttgcacagt attaagaaat atgccgcaga cagcgtggaa 360
cgcgtggttc tgacttcatc ttacgccgcg gtatttgata tggcgaagga aaacgataag 420
agcctgacct tcaacgaaga atcctggaat ccggcgacct gggaatcgtg tcagagtgat 480
ccggtgaacg cttattgcgg ttctaaaaaa ttcgcagaga aagcagcgtg ggaattcttg 540
gaagaaaacc gtgatagcgt gaaatttgag ctgacagcgg tcaacccagt ttacgttttt 600
ggtccgcaga tgttcgataa agatgttaaa aaacacttga acaccagctg cgaactggtg 660
aactctctga tgcatctgag ccctgaagat aaaattccgg aactgtttgg cggttacatc 720
gacgtccgtg acgttgcgaa agctcatctg gttgcatttc agaaacgtga aacaatcggt 780
cagcgcctga tcgtgtcgga ggcacgtttc acgatgcagg acgttctgga cattctgaac 840
gaagactttc cagtactgaa gggcaatatc ccggtcggca agcctggcag cggcgccacc 900
cataatactc tgggcgccac cctggacaat aaaaaaagca aaaaattgct gggcttcaaa 960
ttccgtaatc tgaaagagac tattgacgat actgcgtccc agatcctgaa attcgaaggt 1020
cgcatttaa 1029

<210> 118
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> GRE ADH from Saccharomyces cervisiae

<400> 118
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
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> 119
<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 polar, non-polar, acidic, aromatic, constrained, or basic residue

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE
<222> (43)..(43)
<223> Xaa is a nonpolar or polar residue

<220>
<221> MISC_FEATURE
<222> (60)..(60)
<223> Xaa is an aromatic, non-polar, or aliphatic residue

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

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

<220>
<221> MISC_FEATURE
<222> (96)..(96)
<223> Xaa is an acidic or polar residue

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa is an basic, aliphatic, non-polar, or polar residue

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa is aromatic, aliphatic, or non-polar residue

<220>
<221> MISC_FEATURE

<222> (125)..(125)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (142)..(142)
<223> Xaa is a polar residue

<220>
<221> MISC_FEATURE
<222> (147)..(147)
<223> Xaa is an aromatic, aliphatic, polar, or non-polar residue

<220>
<221> MISC_FEATURE
<222> (149)..(149)
<223> Xaa is a non-polar or aromatic residue

<220>
<221> MISC_FEATURE
<222> (150)..(150)
<223> Xaa is an acidic or constrained residue

<220>
<221> MISC_FEATURE
<222> (152)..(152)
<223> Xaa is a polar or non-polar residue

<220>
<221> MISC_FEATURE
<222> (190)..(190)
<223> Xaa is a non-aromatic residue

<220>
<221> MISC_FEATURE
<222> (196)..(196)
<223> Xaa is an aliphatic, non-polar, or aromatic residue

<220>
<221> MISC_FEATURE
<222> (202)..(202)
<223> Xaa is an aromatic, non-polar, or aliphatic residue

<220>
<221> MISC_FEATURE
<222> (205)..(205)
<223> Xaa is a basic, nonpolar or aliphatic residue

<220>
<221> MISC_FEATURE
<222> (206)..(206)
<223> Xaa is an aromatic or non-polar residue

<400> 119
Met Thr Asp Arg Leu Lys Xaa Lys Val Ala Ile Val Thr Gly Gly Xaa
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 Xaa Gly Glu Lys Ala Ala
35 40 45
Arg Ser Ile Gly Gly Thr Asp Val Ile Arg Phe Xaa 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 Xaa Xaa Xaa
85 90 95
Xaa 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 Xaa Gly Thr Arg Leu Xaa Ile Gln Arg
115 120 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Xaa Ser Ile
130 135 140
Glu Gly Xaa Val Xaa Xaa Pro Xaa 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 Xaa Ile Lys
180 185 190
Thr Pro Leu Xaa Asp Asp Leu Glu Gly Xaa Glu Glu Xaa Xaa 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