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(54) **PRODUCING ALPHA-OLEFINS USING POLYKETIDE SYNTHASES**

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C12P 5/00	(2006.01)

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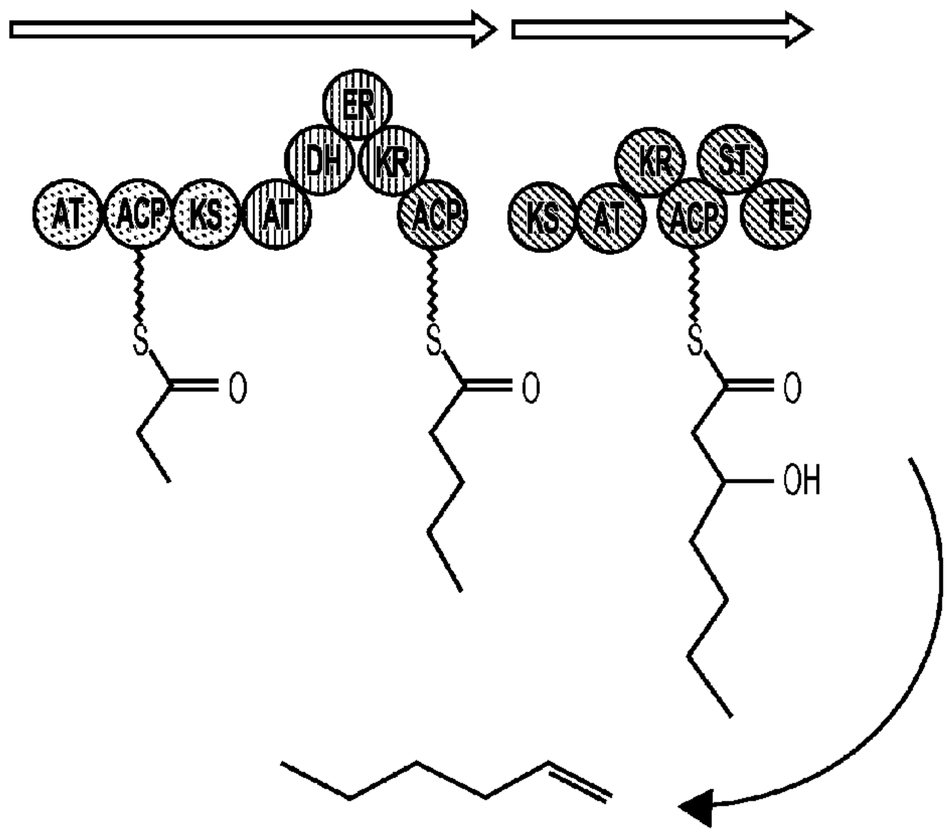
(57) **ABSTRACT**

The present invention provides for a polyketide synthase (PKS) capable of synthesizing an α-olefin, such as 1-hexene or butadiene. The present invention also provides for a host cell comprising the PKS and when cultured produces the α-olefin.



DEBS.LD-Nys.m5 CurM

FIG. 1

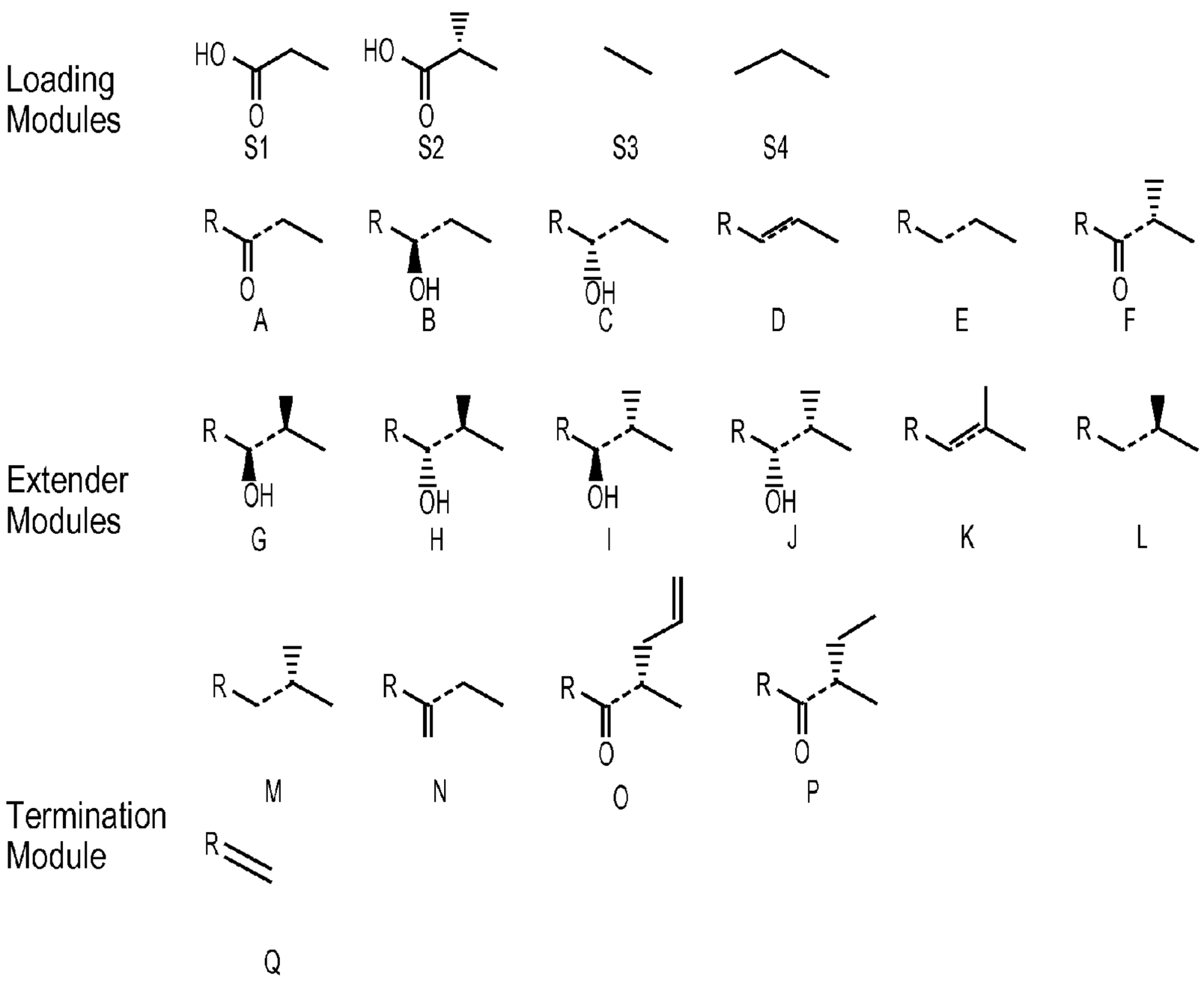


FIG. 2

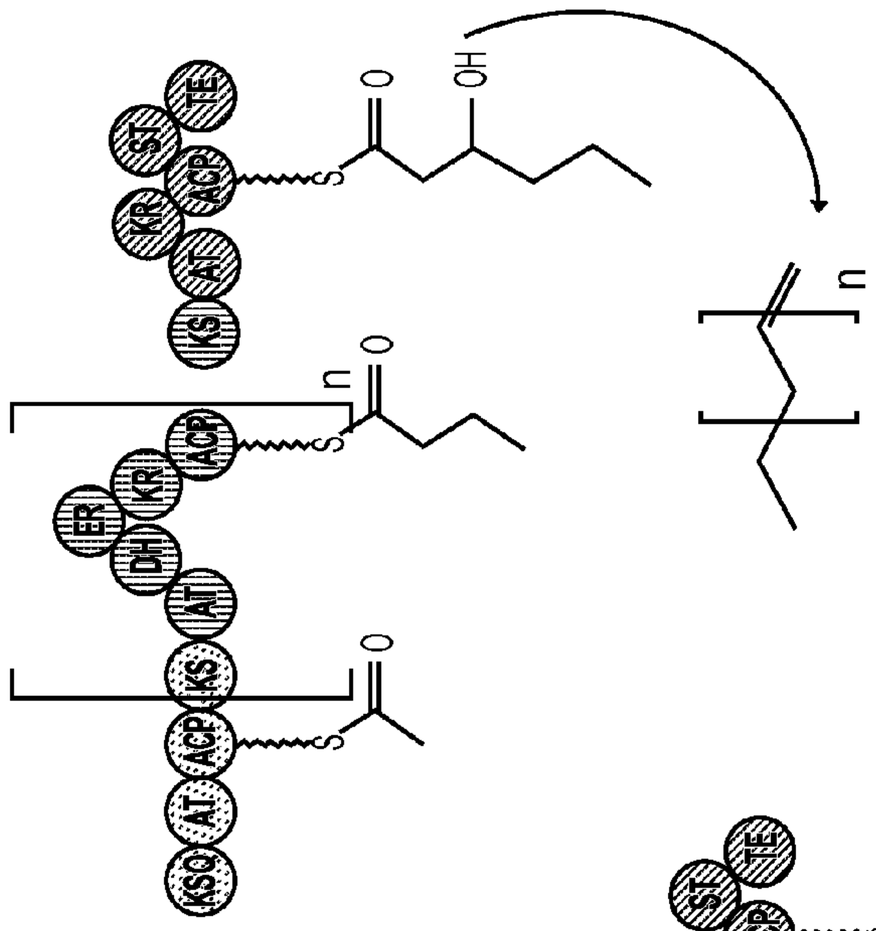


FIG. 3C

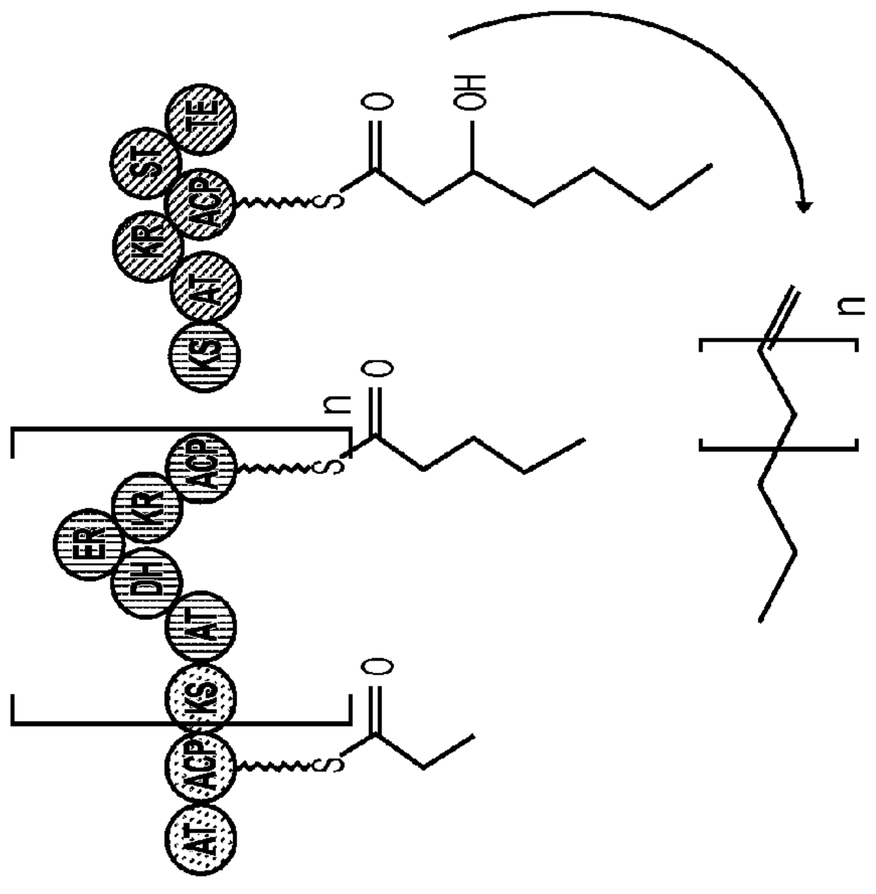


FIG. 3B

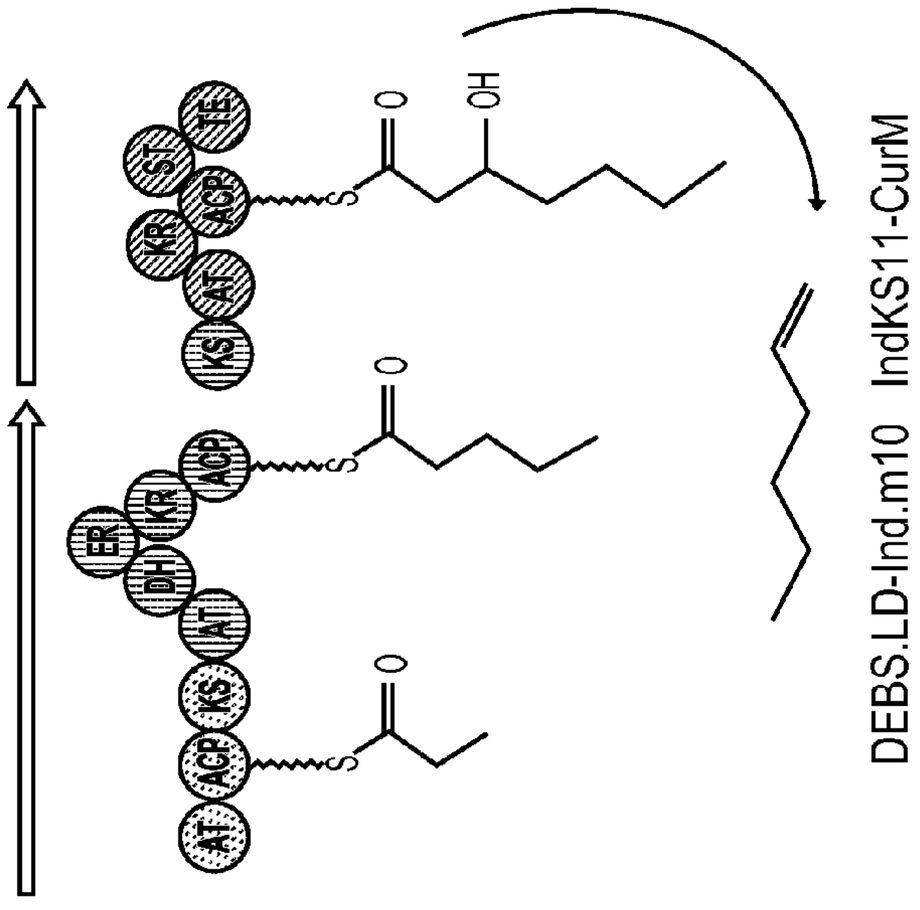


FIG. 3A

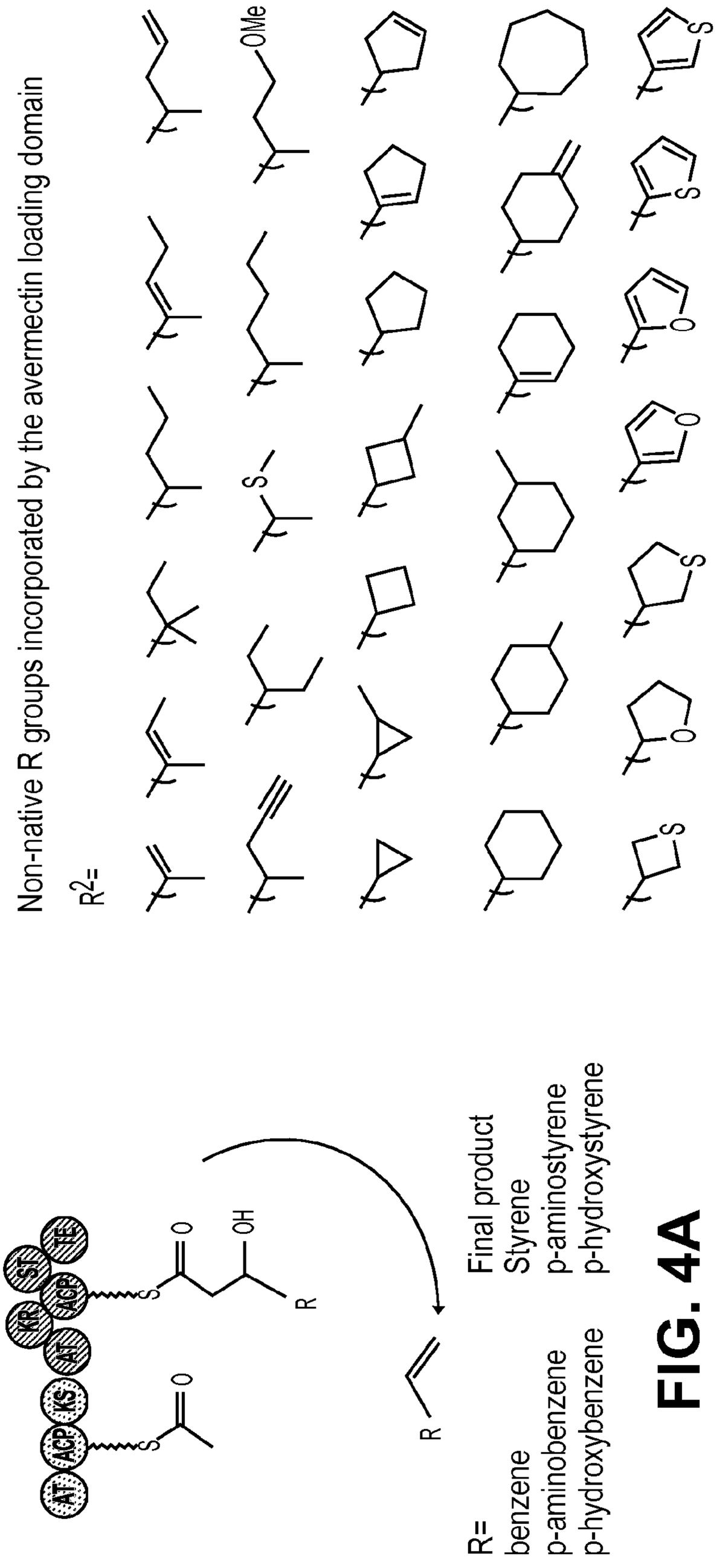
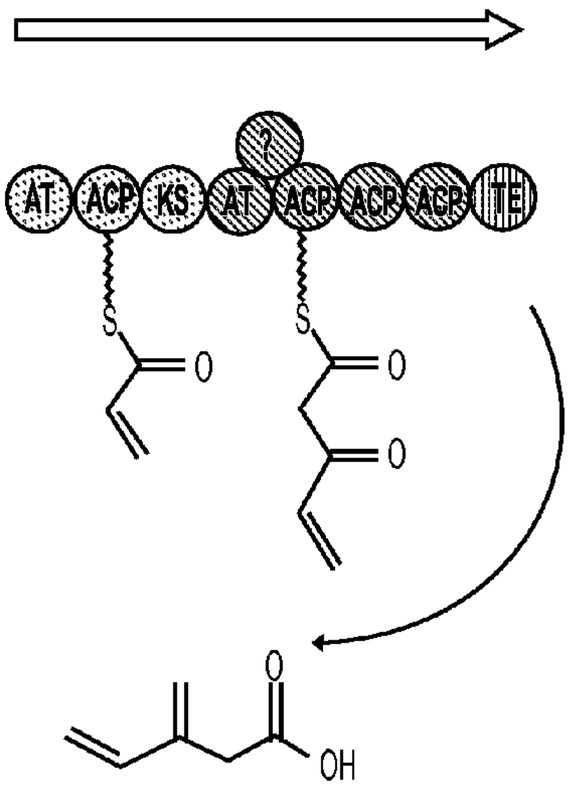

Non-native R groups incorporated by the avermectin loading domain
R2=
OMe
S
S
O
S
S
O
S
O
S
S

FIG. 4B

AT
ACP
KS
AT
KR
ST
ACP
TE
O
O
OH
R
R
R=
benzene
p-aminobenzene
p-hydroxybenzene
Final product
Styrene
p-aminostyrene
p-hydroxystyrene

FIG. 4A



DEBS.LD-JamE-DEBS TE

FIG. 5A

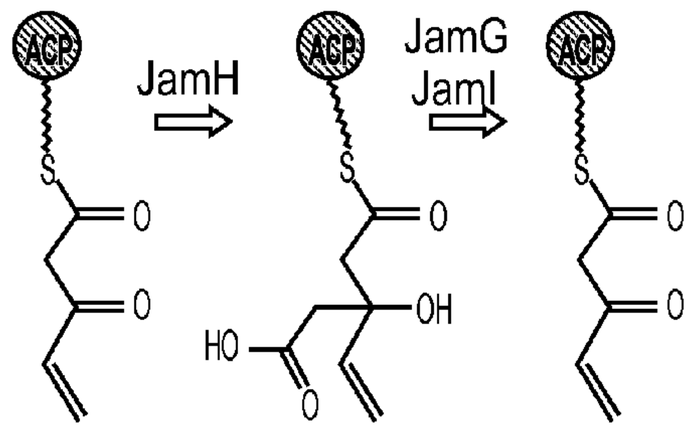


FIG. 5B

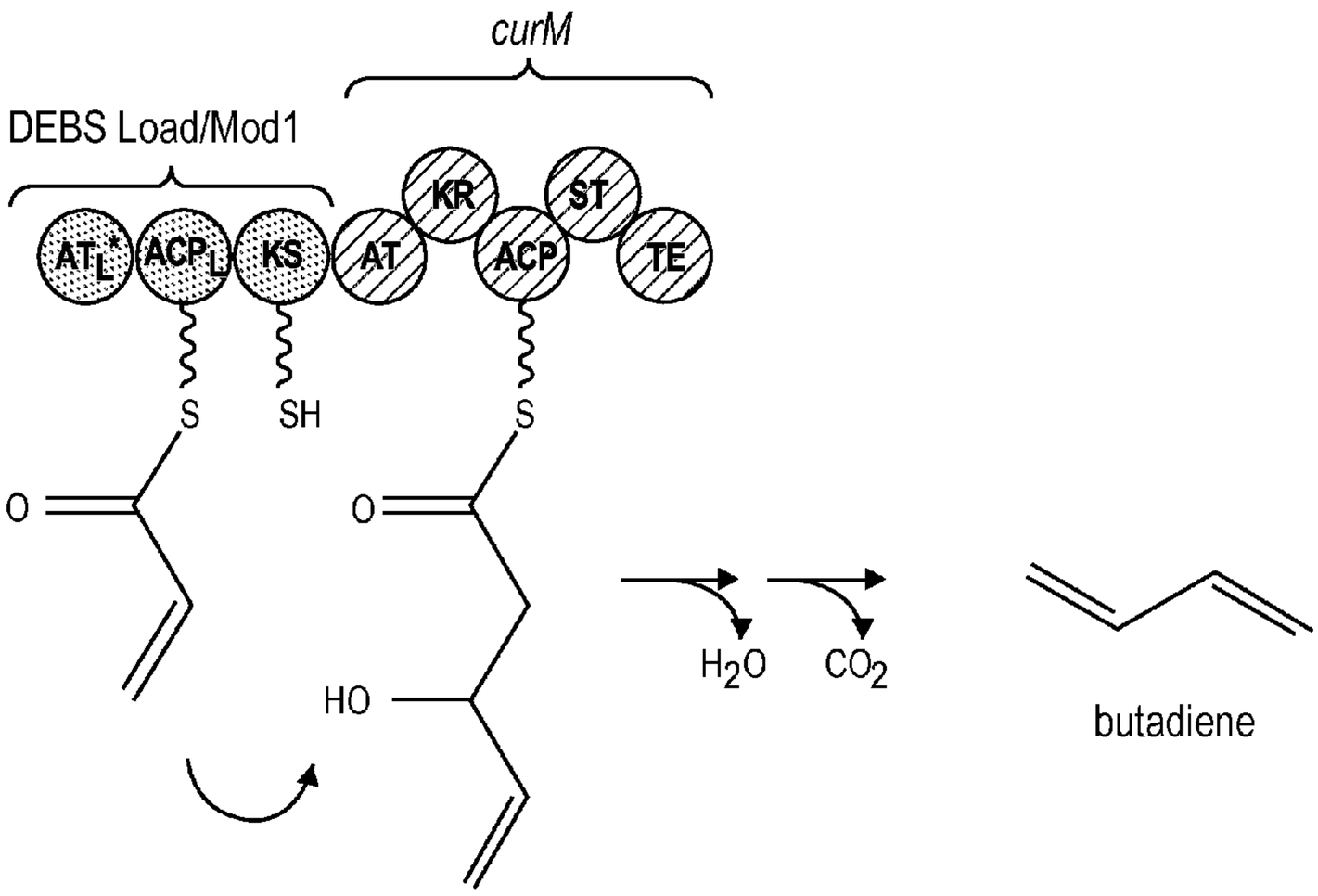


FIG. 6

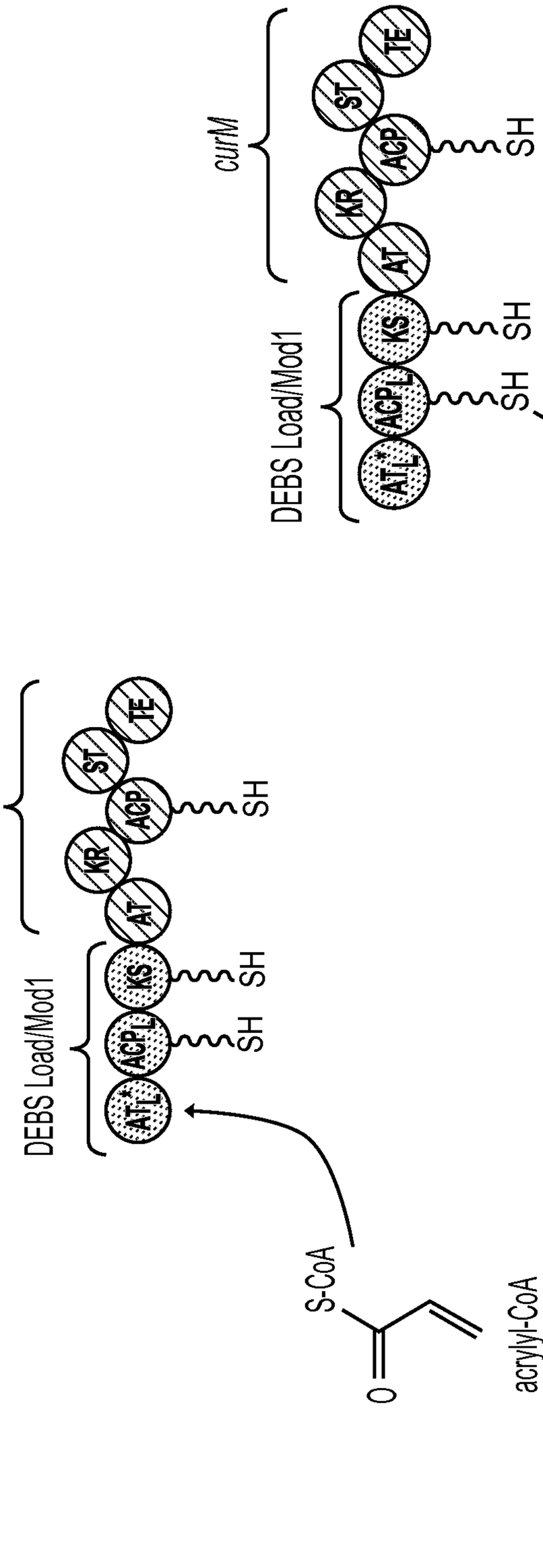

DEBS Load/Mod1
curM
AT*L
ACPL
KS
AT
KR
ACP
ST
TE
SH
SH SH
S-CoA
O
acrylyl-CoA
= DEBS propionyl-CoA specific loading domain, modified to accept acrylyl-CoA (if necessary)

FIG. 7A

DEBS Load/Mod1
curM
AT*L
ACPL
KS
AT
KR
ACP
ST
TE
SH
SH
O

FIG. 7B

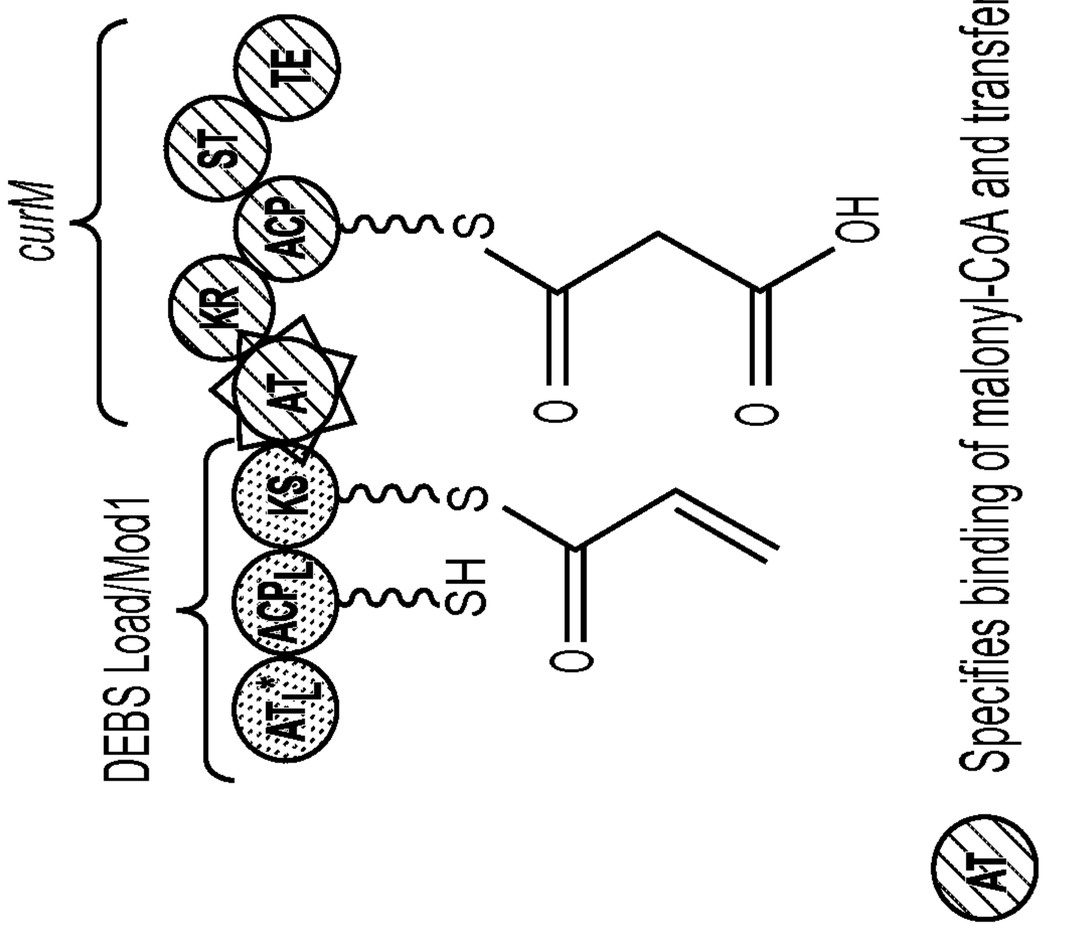

curM
DEBS Load/Mod1
AT*L
ACP L
KS
AT
KR
ACP
ST
TE
SH
S
O
OH
Specifies binding of malonyl-CoA and transfer to ACP domain
AT

FIG. 7D

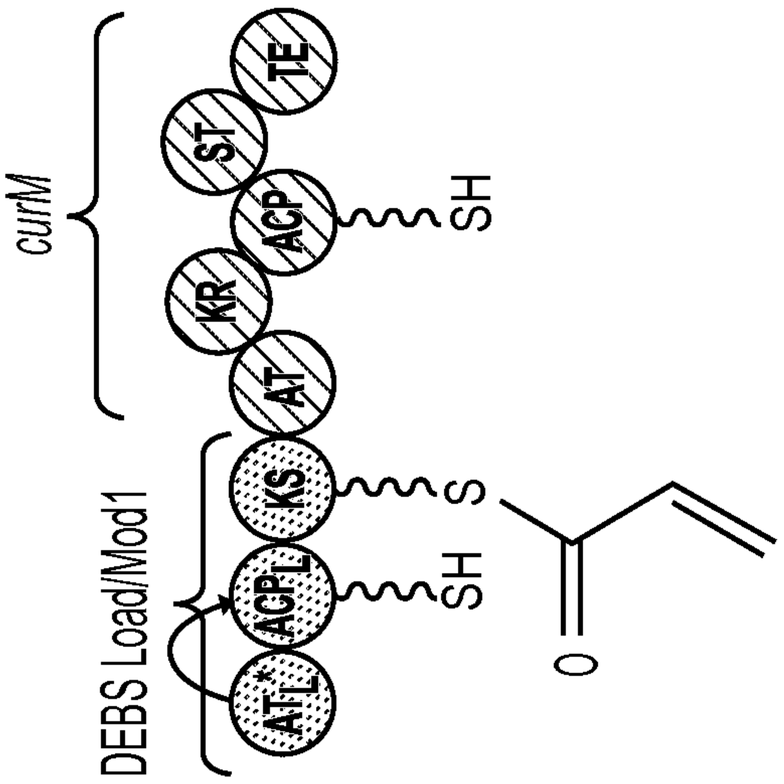

curM
DEBS Load/Mod1
AT*L
ACP L
KS
AT
KR
ACP
ST
TE
SH
S
O
Thiotransfer of acrylate moiety to KS domain

FIG. 7C

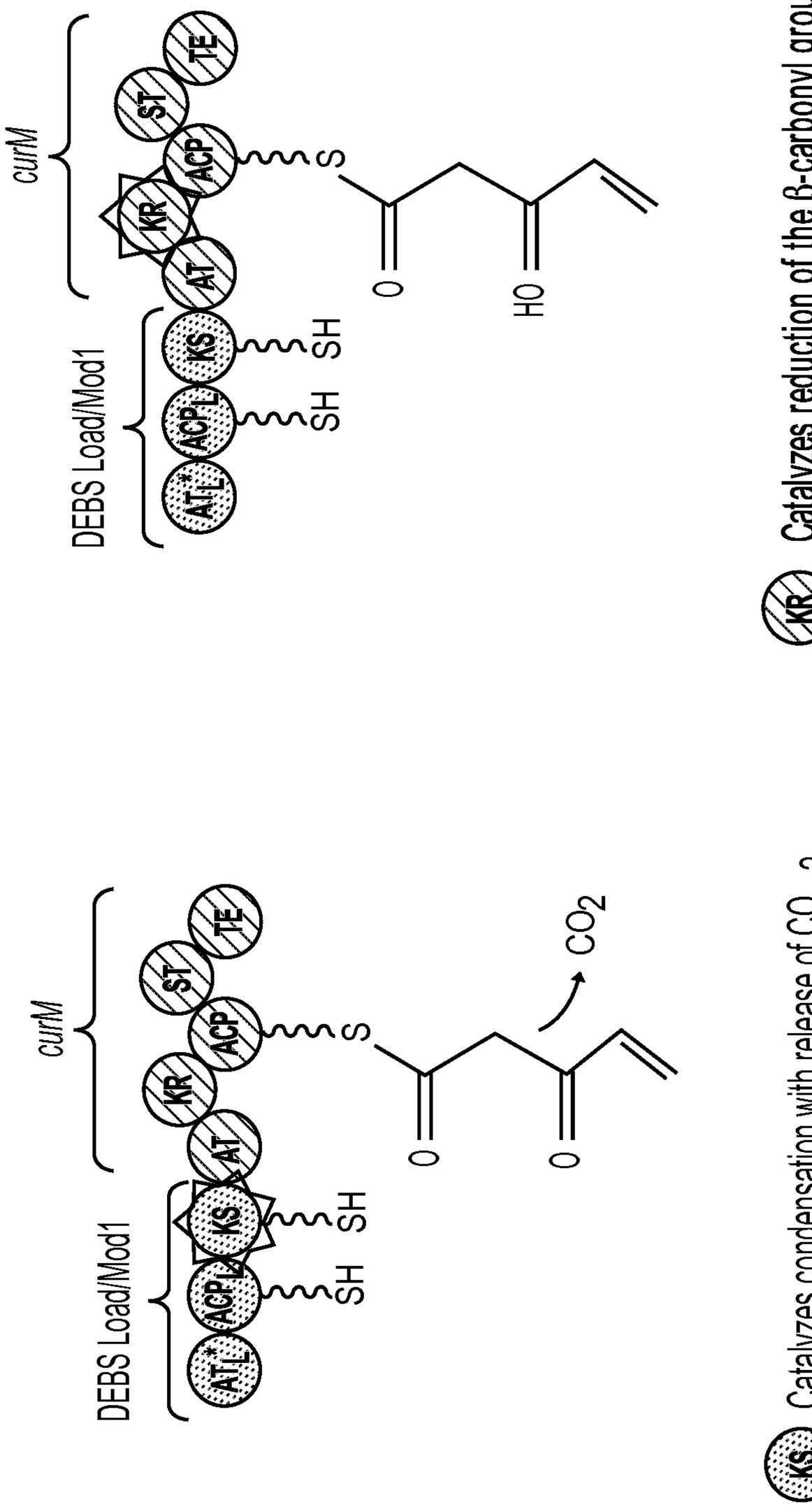

curM
DEBS Load/Mod1
AT*L
ACPL
KS
AT
KR
ACP
ST
TE
SH
S
O
HO
CO2
Catalyzes reduction of the β-carbonyl group
Catalyzes condensation with release of CO2

FIG. 7F

FIG. 7E

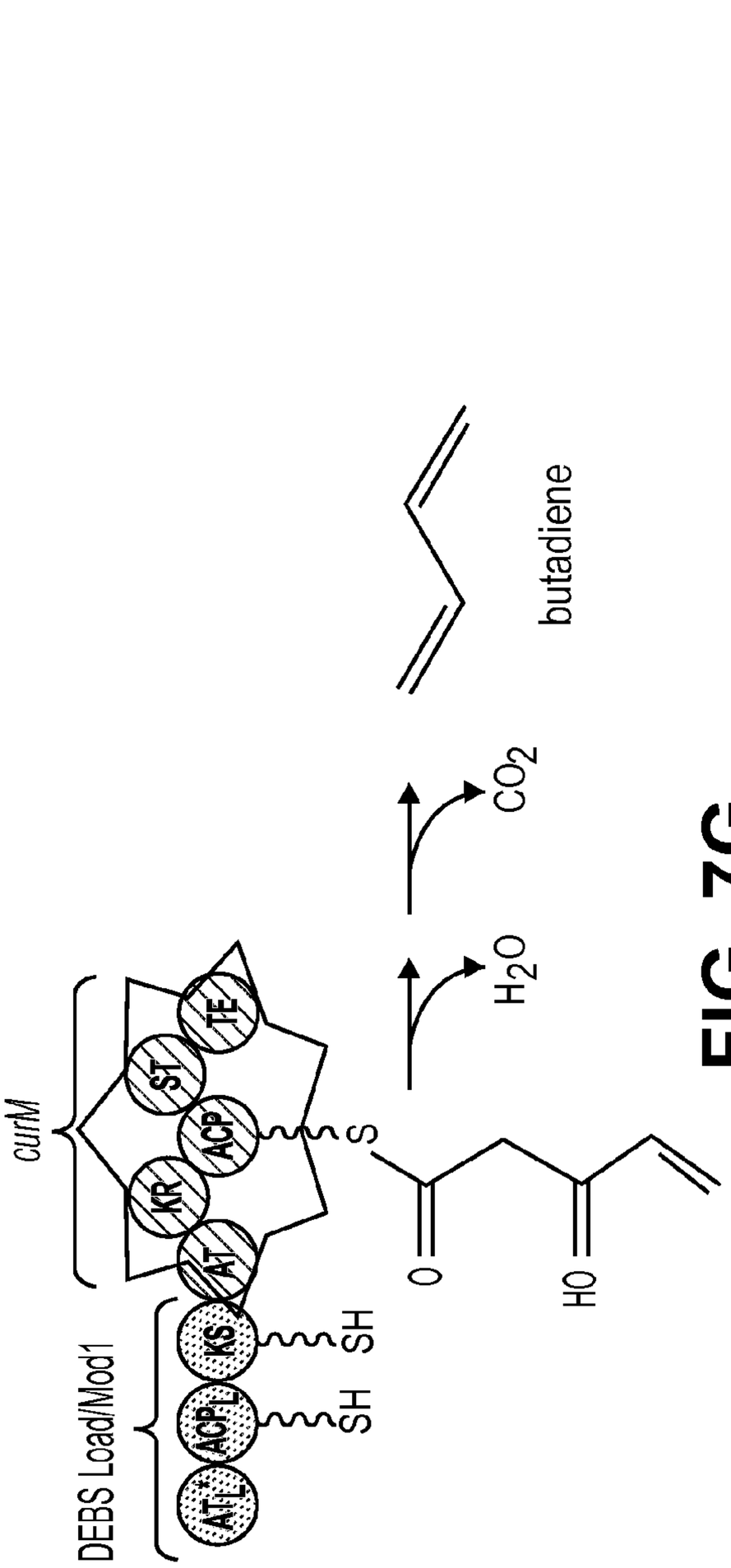

DEBS Load/Mod1
AT
ACP
KS
SH
SH
curM
AT
KR
ACP
ST
TE
S
O
HO
H2O
CO2
butadiene

FIG. 7G

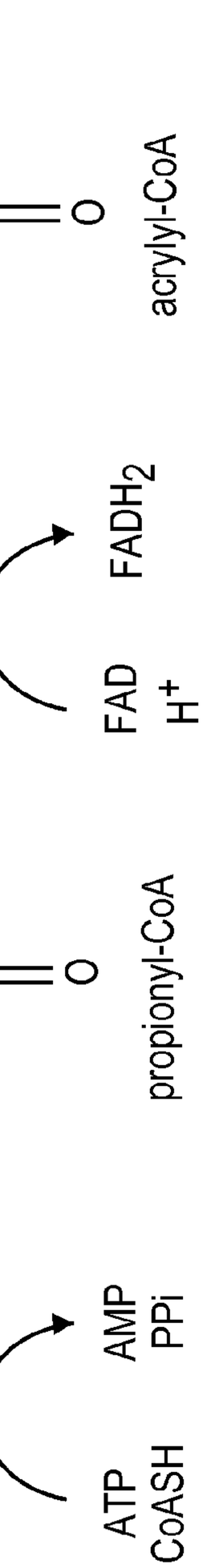
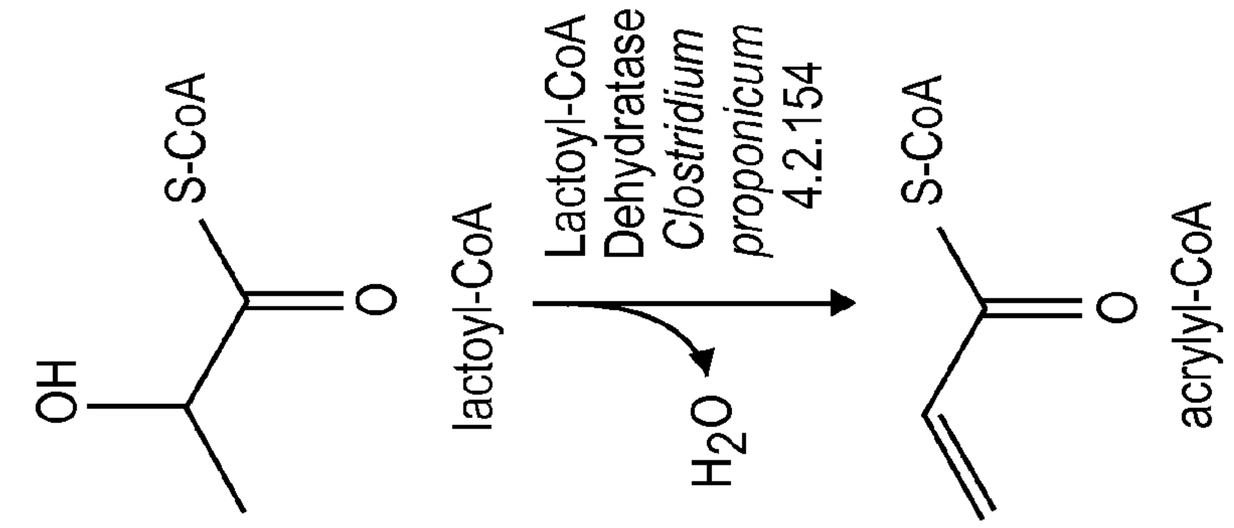
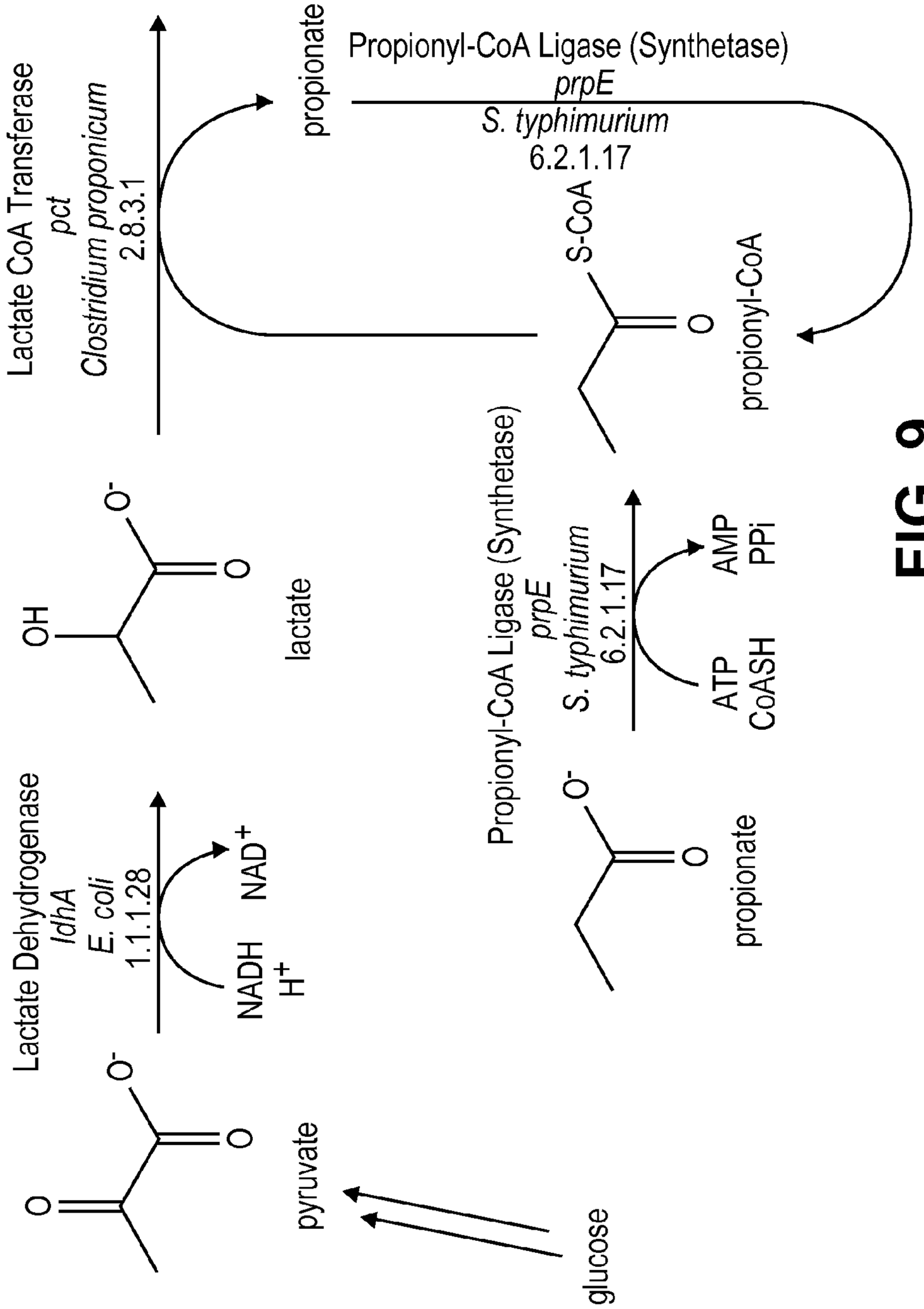

Propionyl-CoA Ligase (Synthetase)
prpE
S. typhimurium
6.2.1.17
ATP
CoASH
AMP
PPi
propionate
O-
O
Acyl-CoA Dehydrogenase
(mammalian)
1.3.99.3
FAD
H+
FADH2
S-CoA
O
propionyl-CoA
S-CoA
O
acrylyl-CoA

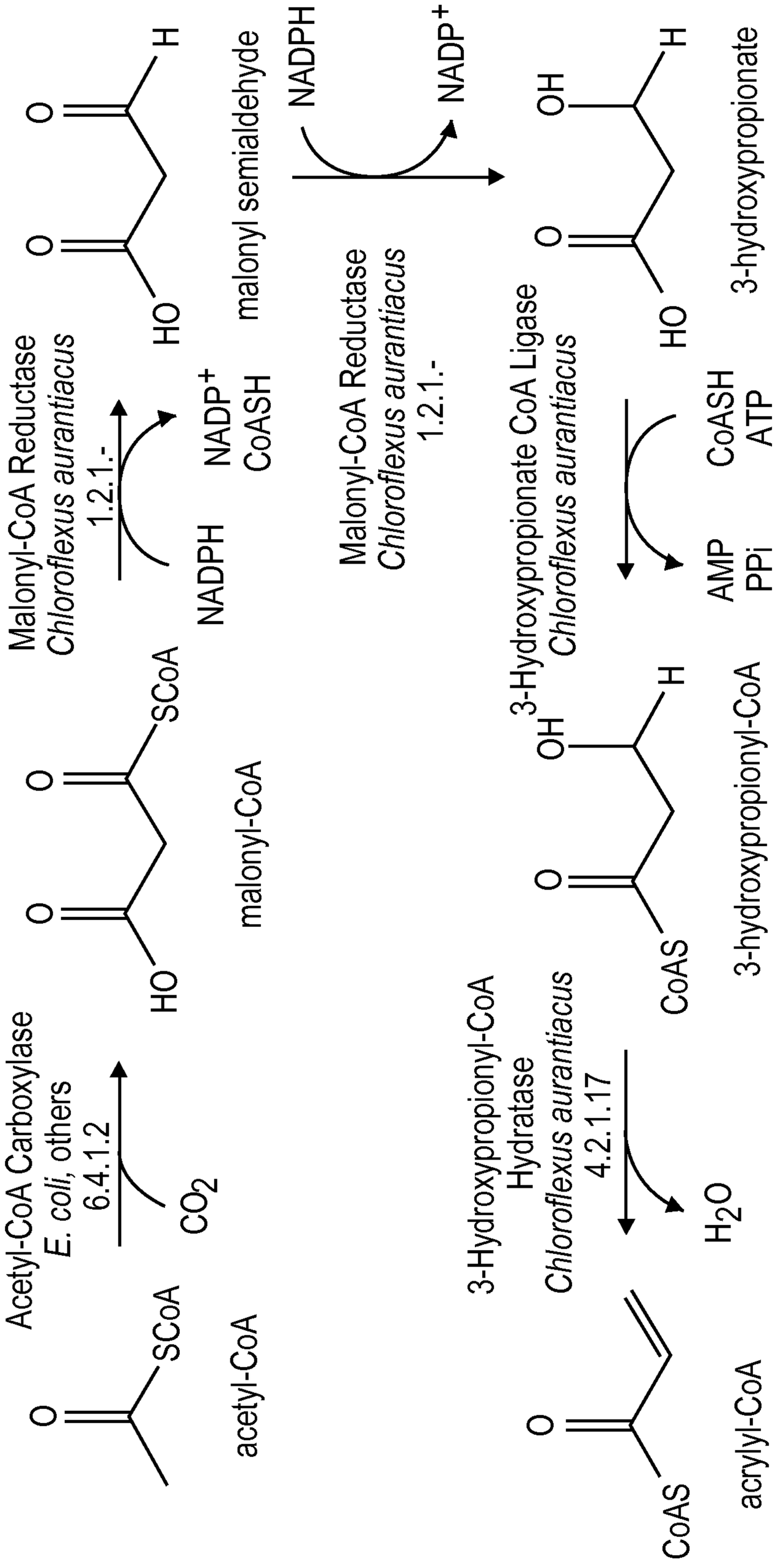
FIG. 8


S-CoA
O
OH
lactoyl-CoA
Lactoyl-CoA Dehydratase
Clostridium proponicum
4.2.154
H2O
S-CoA
O
acrylyl-CoA


Lactate CoA Transferase
pct
Clostridium proponicum
2.8.3.1
propionate
Propionyl-CoA Ligase (Synthetase)
prpE
S. typhimurium
6.2.1.17
S-CoA
O
propionyl-CoA
O-
O
OH
lactate
Propionyl-CoA Ligase (Synthetase)
prpE
S. typhimurium
6.2.1.17
ATP
CoASH
AMP
PPi

Lactate Dehydrogenase
IdhA
E. coli
1.1.1.28
NADH
H+
NAD+
O-
O
O
pyruvate
glucose
Propionate
O-
O
propionate

FIG. 9



- Four genes to clone / express

FIG. 10

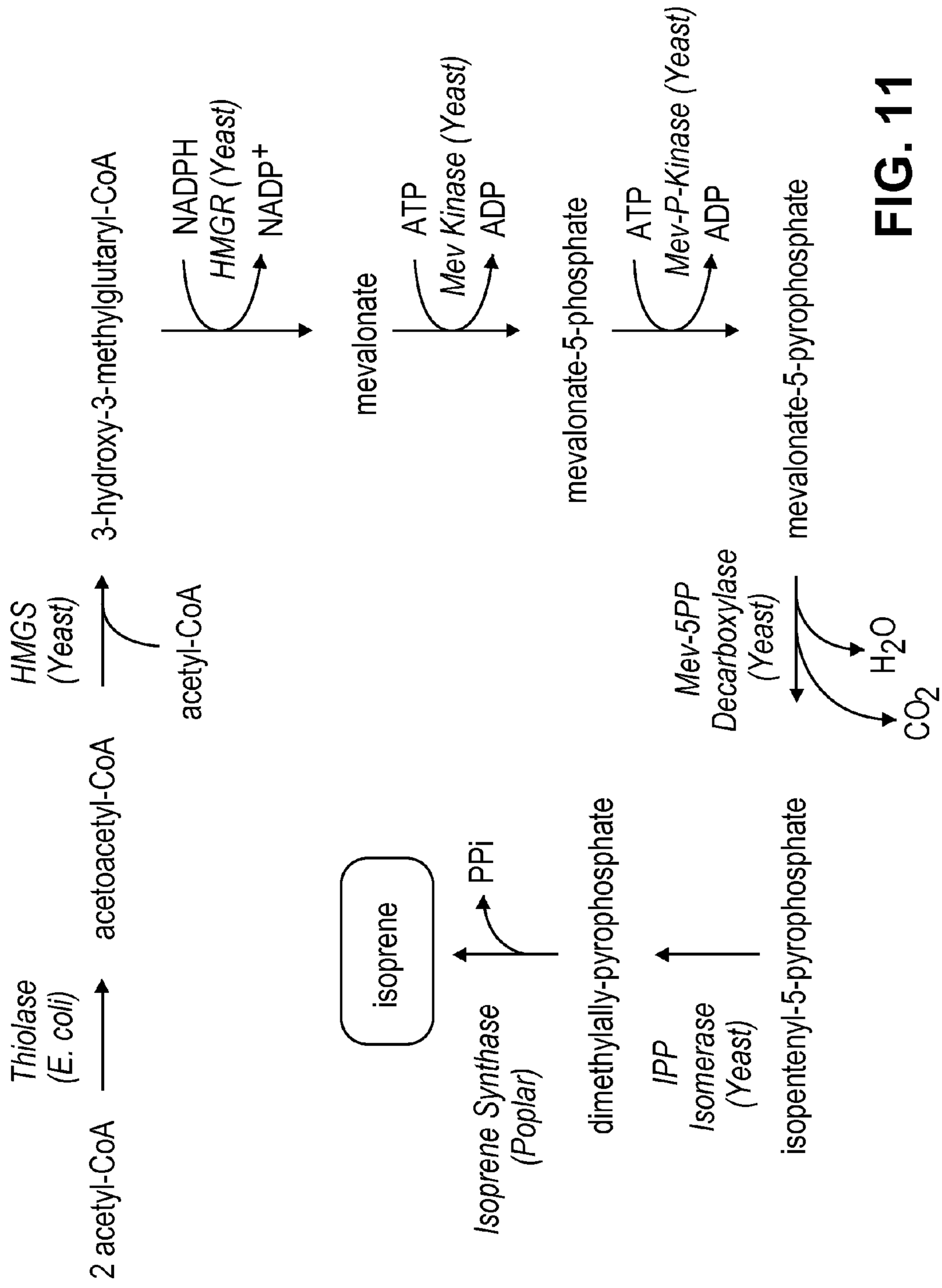

Thiolase
(E. coli)
2 acetyl-CoA
acetoacetyl-CoA
HMGS
(Yeast)
acetyl-CoA
3-hydroxy-3-methylglutaryl-CoA
HMGR (Yeast)
NADPH
NADP+
mevalonate
Mev Kinase (Yeast)
ATP
ADP
mevalonate-5-phosphate
Mev-P-Kinase (Yeast)
ATP
ADP
mevalonate-5-pyrophosphate
Mev-5PP
Decarboxylase
(Yeast)
H2O
CO2
isopentenyl-5-pyrophosphate
IPP
Isomerase
(Yeast)
dimethylally-pyrophosphate
Isoprene Synthase
(Poplar)
PPi
isoprene

FIG. 11

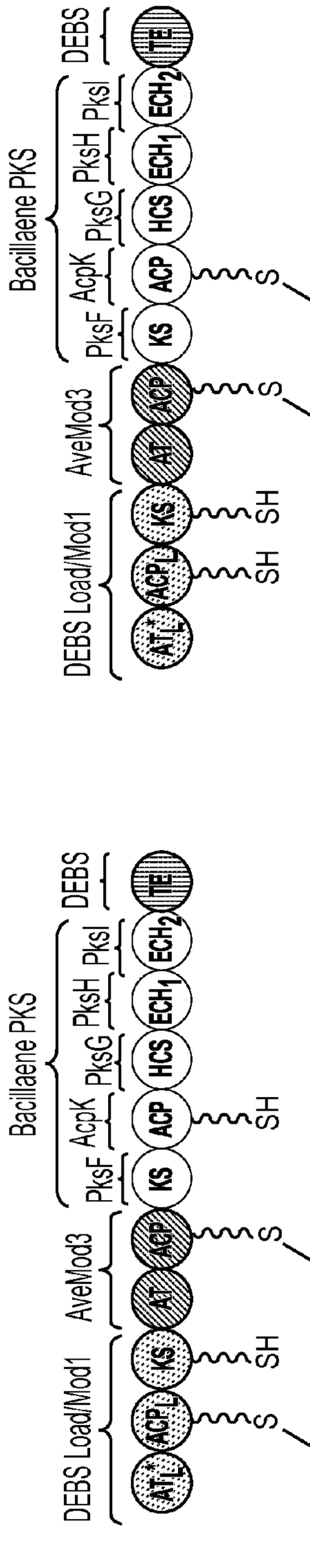


FIG. 12A

FIG. 12B

FIG. 12C

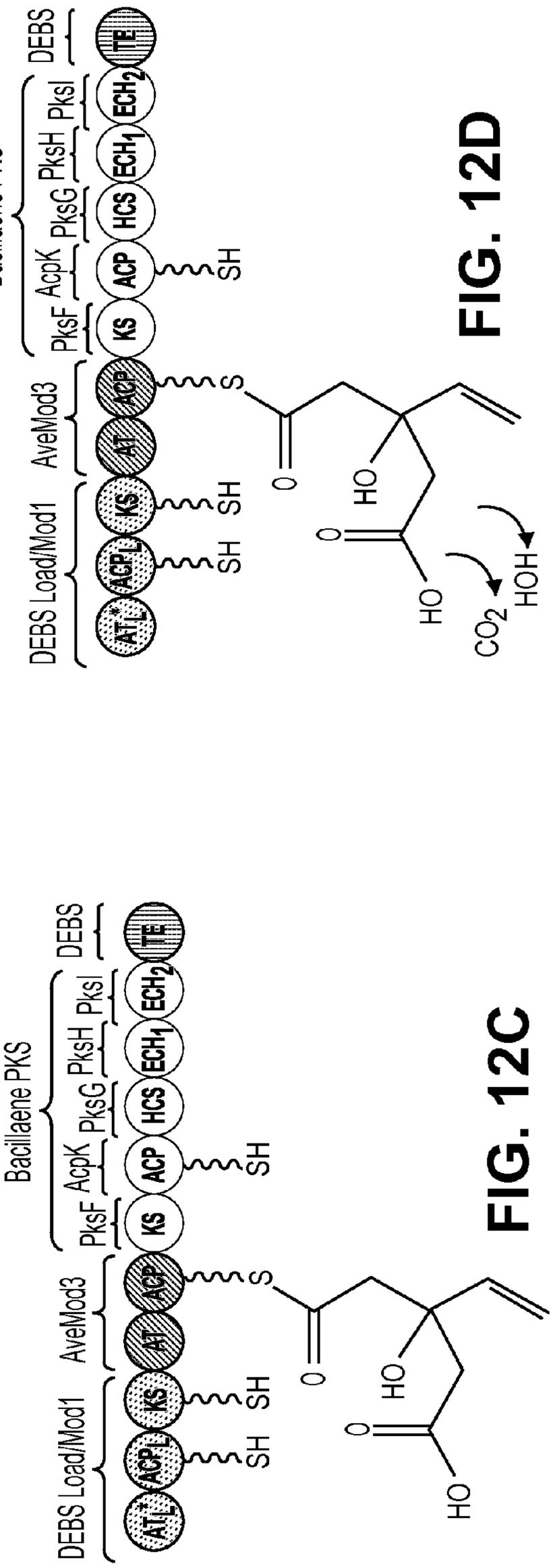


FIG. 12D

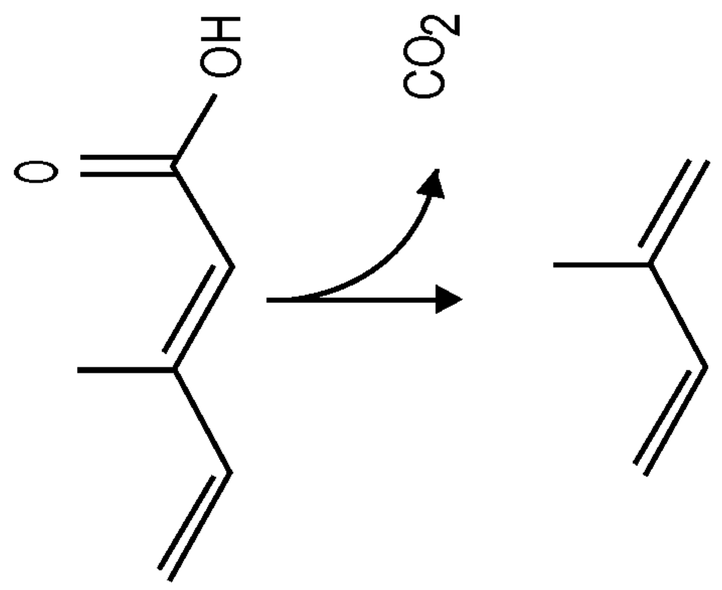


FIG. 12F

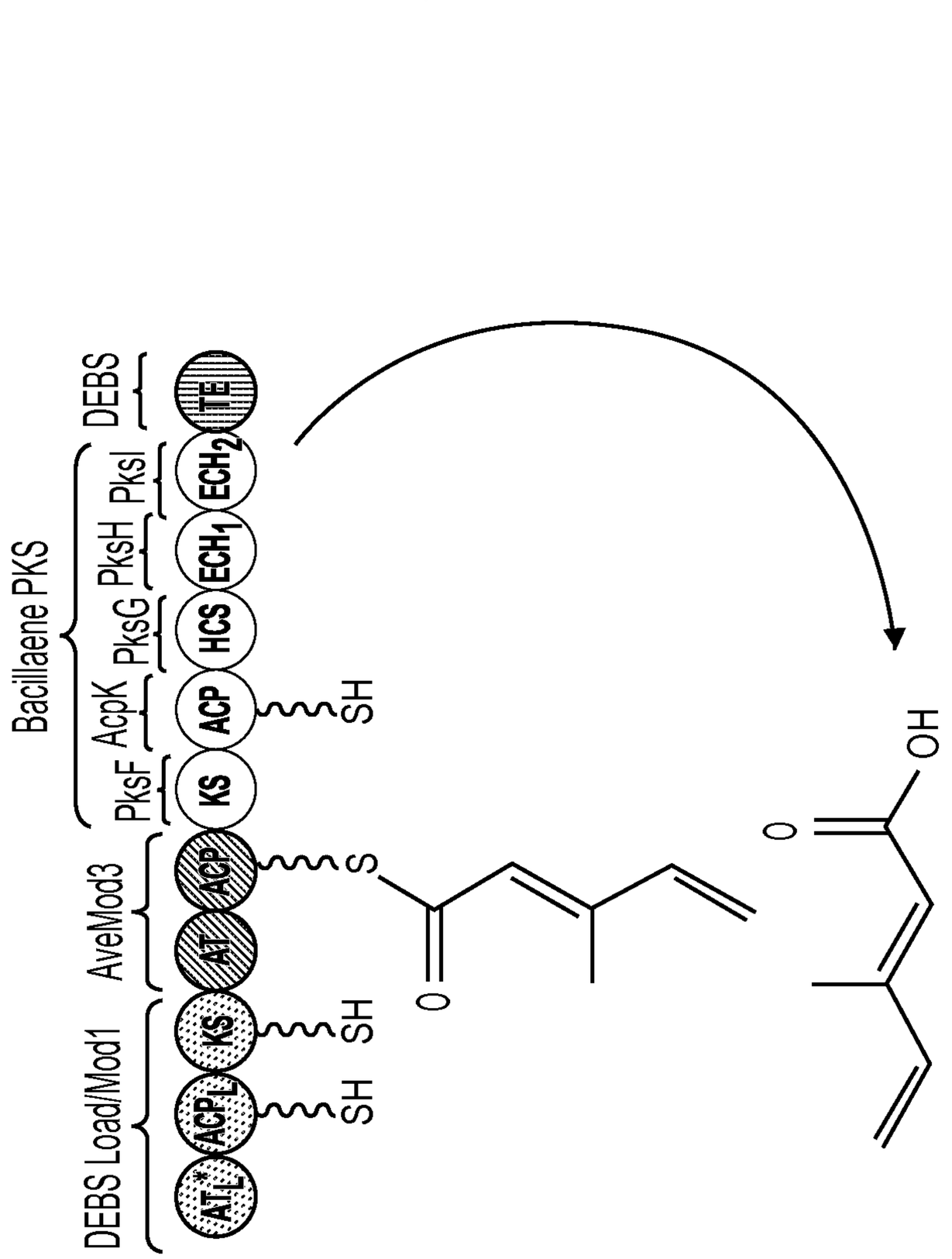


FIG. 12E

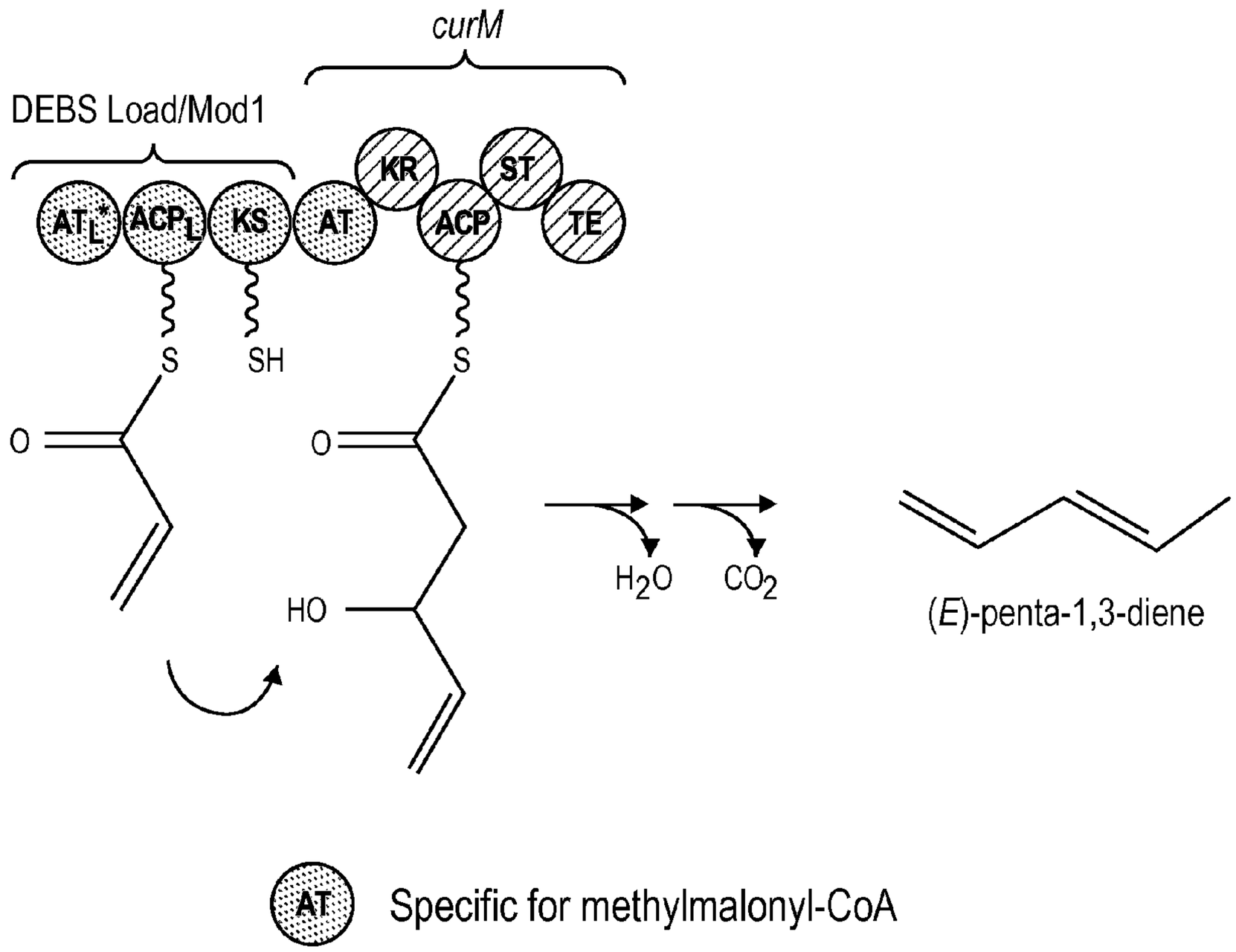

curM
DEBS Load/Mod1
AT*L
ACPL
KS
AT
KR
ACP
ST
TE
S
SH
S
O
O
HO
H2O
CO2
(E)-penta-1,3-diene
AT
Specific for methylmalonyl-CoA

FIG. 13

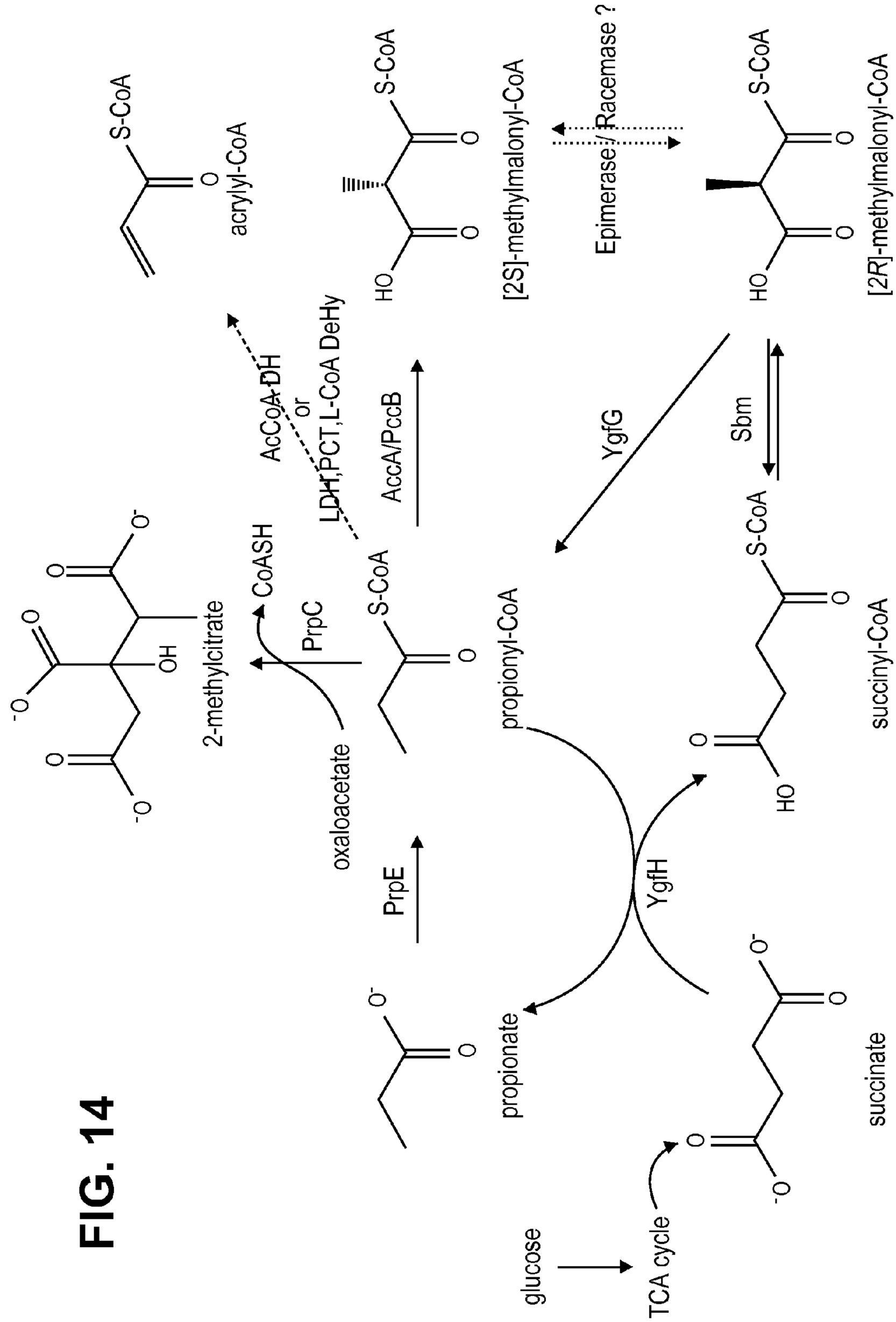

S-CoA
O
acrylyl-CoA
S-CoA
O
O
HO
[2S]-methylmalonyl-CoA
Epimerase / Racemase ?
S-CoA
O
O
HO
[2R]-methylmalonyl-CoA
AcCoA-DH
or
LDH, PCT, L-CoA DeH
AccA/PccB
YgfG
Sbm
O-
O
O
-O
OH
2-methylcitrate
CoASH
PrpC
S-CoA
O
oxaloacetate
propionyl-CoA
S-CoA
O
O
HO
succinyl-CoA
PrpE
O-
O
propionate
YgfH
glucose
TCA cycle
O
O
-O
O-
O
succinate

FIG. 14

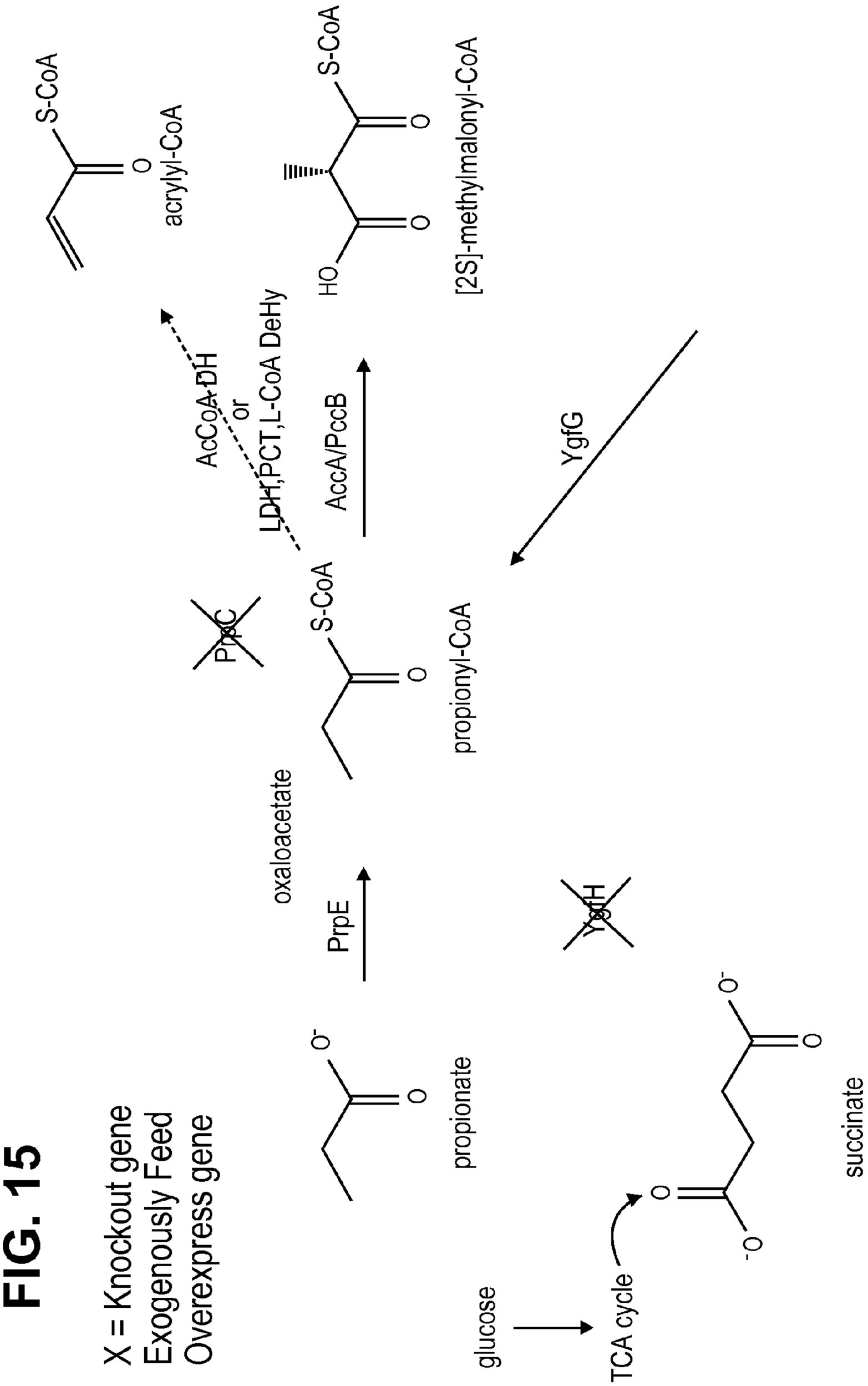


FIG. 15

X = Knockout gene
Exogenously Feed
Overexpress gene


OH

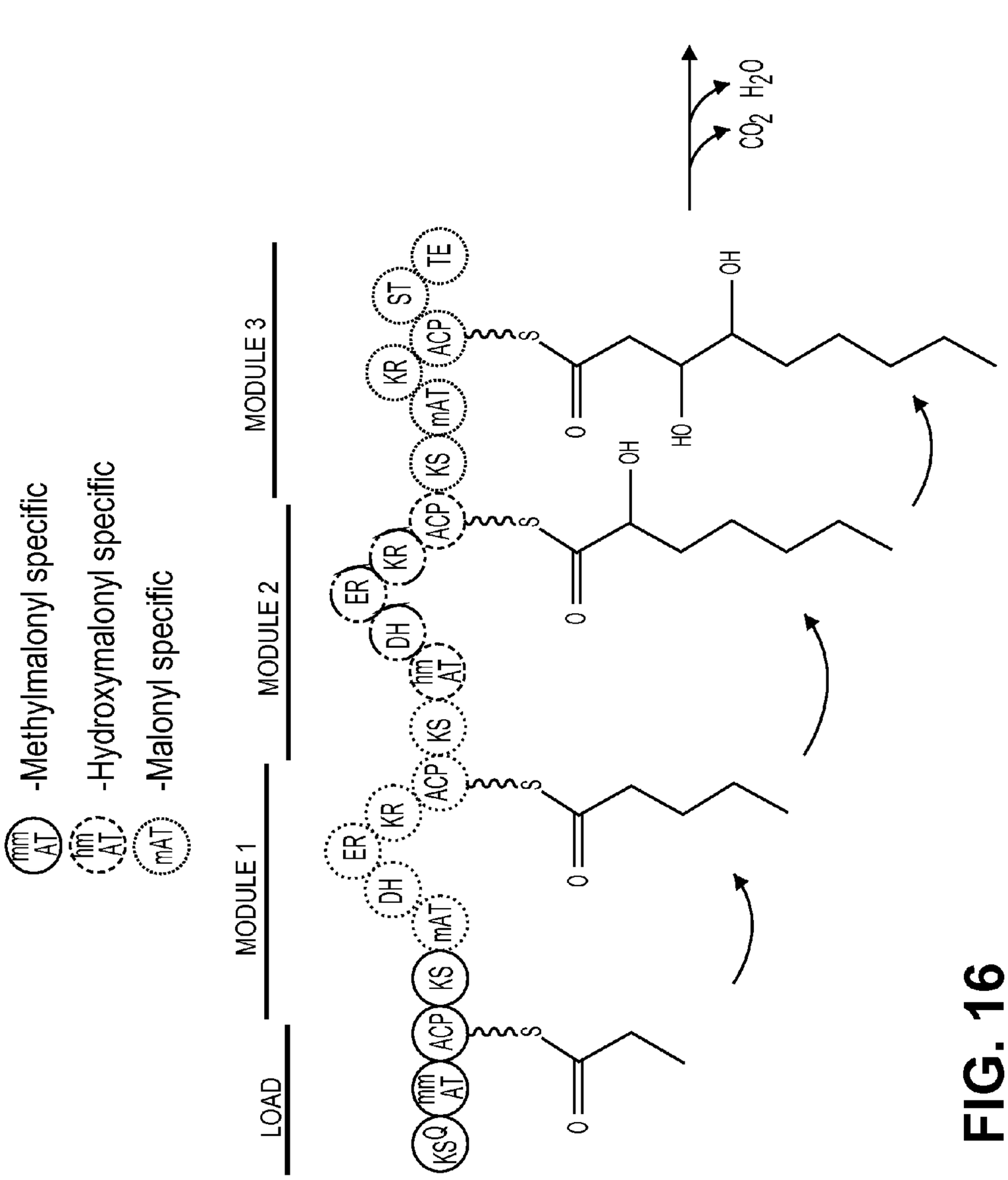

-Methylmalonyl specific
-Hydroxymalonyl specific
-Malonyl specific
LOAD
MODULE 1
MODULE 2
MODULE 3
mm AT
hm AT
mAT
KS
ACP
DH
ER
KR
ST
TE
KSQ
S
O
OH
HO
CO_2 H_2O

FIG. 16

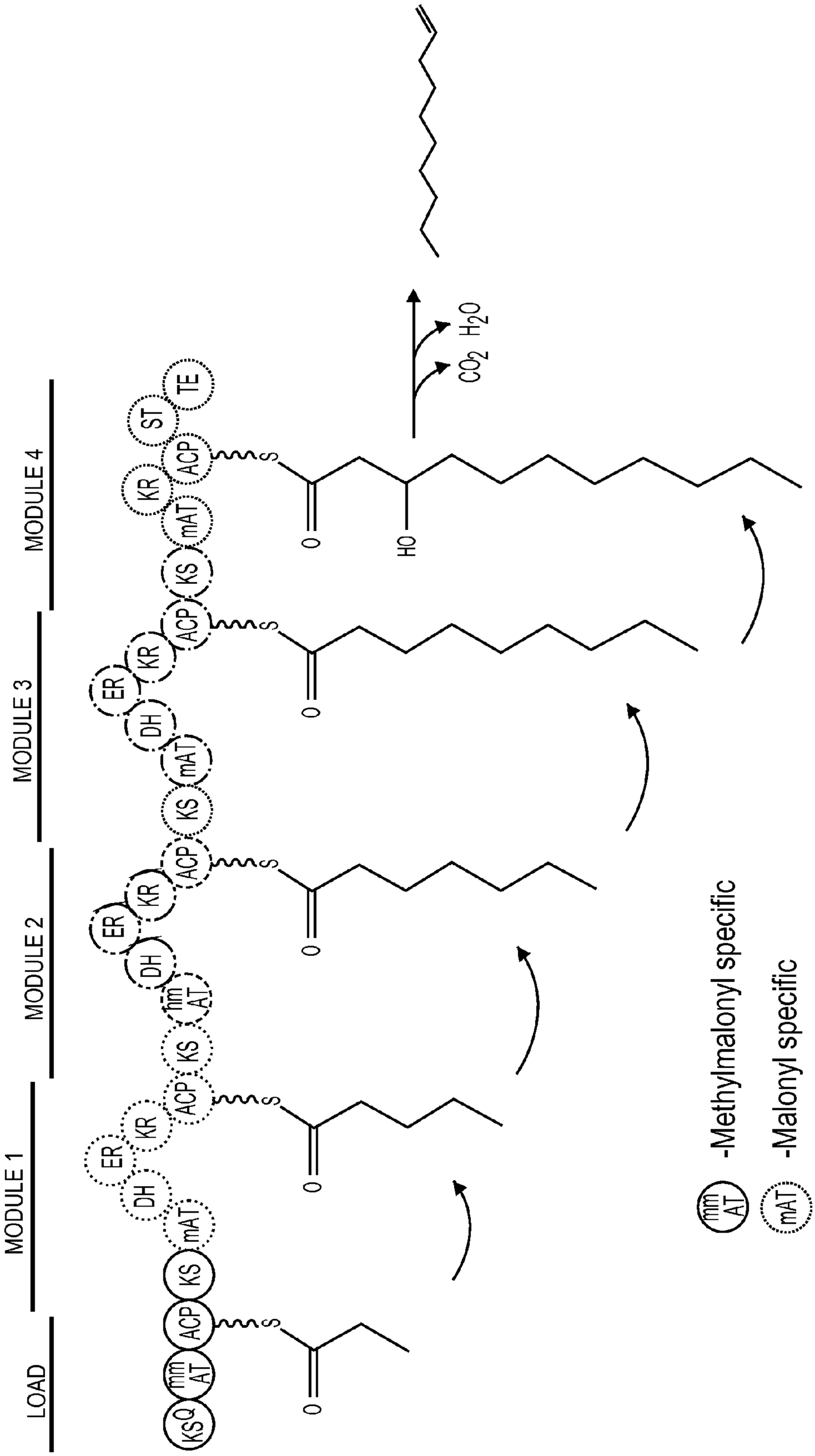

LOAD
MODULE 1
MODULE 2
MODULE 3
MODULE 4
KSQ
mm AT
ACP
KS
mAT
DH
ER
KR
TE
ST
H_2O
CO_2
HO
-Methylmalonyl specific
-Malonyl specific

FIG. 17

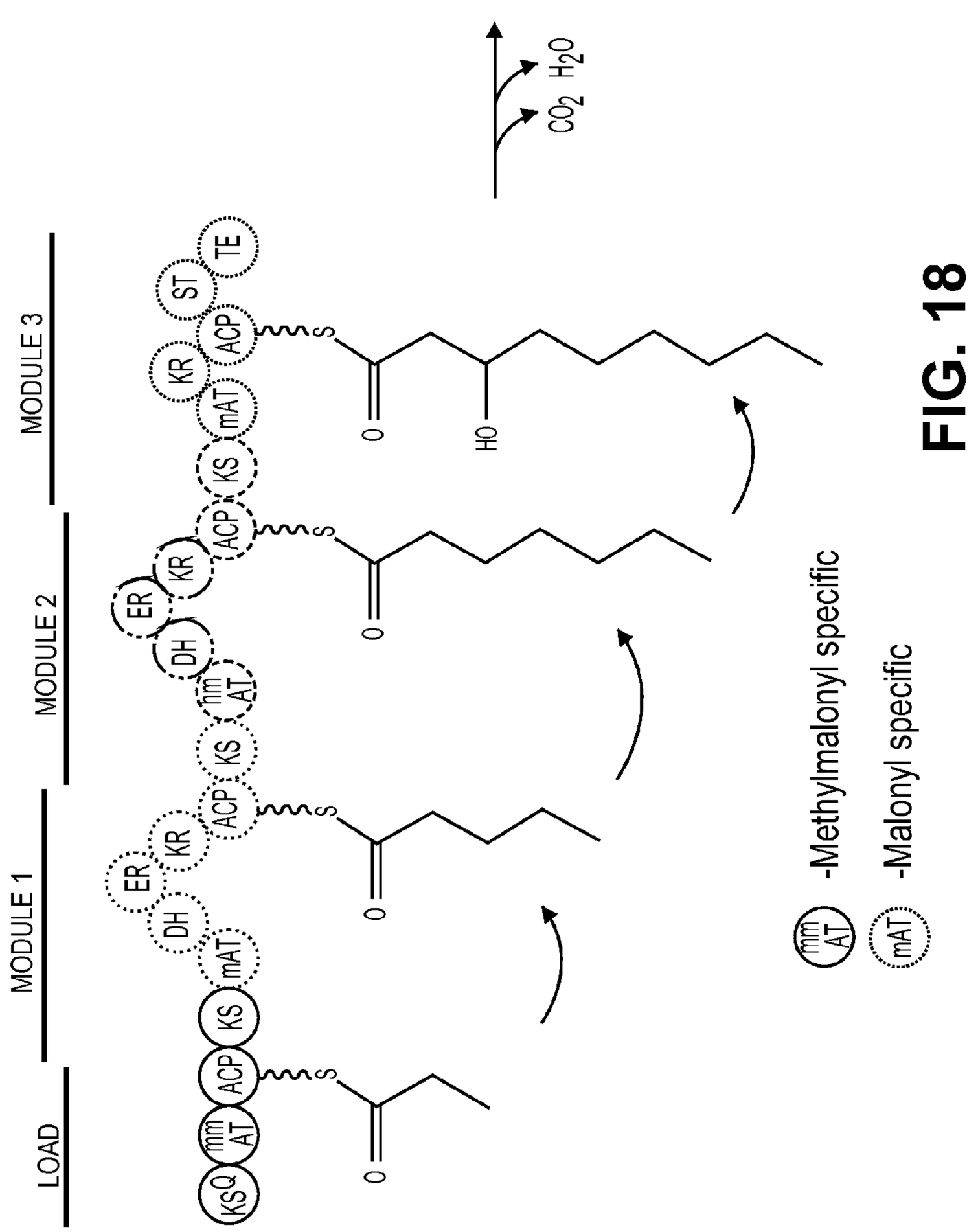

LOAD
MODULE 1
MODULE 2
MODULE 3
KS
Q
mm AT
ACP
DH
ER
KR
mAT
ST
TE
S
O
HO
CO_2 H_2O
-Methylmalonyl specific
-Malonyl specific

FIG. 18

PRODUCING ALPHA-OLEFINS USING POLYKETIDE SYNTHASES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application Ser. No. 61/387,435, filed Sep. 28, 2010, which is hereby incorporated by reference in its entirety.

STATEMENT OF GOVERNMENTAL SUPPORT

[0002] This invention was made with government support under Contract No. DE-AC02-05CH11231 awarded by the U.S. Department of Energy and Award No. 0540879 awarded by the National Science Foundation. The government has certain rights in the invention

FIELD OF THE INVENTION

[0003] This invention relates generally to α-olefin production using polyketide synthases and so relates to the fields of chemistry, microbiology, and molecular biology.

BACKGROUND OF THE INVENTION

[0004] Type I polyketide synthases (PKSs) are programmable, multifunctional enzymes capable of possessing all of the catalytic capacity of fatty-acid synthases (FASs). However, unlike the FAS enzyme, which iteratively extends and fully reduces the β-carbonyl generated with each extension of the hydrocarbon backbone, PKS systems utilize discrete sets of enzymatic domains for each extension and reduction of the nascent chain. These sets, commonly referred to as modules, can incorporate a variety of extenders units resulting in different side chains. They also can encode between zero and three of the reducing domains associated with FASs, respectively leading to a ketone, hydroxy, double bond, or fully saturated carbon at the beta position of the growing polyketide chain (Hopwood and Sherman. 1990. Annual Review of Genetics 24:37-66).

[0005] Due to their modularity, PKS systems have been extensively explored for production of "unnatural" natural products (Weissman and Leadlay. 2005. Nature Reviews Microbiology 3:925-936). Hundreds of these molecules have been produced, ranging from basic lactones to modified versions of drugs and drug-like compounds.

SUMMARY OF THE INVENTION

[0006] The present invention provides polyketide synthases (PKSs) capable of synthesizing α-olefins, recombinant expression vectors for producing them, recombinant host cells that express them and produce the desired alpha olefin, methods for making alpha olefins, and alpha olefins produced by the methods. The PKSs of the invention are not naturally occurring and so are referred to as "recombinant" PKS enzymes. In some embodiments of the invention, the α-olefin is not a compound synthesized by a naturally occurring PKS. In some embodiments of the invention, the PKS is a hybrid PKS comprising modules and/or portions thereof, from two, three, four or more naturally occurring PKSs. A hybrid PKS can contain naturally occurring modules from two or more naturally occurring PKSs and/or it can contain one or more modules composed of portions, including intact domains, of two or more modules from the same naturally occurring PKS or from two or more naturally occurring PKS, or both. In some embodiments of the invention, a recombinant nucleic acid comprising a CurM module or portion thereof, which may be either naturally occurring or recombinant, is employed.

[0007] The present invention provides recombinant nucleic acids that encode PKSs of the invention. The recombinant nucleic acids include nucleic acids that include a portion or all of a PKS of the invention, nucleic acids that further include regulatory sequences, such as promoter and translation initiation and termination sequences, and can further include sequences that facilitate stable maintenance in a host cell, i.e., sequences that provide the function of an origin of replication or facilitate integration into host cell chromosomal or other DNA by homologous recombination. In some embodiments, the recombinant nucleic acid is stably integrated into a chromosome of a host cell. In some embodiments, the recombinant nucleic acid is a plasmid. Thus, the present invention also provides vectors, including expression vectors, comprising a recombinant nucleic acid of the present invention. The present invention also provides host cells comprising any of the recombinant nucleic acid and/or PKS of the present invention. In some embodiments, the host cell, when cultured under suitable conditions, is capable of producing the α-olefin. These host cells include, for example and without limitation, prokaryotes such as *E. coli* species, *Bacillus* species, *Streptomyces* species, Myxobacterial species, as well as eukaryotes including but not limited to yeast and fungal strains.

[0008] Thus, the present invention provides a wide variety of host cell comprising one or more of the recombinant nucleic acids and/or PKSs of the present invention. In some embodiments, the host cell, when cultured, is capable of producing an α-olefin that it otherwise does not produce, or produces at a lower level, in the absence of a nucleic acid of the invention.

[0009] The present invention provides methods for producing α-olefins, said methods generally comprising: providing a host cell of the present invention, and culturing said host cell in a suitable culture medium under suitable conditions such that the α-olefin is produced.

[0010] The present invention also provides compositions comprising an α-olefin from a host cell in which the α-olefin was produced, and in some embodiments may include trace residues and/or other components of the host cell. Such trace residues and/or other components may include, for example, cellular material produced by the lysis of the host cell. The present invention also provides methods of purifying α-olefins and methods for converting them to other useful products.

BRIEF DESCRIPTION OF THE DRAWINGS

[0011] The foregoing aspects and embodiments of the invention as well as others will be readily appreciated by the skilled artisan from the following detailed description of illustrative embodiments when read in conjunction with the accompanying drawings.

[0012] FIG. **1** shows an illustrative example of the modular organization of a biosynthetic pathway suitable for synthesizing 1-hexene in accordance with the invention. In this illustration, the proposed modules are sourced from the loading module of DEBS1 from the erythromycin PKS, module 5 from the nystatin PKS NysC, and CurM the terminal module of the curacin PKS. In another embodiment of the invention, the nystatin PKS module 5 is replaced with portions of mod-

ules 9 and 10 from the indanomycin PKS; this alternative embodiment has actually been used to produce 1-hexene.

[0013] FIG. **2** shows types of modules employed and corresponding precursors utilized for incorporation into polyketide chains. The loading module is designated S. While any suitable loading domain can be used (such as those loading acetate and benzoic acid), only two examples are illustrated in this figure. The remaining compounds represent the structures incorporated into the growing polyketide chain employing extender modules A-P. The dashed line indicates the C—C bond formed through Claisen condensation; atoms to the right of the bond and the C atom at the left of the dashed line represent the structures determined by the module employed. The R group represents the existing acyl chain prior to incorporation determined by the module.

[0014] FIG. **3** shows: (A) a PKS system that can be used to produce 1-hexene in accordance with the invention, (B) how additional modules can be added to yield longer, even-chain α-olefins, and (C) how changing the loading module to incorporate acetate (from malonyl-CoA) will allow access to the saturated, linear, odd-chain α-olefins in accordance with the methods of the invention.

[0015] FIG. **4** shows an embodiment of the invention that illustrates utilization of the avermectin PKS loading module. The side chains illustrated are merely examples and do not constitute the entire pool of side chains that can be incorporated using the avermectin loading module (or similar loading modules) in accordance with the methods and teaching of the invention.

[0016] FIG. **5** shows, in part (A), an example of an illustrative pathway to 3-methylenepent-4-enoic acid, an example of the carboxylated butadiene derivatives accessible using PKSs in accordance with the methods of the invention and how the distance between the diene and carboxylate moieties can be increased via the use of additional PKS modules. FIG. **5**, part (B), shows the proposed mechanism of the exomethylene biosynthesis from the jamaicamide pathway (see Edwards et al. 2004. Chem. Biol. 11(6):817-33; incorporated herein by reference).

[0017] FIG. **6** shows a PKS for producing butadiene in accordance with the methods of the invention. While this invention is not to be limited in any manner by any proposed mechanism of action recited or shown herein, this figure, for simplicity, illustrates loss of the hydroxyl group as a water molecule, the enzymatic mechanism utilizes sulfate as a leaving group.

[0018] FIG. **7** shows a PKS for producing butadiene in accordance with the methods of the invention. Parts (A) and (B) show the loading of the acrylyl-CoA using the DEBS propionyl-CoA specific loading domain modified to accept acrylyl-CoA. Part (C) shows the thiotransfer of the acrylate moiety to KS domain. Part (D) shows the binding of the malonyl-CoA and transfer to ACP domain. Part (E) shows KS catalyzing the condensation of the moiety with release of CO_2. Part (F) shows KR catalyzing the reduction of the β-carbonyl group. Part (G) shows the final step and the release of the butadiene, CO_2, and water (as in FIG. **6**, the loss of the hydroxyl group is illustrated with a water molecule, but the enzymatic mechanism utilizes sulfate as a leaving group).

[0019] FIG. **8** shows an enzymatic pathway accessible by the methods and materials of the invention to produce acrylyl-CoA comprising exogenously supplying propionate, and expressing PrpE and acyl-CoA dehydrogenase activities. A host cell comprising this system would be provided with propionate, which could be exogenously fed to, if not produced endogenously by, the host cell selected for production.

[0020] FIG. **9** shows an enzymatic pathway accessible by the methods and materials of the invention to produce acrylyl-CoA comprising exogenously supplying propionate and glucose. A host cell comprising this system would be provided with propionate, either through exogenous feeding or the introduction of propionate biosynthesis pathway, as above, and a suitable organic molecule that the host cell can directly or indirectly convert into a pyruvate. For example, if the host cell is *E. coli*, the suitable organic molecule can be glucose. This pathway utilizes the central metabolic intermediate pyruvate to produce lactate via a lactate dehydrogenase. Lactate is then converted to lacoyl-CoA by a lactate CoA transferase, utilizing propionyl-CoA as a cofactor and releasing propionate. Lactoyl-CoA is then dehydrated using a lactoyl-CoA dehydratase to yield acrylyl-CoA. One embodiment of this invention includes the lactate dehydrogenase, LdhA, from *E. coli*, the lactate CoA transferase, Pct, from *Clostridium proponicum*, and the lactoyl-CoA dehydratase enzymes, EI and EII, from *C. proponicum*. The introduction of this pathway into *E. coli* or yeast for diene (such as butadiene) production represents a novel application of these enzymes. An embodiment of this invention is use of this pathway for PKS-based acrylate production.

[0021] FIG. **10** shows an enzymatic pathway accessible by the methods and materials of the invention to produce acrylyl-CoA starting from the common metabolic precursor malonyl-CoA. This pathway generates malonyl-CoA using an acetyl-CoA carboxylase, acetyl-CoA and CO_2. Malonyl-CoA is then reduced by a malonyl-CoA reductase releasing malonyl semialdehyde. Malony semialdehyde is converted to 3-hydroxypropionate using a substrate specific oxidoreductase. A 3-hydroxypropionate CoA ligase catalyzes the formation of 3-hydroxypropionyl-CoA. This intermediate is then dehydrated to acryalyl-CoA by the reverse reaction of 3-hydroxypropionyl-CoA hydratase. In one embodiment of the invention, these enzymes are the acetyl-CoA carboxylase complex (AccA/AccD) from *E. coli*, the malonyl-CoA reductase (The introduction of this pathway into *E. coli* or yeast for diene (e.g. butadiene) production represents a novel application of these enzymes and is a unique embodiment of this invention. An embodiment of this invention is use of this pathway for PKS-based acrylate production.

[0022] FIG. **11** shows an enzymatic pathway accessible by the methods and materials of the invention to produce isoprene via the mevalonate pathway.

[0023] FIG. **12** shows an example of an illustrative pathway accessible by a PKS provided by the invention for producing isoprene. (A) shows the loading of the acrylyl-CoA using the DEBS propionyl-CoA specific loading domain modified to accept acrylyl-CoA, and extension with malonyl-CoA to form the beta-keto ACP bound intermediate. Parts (B)-(D) show the HMG-CoA-like mechanism involved in the replacement of the β-carbonyl group with a methyl group using PKS enzymes from the PKSX (Bacillaene) cluster from *Bacillus subtilis* (Butcher, et al. 2007. Proc Natl Acad Sci USA. 104 (5):1506-9; incorporated herein by reference). This invention is not to be limited by any proposed mechanism shown herein. In this embodiment, the penultimate product is released as the free acid and subsequently decarboxylated to isoprene in accordance with the methods of the invention by either a decarboxylase, or extracellular chemical catalysis/pyrolysis.

[0024] FIG. **13** shows a PKS provided by the invention for producing (E)-penta-1,3-diene. This figure illustrates loss of the hydroxyl group as a water molecule, but the enzymatic mechanism utilizes sulfate as a leaving group.

[0025] FIG. **14** shows precursor supply pathways in *E. coli* for producing acrylyl-CoA, as described in previous figures, and [2S]-methylmalonyl-CoA. Each enzymes depicted can be expressed in a host cell wherein each enzyme can be independently either endogenous or native to the host cell, or introduced into recombinant

[0026] FIG. **15** shows methods and materials provided by the invention for maximizing precursor supply pathways in *E. coli*. The means to maximizing acrylyl-CoA can comprise one or more of "knocking out" (eliminating or reducing the expression of) PrpC activity, knocking out YgfH activity, exogenously feeding propionate (or producing propionate endogenously), overexpressing PrpE activity to increase cytosolic pools of propionyl-CoA. From this intermediate, the introduction of the propionyl-CoA carboxylase complex (AccA/PccB) will yield methylmalonyl-CoA (Pfeifer, et al. Science. 2001 Mar. 2; 291(5509):1790-2; incorporated herein by reference). This pool of propionyl-CoA can also be utilized in the pathways described in FIGS. **8** and **9**.

[0027] FIG. **16** shows an illustrative PKS provided by the invention to produce 3-hydroxy-1-octene. The PKS comprises the following elements: (i) Load module and KS1 from PikA1 (pikromycin), followed by (ii) Module 1 and KS2: AT-ACP segment from Module 5 and KS6 domain from the Nystatin PKS, (iii) Module 2: the hydroxymalonate-specific AT and contiguous ACP domains from ZmaA (zwittermicin PKS) from *Bacillus cereus*, DH, ER and KR domains from nanchangmycin PKS Module 2, and (iv) Module 3: AT-TE segment of the CurM module (curacin PKS). For the production of the precursor hydroxymalonyl-ACP, enzymes ZmaD, ZmaG, and ZmaE are also produced by or provided to the host strain. This figure illustrates loss of the hydroxyl group as a water molecule, however, it should be noted that the enzymatic mechanism utilizes sulfate as a leaving group.

[0028] FIG. **17** shows an illustrative PKS provided by the invention to produce 1-decene. The PKS comprises the following elements: (i) Load module and KS 1 from PikA1, followed by (ii) Module 1 and KS2: AT-ACP segment from Module 5 and KS6 domain from the nystatin PKS, (iii) Module 2 and KS3: AT-ACP segment from Module 15 and KS 16 domain from the nystatin PKS, (iv) Module 3 and KS4: AT-ACP segment from Module 3 and K4 domain from the oligomycin PKS, and (v) Module 4: AT-TE segment from CurM. This figure illustrates loss of the hydroxyl group as a water molecule, however, it should be noted that the enzymatic mechanism utilizes sulfate as a leaving group.

[0029] FIG. **18** shows an illustrative PKS provided by the invention to produce 1-octene. The PKS comprises the following elements: (i) Loading Module and KS1 from PikA1, followed by (ii) Module 1 and KS2: AT-ACP segment from Module 5 and KS6 domain from the nystatin PKS Module 2, (iii) and KS3: AT-ACP segment from Module 15 and KS16 domain from the nystatin PKS, and then (iv) Module 3: AT-ST segment from the CurM module. This figure illustrates loss of the hydroxyl group as a water molecule, however, it should be noted that the enzymatic mechanism utilizes sulfate as a leaving group.

DETAILED DESCRIPTION

[0030] This invention is not limited to particular embodiments described, as such may, of course, vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, because the scope of the present invention will be limited only by the appended claims.

[0031] Where a range of values is provided, each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limits of that range is also specifically disclosed. Each smaller range between any stated value or intervening value in a stated range and any other stated or intervening value in that stated range is encompassed within the invention.

[0032] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in practicing the present invention, suitable methods and materials are now described. All publications cited are incorporated herein by reference to disclose and describe the methods and/or materials and/or results therein.

[0033] As used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "an α-olefin" includes a plurality of such α-olefins, and so forth.

[0034] The term "even-chain α-olefin" refers to an α-olefin with a carbon backbone, which, disregarding any functional groups or substituents, has an even number of carbon atoms.

[0035] The term "odd-chain α-olefin" refers to an α-olefin with a carbon backbone, which, disregarding any functional groups or substituents, has an odd number of carbon atoms.

[0036] The term "functional variant" describes an enzyme that has a polypeptide sequence that is at least 70%, 75%, 80%, 85%, 90%, 95% or 99% identical to an enzyme described herein. A "functional variant" enzyme may retain amino acids residues recognized as conserved for the enzyme in nature, and/or may have non-conserved amino acid residues. Amino acids can be, relative to the native enzyme, substituted (different), inserted, or deleted, but the variant has generally similar enzymatic activity as compared to an enzyme described herein. A "functional variant" enzyme may be found in nature or be an engineered mutant (recombinant) thereof.

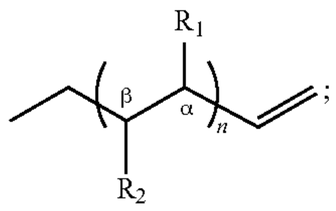
[0037] The objects, advantages, and features of the invention will become more apparent to those persons skilled in the art upon reading the details of the invention as more fully described below.

Polyketide Synthases (PKS)

[0038] The present invention provides recombinant polyketide synthase (PKS) enzymes capable of synthesizing an α-olefin. The PKS enzymes of the invention are not naturally occurring PKS. In some embodiments of the invention, the α-olefin is not a compound synthesized by a naturally occurring PKS. In some embodiments of the invention, the PKS is a hybrid PKS comprising modules, domains, and/or portions thereof, or functional variants thereof, from two or more PKSs. Such α-olefins include the diketides and triketides, and polyketides of more than three ketide units, such as 4, 5, or 6 or more ketide units. The α-olefin can further

include one or more functional groups in additional to the double bond that characterizes them. Such functional groups include, but are not limited to, ethyl, methyl and hydroxy side chains, internal olefins, and ketones.

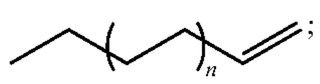
[0039] In some embodiments of the invention, the α-olefin is an even-chain α-olefin having the following chemical structure:



(I)

wherein each R_1 is independently —H or —CH_3, each R_2 is independently —H or —OH, n is an integer, and αβ is a single or double bond, with the proviso that when an αβ is a double bond then the corresponding R_2 is H. In some embodiments of the invention, n is an integer from 1 to 10. n indicates the number of two-carbon-chain subunits in the carbon backbone of the α-olefin. The R_1, R_2, and αβ within each two-carbon-subunit of a multiple subunit α-olefin is independent of the R_1, R_2, and αβ of any other two-carbon-subunit in the molecule. In some embodiments, however, one or more, up to all, subunits have identical R_1, R_2, and αβ.

[0040] In some embodiments of the invention, the α-olefin has the following chemical structure:



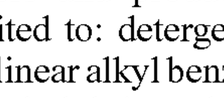
(II)

wherein n is an integer from 0 to 10.

[0041] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C3-alpha olefins propylene (propene) and polymers and products derived therefrom, including but not limited to: polypropylene, acylonitrile, propylene oxide, alcohols, cumene, acrylic acid, injection molded plastics, electronics, electrical appliances, housewares, bottle caps, toys, luggage, films, fibers, carpets, clothing, ropes, pipes, conduit, wire, cable, elastomeric polymers, acrylic fibers, nitrile rubber, acrylonitrile-butadiene-styrene (ABS) resins, styrene-acrylonitrile (SAN) resins, acrylamide, adiponitrile, polyether polyols, polyurethanes, flexible foams, rigid foams, insulation, propylene glycol, polyester resins, antifreeze, de-icing fluids, propylene glycol ethers, paints, coatings, inks, resins, cleaners, isopropanol, cosmetics, pharmaceuticals, food, ink, adhesives, 2-ethylhexanol, phthalate plasticizers, phenol, acetone, polycarbonate, phenolic resins, epoxy resins, methyl methacrylate (MMA), and acrylic esters.

[0042] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C4-alpha olefin butene and polymers and products derived therefrom, including but not limited to: polybutylene, copolymers with ethylene and/or propene, hot-melt adhesives, synthetic rubber, diesel fuel, and jet fuel.

[0043] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C4 diolefin butadiene and polymers and products derived therefrom, including but not limited to: styrene butadiene rubber (SBR), polybutadiene rubber, acrylonitrile butadiene styrene (ABS), styrene butadiene (SB) copolymer latex, nitrile rubber, adiponitrile, chloroprene, butanediol, tetrahydrofuran, tires, adhesives; coatings, high impact polystyrene, thermoplastic resins, engineering nylons (from C12 lactam), paper coating, gaskets and seals, hoses, gloves, nylon fibers, polymers, wet suits, electrical insulation, polybutylene terephthalate, spandex, and binders. Butadiene has the following chemical structure:

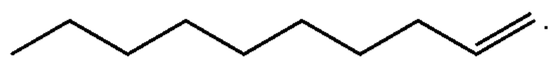


[0044] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C5 α olefin: 1-pentene and polymers and products derived therefrom, including but not limited to: gasoline, polymers; adhesives, sealants, diesel fuel, and jet fuel.

[0045] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C6 α-olefin (see FIG. **1**, example): 1-hexene and polymers and products derived therefrom, including but not limited to comonomer, polyethylene, polymer, high density polyethylene (IIDPE), linear low density polyethene (LLDPE), 1-heptanal, heptanoic acid, resin, film, plastic pipe, containers, diesel fuel, and jet fuel. 1-hexene has the following chemical structure:

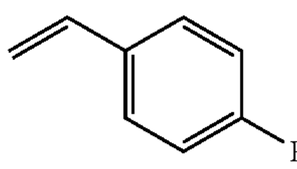
and an illustration of a 1-hexene producing PKS is provided in FIG. **1**.

[0046] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C10 α-olefin: 1-decene and polymers and products derived therefrom, including but not limited to: detergent formulations, linear alkyl benzene (LAB), linear alkyl benzene sulfonate (LABS), polyalphaolefin synthetic lubricant basestocks (PAO), heat-shrink materials, electrical insulation sleeves, rash guards in clothing, polyolefin elastomers (POE), flexible foams, footwear, seat cushions, armrests, pillows, radar coolants, strings, polyol esters, detergent alcohols, plasticizer alcohols, specialty chemicals, epoxides, derivatives thereof, comonomer, intermediate in production of epoxides, amines, oxo alcohols, synthetic lubricants, synthetic fatty acids, alkylated aromatics, emulsifiers, performance waxes, cosmetic formulations, viscosity controller, solvent, decene butene copolymer, binder, film forming, decene/PVP copolymer, food additives, glazing agent, anti-foaming agent, anti-dusting agent, white mineral oil substitute, polishing agent, well fluids, alpha olefin oligomers, and the like. 1-decene has the following chemical structure:



[0047] In one embodiment, the invention provides methods, host cells, and nucleic acids for making the C8 aromatic α-olefin: styrene and polymers and products derived therefrom, including but not limited to: homopolymers, copolymers, polystyrene, expandable polystyrene (EPS), acryloni-

trile-butadiene-styrene (ABS), resins, styrene-acrylonitrile (SAN), acrylonitrile-styrene-acrylate (ASA), styrene butadiene, styrene butadiene rubber, copolymer with maleic anhydride, terephthalate, unsaturated polyester resins, containers, closures, lids and vending cups, construction; electrical and electronic parts; domestic appliances and housings; household goods and home furnishings; and toys, sporting goods and recreational articles, packaging, thermoplastics, cutlery, CDs, insulating materials, polymer bonded explosives, consumer products, renewable plastics, renewable products, hardhats, tires, etc. In some embodiments of the invention, the aromatic α-olefin has the following chemical structure:



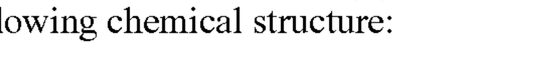
(III)

wherein R_3 is —H, —OH, —NH_3, or —NO_2.

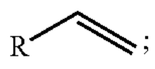
[0048] Alpha olefins are commonly used in the cosmetics and skin care industry, and the present invention therefore provides useful starting materials for making cosmetics and skin care products. For example, alpha olefin sulfonate, sulfate free personal cleaners, soap, copolymer maleic acid, and the like are all used in these industries and provided by the invention. Alpha olefins provide by the invention can also be used in the flavor and fragrance industry. For example, 3-hydroxy-1-octene and 3-oxo-1-octene can be made using the methods and materials of the invention and are used in applications where a mushroom flavor/fragrance is desired.

[0049] The present invention can also be used to generate intermediates useful in the synthesis of pharmaceuticals. These olefins can be coupled via olefin metathesis to one another or other olefin intermediates obtained via traditional chemical syntheses to yield bioactive molecules useful as drugs.

[0050] In some embodiments, the α-olefin produced in accordance with the invention is (E)-deca-1,5-diene, which has the following chemical structure:

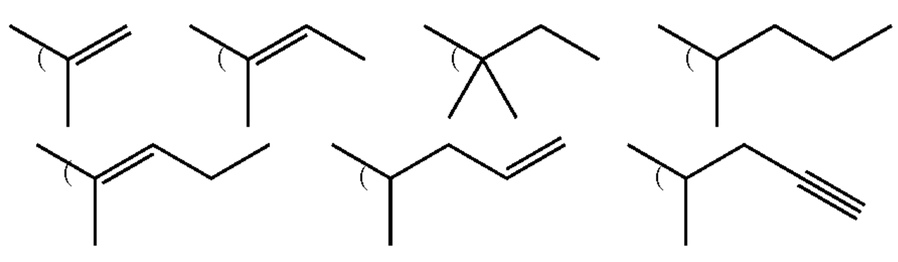


[0051] In some embodiments, the α-olefin produced in accordance, with the invention has the following chemical structure:

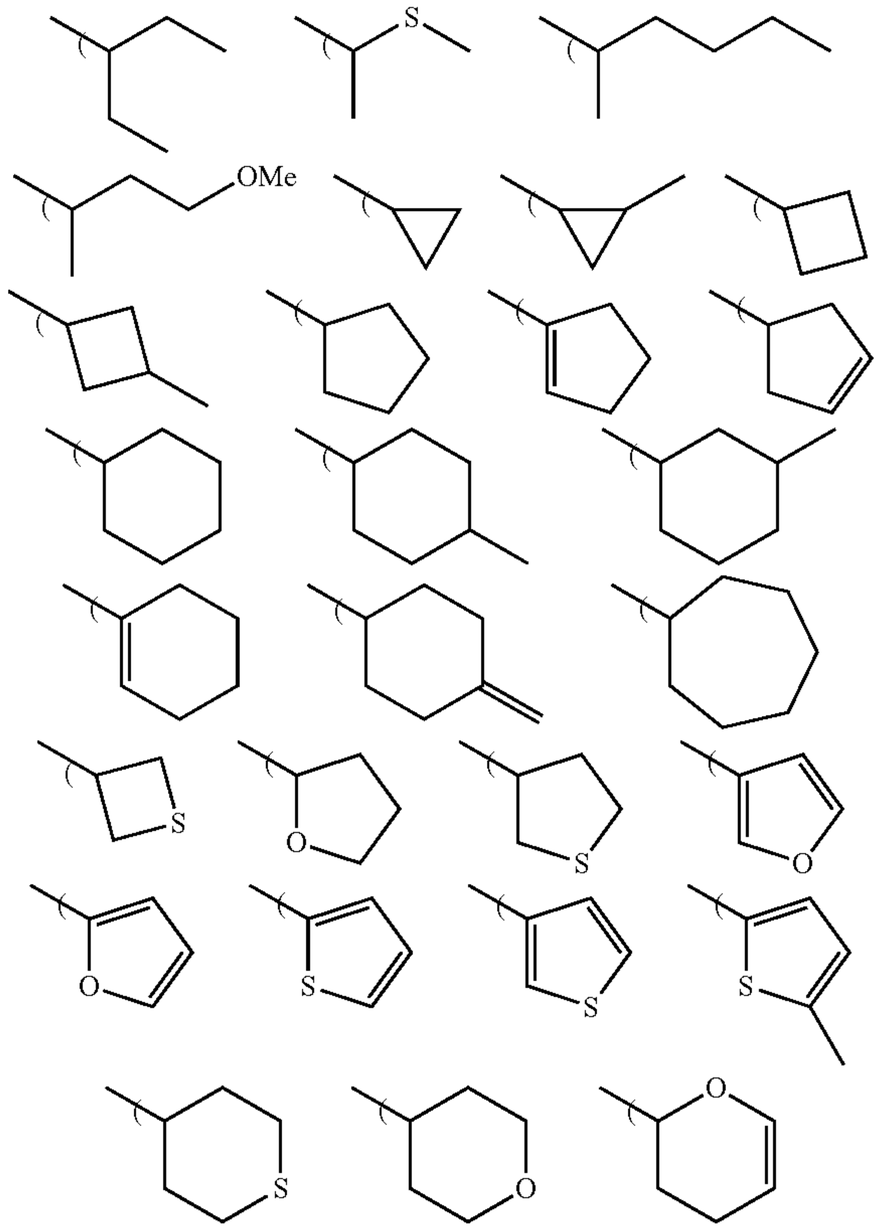


(IV)

wherein R is one of the following structures:

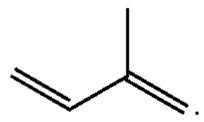


-continued

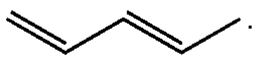


[0052] In some embodiments, the α-olefin produced in accordance with the invention is a polyolefin having chemical structure (I) and comprising at least two, three, four, five, or more C—C double bonds. Such α-olefins include, but are not limited to, diolefins, such as diolefins with two C—C double bonds on the carbon backbone. Such diolefins include, but are not limited to, butadiene, isoprene, and penta-1,3-diene. Butadiene has the chemical structure shown in [0043], above.

[0053] In some embodiments, the α-olefin produced in accordance with the invention is isoprene, which has the following chemical structure:



[0054] In some embodiments, the α-olefin produced in accordance with the invention is penta-1,3-diene, which has the following chemical structure:



[0055] Complex polyketides comprise a large class of natural products that are synthesized in bacteria (mainly members of the actinomycete family; e.g. *Streptomyces*), fungi and plants. Polyketides form the macrolactone component of a large number of clinically important drugs, such as antibiotics (e.g. erythromycin, tylosin), antifungal agents (e.g. nystatin), anticancer agents (e.g. epothilone), immunosuppressives

(e.g. rapamycin), etc. Though these compounds do not resemble each other either in their structure or their mode of action, they share a common basis for their biosynthesis, which is carried out by a group of enzymes designated polyketide synthases.

[0056] Polyketide synthases (PKS) employ short chain fatty acyl CoAs in Claisen condensation reactions to produce polyketides. Unlike fatty acid synthases that utilize acetyl CoA as the starter and malonyl CoA as the extender units, and use a single module iteratively to produce the nascent acyl chains, PKSs are composed of discrete modules, each catalyzing the chain growth of a single step. Modules can differ from each other in composition, so that, overall, a number of different starters (e.g. acetyl CoA, propionyl CoA) and extenders, some of which contain stereospecific methyl (or ethyl) side chains can be incorporated into a polyketide. In addition, PKS modules do not always reduce the 3-carbonyl formed from condensation but may leave it either unreduced (ketone), partially reduced (hydroxyl, 2,3-ene), or fully reduced (3-methylene). Many PKSs employ malonyl CoA or [S]-2-methylmalonyl CoA as the starter for polyketide synthesis. In such cases, the terminal carboxyl group is usually removed by a decarboxylase domain present at the N-terminus of the loading domain of the PKS. Thus, the structure (and chirality) of the α-carbon and β-carbonyl is determined by the module of the PKS employed in the synthesis of the growing chain at each particular step. Because of the correspondence between the modules used in the synthesis and the structure of the polyketide produced, it is possible to program PKS synthesis to produce a compound of desired structure by selection and genetic manipulation of polyketide synthases.

[0057] FIG. **2** shows the various modules and the precursor utilized by each module for incorporation into the corresponding nascent acyl (polyketide) chain to give rise to a range of compounds of interest. Table 1, below, provides illustrative PKS sources for each module in FIG. **2**. Each PKS source (amino acid sequence and corresponding coding sequence) is well-known to one skilled in the art and readily available. In addition, for each module in Table 1, there are other modules from other PKS (or from recombinant DNA technology) that can be used. In addition, other structures can be incorporated in the ketide or polyketide that are not shown in Table 1 and FIG. **2**. For example, useful loading modules includes the benzoate loading module of soraphen PKS, the isobutyrate loading module of the lipomycin PKS and bafilomycin PKS, and the acrylate loading module from the dificidin pathway. The acrylate loading module from the dificidin PKS loads and dehydrates a hydroxypropionate molecule by the use of enzymes difA-E to yield a PKS with an arylyl-ACP (Chen, 2006, J. Bact. 188:4024-4036; incorporated herein by reference).

[0058] The present invention also contemplates the use of functional variants of PKS modules, domains, and portions thereof. In one important embodiment, the invention provides a variety of recombinant modules that carry out the same enzymatic reactions conducted by the CurM module.

TABLE 1

PKS sources of the various modules.

Module	PKS Source
S1	Spiramycin PKS Loading Domain (with and without

TABLE 1-continued

PKS sources of the various modules.

Module	PKS Source
	inactivation or deletion of the KS^Q domain)
S2	Pikromycin PKS Loading Domain (with and without inactivation or deletion of the KS^Q domain)
S3	Spiramycin PKS Loading Domain
S4	Erythromycin PKS Loading Domain
A	Rifamycin PKS Module 2
B	Oligomycin PKS Module 1
C	Spiramycin PKS Module 1
D	Pikromycin PKS Module 2
E	Oligomycin PKS Module 3
F	Erythromycin PKS Module 3
G	Oligomycin PKS Module 5
H	Primaricin PKS Module 7
I	Tylosin PKS Module 1
J	Erythromycin PKS Module 1
K	Avermectin PKS Module 7
L	Rapamycin PKS Module 1
M	Erythromycin PKS Module 4
N	Pederin Module 2
O	Ascomycin Module 4
P	FK506 Module 4
Q	Curacin A Chain Termination Module (CurM)

[0059] All extender modules carry the β-acyl ACP synthase (commonly called the ketosynthase or KS) domain, which conducts the decarboxylative condensation step between the extender and the growing polyketide chain, and the acyl carrier protein (ACP) domain that carries the growing acyl chain and presents it to any cognate reductive domains for reduction of the β-carbonyl. Modules can differ from each other in composition so that a number of different starter and extender units, some of which contain stereospecific side chains (e.g. methyl, ethyl, propylene) can be incorporated. The acyltransferase (AT) domain of each module determines the extender unit (e.g. malonyl CoA, methylmalonyl CoA, and the like) incorporated. In addition, PKS modules do not always reduce the (3-carbonyl formed from condensation but may leave it either unreduced (ketone), partially reduced (hydroxyl, 2,3-ene) or fully reduced (3-methylene), as shown in FIG. **2**. The ketoreductase (KR) domain reduces the ketone to the OH function (stereospecifically); the dehydratase (DH) domain removes water from the α and β carbons leaving an α,β trans-double bond; the enoylreductase (ER) domain reduces the double bond to a β-methylene center; the reductive state of the β-carbonyl, therefore, is determined by the presence of functional reductive domains in the corresponding module. Less commonly, modules may contain an additional C-methylation domain (yielding an additional α-methyl side chain, as in epothilone).

[0060] The Curacin A Chain Termination Module is annotated as CurM. CurM catalyzes an extension of the nascent polyketide molecule with acetate (from malonyl-CoA). The resulting beta carbonyl is reduced to a hydroxyl group by a KR domain. The resulting beta hydroxyl group is then sulfonated by the ST domain (from the common metabolic precursor 3'-phosphoadenosine-5'-phosphosulfate). The TE domain releases the 3-sulfo polyketide which then undergoes loss of sulfate and a decarboxylation to form a terminal olefin

moiety. The chain termination module of the PKS of the present invention can comprise the ST and TE domains of the CurM Chain Termination Module and variants thereof with similar activity. Additional PKS modules carrying the combination of a sulfotransferase (pfam00685)/thioesterase have been identified in nature and can be used in additional embodiments of the invention. One such olefination module (Ols) has been characterized from *Synechococcus* sp. strain PCC 7002 (Mendez-Perez et al. 2011. Appl. Env. Microbiol. 77:4264-4267 2011). Others include, but are not limited to, PKS enzymes from *Cyanothece* sp. PCC 7424, *Cyanothece* sp. PCC 7822, *Prochloron didemni* P1-Palau, *Pseudomonas entomophila* L48, and *Haliangium ochraceum* DSM 14365. The present invention also provides consensus sequences that differ from these naturally occurring sequences but encode similar enzymatic activities.

[0061] The makeup of the PKS, therefore, determines the choice of starter and extender acyl units incorporated, the extent of reduction at each condensation step, and the total number of units added to the chain. The wide diversity of structures of polyketides seen in nature is thus attributable to the diversity in PKS enzymes.

[0062] A partial list of PKS amino acid and corresponding nucleic acid coding sequences that can be used in the PKSs of the present invention includes, for illustration and not limitation, Ambruticin (U.S. Pat. No. 7,332,576); Avermectin (U.S. Pat. No. 5,252,474; MacNeil et al., 1993, Industrial Microorganisms: Basic and Applied Molecular Genetics, Baltz, Hegeman, & Skatrud, eds. (ASM), pp. 245-256; MacNeil et al., 1992, Gene 115: 119-25); Candicidin (FRO008) (Hu et al., 1994, Mol. Microbiol. 14: 163-72); Curacin A (Chang et al., 2004, *J. Nat. Prod.,* 67 (8), pp 1356-1367; Gu et al., 2009, *J. Am. Chem. Soc.,* 131 (44), pp 16033-16035); Epothilone (U.S. Pat. No. 6,303,342); Erythromycin (WO 93/13663; U.S. Pat. No. 5,824,513; Donadio et al., 1991, Science 252: 675-79; Cortes et al., 1990, Nature 348:176-8); FK506 (Motamedi et al., 1998, Eur. J. Biochem. 256:528-34; Motamedi et al., 1997, Eur. J. Biochem. 244:74-80); FK520 or ascomycin (U.S. Pat. No. 6,503,737; see also Nielsen et al., 1991, Biochem. 30:5789-96); Jerangolid (U.S. Pat. No. 7,285,405); Leptomycin (U.S. Pat. No. 7,288,396); Lovastatin (U.S. Pat. No. 5,744,350); Nemadectin (MacNeil et al., 1993, supra); Niddamycin (Kakavas et al., 1997, J. Bacteriol. 179:7515-22); Oleandomycin (Swan et al., 1994, Mol. Gen. Genet. 242:358-62; U.S. Pat. No. 6,388,099; Olano et al., 1998, Mol. Gen. Genet. 259:299-308); Pederin (PCT publication no. WO 2003/044186); Pikromycin (Xue et al., 2000, Gene 245:203-211); Pimaricin (PCT publication no. WO 2000/077222); Platenolide (EP Pat. App. 791,656); Rapamycin (Schwecke et al., 1995, Proc. Natl. Acad. Sci. USA 92:7839-43); Aparicio et al., 1996, Gene 169:9-16); Rifamycin (August et al., 1998, Chemistry & Biology, 5: 69-79); Soraphen (U.S. Pat. No. 5,716,849; Schupp et al., 1995, J. Bacteriology 177: 3673-79); Spiramycin (U.S. Pat. No. 5,098,837); and Tylosin (EP 0 791,655; Kuhstoss et al., 1996, Gene 183:231-36; U.S. Pat. No. 5,876,991); each of the foregoing references is incorporated herein by reference. Additional suitable PKS coding are readily available to one skilled in the art (e.g., by cloning and sequencing of DNA from polyketide producing organisms or by reference to GenBank).

[0063] Of the more than one hundred PKSs studies and reported on in the scientific literature, the correspondence between the modules used in the biosynthesis of, and the structure of, the polyketide produced is understood both at the level of the protein sequence of the PKS and the DNA sequence of the corresponding genes. The organization of modules and correspondence with polyketide structure can be identified by amino acid and/or nucleic acid sequence determination. One can thus clone (or synthesize) DNA sequences corresponding to desired modules and transfer them as fully functioning units to heterologous hosts, including otherwise non-polyketide producing hosts such as *E. coli* (Pfeifer, et al., *Science* 291, 1790 (2001); incorporated herein by reference), and polyketide-producing hosts, such as *Streptomyces* (Kao et al., *Science* 265, 509 (1994); incorporated herein by reference).

[0064] Additional genes employed in polyketide biosynthesis have also been identified. Genes that determine phosphopantetheine:protein transferase (PPTase) that transfer the 4-phosphopantetheine co-factor of the ACP domains, commonly present in polyketide producing hosts, have been cloned in *E. coli* and other hosts (Weissman et al., *Chembiochem* 5, 116 (2004); incorporated herein by reference). While it is possible to re-program polyketide biosynthesis to produce a compound of desired structure by either genetic manipulation of a single PKS or by construction of a hybrid PKS composed of modules from two or more sources (see Weissman et al., supra), the present invention provides the first means for making an alpha-olefin by a recombinant PKS.

[0065] Recombinant methods for manipulating modular PKS genes to make the PKSs of the present invention are described in U.S. Pat. Nos. 5,672,491; 5,843,718; 5,830,750; 5,712,146; and 6,303,342; and in PCT publication nos. WO 98/49315 and WO 97/02358; each of which is incorporated herein by reference. A number of genetic engineering strategies have been used with various PKSs to demonstrate that the structures of polyketides can be manipulated to produce novel polyketides (see the patent publications referenced supra and Hutchinson, 1998, Curr. Opin. Microbiol. 1:319-329, and Baltz, 1998, Trends Microbiol. 6:76-83; incorporated herein by reference). In some embodiments, the components of the hybrid PKS are arranged onto polypeptides having interpolypeptide linkers that direct the assembly of the polypeptides into the functional PKS protein, such that it is not required that the PKS have the same arrangement of modules in the polypeptides as observed in natural PKSs. Suitable interpolypeptide linkers to join polypeptides and intrapolypeptide linkers to join modules within a polypeptide are described in PCT publication No. WO 00/47724, incorporated herein by reference.

[0066] The vast number of polyketide pathways that have been elucidated to date and the present invention in combination provide a variety of different options to produce α-olefins in accordance with the invention. While the products can be vastly different in size and functionality, all employ similar methods for preparing the PKS and corresponding coding sequence and for producing the desired α-olefin. The interfaces between non-cognate enzyme partners can be optimized on a case-by-case basis. ACP-linker-KS and ACP-linker-TE regions from the proteins of interest will be aligned to examine the least disruptive fusion point for the hybrid synthase. Genetic constructions will employ sequence and ligation independent cloning (SLIC), or other sequence independent cloning techniques, so as to eliminate the incorporation of genetic "scarring".

[0067] In some embodiments, the PKS that produces the α-olefin of interest comprises the sulfotransferase (ST)-

thioesterase (TE) domains from *Lyngbya majuscula* CurM or similar domains from another naturally occurring PKS or one of the recombinant domains provided by the invention. The α-olefins capable of being produced by the invention include, but are not limited to, the diketides propylene, 1-butene, and styrene and the triketides 1-hexene and 1-pentene. In one aspect of the invention, the host cell is fed or exogenously provided or endogenously produces acrylate and so produces diolefins such as 1,5-hexadiene and butadiene. In another aspect, feeding or exogenously providing or endogenous production of benzoic acid to the host cell comprising a PKS of the invention enables the production of styrene derivatives.

[0068] In some embodiments, host cells that are capable of producing diolefins are also capable of producing acrylate or acrylyl-CoA/ACP, thus eliminating the need for exogenous acrylate. By coupling one of many PKS thioesterase domains to the module loading acrylate from these precursor pathways, the PKS system is capable of producing acrylic acid. Acrylic acid can also be obtained from acrylyl-CoA or acrylyl-ACP by use of a non-PKS hydrolase in accordance with the invention. In some embodiments of the invention, host cells that are capable of producing diolefins are also capable of producing benzoate.

[0069] *L. majuscula* CurM ST-TE domains comprise the following amino acid sequence:

(SEQ ID NO: 10)

F ILSSPRSGST LLRVMLAGHS SLFSPPELHL LPFNTMKERQ

EQLNLSYLGE GLQKTFMEVK NLDATASQAL IKDLESQNLS

IQQVYGMLQE NIAPRLLVDK SPTYAMEPTI LERGEALFAN

SKYIYLVRHP YSVIESFVRM RMQKLVGLGE ENPYRVAEQV

WAKSNQNILN FLSQLEPERQ HQIRYEDLVK KPQQVLSQLC

DFLNVPFEPE LLQPYQGDRM TGGVHQKSLS ISDPNFLKHN

TIDESLADKW KTIQLPYPLK SETQRIASQL SYELPNLVTT

PTNQQPQVST TPSTEQPIME EKFLEFGGNQ ICLCSWGSPE

HPVVLCIHGI LEQGLAWQEV ALPLAAQGYR VVAPDLFGHG

RSSHLEMVTS YSSLTFLAQI DRVIQELPDQ PLLLVGHSMG

AMLATAIASV RPKKIKELIL VELPLPAEES KKESAVNQLT

TCLDYLSSTP QHPIFPDVAT AASRLRQAIP SLSEEFSYIL

AQRITQPNQG GVRWSWDAII RTRSILGLNN LPGGRSQYLE

MLKSIQVPTT LVYGDSSKLN RPEDLQQQKM TMTQAKRVFL

SGGHNLHIDA AAALASLILT S

[0070] *L. majuscula* CurM ST domain comprises the following amino acid sequence:

(SEQ ID NO: 11)

F ILSSPRSGST LLRVMLAGHS SLFSPPELHL LPFNTMKERQ

EQLNLSYLGE GLQKTFMEVK NLDATASQAL IKDLESQNLS

IQQVYGMLQE NIAPRLLVDK SPTYAMEPTI LERGEALFAN

SKYIYLVRHP YSVIESFVRM RMQKLVGLGE ENPYRVAEQV

-continued

WAKSNQNILN FLSQLEPERQ HQIRYEDLVK KPQQVLSQLC

DFLNVPFEPE LLQPYQGDRM TGGVHQKSLS ISDPNFLKHN

TIDESLADKW KTIQLPYPLK

[0071] *L. majuscula* CurM TE domain comprise the following amino acid sequence:

(SEQ ID NO: 12)

EKFLEFGGNQ ICLCSWGSPE HPVVLCIHGI LEQGLAWQEV

ALPLAAQGYR VVAPDLFGHG RSSHLEMVTS YSSLTFLAQI

DRVIQELPDQ PLLLVGHSMG AMLATAIASV RPKKIKELIL

VELPLPAEES KKESAVNQLT TCLDYLSSTP QHPIFPDVAT

AASRLRQAIP SLSEEFSYIL AQRITQPNQG GVRWSWDAII

RTRSILGLNN LPGGRSQYLE MLKSIQVPTT LVYGDSSKLN

RPEDLQQQKM TMTQAKRVFL SGGHNLHIDA AAALASLILT

S

[0072] In some embodiments, the PKS of the present invention comprises a naturally occurring sulfotransferase-thioesterase (ST-TE) domains, or ST or TE domain, functionally similar, but not identical, to *L. majuscula* CurM. In some embodiments, the PKS of the present invention comprises the amino acid sequences of the ST and/or TE of any of the proteins/peptides described in Tables 2-4, or functionally variants thereof. One skilled in the art can identify such *L. majuscula* CurM-like ST and/or TE domains using available bioinformatics programs. For example, the *L. majuscula* CurM ST-TE can be split in two separately functional portions by relying on its crystal structure and annotation of catalytic boundaries with programs like protein BLAST, and the sequences can be homology-modeled to get a better grasp of the boundary of catalytic domains, using *L. majuscula* CurM ST-TE as an anchoring template. Together, such methods can be employed to make solid predictions about catalytic activity and responsible amino acid regions within a larger protein.

[0073] In some embodiments, ST and/or TE domains, or functionally variants thereof, comprise one or more of the following amino acid residues (using *L. majuscula* CurM as a reference sequence): R205, H266, S100, E124, N211, and N267. In some embodiments, ST and/or TE domains, or functionally variants thereof, comprise the following amino acid residues (using *L. majuscula* CurM as a reference sequence): 8205 and H266, and optionally one or more of S100, E124, N211, and N267. In some embodiments, the PKS comprises a ST domain and a TE domains that are derived or obtained from two different organisms or sources.

TABLE 2

List of proteins/peptides comprising CurM-like ST-TE domains.

Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
1. polyketide synthase module [*Lyngbya majuscula* 3L]	2211 aa protein	ZP_08432359.1 GI:332712433
2. CurM [*Lyngbya majuscula*]	2147 aa protein	AAT70108.1 GI:50082961
3. beta-ketoacyl synthase [*Cyanothece* sp. PCC 7424]	2762 aa protein	YP_002377174.1 GI:218438845
4. beta-ketoacyl synthase [*Cyanothece* sp. PCC 7822]	2775 aa protein	YP_003887107.1 GI:307151723
5. polyketide synthase [*Prochloron didemni* P1-Palau]	2999 aa protein	AEH57210.1 GI:335387269
6. Chain A, Thioesterase Domain From Curacin Biosynthetic Pathway	286 aa protein	3QIT_A GI:325534050
7. polyketide synthase module [*Lyngbya majuscula* 3L]	2277 aa protein	ZP_08425908.1 GI:332705832
8. polyketide synthase [*Synechococcus* sp. PCC 7002]	2720 aa protein	YP_001734428.1 GI:170077790
9. polyketide synthase [*Pseudomonas entomophila* L48]	1217 aa protein	YP_610919.1 GI:104784421
10. KR domain-containing protein [*Haliangium ochraceum* DSM 14365]	3045 aa protein	YP_003265308.1 GI:262194099
11. OciA [*Planktothrix agardhii* NIES-205]	2858 aa protein	ABW84363.1 GI:158954787
12. OciA [*Planktothrix agardhii* NIVA-CYA 116]	3477 aa protein	ABI26077.1 GI:112824006
13. CurM [*Burkholderia pseudomallei* 668]	358 aa protein	YP_001062692.1 GI:126444569
14. amino acid adenylation domain-containing protein [*Cyanothece* sp. PCC 8802]	1470 aa protein	YP_003137597.1 GI:257059709
15. amino acid adenylation domain-containing protein [*Cyanothece* sp. PCC 8801]	1470 aa protein	YP_002372038.1 GI:218246667
16. polyketide synthase [*Ostreococcus lucimarinus* CCE9901]	18193 aa protein	XP_001416378.1 GI:145343541

TABLE 3

List of proteins/peptides comprising a CurM-like ST domain.

Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
1. polyketide synthase module [*Lyngbya majuscula* 3L]	2211 aa protein	ZP_08432359.1 GI:332712433
2. CurM [*Lyngbya majuscula*]	2147 aa protein	AAT70108.1 GI:50082961
3. beta-ketoacyl synthase [*Cyanothece* sp. PCC 7424]	2762 aa protein	YP_002377174.1 GI:218438845
4. beta-ketoacyl synthase [*Cyanothece* sp. PCC 7822]	2775 aa protein	YP_003887107.1 GI:307151723
5. polyketide synthase [*Prochloron didemni* P1-Palau]	2999 aa protein	AEH57210.1 GI:335387269
6. polyketide synthase module [*Lyngbya majuscula* 3L]	2277 aa protein	ZP_08425908.1 GI:332705832
7. polyketide synthase [*Synechococcus* sp. PCC 7002]	2720 aa protein	YP_001734428.1 GI:170077790
8. polyketide synthase [*Pseudomonas entomophila* L48]	1217 aa protein	YP_610919.1 GI:104784421
9. OciA [*Planktothrix agardhii* NIES-205]	2858 aa protein	ABW84363.1 GI:158954787
10. OciA [*Planktothrix agardhii* NIVA-CYA 116]	3477 aa protein	ABI26077.1 GI:112824006
11. CurM [*Burkholderia pseudomallei* 668]	358 aa protein	YP_001062692.1 GI:126444569
12. KR domain-containing protein [*Haliangium ochraceum* DSM 14365]	3045 aa protein	YP_003265308.1 GI:262194099
16. COG3321: Polyketide synthase modules and related proteins (ISS) [*Ostreococcus tauri*]	11541 aa protein	XP_003074830.1 GI:308800098
17. polyketide synthase [*Ostreococcus lucimarinus* CCE9901]	18193 aa protein	XP_001416378.1 GI:145343541
18. modular polyketide synthase type I [*Micromonas* sp. RCC299]	14149 aa protein	XP_002507643.1 GI:255071123

TABLE 3-continued

List of proteins/peptides comprising a CurM-like ST domain.

Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
19. hypothetical protein RBXJA2T_11932 [*Rubrivivax benzoatilyticus* JA2]	301 aa protein	ZP_08402700.1 GI:332526592
20. hypothetical protein Dshi_1965 [*Dinoroseobacter shibae* DFL 12]	310 aa protein	YP_001533306.1 GI:159044512
21. hypothetical protein glr1901 [*Gloeobacter violaceus* PCC 7421]	301 aa protein	NP_924847.1 GI:37521470
22. hypothetical protein Sros_9233 [*Streptosporangium roseum* DSM 43021]	290 aa protein	YP_003344594.1 GI:271970398
23. hypothetical protein SAV_2309 [*Streptomyces avermitilis* MA-4680]	299 aa protein	NP_823485.1 GI:29828851
24. conserved hypothetical protein [*Streptomyces viridochromogenes* DSM 40736]	289 aa protein	ZP_07307763.1 GI:302555421
25. sulfotransferase [*Frankia* sp. EuI1c]	332 aa protein	YP_004017900.1 GI:312197839
26. hypothetical protein Nit79A3_2110 [*Nitrosomonas* sp. Is79A3]	304 aa protein	YP_004695298.1 GI:339483512
27. sulfotransferase [*Thermobispora bispora* DSM 43833]	346 aa protein	YP_003651260.1 GI:296268628
28. sulfotransferase [*Frankia* sp. EuI1c]	264 aa protein	YP_004017815.1 GI:312197754
29. hypothetical protein gll1899 [*Gloeobacter violaceus* PCC 7421]	320 aa protein	NP_924845.1 GI:37521468
30. SecC motif-containing protein [*Shewanella loihica* PV-4]	359 aa protein	YP_001093305.1 GI:127512108
31. predicted protein [*Micromonas pusilla* CCMP1545]	507 aa protein	XP_003055946.1 GI:303273170
32. Putative protein-tyrosine sulfotransferase [*Plesiocystis pacifica* SIR-1]	305 aa protein	ZP_01905212.1 GI:149916710
33. hypothetical protein PB2503_07444 [*Parvularcula bermudensis* HTCC2503]	310 aa protein	YP_003854688.1 GI:304321045
34. hypothetical protein PPE_01162 [*Paenibacillus polymyxa* E681]	422 aa protein	YP_003869548.1 GI:308067943
35. putative sulfotransferase [*Streptomyces griseus* subsp. *griseus* NBRC 13350]	339 aa protein	YP_001822417.1 GI:182434698
36. hypothetical protein LYNGBM3L_54590 [*Lyngbya majuscula* 3L]	318 aa protein	ZP_08430625.1 GI:332710682
37. SecC motif-containing protein [*Shewanella sediminis* HAW-EB3]	336 aa protein	YP_001473003.1 GI:157374403
38. sulfotransferase domain protein [*Plesiocystis pacifica* SIR-1]	329 aa protein	ZP_01905835.1 GI:149917336
39. sulfotransferase [*Streptomyces* cf. *griseus* XylebKG-1]	339 aa protein	ZP_08234477.1 GI:326775212
40. hypothetical protein Sros_1208 [*Streptosporangium roseum* DSM 43021]	347 aa protein	YP_003336949.1 GI:271962753
41. sulfotransferase [*Trichodesmium erythraeum* IMS101]	430 aa protein	YP_722743.1 GI:113476682
42. hypothetical protein Sros_1207 [*Streptosporangium roseum* DSM 43021]	336 aa protein	YP_003336948.1 GI:271962752
43. sulfotransferase [*Flexistipes sinusarabici* DSM 4947]	322 aa protein	YP_004602630.1 GI:336322663
44. Protein-tyrosine sulfotransferase [*Harpegnathos saltator*]	381 aa protein	EFN77815.1 GI:307196126
45. sulfotransferase domain protein [*Rhodobacterales bacterium* HTCC2083]	346 aa protein	ZP_05076043.1 GI:254462627
46. PREDICTED: similar to Transport and Golgi organization 13 CG32632-PB [*Tribolium castaneum*]	382 aa protein	XP_968004.1 GI:91090216
47. sulfotransferase [*Psychromonas ingrahamii* 37]	335 aa protein	YP_943667.1 GI:119945987
48. hypothetical protein sll5046 [*Synechocystis* sp. PCC 6803]	316 aa protein	NP_942202.1 GI:38505581
49. sulfotransferase domain-containing protein [*Roseobacter denitrificans* OCh 114]	340 aa protein	YP_680960.1 GI:110677953
50. putative sulfotransferase [*Burkholderia multivorans* CGD2M]	271 aa protein	ZP_03574132.1 GI:221201092
51. sulfotransferase [*Kangiella koreensis* DSM 16069]	317 aa protein	YP_003146110.1 GI:256822147
52. Protein-tyrosine sulfotransferase [*Acromyrmex echinatior*]	381 aa protein	EGI65733.1 GI:332025570

TABLE 3-continued

List of proteins/peptides comprising a CurM-like ST domain.

Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
53. sulfotransferase [*Flexistipes sinusarabici* DSM 4947]	325 aa protein	YP_004602624.1 GI:336322657
54. nodulation protein noeE [*Magnetospirillum magneticum* AMB-1]	433 aa protein	YP_420424.1 GI:83310160
55. glycosyl transferase family 2 [*Paenibacillus polymyxa* SC2]	421 aa protein	YP_003945463.1 GI:310640705
56. protein-tyrosine sulfotransferase 2 [*Paenibacillus polymyxa* Ml]	423 aa protein	CCC84070.1 GI:343095861
57. sulfotransferase [*Pedobacter* sp. BAL39]	346 aa protein	ZP_01884054.1 GI:149277914
58. sulfotransferase: SEC-C motif protein [*Shewanella* sp. HN-41)	333 aa protein	ZP_08568256.1 GI:336313314
59. sulfotransferase domain protein [*Lyngbya majuscula* 3L]	344 aa protein	ZP_08430778.1 GI:332710841
60. sulfotransferase domain-containing protein [*Rhodopirellula baltica* WH47]	325 aa protein	EGF25969.1 GI:327539348
61. hypothetical protein MettrDRAFT_3778 [*Methylosinus trichosporium* OB3b]	396 aa protein	ZP_06890062.1 GI:296448163
62. PREDICTED: MGC82552 protein-like [*Saccoglossus kowalevskii*]	436 aa protein	XP_002733820.1 GI:291227699
63. Sulfotransferase domain superfamily [*Microcoleus chthonoplastes* PCC 7420]	318 aa protein	ZP_05029988.1 GI:254416234
64. tyrosylprotein sulfotransferase-2 [*Ictalurus punctatus*]	356 aa protein	NP_001187093.1 GI:318064902
65. family 2 glycosyl transferase [*Nitrosococcus halophilus* Nc4]	1043 aa protein	YP_003528062.1 GI:292492623
66. PREDICTED: protein-tyrosine sulfotransferase [*Apis mellifera*]	380 aa protein	XP_624657.2 GI:328780257
67. tyrosine sulfotransferase [*Culex quinquefasciatus*]	395 aa protein	XP_001864662.1 GI:170057846
68. hypothetical protein L8106_07576 [*Lyngbya* sp. PCC 8106]	281 aa protein	ZP_01622104.1 GI:119489297
69. hypothetical protein NIDE3002 [*Candidatus* Nitrospira defluvii]	375 aa protein	YP_003798623.1 GI:302038301
70. SecC motif-containing protein [*Shewanella frigidimarina* NCIMB 400]	342 aa protein	YP_749583.1 GI:114562070
71. sulfotransferase [*Acaryochloris marina* MBIC11017]	294 aa protein	YP_001519982.1 GI:158338805
72. protein-tyrosine sulfotransferase 2 [*Danio rerio*]	356 aa protein	NP_956713.1 GI:41056257
73. PREDICTED: protein-tyrosine sulfotransferase-like [*Bombus terrestris*]	380 aa protein	XP_003394254.1 GI:340711379
74. GG17794 [*Drosophila erecta*]	504 aa protein	XP_001978257.1 GI:194895457
75. hypothetical protein Swit_1252 [*Sphingomonas wittichii* RW1]	308 aa protein	YP_001261755.1 GI:148554173
76. putative enzyme [*Lyngbya* sp. PCC 8106]	305 aa protein	ZP_01618957.1 GI:119484340
77. sulfotransferase [*Trichodesmium erythraeum* IMS101]	344 aa protein	YP_722339.1 GI:113476278
78. transport and golgi organization 13, isoform C [*Drosophila melanogaster*]	346 aa protein	NP_001096973.1 GI:161077803
79. hypothetical protein BRAFLDRAFT_89531 [*Branchiostoma floridae*]	454 aa protein	XP_002590725.1 GI:260791416
80. hypothetical protein L8106_19296 [*Lyngbya* sp. PCC 8106)	318 aa protein	ZP_01620966.1 GI:119487094
81. TyrosylProtein SulfoTransferase family member (tpst-1) [*Caenorhabditis elegans*]	380 aa protein	NP_499646.3 GI:71992370
82. methionine biosynthesis protein MetW, putative [*Nitrosococcus oceani* AFC27]	1039 aa protein	ZP_05048086.1 GI:254434578
83. tyrosylprotein sulfotransferase 2 [*Xenopus laevis*]	375 aa protein	NP_001088427.1 GI:148235112
84. glycosyl transferase family protein [*Nitrosococcus oceani* ATCC 19707]	1037 aa protein	YP_343263.1 GI:77164738
85. GM17618 [*Drosophila sechellia*]	478 aa protein	XP_002042697.1 GI:195352394
86. GE17090 [*Drosophila yakuba*]	508 aa protein	XP_002100486.1 GI:195478327

TABLE 3-continued

List of proteins/peptides comprising a CurM-like ST domain.

	Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
87.	GI14854 [*Drosophila mojavensis*]	459 aa protein	XP_002010160.1 GI:195131443
88.	GD17135 [*Drosophila simulans*]	501 aa protein	XP_002106871.1 GI:195566606
89.	GF22576 [*Drosophila ananassae*]	498 aa protein	XP_001965589.1 GI:194766965
90.	transport and golgi organization 13, isoform B [*Drosophila melanogaster*]	499 aa protein	NP_727717.1 GI:24641809
91.	GL20242 [*Drosophila persimilis*]	515 aa protein	XP_002023360.1 GI:195165053
92.	PREDICTED: protein-tyrosine sulfotransferase-like [*Acyrthosiphon pisum*]	392 aa protein	XP_001942867.2 GI:328706076
93.	PREDICTED: similar to MGC82552 protein [*Gallus gallus*]	379 aa protein	XP_415794.2 GI:118100226
94.	protein-tyrosine sulfotransferase A [*Loa loa*]	384 aa protein	XP_003139556.1 GI:312073519
95.	GA26942 [*Drosophila pseudoobscura pseudoobscura*]	521 aa protein	XP_001354726.2 GI:198468492
96.	GK16105 [*Drosophila willistoni*]	466 aa protein	XP_002067611.1 GI:195439384
97.	PREDICTED: protein-tyrosine sulfotransferase-like [*Nasonia vitripennis*]	396 aa protein	XP_001606792.1 GI:156543274
98.	PREDICTED: protein-tyrosine sulfotransferase 1-like [*Monodelphis domestica*]	450 aa protein	XP_001362570.2 GI:334324786
99.	predicted protein [*Nematostella vectensis*]	272 aa protein	XP_001630972.1 GI:156378079
100.	AGAP000900-PA [*Anopheles gambiae* str. PEST]	392 aa protein	EAA12079.6 GI:333469474

TABLE 4

List of proteins/peptides comprising a CurM-like TE domain.

	Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
37.	hypothetical protein lpl0509 [*Legionella pneumophila* str. Lens]	282 aa protein	YP_125875.1 GI:54293460
38.	putative lipase LipA [*Legionella pneumophila* 130b]	282 aa protein	AAM73852.1 GI:21666982
39.	Alpha/beta hydrolase [gamma proteobacterium IMCC2047]	294 aa protein	ZP_08648517.1 GI:339055924
40.	hypothetical protein lpp0533 [*Legionella pneumophila* str. Paris]	282 aa protein	YP_122871.1 GI:54296502
41.	Putative hydrolase or acyltransferase of alpha/beta superfamily [*Rheinheimera* sp. A13L]	279 aa protein	ZP_08572335.1 GI:336317483
42.	lipase A [*Legionella pneumophila* subsp. *pneumophila* str. Philadelphia 1]	283 aa protein	YP_094512.1 GI:52840713
43.	alpha/beta fold family hydrolase [*Shewanella oneidensis* MR-1]	288 aa protein	NP_718168.1 GI:24374125
44.	alpha/beta hydrolase [*Azotobacter vinelandii* DJ]	300 aa protein	YP_002798221.1 GI:226943148
45.	lipase [*Pseudomonas syringae* pv. mori str. 301020]	284 aa protein	EGH20834.1 GI:330888173
46.	alpha/beta hydrolase fold protein [*Dechlorosoma suillum* PS]	288 aa protein	EGW60665.1 GI:345129761
47.	hydrolase, alpha/beta fold family [*Moritella* sp. PE36]	291 aa protein	ZP_01900040.1 GI:149911422
48.	lipase [*Pseudomonas syringae* pv. lachrymans str. M301315]	284 aa protein	EGH85562.1 GI:330987459

TABLE 4-continued

List of proteins/peptides comprising a CurM-like TE domain.

	Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
49.	lipase [*Pseudomonas syringae* pv. tabaci ATCC 11528]	284 aa protein	EGH90697.1 GI:331010641
50.	Alpha/beta hydrolase fold [*Pseudomonas syringae* pv. syringae B728a]	284 aa protein	YP_235108.1 GI:66045267
51.	serine hydrolase-like 2 [*Xenopus laevis*]	304 aa protein	NP_001079604.1 GI:147899135
52.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. japonica str. M301072PT]	284 aa protein	EGH30625.1 GI:330899206
53.	alpha/beta hydrolase fold protein [*Shewanella halifaxensis* HAW-EB4]	291 aa protein	YP_001674055.1 GI:167623761
54.	lipase [*Pseudomonas syringae* pv. aesculi str. 0893_23]	284 aa protein	EGH02171.1 GI:330867462
55.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. morsprunorum str. M302280PT]	284 aa protein	EGH09818.1 GI:330875669
56.	putative hydrolase [marine gamma proteobacterium HTCC2143]	308 aa protein	ZP_01616002.1 GI:119475649
57.	alpha/beta fold family hydrolase [*Pseudomonas syringae* pv. actinidiae str. M302091]	284 aa protein	EGH65633.1 GI:330965373
58.	putative alpha/beta hydrolase [*Sphingobium japonicum* UT26S]	290 aa protein	YP_003545632.1 GI:294012172
59.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. aptata str. DSM 50252]	284 aa protein	EGH78853.1 GI:330980750
60.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. pisi str. 1704B]	284 aa protein	EGH43451.1 GI:330940344
61.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. syringae FF5]	284 aa protein	ZP_06500867.1 GI:289679977
62.	hydrolase [gamma proteobacterium NOR51-B]	299 aa protein	ZP_04957287.1 GI:254282319
63.	predicted Hydrolase or acyltransferase (alpha/beta hydrolase superfamily) protein [*Marinobacter algicola* DG893]	305 aa protein	ZP_01893017.1 GI:149375245
64.	lipase A [*Legionella longbeachae* D-4968]	281 aa protein	ZP_06187778.1 GI:270159122
65.	alpha/beta hydrolase fold protein [*Pseudomonas fluorescens* WH6]	284 aa protein	ZP_07774389.1 GI:312959874
66.	alpha/beta hydrolase fold protein [*Alicycliphilus denitrificans* K601]	300 aa protein	YP_004387755.1 GI:330824452
67.	hydrolase [*Sorangium cellulosum* 'So ce 56']	322 aa protein	YP_001615653.1 GI:162453286
68.	alpha/beta fold family hydrolase [*Shewanella violacea* DSS12]	296 aa protein	YP_003557221.1 GI:294141243
69.	lipase [*Pseudomonas syringae* pv. phaseolicola 1448A]	284 aa protein	YP_274221.1 GI:71736540
70.	putative esterase [uncultured microorganism]	293 aa protein	BAI49930.1 GI:269913831
71.	alpha/beta fold family hydrolase [*Cellvibrio japonicus* Ueda107]	298 aa protein	YP_001982425.1 GI:192359104
72.	alpha/beta hydrolase fold protein [*Pseudomonas fulva* 12-X]	287 aa protein	YP_004474637.1 GI:333900764
73.	alpha/beta hydrolase [gamma proteobacterium HdN1]	283 aa protein	YP_003810829.1 GI:304311231
74.	putative hydrolase [*Nocardia farcinica* IFM 10152]	249 aa protein	YP_117116.1 GI:54022874
75.	alpha/beta hydrolase fold protein [*Haliangium ochraceum* DSM 14365]	289 aa protein	YP_003269090.1 GI:262197881
76.	Alpha/beta hydrolase fold protein [*Pseudomonas syringae* pv. syringae 642]	284 aa protein	ZP_07264074.1 GI:302187401
77.	Alpha/beta hydrolase fold protein [*Limnobacter* sp. MED105]	310 aa protein	ZP_01916760.1 GI:149928530
78.	putative lipase LipA [*Legionella drancourtii* LLAP12]	280 aa protein	ZP_05108808.1 GI:254495899
79.	hydrolase, alpha/beta fold family [*Pseudomonas syringae* pv. tomato T1]	284 aa protein	ZP_03396309.1 GI:213968164

TABLE 4-continued

List of proteins/peptides comprising a CurM-like TE domain.

	Ref. Protein/peptide [organism or source]	No. of amino acid residues	Accession No.
80.	alpha/beta hydrolase fold protein [*Rhodopseudomonas palustris* CGA009]	340 aa protein	NP_946347.1 GI:39934071
81.	lipase, putative [*Pseudomonas syringae* pv. glycinea str. B076]	284 aa protein	EFW80985.1 GI:320324913
82.	alpha/beta fold family hydrolase [*Pseudomonas syringae* pv. tomato str. DC3000]	284 aa protein	NP_792039.1 GI:28869420
83.	hydrolase or acytransferase [*Azoarcus* sp. BH72]	300 aa protein	YP_933620.1 GI:119898407
84.	alpha/beta superfamily hydrolase [*Shewanella* piezotolerans WP3]	293 aa protein	YP_002311621.1 GI:212635096
85.	putative hydrolase [*Aromatoleum aromaticum* EbN1]	292 aa protein	YP_158988.1 GI:56477399
86.	putative hydrolase [*Pseudomonas fluorescens* SBW25]	284 aa protein	YP_002871482.1 GI:229589363
87.	alpha/beta hydrolase fold protein [*Rhodopseudomonas palustris* TIE-1]	289 aa protein	YP_001990203.1 GI:192289598
88.	hydrolase [*Pseudomonas aeruginosa* PAO1]	286 aa protein	NP_250313.1 GI:15596819
89.	putative hydrolase [*Pseudomonas aeruginosa* 39016]	286 aa protein	ZP_07792860.1 GI:313106637
90.	hydrolase, alpha/beta fold family protein [marine gamma proteobacterium HTCC2207]	286 aa protein	ZP_01223987.1 GI:90416054
91.	PA1622 [synthetic construct]	287 aa protein	AAT50924.1 GI:49083048
92.	lipase [*Pseudomonas syringae* pv. maculicola str. ES4326]	284 aa protein	EGH59298.1 GI:330959038
93.	hydrolase [*Pseudomonas stutzeri* DSM 4166]	282 aa protein	AEA83820.1 GI:327480510
94.	alpha/beta hydrolase [*Chromohalobacter salexigens* DSM 3043]	289 aa protein	YP_574516.1 GI:92114588
95.	alpha/beta hydrolase fold [*Marinobacter aquaeolei* VT8]	306 aa protein	YP_958843.1 GI:120554492
96.	hydrolase [*Pseudomonas stutzeri* A1501]	285 aa protein	YP_001172415.1 GI:146282262
97.	Hydrolase or acetyltransferase [*Leptospira biflexa* serovar Patoc strain 'Patoc 1 (Ames)']	287 aa protein	YP_001964755.1 GI:189912866
98.	hypothetical hydrolase/acyltransferase [*Photobacterium profundum* 3TCK]	299 aa protein	ZP_01219631.1 GI:90411621
99.	putative hydrolase [*Pseudomonas aeruginosa* PA7]	286 aa protein	YP_001349005.1 GI:152984242
100.	hydrolase [*Oxalobacter formigenes* HOxBLS]	289 aa protein	ZP_04576152.1 GI:237745672

[0074] In some embodiments of the invention, a precursor molecule, such as propionate or acrylate, is provided to the PKS to produce a polyketide of interest. The precursor molecule can be fed or exogenously provided to or endogenously produced by the host cell comprising the PKS, or the host cell can produce the enzymes capable of biosynthesizing the precursor molecule from a simpler molecule that can be fed or exogenously provided to the host cell or the host cell naturally endogenously produces. For example, *Streptomyces* species produces propionyl-CoA as part of its innate metabolism, thus eliminating the need for exogenous propionate provision.

[0075] In some embodiments of the invention, the PKS capable of producing an α-olefin of interest comprises CurM, the terminal PKS from the curacin biosynthesis pathway (Chang, 2004) or a similar module. CurM is a monomodular PKS protein containing an unusual sulfotransferase domain. This domain sulfonates the beta hydroxyl group of the penultimate product and the combination of the ST-TE domains catalyze a decarboxylation and functional dehydration (with sulfate as the leaving group) to yield the terminal olefin. FIG. **1** illustrates how domains from CurM can be coupled to other PKS enzymes to produce an α-olefin, such as 1-hexene, in accordance with the methods and materials of the invention. In the example shown in FIG. **1**, first PKS ORF encodes a loading module specific for propionate (via the CoA) and an extension module that incorporates acetate (via malonyl-CoA) and fully reduces the β-carbonyl. In this example shown in FIG. **1**, the loading domain is from the erythromycin PKS (Donadio et al. 1991. Science 675-679; incorporated herein by reference) and module 5 is from the nystatin PKS (Brautaset et al. 2000. Chemistry & Biology 7:395-403; incorporated herein by reference), but there are other modules that can be used to provide the same product. The second and third proteins that constitute the multi-subunit PKS in this example come from the curacin PKS and corresponding gene

cluster (see Chang et al. 2004. Journal of Natural Products 67:1356-1367; sequence updated in Gu et al. J Am Chem. Soc. 2009 Nov. 11; 131(44):16033-5; both of which are incorporated herein by reference). Using this PKS, the first two modules can be replaced with any of several well characterized modules to yield several dozen different α-olefins. Increasing the number of upstream modules to three or more increases the number of different products into the hundreds and higher.

[0076] To ensure appropriate interactions between the two PKS proteins in this and related examples, one can use the acyl-carrier protein (ACP) and C-terminus from CurM's native enzyme partner, CurL. In general, native C- and N-terminal docking partners can be used in the combinatorial PKS enzymes of the invention. Other cognate domains from different PKS enzymes can also be used.

[0077] FIG. **3**A shows an exemplary PKS for producing a triketide α-olefin. FIGS. **3**B and **3**C show exemplary extensions of this model, demonstrating how additional modules can be employed to yield longer, fully saturated, linear α-olefins.

[0078] Incorporation of the avermectin loading domain into a PKS of the invention provides access to a number of other α-olefins. Some examples of this aspect of the invention to make both known and novel α-olefins are shown in FIG. **4**.

[0079] In some embodiments, the PKS of the invention produces a butadiene with a pendant acid moiety, such that the butadiene is suitable for subsequent crosslinking. FIG. **5** shows such a PKS that comprises a set of enzymes comprising an HMG-like system found in several PKS enzymes and corresponding gene clusters. This system converts the fl-carbonyl to a number of different chemical moieties, most pertinently an exomethylene. Briefly, one of the previously described systems for incorporating an acrylate starter (DEBS (Donadio et al. 1991. supra) or difficidin (Chen et al. 2006. J. Bacteriol. 188(11):4024-36; incorporated herein by reference) loading module) can be fused to an HMG-like module, such as JamE from the jamaicamide cluster (Edwards et al. 2004. ChemBiol. 11(6):817-33; incorporated herein by reference), and a TE domain at the C-terminus. Such a bimodular PKS enzyme can be co-expressed with the genes encoding accessory proteins required for the incorporation of the desired chemistry. In this example these enzymes are JamH, JamG and JamI (Edwards et al., 2004, supra).

[0080] In some embodiments of the invention, the PKS comprises a CurM chain termination module of *Lyngbya majuscula* CurM or functionally equivalent module. In some embodiments of the invention, the PKS comprises the ST and TE domains of the curM chain termination module and sequences derived from a different CurM module or another PKS entirely. In some embodiments of the invention, the PKS comprises the KR, ACP, ST and TE domains of the CurM chain termination module and sequences derived from a different CurM module or another PKS entirely. In some embodiments of the invention, the PKS comprises the AT, KR, ACP, ST and TE domains of the CurM chain termination module and sequences derived from a different CurM module or another PKS entirely.

[0081] In some embodiments, the PKS of the invention comprises an acrylate loading module, such as the acrylate loading module from the dificidin PKS (Chen et al., 2006, supra), which incorporates the acrylyl moiety from a hydroxypropionate precursor involving the enzymes difA-E.

[0082] The present invention also provides a PKS comprising an acrylate loading module coupled to a thioesterase domain, wherein the PKS is capable of producing acrylate (acrylic acid). The erythromycin PKS, for example and without limitation, includes suitable such modules and domains.

[0083] The following depict the amino acid sequences of SEQ ID NO:1-9

[0084] *L. majuscula* CurM (GenBank: ACV42478.1) has the following amino acid sequence (SEQ ID NO:1):

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  1 msnvskttqq dvssqevlqv lqemrsrlea vnkaktepia ivgmacrfpg gandpstywr
 61 llhdgidait pvpphrwdvn ahyepnpeip gkaytkqggf iegvdqfdpl ffgispreai
121 sldpqyrlll evtwealena gqtwtnlkns ktsvfmgvst ddyaslsnpi linnrslgvg
181 rishllglqg sniqldtacs sslvaihlac qs1rsgesnl alvggvnlil spistigrct
241 mkalspdgrc ktfdaaangy gqaegcgvvv lkrlsdaitd gdlisalirg sainhdgpss
301 gltvpngmaq kqviqqalsn arlephqvsy leahgtgtal gdpieieala aiygknrpvd
361 qplvvgsvkt nighleaaag vsalikvvla lqhgeipphl hlkqpnpyvd wdklpikipt
421 slmpwnceak priagissfg isgtnahlll eevpelikgq kakgksendl erplhiltls
481 tktekaleel vsryqnhwet ypelaisdvc ytantgraqf nhrlaviasg seeltqklrq
541 htageevvgv fsgkvpnsgs eskvaflftg ggsqylnmgr qlyetqptfr qaldtcdhil
601 rpyldnplle ilypqdaqks ndspldqtgy tqpalfsiey allklweswg ikpnvvmghs
661 vgeyvaatva gvfsledglk liaargrlmq glpaggemvs vmaseskvle tlkamsledk
721 vaiaaingpe sivisgeaea iramathles vgiktkqlqv shafhsplme pmlaefeava
781 nqityhqpri piisnvtgtk adksiataqy wvnhvrqpvr faqgmatlhq qgyetfleig
841 akpillgmgk qclspdvgvw lpslrhgvde wqqilsslgq lyvqgakvdw sgfdrdysre
901 kvvlptypfq rerywvetsi nqqqvvcsge pnlqgtpegt sttivkllsq gntkelaekv
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961 ektsdlppeq lkllpdllas lsqqhqqela rlttkkwfyk vqwisqaikp qrnksnnqvc

1021 hwliltdskg lgkslathlq qlgnecsvvy qadnyqnyep giyhinpshp qefeqvyqti

1081 fengklplqk vihlwsldta seqdlttetl eqaqlwgcgs tlhllqtivk npnstppklw

1141 mitrgtqpvl sptekltvat splwglgrti asehpqlwgg lvdldpqgse devevllqqi

1201 idsqkedhla vrnrkiyvar llkhipqesq plslrsdaty litgglgalg lktaawmaek

1261 garnlvlisr rqpseqaqqt iqsleelgtq vkvlsadisv esdvanileq igtslppllg

1321 vihaagvldd gllqqtnwer ftkvmapkvn gtwnlhkltq hlsldffvcf ssmssllgsp

1381 gqgnyaaana fmdavvhyrr emglpglsin wggwseggma trlasqhqnr mqtagislis

1441 peqgiqvlee lvrtqstaqv gvlpvdwsvl akqfssanps slllellqqe tssektderi

1501 leklqaapit erqdilknyi qlvvaktlgi npskistddn fvelgmdslm gmevvnklsg

1561 dldfiiypre fyerptidsl tqylsaelse dnlatqpspt sleifatkss psgnsarpas

1621 vssrlpgiif ilssprsgst llrvmlaghs slfsppelhl lpfntmkerq eqlnlsylge

1681 glqktfmevk nldatasgal ikdlesqnls iqqvygmlqe niaprllvdk sptyamepti

1741 lergealfan skyiylvrhp ysviesfvrm rmqklvglge enpyrvaeqv waksnqniln

1801 flsqleperq hqiryedlvk kpqqvlsqlc dflnvpfepe llqpyqgdrm tggvhqksls

1861 isdpnflkhn tidesladkw ktiqlpyplk setqriasql syelpnlvtt ptnqqpqvst

1921 tpsteqpime ekflefggnq icicswgspe hpvvlcihgi leqglawqev alplaaqgyr

1981 vvapdlfghg rsshlemvts yssltflaqi drvigelpdq plllvghsmg amlataiasv

2041 rpkkikelil velplpaees kkesavnqlt tcldylsstp qhpifpdvat aasrlrqaip

2101 slseefsyil agritqpnqg gvrwswdaii rtrsilglnn lpggrsqyle mlksiqvptt

2161 lvygdsskln rpedlqqqkm tmtqakrvfl sgghnlhida aaalaslilt s

[0085] HexORF1 has the following amino acid sequence (SEQ ID NO:2):

-continued

MADLSKLSDSRTAQPGRIVRPWPLSGCNESALRARARQLRAHLDRFPDAG

VEGVGAALAHDEQADAGPHRAVVVASSTSELLDGLAAVADGRPHASVVRG

VARPSAPVVFVFPGQGAQWAGMAGELLGESRVFAAAMDACARAFEPVTDW

TLAQVLDSPEQSRRVEVVQPALFAVQTSLAALWRSFGVTPDAVVGHSIGE

LAAAHVCGAAGAADAARAAALWSREMIPLVGNGDMAAVALSADEIEPRIA

RWDDDVVLAGVNGPRSVLLTGSPEPVARRVQELSAEGVRAQVINVSMAAH

SAQVDDIAEGMRSALAWFAPGGSEVPFYASLTGGAVDTRELVADYWRRSF

RLPVRFDEAIRSALEVGPGTFVEASPHPVLAAALQQTLDAEGSSAAVVPT

LQRGQGGMRRFLLAAAQAFTGGVAVDWTAAYDDVGAEPGSLPEFAPAEEE

DEPAESGVDWNAPPHVLRERLLAVVNGETAALAGREADAEATFRELGLDS

VLAAQLRAKVSAAIGREVNIALLYDHPTPRALAEALAAGTEVAQRETRAR

TNEAAPGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRGWD

LDSLFHPDPTRSGTAHQRGGGFLTEATAFDPAFFGMSPREALAVDPQQRL

MLELSWEVLERAGIPPTSLQASPTGVFVGLIPQEYGPRLAEGGEGVEGYL

MTGTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESS

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LAMAGGVTVMPTPGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGML

LLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQVRVIQQALA

ESGLGPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSN

LGHTQAAAGVAGVIKMVLAMRAGTLPRTLHASERSKEIDWSSGAISLLDE

PEPWPAGARPRRAGVSSFGVSGTNAHVIVEEAPESSADAVAESGVRVPVP

VVPWVVSARSAEGLAAQAERLARFVGERSDQDPVDIGFSLVRSRSLLEHR

AVVLGKGRDDLVAGLASLASDGSATGVVSGVARGRARVAFGFSGQGAQRV

GMGAELASVYPVFAEALAEVTGALGLDPEVFGDVDRLGRTEVTQAALFAF

EVAVVRLLESFGVRPDVLIGHSIGEIAAAYVAGVFSLGDAAALVGARGRL

MQALPAGGVMVAVQAGEAEVVAALEGFADRVSLAAVNGPSSVVVSGEAEA

VEQVVARLGKVKSKRLRVSHAFHSPLMEPMLADFRQVAEQITYNEPQLPV

VSNVSGRLAEPGELTTPDYWVRHVREAVRFGDGVRALAADGVGVLVEVGP

DSVLTALARESLDGEDGLRAVPLLRKDRPEPETLLTGVAQAFTHGVQVDW

PALLPGGRRVELPTYAFQRRRYWLEDADPTGGDPAALGLTAADHPLLGAA

VPLAEDQGIVITSRLSLRTHPWLADHEIGGTVLLPGAGLVEIALRAGDEV

GCGRVEELTLEIPLVVPQEGGVTVQIRVGAPDESGWRPMTVHSRTDPEEE

WTRHVSGVLSPDVPTERYDLGAWPPAGATPVELDGFYEAYARLGYAYGPS

-continued

FQGLRAAWRRGDEVFAEVSLPVEEQETAGRFTLHPALLDAALQSAGAGAF

FDSGGSMRLPFAWSGVSVFAAGASTVRVRLSPAGPDAVTVALADPTGAPV

ALVERLLIPEMSPEQLERVRGEEKEAPYVLDWVPVEVPADDLVRPERWTL

LGGADAGVGLDVAGAFASLEPSDGAPEFVVLPCVPPTSPTRAADVRQSTL

QALTVLQNWVTDERHADSRLVLVTRRAVGVGAHDDVPDLTHAALWGLVRS

AQTENPGRFLLVDLDEGAELAEVLPGALGSGESQVAVRAGRVLAARLARS

GSGGAELVPPAGAPWRLDTTSPGTLENLALVPSAEEPLGPLDVRVSVRAA

GLNFRDVLIALGMYPGDARMGGEGAGVVTDVGSEVTTLAPGDRVMGMLSS

AFGPTAVSDHRALVRVPDDWSFEQAASVPTVFATAYYGLVDLAELRAGQS

VLVHAAAGGVGMAAVQLARHLGAEVFGTASTGKWDSLRAGGLDAEHIASS

RTVEFEETFLAATAGRGVDVVLDSLAGEFVDASLRLLPRGGRFVEMGKAD

IRDAERVAADHPGVTYRSFDLLEAGLDRFQEILTEVVRLFERGVLRHLPV

TAWDVRRAAEAFRFVSQARHVGKNVLVMPRVWDRDGTVLITGGTGALGAL

VARHLVAEHGMRNVLLAGRRGVDAPGARELLAELETAGAQVSVVACDVAD

RDAVAELIAKVPVEHPLTAVVHTAGVVADATLTALDAERVDTVLRAKVDA

VLHLHEATRGLDLAGFVLFSSASGIFGSPGQGNYAAANSFIDAFAHHRRA

QGLPALSLAWGLWARTSGMAGQLGHDDVARISRTGLAPITDDQGMALLDA

ALGAGRPLLVPVRLDRAALRSQATAGTLPPILRGLVRATVRRAASTAAAQ

GPSLAERLAGLPVTEHERIVVELVRADLAAVLGHSSSAGIDPGRAFQDMG

IDSLTAVELRNRLNGATGLRLAASLVFDYPTPNALATHILDELALDTAGA

GAAGEPDGPAPAPADEARFRRVINSIPLDRIRRAGLLDALLGLAGTSADT

AASDDFDQEEDGPAIASMDVDDLVRIALGESDTTADITEGTDRS*

[0086] HexORF1' has the following amino acid sequence (SEQ ID NO:3):

MADLSKLSDSRTAQPGRIVRPWPLSGCNESALRARARQLRAHLDRFPDAG

VEGVGAALAHDEQADAGPHRAVVVASSTSELLDGLAAVADGRPHASVVRG

VARPSAPVVFVFPGQGAQWAGMAGELLGESRVFAAAMDACARAFEPVTDW

TLAQVLDSPEQSRRVEVVQPALFAVQTSLAALWRSFGVTPDAVVGHSIGE

LAAAHVCGAAGAADAARAAALWSREMIPLVGNGDMAAVALSADEIEPRIA

RWDDDVVLAGVNGPRSVLLTGSPEPVARRVQELSAEGVRAQVINVSMAAH

SAQVDDIAEGMRSALAWFAPGGSEVPFYASLTGGAVDTRELVADYWRRSF

RLPVRFDEAIRSALEVGPGTFVEASPHPVLAAALQQTLDAEGSSAAVVPT

LQRGQGGMRRFLLAAAQAFTGGVAVDWTAAYDDVGAEPGSLPEFAPAEEE

DEPAESGVDWNAPPHVLRERLLAVVNGETAALAGREADAEATFRELGLDS

VLAAQLRAKVSAAIGREVNIALLYDHPTPRALAEALAAGTEVAQRETRAR

TNEAAPGEPVAVVAMACRLPGGVSTPEEFWELLSEGRDAVAGLPTDRGWD

LDSLFHPDPTRSGTAHQRGGGFLTEATAFDPAFFGMSPREALAVDPQQRL

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MLELSWEVLERAGIPPTSLQASPTGVFVGLIPQEYGPRLAEGGEGVEGYL

MTGTTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESS

LAMAGGVTVMPTPGMLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGML

LLERLSDARRNGHPVLAVLRGTAVNSDGASNGLSAPNGRAQVRVIQQALA

ESGLGPADIDAVEAHGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSN

LGHTQAAAGVAGVIKMVLAMRAGTLPRTLHASERSKEIDWSSGAISLLDE

PEPWPAGARPRRAGVSSFGVSGTNAHVIVEEAPESSADAVAESGVRVPVP

VVPWVVSARSAEGLAAQAERLARFVGERSDQDPVDIGFSLVRSRSLLEHR

AVVLGKGRDDLVAGLASLASDGSATGVVSGVARGRARVAFGFSGQGAQRV

GMGAELASVYPVFAEALAEVTGALGLDPEVFGDVDRLGRTEVTQAALFAF

EVAVVRLLESFGVRPDVLIGHSIGEIAAAYVAGVFSLGDAAALVGARGRL

MQALPAGGVMVAVQAGEAEVVAALEGFADRVSLAAVNGPSSVVVSGEAEA

VEQVVARLGKVKSKRLRVSHAFHSPLMEPMLADFRQVAEQITYNEPQLPV

VSNVSGRLAEPGELTTPDYWVRHVREAVRFGDGVRALAADGVGVLVEVGP

DSVLTALARESLDGEDGLRAVPLLRKDRPEPETLLTGVAQAFTHGVQVDW

PALLPGGRRVELPTYAFQRRRYWLEDADPTGGDPAALGLTAADHPLLGAA

VPLAEDQGIVITSRLSLRTHPWLADHEIGGTVLLPGAGLVEIALRAGDEV

GCGRVEELTLEIPLVVPQEGGVTVQIRVGAPDESGWRPMTVHSRTDPEEE

WTRHVSGVLSPDVPTERYDLGAWPPAGATPVELDGFYEAYARLGYAYGPS

FQGLRAAWRRGDEVFAEVSLPVEEQETAGRFTLHPALLDAALQSAGAGAF

FDSGGSMRLPFAWSGVSVFAAGASTVRVRLSPAGPDAVTVALADPTGAPV

ALVERLLIPEMSPEQLERVRGEEKEAPYVLDWVPVEVPADDLVRPERWTL

LGGADAGVGLDVAGAFASLEPSDGAPEFVVLPCVPPTSPTRAADVRQSTL

QALTVLQNWVTDERHADSRLVLVTRRAVGVGAHDDVPDLTHAALWGLVRS

AQTENPGRFLLVDLDEGAELAEVLPGALGSGESQVAVRAGRVLAARLARS

GSGGAELVPPAGAPWRLDTTSPGTLENLALVPSAEEPLGPLDVRVSVRAA

GLNFRDVLIALGMYPGDARMGGEGAGVVTDVGSEVTTLAPGDRVMGMLSS

AFGPTAVSDHRALVRVPDDWSFEQAASVPTVFATAYYGLVDLAELRAGQS

VLVHAAAGGVGMAAVQLARHLGAEVFGTASTGKWDSLRAGGLDAEHIASS

RTVEFEETFLAATAGRGVDVVLDSLAGEFVDASLRLLPRGGRFVEMGKAD

IRDAERVAADHPGVTYRSFDLLEAGLDRFQEILTEVVRLFERGVLRHLPV

TAWDVRRAAEAFRFVSQARHVGKNVLVMPRVWDRDGTVLITGGTGALGAL

VARHLVAEHGMRNVLLAGRRGVDAPGARELLAELETAGAQVSVVACDVAD

RDAVAELIAKVPVEHPLTAVVHTAGVVADATLTALDAERVDTVLRAKVDA

VLHLHEATRGLDLAGFVLFSSASGIFGSPGQGNYAAANSFIDAFAHHRRA

QGLPALSLAWGLWARTSGMAGQLGHDDVARISRTGLAPITDDQGMALLDA

ALGAGRPLLVPVRLDRAALRSQATAGTLPPILRGLVRATVRRAASTAAAQ

GPSLAERLAGLPVTEHERIVVELVRADLAAVLGHASAERVPADQAFAELG

VDSLTAVELRNRLNGATGLRLAASLVFDYPTPNALATHILDELALDTAGA

-continued

GAAGEPDGPAPAPADEARFRRVINSIPLDRIRRAGLLDALLGLAGTSADT

AASDDFDQEEDGPAIASMDVDDLVRIALGESDTTADITEGTDRS*

[0087] HexORF2 has the following amino acid sequence (SEQ ID NO:4):

MSSASSEKIVEALRASLTENERLRRLNQELAAAAHEPVAIVSMACRFP

GGVESPEDFWDLISEGRDAVSGLPDNRGWDLDALYDPDPEAQGKTYVR

EGAFLYDAAEFDAELFGISPREALAMDPQQRLLMETSWEVLERAGIRP

DSLRGKPVGVFTGGITSDYVTRHYASGTAPQLPSGVESHFMTGSAGSV

FSGRIAYTYGFEGPAVTVDTACSSSLVALHMAAQSLRQGECSLAFAGG

VAVLPNPGTFVGFSRQRALSPDGRCKAFSADADGTGWGEGAGLVLLEK

LSDARRNGHPVLAILRGSAVNQDGASNGLTAPNGPSQQRVIRAALANA

RLSPDDVDVVEAHGTGTPLGDPIEAQALQATYGRSRSAERPLWLGSVK

SNVAHAQAAAGVASVIKVVMALRHRLLPKTLHADERSPHIDWHSGAVE

LLTEAREWSRTEGRARRAGVSSFGISGTNAHVIIEEAPELIKGQKAKG

KSENDLERPLHILTLSTKTEKALEELVSRYQNHWETYPELAISDVCYT

ANTGRAQFNHRLAVIASGSEELTQKLRQHTAGEEVVGVFSGKVPNSGS

ESKVAFLFTGQGSQYLNMGRQLYETQPTFRQALDTCDHILRPYLDNPL

LEILYPQDAQKSNDSPLDQTGYTQPALFSIEYALLKLWESWGIKPNVV

MGHSVGEYVAATVAGVFSLEDGLKLIAARGRLMQGLPAGGEMVSVMAS

ESKVLETLKAMSLEDKVAIAAINGPESIVISGEAEAIRAMATHLESVG

IKTKQLQVSHAFHSPLMEPMLAEFEAVANQITYHQPRIPIISNVTGTK

ADKSIATAQYWVNHVRQPVRFAQGMATLHQQGYETFLEIGAKPILLGM

GKQCLSPDVGVWLPSLRHGVDEWQQILSSLGQLYVQGAKVDWSGFDRD

YSREKVVLPTYPFQRERYWVETSINQQQVVCSGEPNLQGTPEGTSTTI

VKLLSQGNTKELAEKVEKTSDLPPEQLKLLPDLLASLSQQHQQELARL

TTKKWFYKVQWISQAIKPQRNKSNNQVCHWLILTDSKGLGKSLATHLQ

QLGNECSVVYQADNYQNYEPGIYHINPSHPQEFEQVYQTIFENGKLPL

QKVIHLWSLDTASEQDLTTETLEQAQLWGCGSTLHLLQTLVKNPNSTP

PKLWMITRGTQPVLSPTEKLTVATSPLWGLGRTIASEHPQLWGGLVDL

DPQGSEDEVEVLLQQIIDSQKEDHLAVRNRKIYVARLLKHIPQESQPL

SLRSDATYLITGGLGALGLKTAAWMAEKGARNLVLISRRQPSEQAQQT

IQSLEELGTQVKVLSADISVESDVANILEQIQTSLPPLLGVIHAAGVL

DDGLLQQTNWERFTKVMAPKVNGTWNLHKLTQHLSLDFFVCFSSMSSL

LGSPGQGNYAAANAFMDAVVHYRREMGLPGLSINWGGWSEGGMATRLA

SQHQNRMQTAGISLISPEQGIQVLEELVRTQSTAQVGVLPVDWSVLAK

QFSSANPSSLLLELLQQETSSEKTDERILEKLQAAPITERQDILKNYI

QLVVAKTLGINPSKISTDDNFVELGMDSLMGMEVVNKLSGDLDFIIYP

REFYERPTIDSLTQYLSAELSEDNLATQPSPTSLEIFATKSSPSGNSA

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RPASVSSRLPGIIFILSSPRSGSTLLRVMLAGHSSLFSPPELHLLPFN

TMKERQEQLNLSYLGEGLQKTFMEVKNLDATASQALIKDLESQNLSIQ

QVYGMLQENIAPRLLVDKSPTYAMEPTILERGEALFANSKYIYLVRHP

YSVIESFVRMRMQKLVGLGEENPYRVAEQVWAKSNQNILNFLSQLEPE

RQHQIRYEDLVKKPQQVLSQLCDFLNVPFEPELLQPYQGDRMTGGVHQ

KSLSISDPNFLKHNTIDESLADKWKTIQLPYPLKSETQRIASQLSYEL

PNLVTTPTNQQPQVSTTPSTEQPIMEEKFLEFGGNQICLCSWGSPEHP

VVLCIHGILEQGLAWQEVALPLAAQGYRVVAPDLFGHGRSSHLEMVTS

YSSLTFLAQIDRVIQELPDQPLLLVGHSMGAMLATAIASVRPKKIKEL

ILVELPLPAEESKKESAVNQLTTCLDYLSSTPQHPIFPDVATAASRLR

QAIPSLSEEFSYILAQRITQPNQGGVRWSWDAIIRTRSILGLNNLPGG

RSQYLEMLKSIQVPTTLVYGDSSKLNRPEDLQQQKMTMTQAKRVFLSG

GHNLHIDAAAALASLILTS*

[0088] The amino acid sequence of a PKS capable of producing 1-butene has the following amino acid sequence (SEQ ID NO:5):

MADLSKLSDSRTAQPGRIVRPWPLSGCNESALRARARQLRAHLDRFPD

AGVEGVGAALAHDEQADAGPHRAVVVASSTSELLDGLAAVADGRPHAS

VVRGVARPSAPVVFVFPGQGAQWAGMAGELLGESRVFAAAMDACARAF

EPVTDWTLAQVLDSPEQSRRVEVVQPALFAVQTSLAALWRSFGVTPDA

VVGHSIGELAAAHVCGAAGAADAARAAALWSREMIPLVGNGDMAAVAL

SADEIEPRIARWDDDVVLAGVNGPRSVLLTGSPEPVARRVQELSAEGV

RAQVINVSMAAHSAQVDDIAEGMRSALAWFAPGGSEVPFYASLTGGAV

DTRELVADYWRRSFRLPVRFDEAIRSALEVGPGTFVEASPHPVLAAAL

QQTLDAEGSSAAVVPTLQRGQGGMRRFLLAAAQAFTGGVAVDWTAAYD

DVGAEPGSLPEFAPAEEEDEPAESGVDWNAPPHVLRERLLAVVNGETA

ALAGREADAEATFRELGLDSVLAAQLRAKVSAAIGREVNIALLYDHPT

PRALAEALSSGTEVAQRETRARTNEAAPGEPIAVVAMACRLPGGVSTP

EEFWELLSEGRDAVAGLPTDRGWDLDSLFHPDPTRSGTAHQRGGGFLT

EATAFDPAFFGMSPREALAVDPQQRLMLELSWEVLERAGIPPTSLQAS

PTGVFVGLIPQEYGPRLAEGGEGVEGYLMTGTTTSVASGRIAYTLGLE

GPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPTPGMLVD

FSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLSDARRNGHPVL

AVLRGTAVNSDGASNGLSAPNGRAQVRVIQQALAESGLGPADIDAVEA

HGTGTRLGDPIEARALFEAYGRDREQPLHLGSVKSNLGHTQAAAGVAG

VIKMVLAMRAGTLPRTLHASERSKEIDWSSGAISLLDEPEPWPAGARP

RRAGVSSFGISGTNAHAIIEEAPELIKGQKAKGKSENDLERPLHILTL

STKTEKALEELVSRYQNHWETYPELAISDVCYTANTGRAQFNHRLAVI

ASGSEELTQKLRQHTAGEEVVGVFSGKVPNSGSESKVAFLFTGQGSQY

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LNMGRQLYETQPTFRQALDTCDHILRPYLDNPLLEILYPQDAQKSNDS

PLDQTGYTQPALFSIEYALLKLWESWGIKPNVVMGHSVGEYVAATVAG

VFSLEDGLKLIAARGRLMQGLPAGGEMVSVMASESKVLETLKAMSLED

KVAIAAINGPESIVISGEAEAIRAMATHLESVGIKTKQLQVSHAFHSP

LMEPMLAEFEAVANQITYHQPRIPIISNVTGTKADKSIATAQYWVNHV

RQPVRFAQGMATLHQQGYETFLEIGAKPILLGMGKQCLSPDVGVWLPS

LRHGVDEWQQILSSLGQLYVQGAKVDWSGFDRDYSREKVVLPTYPFQR

ERYWVETSINQQQVVCSGEPNLQGTPEGTSTTIVKLLSQGNTKELAEK

VEKTSDLPPEQLKLLPDLLASLSQQHQQELARLTTKKWFYKVQWISQA

IKPQRNKSNNQVCHWLILTDSKGLGKSLATHLQQLGNECSVVYQADNY

QNYEPGIYHINPSHPQEFEQVYQTIFENGKLPLQKVIHLWSLDTASEQ

DLTTETLEQAQLWGCGSTLHLLQTLVKNPNSTPPKLWMITRGTQPVLS

PTEKLTVATSPLWGLGRTIASEHPQLWGGLVDLDPQGSEDEVEVLLQQ

IIDSQKEDHLAVRNRKIYVARLLKHIPQESQPLSLRSDATYLITGGLG

ALGLKTAAWMAEKGARNLVLISRRQPSEQAQQTIQSLEELGTQVKVLS

ADISVESDVANILEQIQTSLPPLLGVIHAAGVLDDGLLQQTNWERFTK

VMAPKVNGTWNLHKLTQHLSLDFFVCFSSMSSLLGSPGQGNYAAANAF

MDAVVHYRREMGLPGLSINWGGWSEGGMATRLASQHQNRMQTAGISLI

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SPEQGIQVLEELVRTQSTAQVGVLPVDWSVLAKQFSSANPSSLLLELL

QQETSSEKTDERILEKLQAAPITERQDILKNYIQLVVAKTLGINPSKI

STDDNFVELGMDSLMGMEVVNKLSGDLDFIIYPREFYERPTIDSLTQY

LSAELSEDNLATQPSPTSLEIFATKSSPSGNSARPASVSSRLPGIIFI

LSSPRSGSTLLRVMLAGHSSLFSPPELHLLPFNTMKERQEQLNLSYLG

EGLQKTFMEVKNLDATASQALIKDLESQNLSIQQVYGMLQENIAPRLL

VDKSPTYAMEPTILERGEALFANSKYIYLVRHPYSVIESFVRMRMQKL

VGLGEENPYRVAEQVWAKSNQNILNFLSQLEPERQHQIRYEDLVKKPQ

QVLSQLCDFLNVPFEPELLQPYQGDRMTGGVHQKSLSISDPNFLKHNT

IDESLADKWKTIQLPYPLKSETQRIASQLSYELPNLVTTPTNQQPQVS

TTPSTEQPIMEEKFLEFGGNQICLCSWGSPEHPVVLCIHGILEQGLAW

QEVALPLAAQGYRVVAPDLFGHGRSSHLEMVTSYSSLTFLAQIDRVIQ

ELPDQPLLLVGHSMGAMLATAIASVRPKKIKELILVELPLPAEESKKE

SAVNQLTTCLDYLSSTPQHPIFPDVATAASRLRQAIPSLSEEFSYILA

QRITQPNQGGVRWSWDAIIRTRSILGLNNLPGGRSQYLEMLKSIQVPT

TLVYGDSSKLNRPEDLQQQKMTMTQAKRVFLSGGHNLHIDAAAALASL

ILTS*

[0089] The amino acid sequence of a PKS capable of producing propene has the following amino acid sequence (SEQ ID NO:6):

MAGHGDATAQKAQDAEKSEDGSDAIAVIGMSCRFPGAPGTAEFWQLLSSGADAVVTAADGRR

RGTIDAPADFDAAFFGMSPREAAATDPQQRLVLELGWEALEDAGIVPESLRGEAASVFVGAM

NDDYATLLHRAGAPTDTYTATGLQHSMIANRLSYFLGLRGPSLVVDTGQSSSLVAVALAVES

LRGGTSGIALAGGVNLVLAEEGSAAMERVGALSPDGRCHTFDARANGYVRGEGGAIVVLKPL

ADALADGDRVYCVVRGVATGNDGGGPGLTVPDRAGQEAVLRAACDQAGVRPADVRFVELHGT

GTPAGDPVEAEALGAVYGTGRPANEPLLVGSVKTNIGHLEGAAGIAGFVKAALCLHERALPA

SLNFETPNPAIPLERLRLKVQTAHAALQPGTGGGPLLAGVSAFGMGGTNCHVVLEETPGGRQ

PAETGQADACLFSASPMLLLSARSEQALRAQAARLREHLEDSGADPLDIAYSLATTRTRFEH

RAAVPCGDPDRLSSALAALAAGQTPRGVRIGSTDADGRLALLFTGQGAQHPGMGQELYTTDP

HFAAALDEVCEELQRCGTQNLREVMFTPDQPDLLDRTEYTQPALFALQTALYRTLTARGTQA

HLVLGHSVGEITAAHIAGVLDLPDAARLITARAHVMGQLPHGGAMLSVQAAEHDLDQLAHTH

GVEIAAVNGPTHCVLSGPRTALEETAQHLREQNVRHTWLKVSHAFHSALMDPMLGAFRDTLN

TLNYQPPTIPLISNLTGQIADPNHLCTPDYWIDHARHTVRFADAVQTAHHQGTTTYLEIGPH

PTLTTLLHHTLDNPTTIPTLHRERPEPETLTQAIAAVGVRTDGIDWAVLCGASRPRRVELPT

YAFQRRTHWAPGLTPNHAPADRPAAEPQRAMAVGPVSREALVRLVGETTASVLGLDGPDEVA

LDRPFTSQGLDSMTAVELAGLLGTAAGVALDPTLVYELPTPRAVADHLAKTLLGESAADADQ

EVNGRTGEAEAKAGDPIAVIGIGCRFPGGVATPDDLWELVASGTDAISTFPTDRGWDLDGLY

DPDPSTPGKSYVRHGGFLHDAAQFDAEFFGISPREATAMDPQQRLLLETSWEALERAGVVPE

SLRGGRTGVFVGTTAPEYGPRLHEGTDGYEGFLLTGTTASVASGRIAYALGTRGPALTVDTA

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CSSSLVALHLAVQSLRRGECDLALAGGTTVMSGPGMFVEFSRQRGLAPDGRCKAFSADADGT

AWAEGVGMLLVERLSDAERLGHRVLAVVRGTAVNQDGASNGLTAPSGPAQQQVIRDALSDAG

LSADDIDAVEAHGTGTALGDPIEAGALLATYGHPKRQTPVWLGSLKSNIGHTQAAAGIAGII

KMVQALRHDTLPRTLHADHPSSKVDWDAGPLQLLTDARPWPADPDRPRRAGISAFGVSGTNA

HVVLEEPPELIKGQKAKGKSENDLERPLHILTLSTKTEKALEELVSRYQNHWETYPELAISD

VCYTANTGRAQFNHRLAVIASGSEELTQKLRQHTAGEEVVGVFSGKVPNSGSESKVAFLFTG

QGSQYLNMGRQLYETQPTFRQALDTCDHILRPYLDNPLLEILYPQDAQKSNDSPLDQTGYTQ

PALFSIEYALLKLWESWGIKPNVVMGHSVGEYVAATVAGVFSLEDGLKLIAARGRLMQGLPA

GGEMVSVMASESKVLETLKAMSLEDKVAIAAINGPESIVISGEAEAIRAMATHLESVGIKTK

QLQVSHAFHSPLMEPMLAEFEAVANQITYHQPRIPIISNVTGTKADKSIATAQYWVNHVRQP

VRFAQGMATLHQQGYETFLEIGAKPILLGMGKQCLSPDVGVWLPSLRHGVDEWQQILSSLGQ

LYVQGAKVDWSGFDRDYSREKVVLPTYPFQRERYWVETSINQQQVVCSGEPNLQGTPEGTST

TIVKLLSQGNTKELAEKVEKTSDLPPEQLKLLPDLLASLSQQHQQELARLTTKKWFYKVQWI

SQAIKPQRNKSNNQVCHWLILTDSKGLGKSLATHLQQLGNECSVVYQADNYQNYEPGIYHIN

PSHPQEFEQVYQTIFENGKLPLQKVIHLWSLDTASEQDLTTETLEQAQLWGCGSTLHLLQTL

VKNPNSTPPKLWMITRGTQPVLSPTEKLTVATSPLWGLGRTIASEHPQLWGGLVDLDPQGSE

DEVEVLLQQIIDSQKEDHLAVRNRKIYVARLLKHIPQESQPLSLRSDATYLITGGLGALGLK

TAAWMAEKGARNLVLISRRQPSEQAQQTIQSLEELGTQVKVLSADISVESDVANILEQIQTS

LPPLLGVIHAAGVLDDGLLQQTNWERFTKVMAPKVNGTWNLHKLTQHLSLDFFVCFSSMSSL

LGSPGQGNYAAANAFMDAVVHYRREMGLPGLSINWGGWSEGGMATRLASQHQNRMQTAGISL

ISPEQGIQVLEELVRTQSTAQVGVLPVDWSVLAKQFSSANPSSLLLELLQQETSSEKTDERI

LEKLQAAPITERQDILKNYIQLVVAKTLGINPSKISTDDNFVELGMDSLMGMEVVNKLSGDL

DFIIYPREFYERPTIDSLTQYLSAELSEDNLATQPSPTSLEIFATKSSPSGNSARPASVSSR

LPGIIFILSSPRSGSTLLRVMLAGHSSLFSPPELHLLPFNTMKERQEQLNLSYLGEGLQKTF

MEVKNLDATASQALIKDLESQNLSIQQVYGMLQENIAPRLLVDKSPTYAMEPTILERGEALF

ANSKYIYLVRHPYSVIESFVRMRMQKLVGLGEENPYRVAEQVWAKSNQNILNFLSQLEPERQ

HQIRYEDLVKKPQQVLSQLCDFLNVPFEPELLQPYQGDRMTGGVHQKSLSISDPNFLKHNTI

DESLADKWKTIQLPYPLKSETQRIASQLSYELPNLVTTPTNQQPQVSTTPSTEQPIMEEKFL

EFGGNQICLCSWGSPEHPVVLCIHGILEQGLAWQEVALPLAAQGYRVVAPDLFGHGRSSHLE

MVTSYSSLTFLAQIDRVIQELPDQPLLLVGHSMGAMLATAIASVRPKKIKELILVELPLPAE

ESKKESAVNQLTTCLDYLSSTPQHPIFPDVATAASRLRQAIPSLSEEFSYILAQRITQPNQG

GVRWSWDAIIRTRSILGLNNLPGGRSQYLEMLKSIQVPTTLVYGDSSKLNRPEDLQQQKMTM

TQAKRVFLSGGHNLHIDAAAALASLILTS

[0090] The amino acid sequence of a PKS capable of producing styrene has the following amino acid sequence (SEQ ID NO:7):

MTKEYTRPQSAPLTEGDLLTLIVAHLAERLRMDARFIDVHEPFSRHGLDSRGAVDLVVDLRT

ALGRPLSPVVVWQHPTPDALARHLAGGADAREGQARADSAYERPGAPNEPIAIVGMACRFPG

APDVDSYWRLLSGGVDAVTEVPAGRWDMDAFYDRDPRSLGDVSTLRGGFIDDVDRFDAMFFG

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ISPREAVSMDPQQRLMLELAWEALEDAGIVAERLKESLTGVFFGCIWDDYVTLIHQRGRGAI

AQHTVTGNHRSIIANRVSYTLDLRGPSMTVDSACSSALVTIHMACESLRSGESTLALAGGVN

LNIAPESTIGVHKFGGLSPDGRCFTFDARANGYVRGEGGGVVVLKRLSSAIADGDPIICVIR

GSAVNNDGASNGLTGPNPLAQEAVLRTAYERAGVNPADVQYVELHGTGTQLGDPVEASALGA

VLGKRRPAERPLLVGSAKTNVGHLEGAAGIVGLLKAALCLKHKQLAPNLNFETPNPHIPFAE

LNLKVQGALGPWPDMDRPLVCGVSSFGLGGTNAHVVLSEWASLEAELHPLAAESPEALREEV

QRRLLTMTSLVGRAPLSFLCGRSAAQRSAKEHRLAVTARSFEELKQRLLGFLEHEKHVSVSA

GRVDLGAAPKVVFVFAGQGAQWFGMGRALLQREPVFRTTIEQCSSFIQQNLGWSLLDELMTD

RESSRLDEIDVSLPAIISIEIALAAQWRAWGVEPAFVVGHSTGEIAAAHVAGVLSIEDAMRT

ICAYGRIIRKLRGKGGMGLVALSWEDAGKELTGYEGRLFRAIEHSADSTVLAGEPDALDALL

QALERKNVFCRRVAMDVAPHCPQVDCLRDELFDALREVRPNKAQIPIVSEVTGTALDGERFD

ASHWVRNFGDPALFSTAIDHLLQEGFDIFLELTPHPLALPAIESNLRRSGRRGVVLPSLRRN

EDERGVMLDTLGVLYVRGAPVRWDNVYPAAFESMPLPSTAGGGKPLPPMPLLISARTDAALA

AQAARLRAHLDSHLDLELVDVAYSLAATRTHFERRAVVVARDRAGILDGLDALAHGGSAALL

GRSAAHGKLAILFTGQGSQRPTMGRALYDAFPVFRGALDAAAAHLDRDLDRPLRDVLFAPDG

SEQAARLDQTAFTQPALFALEVALFELLQSFGLKPALLLGHSIGELVAAHVAGVLSLQDACT

LVAARAKLMQALPQGGAMVTLQASEQEARDLLQAAEGRVSLAAVNGHLSTVVAGDEDAVLKI

ARQVEALGRKATRLRVSHAFHSPHMDGMLDDFRRVAQGLTFHPARIPIISNVTGARATDQEL

ASPETWVRHVRDTVRFLDGVRTLHAEGARAFLELGPHPVLSALAQDALGHDEGPSPCAFLPT

LRKGRDDAEAFTAALGALHAAGLTPDWNAFFAPFAPCKVPLPTYTFQRERFWLDASTAHAAS

ATPAAALEGRFWQAVESGDIDTLSSELHVDGDEQRAALALVLPTLSSFRHKRQEQSTVDAWR

YRVTWKPLTTAATPADLAGTWLLVVPSALGDDALLATLTEALTRRGARVLALRVSDIHIGRS

ALVEHLREALAETAPLRGVLSLLALDEHRLADRSALPAGLALSLALVQGLDDLAIEAPLWLF

TRGAVSIGHSDPITHPTQAMIWGLGRVVGLEHPERWGGLVDVSAGVDESAVGRLLPALAQRH

DEDQLALRPAGLYARRIVRAPLGDAPPAREFRPRGTILITGGTGALGAHVARWLARQGAEHL

ILISRRGAEAPGASELHAELNALGVRTTLAACDVADRSALQALLDSIPSDCPLTAVFHTAGA

RDDGLIGDMTPERIERVLAPKLDSALHLHELTKNSALDAFVLYASLSGVLGNPGQANYAAAN

AFLDALAEHRRSLGLTATSVAWGGWGGGGMATERVAAQLQQRGLLQMAPSLALAALAQALQQ

DETTITVADIDWSRFAPAFSVARQRPLLRDLPEAQRALQASEGASSEHGPATGLLDELRSRS

ESEQLDLLATLVRGETATVLGHAEASHVDPDKGFMDLGLDSLMTVELRRRLQKATGVKLPPT

LAFDHPSPHRVAFFLRDSLSEDNLATQPSPTSLEIFATKSSPSGNSARPASVSSRLPGIIFI

LSSPRSGSTLLRVMLAGHSSLFSPPELHLLPFNTMKERQEQLNLSYLGEGLQKTFMEVKNLD

ATASQALIKDLESQNLSIQQVYGMLQENIAPRLLVDKSPTYAMEPTILERGEALFANSKYIY

LVRHPYSVIESFVRMRMQKLVGLGEENPYRVAEQVWAKSNQNILNFLSQLEPERQHQIRYED

LVKKPQQVLSQLCDFLNVPFEPELLQPYQGDRMTGGVHQKSLSISDPNFLKHNTIDESLADK

WKTIQLPYPLKSETQRIASQLSYELPNLVTTPTNQQPQVSTTPSTEQPIMEEKFLEFGGNQI

CLCSWGSPEHPVVLCIHGILEQGLAWQEVALPLAAQGYRVVAPDLFGHGRSSHLEMVTSYSS

LTFLAQIDRVIQELPDQPLLLVGHSMGAMLATAIASVRPKKIKELILVELPLPAEESKKESA

VNQLTTCLDYLSSTPQHPIFPDVATAASRLRQAIPSLSEEFSYILAQRITQPNQGGVRWSWD

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AIIRTRSILGLNNLPGGRSQYLEMLKSIQVPTTLVYGDSSKLNRPEDLQQQKMTMTQAKRVF

LSGGHNLHIDAAAALASLILTS

[0091] The amino acid sequence of a PKS (pentene ORF1) capable of producing pentene has the following amino acid sequence (SEQ ID NO:8):

MRAPYGNRQVNRRFLREFRAKRPHCVSPLHFLAEFSESRQTTGSAGVTAPIDRPGVSMAPKS

GAQRSSDIAVVGMSCRLPGAPGIDEFWHLLTTGGSAIERRADGTWRGSLDGAADFDAAFFDM

TPRQAAAADPQQRLMLELGWTALENAGIVPGSLAGTDTGVFVGIAADDYAALLHRSATPVSG

HTATGLSRGMAANRLSYLLGLGGPSLAVDSAQSSSLVAVHLACESLRRGESDLAIVGGVSLI

LAEDSTAGMELMGALSPDGRCHTFDARANGYVRGEGGACVVLKPLERALADGDRVHCVVRGS

AVNNDGGGSTLTTPHREAQAAVLRAAYERAGVGPDQVSYVELHGTGTPVGDPVEAAALGAVL

GTAHGRNAPLSVGSVKTNVGHLEAAAGLVGFVKAALCVREGVVPPSLNHATPNPAIPMDRLN

LRVPTRLEPWPHPDDRATGRLRLAGVSSFGMGGTNAHVVVEEAPLPEAGEPVGAGVPLAVVP

VVVSGRSAGAVAELASRLNESVRSDRLVDVGLSSVVSRSVFEHRSVVLAGDSAELSAGLDAL

AADGVSPVLVSGVASVGGGRSVFVFPGAGVKWAGMALGLWAESAVFAESMARCEAAFAGLVE

WRLADVLGDGAALEREDVVQPASFAVMVSLAALWRSLGVVPDAVVGHSQGEIAAAVVAGGLS

LEDGARVVVLRARVAEEVLSGGGIASVRLSRAEVEERLAGGGGGLSVAVVNAPSSTVVAGEL

GDLDRFVAACEAEGVRARRLEFGYASHSRFVEPVRERLLEGLADVRPVRGRIPFYSTVEAAE

FDTAGLDAEYWFGNLRRPVRFQETVERLLADGFRVFVECGAHPVLTGAVQETAETAGREICS

VGSLRRDEGGLRRFLTSAAEAFVQGVEVSWPVLFDGTGARTVDLPTYPFQRRHHWAPDGSAS

AAPTRDIRPDETAAVPADTMDLAGQLRADVASLPTTEQIARLLDQVRDGVATVLGLDARDEV

RAEATFKELGVESLTGVELKNHLRARTGLHVPTSLIYDCPTPLAAAHYLRDELLGRPAEQAV

VPAGIPVDEPIAIVGMGCRLPGGVSSPEGLWDLVASGVDAVSPFPTDRGWDVGGLFDPEPGV

PGRSYVREGGFLHEAGEFDAGFFGISPREALAMDPQQRLLLETSWEALERAGIDPHTLRGSR

TGVYAGVMAQEYGPRLHEGADGYEGYLLTGSSSSVASGRISYVLGLEGPAVTVDTACSSSLV

ALHLAVRALRSGECDLALAGGATVMAEPGMFVEFSRQRGLSAHGRCKAYSDSADGTGWAEGA

GVLLVERLSDAVRHGRRVLAVVRGSAVNQDGASNGLTAPNGRSQSRLIRQALADARLGVADV

DVVEGHGTGTRLGDPIEAQALLATYGQRDAGRPLRLGSLKSNVGHTQAAAGVAGVIKMVMAM

RHGVLPKTLHVDEPTAEVDWSAGAVSLLREQEAWPRGERVRRAGVSSFGVSGTNAHVILEQP

PGVPSQSAGPGSGSVVDVPVVPWMVSGKTPEALSAQATALMTYLDERPDVSSLDVGYSLALT

RSALDERAVVLGSDRETLLCGVKALSAGHEASGLVTGSVGAGGRIGFVFSGQGGQWLGMGRG

LYRAFPVFAAAFDEACAELDAHLGQEIGVREVVSGSDAQLLDRTLWAQSGLFALQVGLLKLL

DSWGVRPSVVLGHSVGELAAAFAAGVVSLSGAARLVAGRARLMQALPSGGGMLAVPAGEELL

WSLLADQGDRVGIAAVNAAGSVVLSGDRDVLDDLAGRLDGQGIRSRWLRVSHAFHSYRMDPM

LAEFAELARTVDYRRCEVPIVSTLTGDLDDAGRMSGPDYWVRQVREPVRFADGVQALVEHDV

ATVVELGPDGALSALIQECVAASDHAGRLSAVPAMRRNQDEAQKVMTALAHVHVRGGAVDWR

SFFAGTGAKQIELPTYAFQRQRYWLVPSDSGDVTGAGLAGAEHPLLGAVVPVAGGDEVLLTG

RISVRTHPWLAEHRVLGEVIVAGTALLEIALHAGERLGCERVEELTLEAPLVLPERGAIQVQ

-continued

LRVGAPENSGRRPMALYSRPEGAAEHDWTRHATGRLAPGRGEAAGDLADWPAPGALPVDLDE

FYRDLAELGLEYGPIFQGLKAAWRQGDEVYAEAALPGTEDSGFGVHPALLDAALHATAVRDM

DDARLPFQWEGVSLHAKAAPALRVRVVPAGDDAKSLLVCDGTGRPVISVDRLVLRSAAARRT

GARRQAHQARLYRLSWPTVQLPTSAQPPSCVLLGTSEVSADIQVYPDLRSLTAALDAGAEPP

GVVIAPTPPGGGRTADVRETTRHALDLVQGWLSDQRLNESRLLLVTQGAVAVEPGEPVTDLA

QAALWGLLRSTQTEHPDRFVLVDVPEPAQLLPALPGVLACGEPQLALRRGGAHAPRLAGLGS

DDVLPVPDGTGWRLEATRPGSLDGLALVDEPTATAPLGDGEVRIAMRAAGVNFRDALIALGM

YPGVASLGSEGAGVVVETGPGVTGLAPGDRVMGMIPKAFGPLAVADHRMVTRIPAGWSFARA

ASVPIVFLTAYYALVDLAGLRPGESLLVHSAAGGVGMAAIQLARHLGAEVYATASEDKWQAV

ELSREHLASSRTCDFEQQFLGATGGRGVDVVLNSLAGEFADASLRMLPRGGRFLELGKTDVR

DPVEVADAHPGVSYQAFDTVEAGPQRIGEMLHELVELFEGRVLEPLPVTAWDVRQAPEALRH

LSQARHVGKLVLTMPPVWDAAGTVLVTGGTGALGAEVARHLVIERGVRNLVLVSRRGPAASG

AAELVAQLTAYGAEVSLQACDVADRETLAKVLASIPDEHPLTAVVHAAGVLDDGVSESLTVE

RLDQVLRPKVDGARNLLELIDPDVALVLFSSVSGVLGSGGQGNYAAANSFLDALAQQRQSRG

LPTRSLAWGPWAEHGMASTLREAEQDRLARSGLLPISTEEGLSQFDAACGGAHTVVAPVRFS

RLSDGNAIKFSVLQGLVGPHRVNKAATADDAESLRKRLGRLPDAEQHRILLDLVRMHVAAVL

GFAGSQEITADGTFKVLGFDSLTVVELRNRINGATGLRLPATLVFNYPTPDALAAHLVTALS

ADRLAGTFEELDRWAANLPTLARDEATRAQITTRLQAILQSLADVSGGTGGGSVPDRLRSAT

DDELFQLLDNDLELP

[0092] The amino acid sequence of a PKS (pentene ORF2) capable of producing pentene has the following amino acid sequence (SEQ ID NO:9):

MSNEEKLREYLRRALVDLHQARERLHEAESGEREPIAIVAMGCRYPGGVQDPEGLWKLVASG

GDAIGEFPADRGWHLDELYDPDPDQPGTCYTRHGGFLHDAGEFDAGFFDISPREALAMDPQQ

RLLLEISWETVESAGMDPRSLRGSRTGVFAGLMYEGYDTGAHRAGEGVEGYLGTGNAGSVAS

GRVAYAFGFEGPAVTVDTACSSSLVALHLACQSLRQGECDLALAGGVTVMSTPERFVEFSRQ

RGLAPDGRCKSFAAAADGTGWGEGAGLVLLERLSDARRNGHRVLAVVRGSAVNQDGASNGLT

APNGLAQERVIQQVLTSAGLSASDVDAVEAHGTGTRLGDPIEAQALIAAYGQDRDRDRPLWL

GSVKSNIGHTQAAAGVAGVIKMVMAMRHGELPRTLHVDEPNSHVDWSAGAVRLLTENIRWPG

TGTRRAGVSSFGVSGTNAHVIVGDYAQQKSPLAPPATQDRPWHLLTLSAKNAQALNALQKSY

GDYLAQHPSVDPRDLCLSANTGRSPLKERRFFVFKQVADLQQTLNQDFLAQPRLSSPAKIAF

LFTGQGSQYYGMGQQLYQTSPVFRQVLDECDRLWQTYSPEAPALTDLLYGNHNPDLVHETVY

TQPLLFAVEYAIAQLWLSWGVTPDFCMGHSVGEYVAACLAGVFSLADGMKLITARGKLMHAL

PSNGSMAAVFADKTVIKPYLSEHLTVGAENGSHLVLSGKTPCLEASIHKLQSQGIKTKPLKV

SHAFHSPLMAPMLAEFREIAEQITFHPPRIPLISNVTGGQIEAEIAQADYWVKHVSQPVKFV

QSIQTLAQAGVNVYLEIGVKPVLLSMGRHCLAEQEAVWLPSLRPHSEPWPEILTSLGKLYEQ

GLNIDWQTVEAGDRRRKLILPTYPFQRQRYWFNQGSWQTVETESVNPGPDDLNDWLYQVAWT

PLDTLPPAPEPSAKLWLILGDRHDHQPIEAQFKNAQRVYLGQSNHFPTNAPWEVSADALDNL

FTHVGSQNLAGILYLCPPGEDPEDLDEIQKQTSGFALQLIQTLYQQKIAVPCWFVTHQSQRV

-continued

LETDAVTGFAQGGLWGLAQAIALEHPELWGGIIDVDDSLPNFAQICQQRQVQQLAVRHQKLY

GAQLKKQPSLPQKNLQIQPQQTYLVTGGLGAIGRKIAQWLAAAGAEKVILVSRRAPAADQQT

LPTNAVVYPCDLADAAQVAKLFQTYPHIKGIFHAAGTLADGLLQQQTWQKFQTVAAAKMKGT

WHLHRHSQKLDLDFFVLFSSVAGVLGSPGQGNYAAANRGMAAIAQYRQAQGLPALAIHWGPW

AEGGMANSLSNQNLAWLPPPQGLTILEKVLGAQGEMGVFKPDWQNLAKQFPEFAKTHYFAAV

IPSAEAVPPTASIFDKLINLEASQRADYLLDYLRRSVAQILKLEIEQIQSHDSLLDLGMDSL

MIMEAIASLKQDLQLMLYPREIYERPRLDVLTAYLAAEFTKAHDSEAATAAAAIPSQSLSVK

TKKQWQKPDHKNPNPIAFILSSPRSGSTLLRVMLAGHPGLYSPPELHLLPFETMGDRHQELG

LSHLGEGLQRALMDLENLTPEASQAKVNQWVKANTPIADIYAYLQRQAEQRLLIDKSPSYGS

DRHILDHSEILFDQAKYIHLVRHPYAVIESFTRLRMDKLLGAEQQNPYALAESIWRTSNRNI

LDLGRTVGADRYLQVIYEDLVRDPRKVLTNICDFLGVDFDEALLNPYSGDRLTDGLHQQSMG

VGDPNFLQHKTIDPALADKWRSITLPAALQLDTIQLAETFAYDLPQEPQLTPQTQSLPSMVE

RFVTVRGLETCLCEWGDRHQPLVLLLHGILEQGASWQLIAPQLAAQGYWVVAPDLRGHGKSA

HAQSYSMLDFLADVDALAKQLGDRPFTLVGHSMGSIIGAMYAGIRQTQVEKLILVETIVPND

IDDAETGNHLTTHLDYLAAPPQHPIFPSLEVAARRLRQATPQLPKDLSAFLTQRSTKSVEKG

VQWRWDAFLRTRAGIEFNGISRRRYLALLKDIQAPITLIYGDQSEFNRPADLQAIQAALPQA

QRLTVAGGHNLHFENPQAIAQIVYQQLQTPVPKTQ

Nucleic Acids Encoding the PKS

[0093] The present invention provides recombinant nucleic acids that encode the PKSs of the invention. The recombinant nucleic acids include double-stranded and single:stranded DNAs and RNA derived therefrom. The recombinant nucleic acids of the invention include those that encode an open reading frame (ORF) of a PKS of the present invention. The recombinant nucleic acids of the invention also include, in a variety of embodiments, promoter sequences for transcribing the ORF in a suitable host cell. The recombinant nucleic acids of the invention include, in some embodiments, sequences sufficient for having the recombinant nucleic acid stably replicate in a host cell, such as sequences that provide a replicon capable of stable maintenance in a host cell or sequences that direct homologous recombination of the nucleic acid into a chromosome of the host cell. In some embodiments, the nucleic acid is a plasmid, including but not limited to plasmids containing an origin of replication. The present invention also provides vectors, such as expression vectors, comprising another recombinant nucleic acid of the present invention. The present invention provides host cell comprising any of the recombinant nucleic acids and/or capable of expressing a PKS of the present invention. In some embodiments, the host cell, when cultured under suitable conditions, is capable of producing an α-olefin of the invention.

[0094] It will be apparent to one of skill in the art that a variety of recombinant vectors can be utilized in the practice of the invention. As used herein, "vector" refers to polynucleotide elements that are used to introduce recombinant nucleic acid into cells for either expression or replication (or both). Selection and use of such vectors generally is routine in the art. An "expression vector" is a recombinant nucleic acid capable of expressing (producing proteins encoded by) DNA coding sequences (and corresponding mRNA) that are operatively linked with regulatory sequences, such as promoters. Thus, an expression vector refers to a recombinant DNA or RNA construct, such as a plasmid, a phage, a recombinant virus, or other vector that, upon introduction into an appropriate host cell that when cultured under appropriate conditions, results in expression of the DNA coding sequence. Appropriate expression vector elements suitable for use in accordance with the present invention are well known to those of skill in the art and include those that are replicable in eukaryotic cells and/or prokaryotic cells and those that remain episomal as well as those that integrate into the host cell genome.

[0095] The vectors of the invention include those chosen to contain control sequences operably linked to the resulting coding sequences in a manner that expression of the coding sequences may be effected in an appropriate host. Suitable control sequences include those that function in eukaryotic and prokaryotic host cells. If the cloning vectors employed to obtain PKS genes lack control sequences for expression operably linked to the PKS-encoding nucleotide sequences, the nucleotide sequences are inserted into appropriate expression vectors. This can be done individually, or using a pool of isolated encoding nucleotide sequences, which can be inserted into "host" vectors, the resulting vectors transformed or transfected into host cells, and the resulting cells plated out into individual colonies. Suitable control sequences for single cell cultures of various types of organisms are well known in the art. Control systems for expression in yeast are widely available and are routinely used. Control elements include promoters, optionally containing operator sequences, and other elements depending on the nature of the host, such as ribosome binding sites. Particularly useful promoters for prokaryotic hosts include those from PKS gene clusters that result in the production of polyketides as secondary metabo-

lites, including those from Type I or aromatic (Type II) PKS gene clusters. Examples are act promoters, tcm promoters, spiramycin promoters, and the like. However, other bacterial promoters, such as those derived from the genes encoding sugar metabolizing enzymes, such as those that metabolize galactose, lactose (lac) and maltose, are also useful. Additional examples include promoters derived from the genes encoding biosynthetic enzymes such as those that encode the enzymes for tryptophan (trp) biosynthesis, the β-lactamase (bla) gene promoter, bacteriophage lambda PL promoter, and the T5 promoter. In addition, synthetic promoters, such as the tac promoter (U.S. Pat. No. 4,551,433; incorporated herein by reference), can be used to construct an expression vector of the invention.

[0096] As noted, particularly useful control sequences are those which themselves, or with suitable regulatory systems, activate expression during transition from growth to stationary phase in the vegetative mycelium. Illustrative control sequences, vectors, and host cells of these types include the modified *Streptomyces coelicolor* CH999 and vectors described in PCT publication No. WO 96/40968 and similar strains of *Streptomyces lividans*. See U.S. Pat. Nos. 5,672,491; 5,830,750; 5,843,718; and 6,177,262, each of which is hereby incorporated by reference. Other regulatory sequences may also be desirable; these include those that allow for regulation of expression of the PKS sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

[0097] Selectable markers can also be included in the recombinant expression vectors of the invention. A variety of markers are known that are useful in selecting for transformed cell lines; these generally are any gene whose expression confers a selectable phenotype on transformed cells when the cells are grown in an appropriate selective medium. Such markers include, for example, genes that confer antibiotic resistance or sensitivity to a host cell.

[0098] The various PKS nucleotide sequences, or a mixture of such sequences, can be cloned into one or more recombinant vectors as individual cassettes, with separate control elements or under the control of a single promoter. The PKS encoding subunits or components can include flanking restriction sites to allow for the easy deletion and insertion of other PKS encoding subunits. The design of such restriction sites is known to those of skill in the art and can be accomplished using the techniques described in the scientific literature, such as site-directed mutagenesis and PCR. Methods for introducing the recombinant vectors of the present invention into suitable hosts are known to those of skill in the art and include the use of $CaCl_2$ or other agents, such as other divalent cations, lipofection, DMSO, protoplast transformation, conjugation, and electroporation.

Host Cells Comprising the PKS

[0099] The present invention provides host cells comprising the recombinant nucleic acid and/or PKS of the present invention. In many embodiments, the host cell, when cultured, is capable of producing an α-olefin. The host cell can be a eukaryotic or a prokaryotic cell. Suitable eukaryotic cells include yeast cells, such as from the genus *Saccharomyces, Candida*, or *Schizosaccharomyces*. A suitable species from the genus *Saccharomyces* is *Saccharomyces cerevisiae*. A suitable species from the genus *Schizosaccharomyces* is *Schizosaccharomyces pombe*. Suitable prokaryotic cells include, but are not limited to, the gram negative *Escherichia coli* and the gram positive *Streptomyces* species, such as *S. coelicolor* and *S. lividans*.

[0100] The PKSs of the invention can be in a host cell, and can isolated and purified. The PKS can synthesize the α-olefin in vivo (in a host cell) or in vitro (in a cell extract or where all necessary chemical components or starting materials are provided). The present invention provides methods of producing the α-olefin using any of these in vivo or in vitro means.

[0101] In some embodiments of the invention, the host cell comprises a PKS which produces butadiene comprising a loading module comprising an acrylyl-ACP starter, such as a DEBS proprionyl-CoA specific loading domain which is modified to accept acrylyl-CoA, and one or more nucleic acids encoding and capable of expressing biosynthetic enzymes for synthesizing acrylyl-CoA from propionate (see FIG. **8**). An example of a set of such enzymes is propionyl-CoA ligase (synthetase) (EC 6.2.1.17) and acyl-CoA dehydrogenase (mammalian) (EC 1.3.99.3), and functional variants thereof. In some embodiments, the host cell comprises a nucleic acid encoding and capable of expressing an enzyme, or functional variant thereof, capable of converting propionate into propionyl-CoA, and an enzyme, or functional variant thereof, capable of converting propionyl-CoA into acrylyl-CoA. An enzyme capable of converting propionate into propionyl-CoA is the propionyl-CoA ligase encoded by the prpE gene of *Salmonella typhimurium*. An enzyme capable of converting propionyl-CoA into acrylyl-CoA is the mammalian acyl-CoA dehydrogenase. A host cell comprising this system is provided with propionate, such as by exogenously feeding propionate to the host cell, or produces propionate endogenously.

[0102] The amino acid sequence of the propionyl-CoA ligase encoded by the prpE gene in *Salmonella typhimurium* (GenBank accession no. NP_459366) comprises:

(SEQ ID NO: 13)

```
  1 msfsefyqrs inepeafwae qarridwrqp ftqtldhsrp pfarwfcggt tnlchnavdr

 61 wrdkqpeala liayssetde ertftfsqlh devnivaaml lslgvqrgdr vlvympmiae

121 aqitllacar igaihsvvfg gfashsvaar iddarpaliv sadagarggk ilpykklldd

181 aiaqaqhqpk hvllvdrgla kmawvdgrdl dfatlrqqhl gasvpvawle snetscilyt

241 sgttgkpkgv qrdvggyava latsmdtifg gkaggvffca sdigwvvghs yivyapllag

301 mativyeglp typdcgvwwk ivekyqvnrm fsaptairvl kkfptaqirn hdlsslealy
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361 lagepldept aswvtetlgv pvidnywqte sgwpimalar alddrpsrlg spgvpmygyn

421 vqllnevtge pcginekgml viegplppgc iqtiwgddar fvktywslfn rqvyatfdwg

481 irdaegyyfi lgrtddvini aghrlgtrei eesissypnv aevavvgikd alkgqvavaf

541 vipkqsdtla dreaardeen aimalvdnqi ghfgrpahvw fvsqlpktrs gkmlrrtiqa

601 egrdpgdl ttiddpaslq qirqaiee
```

[0103] The amino acid sequence of the acyl-CoA dehydrogenase of *Mus musculus* (GenBank accession no. Q07417) comprises:

(SEQ ID NO: 14)

```
  1 maaallarar gplrralgvr dwrrlhtvyq svelpethqm lrqtcrdfae kelvpiaaql

 61 drehlfptaq vkkmgelgll amdvpeelsg aglgylaysi aleeisraca stgvimsvnn

121 slylgpilkf gsaqqkqqwi tpftngdkig cfalsepgng sdagaastta reegdswvin

181 gtkawitnsw easatvvfas tdrsrqnkgi saflvpmptp gltlgkkedk lgirasstan

241 lifedcripk enllgepgmg fkiamqtldm grigiasqal giaqasldca vkyaenrnaf

301 gapltklqni qfkladmala lesarlltwr aamlkdnkkp ftkesamrkl aaseaatais

361 aiqilgsm gyvtempaer yyrdaritei yegtseiqrl viaghllrsy rs
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[0104] In some embodiments, the host cell of the invention comprises a PKS which produces butadiene and comprises a loading module comprising an acrylyl-ACP starter, such as a DEBS proprionyl-CoA specific loading domain which is modified to accept acrylyl-CoA, and one or more nucleic acids encoding and capable of expressing biosynthetic enzymes for synthesizing acrylyl-CoA from pyruvate (see FIG. **9**). An example of a set of such enzymes is lactate dehydrogenase (EC 6.2.1.17), lactate CoA transferase (EC 2.8.3.1), propionyl-CoA ligase (synthetase) (EC 6.2.1.17), and lactoyl-CoA dehydratase (EC 4.2.164), or functional variants thereof. In some embodiments, the host cell comprises one or more nucleic acids encoding and capable of expressing these four enzymes. A host cell comprising this system is provided with propionate and a suitable organic molecule that the host cell can directly or indirectly convert into a pyruvate, and these compounds are either exogenously fed to or produced by the host cell. For example, if the host cell is *E. coli*, a suitable organic molecule is glucose.

[0105] The amino acid sequence of the lactate dehydrogenase encoded by the IdhA gene of *E. coli* (GenBank accession no. CAQ31881) comprises:

(SEQ ID NO: 15)

```
  1 taktangcea vcifvnddgs rpvleelkkh gvkyialrca gfnnvdldaa kelglkvvry

 61 paydpeavae haigmmmtln rrihrayqrt rdanfslegl tgftmygkta gvigtgkigv

121 amlrilkgfg mrllafdpyp saaalelgve yvdlptlfse sdvislhcpl tpenyhllne

181 aafdqmkngv mivntsrgal idsqaaieal knqkigslgm dvyenerdlf fedksndviq

241 ddvfrrlsac hnvlftghqa fltaealtsi sqttlqnlsn lekgetcpne lv
```

[0106] The amino acid sequence of the lactate CoA transferase encoded by the pct gene of *Clostridium proponicum* (GenBank accession no. CAB77207) comprises:

(SEQ ID NO: 16)

```
  1 mrkvpiitad eaaklikdgd tvttsgfvgn aipealdrav ekrfletgep knityvycgs

 61 qgnrdgrgae hfahegllkr yiaghwatvp algkmamenk meaynvsqga lchlfrdias

121 hkpgvftkvg igtfidprng ggkvnditke divelveikg qeylfypafp ihvalirgty

181 adesgnitfe kevaplegts vcqavknsgg ivvvqvervv kagtldprhv kvpgiyvdyv

241 vvadpedhqq sldceydpal sgehrrpevv geplplsakk vigrrgaiel ekdvavnlgv
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301 gapeyvasva deegivdfmt ltaesgaigg vpaggvrfga synadalidq gyqfdyydgg

361 gldlcylgla ecdekgninv srfgpriagc ggfinitqnt pkvffcgtft agglkvkied

421 gkviivqegk qkkflkaveq itfngdvala nkqqvtyite rcvfllkedg lhlseiapgi

481 qtqildvm dfapiidrda ngqiklmdaa lfaeglmglk emks
```

[0107] The amino acid sequence of the lactoyl-CoA dehydratase encoded by the pct gene of *Clostridium proponicum* (GenBank accession no. CAB77206) comprises:

(SEQ ID NO: 17)

```
  1 efkiaivddd laqesrqiry dvldgeggpl yrmakawqqm ygcslatdtk kgrgrmlink

 61 tiqtgadaiv vammkfcdpe ewdypvmyre feekgvkslm ievdqevssf eqiktrlqsf

121 veml
```

[0108] In some embodiments, the host cell of the invention comprises a PKS which produces butadiene and comprises a loading module comprising an acrylyl-ACP starter, such as a DEBS proprionyl-CoA specific loading domain which is modified to accept acrylyl-CoA, and one or more nucleic acids encoding and capable of expressing biosynthetic enzymes for synthesizing acrylyl-CoA from acetyl CoA (see FIG. **10**). An example of a set of such enzymes is acetyl-CoA carboxylase (EC 6.4.1.2), malonyl-CoA reductase (EC 1.2.1.75), 3-hydroxypropionate:CoA ligase, and 3-hydroxypropionyl-CoA hydratase (EC 4.2.1.17), or functional variants thereof. In some embodiments, the host cell comprises one or more nucleic acids encoding and capable of expressing the four enzymes described. A host cell comprising this system can be engineered to produce increased titers of acetyl-CoA.

[0109] In some embodiments, the host cell of the invention comprises a PKS which produces butadiene and comprises a loading module comprising an acrylyl-ACP starter, such as a DEBS proprionyl-CoA specific loading domain which is modified to accept acrylyl-CoA, and one or more nucleic acids encoding and capable of expressing biosynthetic enzymes for synthesizing acrylyl-CoA from propionate (see FIG. **15**). An example of a set of such enzymes is propionyl-CoA ligase (synthetase) (EC 6.2.1.17), lactoyl-CoA dehydratase (EC 4.2.164), lactate dehydrogenase (EC 6.2.1.17), lactate CoA transferase (EC 2.8.3.1), or functional variants thereof. A host cell comprising this system is provided with propionate, either by exogenous feeding or by endogenous production.

[0110] In some embodiments, the host cell of the invention comprises a PKS which produces 3-methyl-2,4-pentadienoic acid and comprises the modules shown in FIG. **12** including a loading module comprising an acrylyl-ACP starter, such as a DEBS proprionyl-CoA specific loading domain which is modified to accept acrylyl-CoA, and one or more nucleic acids encoding and capable of expressing biosynthetic enzymes for synthesizing acrylyl-CoA (see FIG. **12**). There are several methods for enabling a host cell to synthesize acrylyl-CoA described above. 3-methyl-2,4-pentadienoic acid can be enzymatically, catalytically, or pyrolytically converted to isoprene.

Methods of Producing α-olefins Using the PKS

[0111] The present invention provides a method of producing an α-olefin comprising: providing a host cell of the present invention, and culturing said host cell in a suitable culture medium such that the α-olefin is produced. The method can further comprise isolating said α-olefin from the host cell and/or the culture medium. The method can further comprise polymerizing the α-olefin to itself and/or any other suitable organic molecule(s), including but not limited to other compounds comprising a C—C double bond. A variety of methods for heterologous expression of PKS genes and host cells suitable for expression of these genes and production of polyketides are described, for example, in U.S. Pat. Nos. 5,843,718; 5,830,750 and 6,262,340; WO 01/31035, WO 01/27306, and WO 02/068613; and U.S. Patent Application Pub. Nos. 20020192767 and 20020045220; each of which is incorporated herein by reference.

[0112] The present invention provides for a composition comprising an α-olefin isolated from a host cell from which the α-olefin is produced, and trace residues and/or contaminants of the host cell. Such trace residues and/or contaminants include cellular material produced by the lysis of the host cell. The present invention also provides α-olefins in substantially pure form.

[0113] Certain α-olefins produced by the PKSs of the present invention can be used as fuels. In some embodiments of the invention, an α-olefin produced in accordance with the invention can be used as a "green" jet fuel. The α-olefin can be catalytically oligomerized, including but not limited to dimerized, and optionally purified. The resulting products can be dimerized again to yield a mixture of branched molecules that are then catalytically hydrogenated. For example, 1-butene produced by a PKS of the present invention can be catalytically dimerized and purified. The resulting octene products can be dimerized again to yield a mixture of branched C16 molecules that are then catalytically hydrogenated. Oligomers of butene have been validated by the US Navy as both jet and diesel fuel replacements (Harvey, 2011. Journal of Chemical Technology and Biotechnology 86(1): 2-9.). Additional benefit may come from making branched, or aromatic, α-olefins using the avermectin (or other) loading modules, as described herein.

[0114] Thus, among others, the present invention has one or more of the following advantages: (1) it reduces the dependence on oil for producing certain chemicals, and (2) it serves as a means of capture and sequestration of carbon from the atmosphere.

[0115] The invention having been described, the following examples are offered to illustrate and not limit the subject invention.

EXAMPLES

[0116] Constructs can be conveniently designed at the amino acid level and then, back translation and DNA synthesis, such as that offered commercially by service providers such as DNA 2.0, can be conducted to yield the desired nucleic acid, which may be optimized for expression in a particular host cell type. Subsequent plasmid assembly can be conducted using standard molecular biology techniques.

Example 1

Production of 1-Hexene Using a PKS-Based Enzyme System

[0117] In one embodiment of the invention, PKS modules from three different organisms were used to construct a triketide pathway designed for the production of 1-hexene. In this embodiment, the 1-hexene synthase consists of two ORFs. HexORF1 combines EryA1 loading module+KS1 and AT-ACP from IdmO, HexORF2 utilizes the KS domain from IdmP and AT-TE domains from CurM. In another embodiment of this invention the loop I region of the indanomycin sourced ACP in HexORF1, SSSAGIDPGRAFQDMGI, is swapped with ASAERVPADQAFAELGV, the segment of ACP directly following EryA1. Both of these designs were back translated using software designed to optimize expression in *E. coli*. The genes are synthesized and ligated into two pairs of compatible, *E. coli* expression vectors that are subsequently transformed into *E. coli* BAP-1. The amino acid sequences for HexORF1, HexORF1', and HexORF2 are provided as SEQ ID NOs: 2-4, respectively.

[0118] Experiments have been performed demonstrating *E. coli* BAP-1 utilizing exogenously added propionate. In both examples of 1-hexene production, overnight cultures of a pBbA7C-HexORF1' (or pBbA7C-HexORF1)+pBbS7k-HexORF2 cotransformed strain were grown from a single colony and used to inoculate (1% v/v) three 50-mL cultures of LB medium supplemented with 0.5% glucose and 10% glycerol in 250 mL screw cap (unsealed) flask. Cultures were grown to an OD600 of 1.0 to 1.2, induced with 50 uM IPTG and grown at (30° C.) for an additional 3 hours. Then 100 mM propionate was supplemented to the culture and a Teflon septum was used to seal the cap. The cultures were then grown at 20° C. for 24 hours after which 1-butene was detectable in the headspace of the culture using solid phase micro extraction followed by GC-MS.

Example 2

Production of Butadiene Using a PKS-Based Enzyme System

[0119] An example of a PKS system for producing butadiene is shown in FIGS. **6** and **7**. The system built to produce 1-butene, described below, was fed acrylate to produce butadiene. Otherwise, all experimental details are as described as that for 1-butene production, above. While the limits of detection were inadequate to determine productivity in this instance, the invention provides several routes to increasing butadiene productivity, including: adding an acrylate specific CoA ligase to the host strain, adding an acrylate importer to the host strain, and/or utilizing a host strain less sensitive to acrylate toxicity.

Example 3

Production of 1-Butene Using a PKS-Based Enzyme System

[0120] An illustrative PKS system for producing 1-butene was constructed using the AT-TE PKS domains from CurM and the loading module for propionyl-CoA+KS1 from EryA1. For in vivo 1-butene production, overnight cultures of *E. coli* BAP1 carrying pBbS7k-Butene (PKS protein sequence provided as SEQ ID NO:5) were grown from a single colony and used to inoculate (1% v/v) three 50-mL cultures of LB medium supplemented with 0.5% glucose and 10% glycerol in 250 mL screw cap (unsealed) flask. Cultures were grown to an OD600 of 1.0 to 1.2, induced with 50 uM IPTG and grown at (30° C.) for an additional 3 hours. Then 100 mM propionate was supplemented to the culture and a Teflon septum was used to seal the cap. The cultures were then grown at 20° C. for 24 hours after which 1-butene was detectable in the headspace of the culture using solid phase micro extraction followed by GC-MS.

Example 4

Production of Isoprene Using a PKS-Based Enzyme System

[0121] An example of a PKS system for producing isoprene is shown in FIG. **12**.

Example 5

Production of (E)-penta-1,3-diene Using a PKS-Based Enzyme System

[0122] An example of a PKS system for producing (E)-penta-1,3-diene is shown in FIG. **13**.

Example 6

Production of Propene (Propylene) Using a PKS-Based Enzyme System

[0123] An illustrative propene synthase of the invention is a single enzyme consisting of the loading module+KS1 from the niddamycin PKS (Kakavas, 1997) fused to AT-TE domains from CurM (Chang, 2004; Gu, 2009) (the amino acid sequence for this construct is provided as SEQ ID NO:6). For in vivo propene production, overnight cultures of *E. coli* BAP1 carrying pBbS7k-propene were grown from a single colony and used to inoculate (1% v/v) three 50-mL cultures of LB medium supplemented with 0.5% glucose and 10% glycerol in 250 mL screw cap (unsealed) flask. Cultures were grown to an OD600 of 1.0 to 1.2, induced with 50 uM IPTG and grown at (30° C.) for an additional 3 hours. Then a Teflon septum was used to seal the cap. The cultures were then grown at 20° C. for 24 hours after which propene was detectable in the headspace of the culture using solid phase micro extraction followed by GC-MS.

Example 7

Production of Styrene Using a PKS-Based Enzyme System

[0124] An illustrative styrene synthase of the invention was constructed by fusing the ST and TE domains from CurM onto the loading and first extension modules from the soraphen PKS (Schupp, 1995; Wilkinson, 2001). The amino acid sequence for this construct is provided as SEQ ID NO:7. For styrene biosynthesis in the system illustrated, a pool of benzoyl-CoA is provided. To facilitate production of this essential precursor, the styrene synthase construct was coexpressed with an *E. coli* codon optimized gene encoding benzoate-CoA ligase, badA, from *Rhodopseudomonas palustris* (Egland, et al., J. Bacteriol. 1995 November; 177(22):6545-51.) and fed exogenous benzoate. For in vivo styrene production, overnight cultures of *E. coli* BAP1 carrying pBbS7k-SS1 (SS1 encodes SEQ ID NO:7) were grown from a single colony and used to inoculate (1% v/v) three 50-mL cultures of LB medium supplemented with 0.5% glucose and 10% glycerol in 250 mL screw cap (unsealed) flask. Cultures were grown to an OD600 of 1.0 to 1.2, induced with 50 uM IPTG and grown at (30° C.) for an additional 3 hours. Then 100 mM benzoic acid was supplemented to the culture and a Teflon septum was used to seal the cap. The cultures were then grown at 20° C. for 24 hours after which styrene was detectable in the headspace of the culture using solid phase micro extraction followed by GC-MS.

Example 8

Production of Pentene Using a PKS-Based Enzyme System

[0125] An illustrative pentene synthase of the invention was designed as two ORFs. The first ORF is built using the chalcomycin PKS loading module+KS 1 fused to spinosad AT-ACP PKS module two. The second ORF is the KS from spinosad M3 fused to the olefination module (Ols) from *Synechococcus* sp. PCC7002 (Mendez-Perez, et al., Appl Environ Microbiol. 2011 June; 77(12):4264-7). The amino acid sequences for these chimeric proteins are provided as SEQ ID NO:8 and 9.

[0126] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

SEQUENCE LISTING

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<210> SEQ ID NO 1
<211> LENGTH: 2211
<212> TYPE: PRT
<213> ORGANISM: Lyngbya majuscula

<400> SEQUENCE: 1

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Val Leu Gln Val Leu Gln Glu Met Arg Ser Arg Leu Glu Ala Val Asn
            20                  25                  30

Lys Ala Lys Thr Glu Pro Ile Ala Ile Val Gly Met Ala Cys Arg Phe
        35                  40                  45

Pro Gly Gly Ala Asn Asp Pro Ser Thr Tyr Trp Arg Leu Leu His Asp
    50                  55                  60

Gly Ile Asp Ala Ile Thr Pro Val Pro Pro His Arg Trp Asp Val Asn
65                  70                  75                  80

Ala His Tyr Glu Pro Asn Pro Glu Ile Pro Gly Lys Ala Tyr Thr Lys
                85                  90                  95

Gln Gly Gly Phe Ile Glu Gln Val Asp Gln Phe Asp Pro Leu Phe Phe
            100                 105                 110

Gly Ile Ser Pro Arg Glu Ala Ile Ser Leu Asp Pro Gln Tyr Arg Leu
        115                 120                 125

Leu Leu Glu Val Thr Trp Glu Ala Leu Glu Asn Ala Gly Gln Thr Trp
    130                 135                 140

Thr Asn Leu Lys Asn Ser Lys Thr Ser Val Phe Met Gly Val Ser Thr
145                 150                 155                 160

Asp Asp Tyr Ala Ser Leu Ser Asn Pro Ile Leu Ile Asn Asn Arg Ser
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                165                 170                 175

Leu Gly Val Gly Arg Ile Ser His Leu Leu Gly Leu Gln Gly Ser Asn
            180                 185                 190

Ile Gln Leu Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Ile His Leu
        195                 200                 205

Ala Cys Gln Ser Leu Arg Ser Gly Glu Ser Asn Leu Ala Leu Val Gly
    210                 215                 220

Gly Val Asn Leu Ile Leu Ser Pro Ile Ser Thr Ile Gly Arg Cys Thr
225                 230                 235                 240

Met Lys Ala Leu Ser Pro Asp Gly Arg Cys Lys Thr Phe Asp Ala Ala
                245                 250                 255

Ala Asn Gly Tyr Gly Gln Ala Glu Gly Cys Gly Val Val Val Leu Lys
            260                 265                 270

Arg Leu Ser Asp Ala Ile Thr Asp Gly Asp Leu Ile Ser Ala Leu Ile
        275                 280                 285

Arg Gly Ser Ala Ile Asn His Asp Gly Pro Ser Ser Gly Leu Thr Val
    290                 295                 300

Pro Asn Gly Met Ala Gln Lys Gln Val Ile Gln Gln Ala Leu Ser Asn
305                 310                 315                 320

Ala Arg Leu Glu Pro His Gln Val Ser Tyr Leu Glu Ala His Gly Thr
                325                 330                 335

Gly Thr Ala Leu Gly Asp Pro Ile Glu Ile Glu Ala Leu Ala Ala Ile
            340                 345                 350

Tyr Gly Lys Asn Arg Pro Val Asp Gln Pro Leu Val Val Gly Ser Val
        355                 360                 365

Lys Thr Asn Ile Gly His Leu Glu Ala Ala Ala Gly Val Ser Ala Leu
    370                 375                 380

Ile Lys Val Val Leu Ala Leu Gln His Gln Glu Ile Pro Pro His Leu
385                 390                 395                 400

His Leu Lys Gln Pro Asn Pro Tyr Val Asp Trp Asp Lys Leu Pro Ile
                405                 410                 415

Lys Ile Pro Thr Ser Leu Met Pro Trp Asn Cys Glu Ala Lys Pro Arg
            420                 425                 430

Ile Ala Gly Ile Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu
        435                 440                 445

Leu Leu Glu Glu Val Pro Glu Leu Ile Lys Gly Gln Lys Ala Lys Gly
    450                 455                 460

Lys Ser Glu Asn Asp Leu Glu Arg Pro Leu His Ile Leu Thr Leu Ser
465                 470                 475                 480

Thr Lys Thr Glu Lys Ala Leu Glu Glu Leu Val Ser Arg Tyr Gln Asn
                485                 490                 495

His Trp Glu Thr Tyr Pro Glu Leu Ala Ile Ser Asp Val Cys Tyr Thr
            500                 505                 510

Ala Asn Thr Gly Arg Ala Gln Phe Asn His Arg Leu Ala Val Ile Ala
        515                 520                 525

Ser Gly Ser Glu Glu Leu Thr Gln Lys Leu Arg Gln His Thr Ala Gly
    530                 535                 540

Glu Glu Val Val Gly Val Phe Ser Gly Lys Val Pro Asn Ser Gly Ser
545                 550                 555                 560

Glu Ser Lys Val Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln Tyr Leu
                565                 570                 575
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Asn Met Gly Arg Gln Leu Tyr Glu Thr Gln Pro Thr Phe Arg Gln Ala
            580                 585                 590

Leu Asp Thr Cys Asp His Ile Leu Arg Pro Tyr Leu Asp Asn Pro Leu
        595                 600                 605

Leu Glu Ile Leu Tyr Pro Gln Asp Ala Gln Lys Ser Asn Asp Ser Pro
    610                 615                 620

Leu Asp Gln Thr Gly Tyr Thr Gln Pro Ala Leu Phe Ser Ile Glu Tyr
625                 630                 635                 640

Ala Leu Leu Lys Leu Trp Glu Ser Trp Gly Ile Lys Pro Asn Val Val
                645                 650                 655

Met Gly His Ser Val Gly Glu Tyr Val Ala Ala Thr Val Ala Gly Val
            660                 665                 670

Phe Ser Leu Glu Asp Gly Leu Lys Leu Ile Ala Ala Arg Gly Arg Leu
        675                 680                 685

Met Gln Gly Leu Pro Ala Gly Gly Glu Met Val Ser Val Met Ala Ser
    690                 695                 700

Glu Ser Lys Val Leu Glu Thr Leu Lys Ala Met Ser Leu Glu Asp Lys
705                 710                 715                 720

Val Ala Ile Ala Ala Ile Asn Gly Pro Glu Ser Ile Val Ile Ser Gly
                725                 730                 735

Glu Ala Glu Ala Ile Arg Ala Met Ala Thr His Leu Glu Ser Val Gly
            740                 745                 750

Ile Lys Thr Lys Gln Leu Gln Val Ser His Ala Phe His Ser Pro Leu
        755                 760                 765

Met Glu Pro Met Leu Ala Glu Phe Glu Ala Val Ala Asn Gln Ile Thr
    770                 775                 780

Tyr His Gln Pro Arg Ile Pro Ile Ile Ser Asn Val Thr Gly Thr Lys
785                 790                 795                 800

Ala Asp Lys Ser Ile Ala Thr Ala Gln Tyr Trp Val Asn His Val Arg
                805                 810                 815

Gln Pro Val Arg Phe Ala Gln Gly Met Ala Thr Leu His Gln Gln Gly
            820                 825                 830

Tyr Glu Thr Phe Leu Glu Ile Gly Ala Lys Pro Ile Leu Leu Gly Met
        835                 840                 845

Gly Lys Gln Cys Leu Ser Pro Asp Val Gly Val Trp Leu Pro Ser Leu
    850                 855                 860

Arg His Gly Val Asp Glu Trp Gln Gln Ile Leu Ser Ser Leu Gly Gln
865                 870                 875                 880

Leu Tyr Val Gln Gly Ala Lys Val Asp Trp Ser Gly Phe Asp Arg Asp
                885                 890                 895

Tyr Ser Arg Glu Lys Val Val Leu Pro Thr Tyr Pro Phe Gln Arg Glu
            900                 905                 910

Arg Tyr Trp Val Glu Thr Ser Ile Asn Gln Gln Gln Val Val Cys Ser
        915                 920                 925

Gly Glu Pro Asn Leu Gln Gly Thr Pro Glu Gly Thr Ser Thr Thr Ile
    930                 935                 940

Val Lys Leu Leu Ser Gln Gly Asn Thr Lys Glu Leu Ala Glu Lys Val
945                 950                 955                 960

Glu Lys Thr Ser Asp Leu Pro Pro Glu Gln Leu Lys Leu Leu Pro Asp
                965                 970                 975

Leu Leu Ala Ser Leu Ser Gln Gln His Gln Gln Glu Leu Ala Arg Leu
            980                 985                 990
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Thr Thr Lys Lys Trp Phe Tyr Lys  Val Gln Trp Ile Ser  Gln Ala Ile
        995                 1000                1005

Lys Pro  Gln Arg Asn Lys Ser  Asn Asn Gln Val Cys  His Trp Leu
    1010                1015                1020

Ile Leu  Thr Asp Ser Lys Gly  Leu Gly Lys Ser Leu  Ala Thr His
    1025                1030                1035

Leu Gln  Gln Leu Gly Asn Glu  Cys Ser Val Val Tyr  Gln Ala Asp
    1040                1045                1050

Asn Tyr  Gln Asn Tyr Glu Pro  Gly Ile Tyr His Ile  Asn Pro Ser
    1055                1060                1065

His Pro  Gln Glu Phe Glu Gln  Val Tyr Gln Thr Ile  Phe Glu Asn
    1070                1075                1080

Gly Lys  Leu Pro Leu Gln Lys  Val Ile His Leu Trp  Ser Leu Asp
    1085                1090                1095

Thr Ala  Ser Glu Gln Asp Leu  Thr Thr Glu Thr Leu  Glu Gln Ala
    1100                1105                1110

Gln Leu  Trp Gly Cys Gly Ser  Thr Leu His Leu Leu  Gln Thr Leu
    1115                1120                1125

Val Lys  Asn Pro Asn Ser Thr  Pro Pro Lys Leu Trp  Met Ile Thr
    1130                1135                1140

Arg Gly  Thr Gln Pro Val Leu  Ser Pro Thr Glu Lys  Leu Thr Val
    1145                1150                1155

Ala Thr  Ser Pro Leu Trp Gly  Leu Gly Arg Thr Ile  Ala Ser Glu
    1160                1165                1170

His Pro  Gln Leu Trp Gly Gly  Leu Val Asp Leu Asp  Pro Gln Gly
    1175                1180                1185

Ser Glu  Asp Glu Val Glu Val  Leu Leu Gln Gln Ile  Ile Asp Ser
    1190                1195                1200

Gln Lys  Glu Asp His Leu Ala  Val Arg Asn Arg Lys  Ile Tyr Val
    1205                1210                1215

Ala Arg  Leu Leu Lys His Ile  Pro Gln Glu Ser Gln  Pro Leu Ser
    1220                1225                1230

Leu Arg  Ser Asp Ala Thr Tyr  Leu Ile Thr Gly Gly  Leu Gly Ala
    1235                1240                1245

Leu Gly  Leu Lys Thr Ala Ala  Trp Met Ala Glu Lys  Gly Ala Arg
    1250                1255                1260

Asn Leu  Val Leu Ile Ser Arg  Arg Gln Pro Ser Glu  Gln Ala Gln
    1265                1270                1275

Gln Thr  Ile Gln Ser Leu Glu  Glu Leu Gly Thr Gln  Val Lys Val
    1280                1285                1290

Leu Ser  Ala Asp Ile Ser Val  Glu Ser Asp Val Ala  Asn Ile Leu
    1295                1300                1305

Glu Gln  Ile Gln Thr Ser Leu  Pro Pro Leu Leu Gly  Val Ile His
    1310                1315                1320

Ala Ala  Gly Val Leu Asp Asp  Gly Leu Leu Gln Gln  Thr Asn Trp
    1325                1330                1335

Glu Arg  Phe Thr Lys Val Met  Ala Pro Lys Val Asn  Gly Thr Trp
    1340                1345                1350

Asn Leu  His Lys Leu Thr Gln  His Leu Ser Leu Asp  Phe Phe Val
    1355                1360                1365

Cys Phe  Ser Ser Met Ser Ser  Leu Leu Gly Ser Pro  Gly Gln Gly
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    1370                1375                1380

Asn Tyr  Ala Ala Ala Asn Ala  Phe Met Asp Ala Val  Val His Tyr
    1385                1390                1395

Arg Arg  Glu Met Gly Leu Pro  Gly Leu Ser Ile Asn  Trp Gly Gly
    1400                1405                1410

Trp Ser  Glu Gly Gly Met Ala  Thr Arg Leu Ala Ser  Gln His Gln
    1415                1420                1425

Asn Arg  Met Gln Thr Ala Gly  Ile Ser Leu Ile Ser  Pro Glu Gln
    1430                1435                1440

Gly Ile  Gln Val Leu Glu Glu  Leu Val Arg Thr Gln  Ser Thr Ala
    1445                1450                1455

Gln Val  Gly Val Leu Pro Val  Asp Trp Ser Val Leu  Ala Lys Gln
    1460                1465                1470

Phe Ser  Ser Ala Asn Pro Ser  Ser Leu Leu Leu Glu  Leu Leu Gln
    1475                1480                1485

Gln Glu  Thr Ser Ser Glu Lys  Thr Asp Glu Arg Ile  Leu Glu Lys
    1490                1495                1500

Leu Gln  Ala Ala Pro Ile Thr  Glu Arg Gln Asp Ile  Leu Lys Asn
    1505                1510                1515

Tyr Ile  Gln Leu Val Val Ala  Lys Thr Leu Gly Ile  Asn Pro Ser
    1520                1525                1530

Lys Ile  Ser Thr Asp Asp Asn  Phe Val Glu Leu Gly  Met Asp Ser
    1535                1540                1545

Leu Met  Gly Met Glu Val Val  Asn Lys Leu Ser Gly  Asp Leu Asp
    1550                1555                1560

Phe Ile  Ile Tyr Pro Arg Glu  Phe Tyr Glu Arg Pro  Thr Ile Asp
    1565                1570                1575

Ser Leu  Thr Gln Tyr Leu Ser  Ala Glu Leu Ser Glu  Asp Asn Leu
    1580                1585                1590

Ala Thr  Gln Pro Ser Pro Thr  Ser Leu Glu Ile Phe  Ala Thr Lys
    1595                1600                1605

Ser Ser  Pro Ser Gly Asn Ser  Ala Arg Pro Ala Ser  Val Ser Ser
    1610                1615                1620

Arg Leu  Pro Gly Ile Ile Phe  Ile Leu Ser Ser Pro  Arg Ser Gly
    1625                1630                1635

Ser Thr  Leu Leu Arg Val Met  Leu Ala Gly His Ser  Ser Leu Phe
    1640                1645                1650

Ser Pro  Pro Glu Leu His Leu  Leu Pro Phe Asn Thr  Met Lys Glu
    1655                1660                1665

Arg Gln  Glu Gln Leu Asn Leu  Ser Tyr Leu Gly Glu  Gly Leu Gln
    1670                1675                1680

Lys Thr  Phe Met Glu Val Lys  Asn Leu Asp Ala Thr  Ala Ser Gln
    1685                1690                1695

Ala Leu  Ile Lys Asp Leu Glu  Ser Gln Asn Leu Ser  Ile Gln Gln
    1700                1705                1710

Val Tyr  Gly Met Leu Gln Glu  Asn Ile Ala Pro Arg  Leu Leu Val
    1715                1720                1725

Asp Lys  Ser Pro Thr Tyr Ala  Met Glu Pro Thr Ile  Leu Glu Arg
    1730                1735                1740

Gly Glu  Ala Leu Phe Ala Asn  Ser Lys Tyr Ile Tyr  Leu Val Arg
    1745                1750                1755
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His Pro  Tyr Ser Val Ile Glu  Ser Phe Val Arg Met  Arg Met Gln
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Lys Leu  Val Gly Leu Gly Glu  Glu Asn Pro Tyr Arg  Val Ala Glu
    1775                 1780                 1785

Gln Val  Trp Ala Lys Ser Asn  Gln Asn Ile Leu Asn  Phe Leu Ser
    1790                 1795                 1800

Gln Leu  Glu Pro Glu Arg Gln  His Gln Ile Arg Tyr  Glu Asp Leu
    1805                 1810                 1815

Val Lys  Lys Pro Gln Gln Val  Leu Ser Gln Leu Cys  Asp Phe Leu
    1820                 1825                 1830

Asn Val  Pro Phe Glu Pro Glu  Leu Leu Gln Pro Tyr  Gln Gly Asp
    1835                 1840                 1845

Arg Met  Thr Gly Gly Val His  Gln Lys Ser Leu Ser  Ile Ser Asp
    1850                 1855                 1860

Pro Asn  Phe Leu Lys His Asn  Thr Ile Asp Glu Ser  Leu Ala Asp
    1865                 1870                 1875

Lys Trp  Lys Thr Ile Gln Leu  Pro Tyr Pro Leu Lys  Ser Glu Thr
    1880                 1885                 1890

Gln Arg  Ile Ala Ser Gln Leu  Ser Tyr Glu Leu Pro  Asn Leu Val
    1895                 1900                 1905

Thr Thr  Pro Thr Asn Gln Gln  Pro Gln Val Ser Thr  Thr Pro Ser
    1910                 1915                 1920

Thr Glu  Gln Pro Ile Met Glu  Glu Lys Phe Leu Glu  Phe Gly Gly
    1925                 1930                 1935

Asn Gln  Ile Cys Leu Cys Ser  Trp Gly Ser Pro Glu  His Pro Val
    1940                 1945                 1950

Val Leu  Cys Ile His Gly Ile  Leu Glu Gln Gly Leu  Ala Trp Gln
    1955                 1960                 1965

Glu Val  Ala Leu Pro Leu Ala  Ala Gln Gly Tyr Arg  Val Val Ala
    1970                 1975                 1980

Pro Asp  Leu Phe Gly His Gly  Arg Ser Ser His Leu  Glu Met Val
    1985                 1990                 1995

Thr Ser  Tyr Ser Ser Leu Thr  Phe Leu Ala Gln Ile  Asp Arg Val
    2000                 2005                 2010

Ile Gln  Glu Leu Pro Asp Gln  Pro Leu Leu Leu Val  Gly His Ser
    2015                 2020                 2025

Met Gly  Ala Met Leu Ala Thr  Ala Ile Ala Ser Val  Arg Pro Lys
    2030                 2035                 2040

Lys Ile  Lys Glu Leu Ile Leu  Val Glu Leu Pro Leu  Pro Ala Glu
    2045                 2050                 2055

Glu Ser  Lys Lys Glu Ser Ala  Val Asn Gln Leu Thr  Thr Cys Leu
    2060                 2065                 2070

Asp Tyr  Leu Ser Ser Thr Pro  Gln His Pro Ile Phe  Pro Asp Val
    2075                 2080                 2085

Ala Thr  Ala Ala Ser Arg Leu  Arg Gln Ala Ile Pro  Ser Leu Ser
    2090                 2095                 2100

Glu Glu  Phe Ser Tyr Ile Leu  Ala Gln Arg Ile Thr  Gln Pro Asn
    2105                 2110                 2115

Gln Gly  Gly Val Arg Trp Ser  Trp Asp Ala Ile Ile  Arg Thr Arg
    2120                 2125                 2130

Ser Ile  Leu Gly Leu Asn Asn  Leu Pro Gly Gly Arg  Ser Gln Tyr
    2135                 2140                 2145
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Leu Glu  Met Leu Lys Ser Ile  Gln Val Pro Thr Thr  Leu Val Tyr
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Gly Asp  Ser Ser Lys Leu Asn  Arg Pro Glu Asp Leu  Gln Gln Gln
    2165                 2170                 2175

Lys Met  Thr Met Thr Gln Ala  Lys Arg Val Phe Leu  Ser Gly Gly
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Leu Thr  Ser
    2210
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<210> SEQ ID NO 2
<211> LENGTH: 2694
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: EryA1 loading module + KS1 and AT-ACP from IdmO

<400> SEQUENCE: 2

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            20                  25                  30

Arg Ala Arg Ala Arg Gln Leu Arg Ala His Leu Asp Arg Phe Pro Asp
        35                  40                  45

Ala Gly Val Glu Gly Val Gly Ala Ala Leu Ala His Asp Glu Gln Ala
    50                  55                  60

Asp Ala Gly Pro His Arg Ala Val Val Val Ala Ser Ser Thr Ser Glu
65                  70                  75                  80

Leu Leu Asp Gly Leu Ala Ala Val Ala Asp Gly Arg Pro His Ala Ser
                85                  90                  95

Val Val Arg Gly Val Ala Arg Pro Ser Ala Pro Val Val Phe Val Phe
            100                 105                 110

Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala Gly Glu Leu Leu Gly
        115                 120                 125

Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala Cys Ala Arg Ala Phe
    130                 135                 140

Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val Leu Asp Ser Pro Glu
145                 150                 155                 160

Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala Leu Phe Ala Val Gln
                165                 170                 175

Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly Val Thr Pro Asp Ala
            180                 185                 190

Val Val Gly His Ser Ile Gly Glu Leu Ala Ala Ala His Val Cys Gly
        195                 200                 205

Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala Ala Leu Trp Ser Arg
    210                 215                 220

Glu Met Ile Pro Leu Val Gly Asn Gly Asp Met Ala Ala Val Ala Leu
225                 230                 235                 240

Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg Trp Asp Asp Asp Val
                245                 250                 255

Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu Leu Thr Gly Ser
            260                 265                 270
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Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser Ala Glu Gly Val
        275                 280                 285

Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His Ser Ala Gln Val
    290                 295                 300

Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala Trp Phe Ala Pro
305                 310                 315                 320

Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr Gly Gly Ala Val
                325                 330                 335

Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg Ser Phe Arg Leu
            340                 345                 350

Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu Glu Val Gly Pro
        355                 360                 365

Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Leu Ala Ala Ala Leu
    370                 375                 380

Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala Val Val Pro Thr
385                 390                 395                 400

Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu Leu Ala Ala Ala
                405                 410                 415

Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr Ala Ala Tyr Asp
            420                 425                 430

Asp Val Gly Ala Glu Pro Gly Ser Leu Pro Glu Phe Ala Pro Ala Glu
        435                 440                 445

Glu Glu Asp Glu Pro Ala Glu Ser Gly Val Asp Trp Asn Ala Pro Pro
    450                 455                 460

His Val Leu Arg Glu Arg Leu Leu Ala Val Val Asn Gly Glu Thr Ala
465                 470                 475                 480

Ala Leu Ala Gly Arg Glu Ala Asp Ala Glu Ala Thr Phe Arg Glu Leu
                485                 490                 495

Gly Leu Asp Ser Val Leu Ala Ala Gln Leu Arg Ala Lys Val Ser Ala
            500                 505                 510

Ala Ile Gly Arg Glu Val Asn Ile Ala Leu Leu Tyr Asp His Pro Thr
        515                 520                 525

Pro Arg Ala Leu Ala Glu Ala Leu Ala Ala Gly Thr Glu Val Ala Gln
    530                 535                 540

Arg Glu Thr Arg Ala Arg Thr Asn Glu Ala Ala Pro Gly Glu Pro Val
545                 550                 555                 560

Ala Val Val Ala Met Ala Cys Arg Leu Pro Gly Gly Val Ser Thr Pro
                565                 570                 575

Glu Glu Phe Trp Glu Leu Leu Ser Glu Gly Arg Asp Ala Val Ala Gly
            580                 585                 590

Leu Pro Thr Asp Arg Gly Trp Asp Leu Asp Ser Leu Phe His Pro Asp
        595                 600                 605

Pro Thr Arg Ser Gly Thr Ala His Gln Arg Gly Gly Gly Phe Leu Thr
    610                 615                 620

Glu Ala Thr Ala Phe Asp Pro Ala Phe Phe Gly Met Ser Pro Arg Glu
625                 630                 635                 640

Ala Leu Ala Val Asp Pro Gln Gln Arg Leu Met Leu Glu Leu Ser Trp
                645                 650                 655

Glu Val Leu Glu Arg Ala Gly Ile Pro Pro Thr Ser Leu Gln Ala Ser
            660                 665                 670

Pro Thr Gly Val Phe Val Gly Leu Ile Pro Gln Glu Tyr Gly Pro Arg
        675                 680                 685
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Leu Ala Glu Gly Gly Glu Gly Val Glu Gly Tyr Leu Met Thr Gly Thr
    690                 695                 700

Thr Thr Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Leu Glu
705                 710                 715                 720

Gly Pro Ala Ile Ser Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
                725                 730                 735

Val His Leu Ala Cys Gln Ser Leu Arg Arg Gly Glu Ser Ser Leu Ala
            740                 745                 750

Met Ala Gly Gly Val Thr Val Met Pro Thr Pro Gly Met Leu Val Asp
        755                 760                 765

Phe Ser Arg Met Asn Ser Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe
    770                 775                 780

Ser Ala Gly Ala Asn Gly Phe Gly Met Ala Glu Gly Ala Gly Met Leu
785                 790                 795                 800

Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Pro Val Leu
                805                 810                 815

Ala Val Leu Arg Gly Thr Ala Val Asn Ser Asp Gly Ala Ser Asn Gly
            820                 825                 830

Leu Ser Ala Pro Asn Gly Arg Ala Gln Val Arg Val Ile Gln Gln Ala
        835                 840                 845

Leu Ala Glu Ser Gly Leu Gly Pro Ala Asp Ile Asp Ala Val Glu Ala
    850                 855                 860

His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Arg Ala Leu
865                 870                 875                 880

Phe Glu Ala Tyr Gly Arg Asp Arg Glu Gln Pro Leu His Leu Gly Ser
                885                 890                 895

Val Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly
            900                 905                 910

Val Ile Lys Met Val Leu Ala Met Arg Ala Gly Thr Leu Pro Arg Thr
        915                 920                 925

Leu His Ala Ser Glu Arg Ser Lys Glu Ile Asp Trp Ser Ser Gly Ala
    930                 935                 940

Ile Ser Leu Leu Asp Glu Pro Glu Pro Trp Pro Ala Gly Ala Arg Pro
945                 950                 955                 960

Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser Gly Thr Asn Ala His
                965                 970                 975

Val Ile Val Glu Glu Ala Pro Glu Ser Ser Ala Asp Ala Val Ala Glu
            980                 985                 990

Ser Gly Val Arg Val Pro Val Pro  Val Val Pro Trp Val  Val Ser Ala
        995                 1000                1005

Arg Ser  Ala Glu Gly Leu Ala  Ala Gln Ala Glu Arg  Leu Ala Arg
    1010                1015                1020

Phe Val  Gly Glu Arg Ser Asp  Gln Asp Pro Val Asp  Ile Gly Phe
    1025                1030                1035

Ser Leu  Val Arg Ser Arg Ser  Leu Leu Glu His Arg  Ala Val Val
    1040                1045                1050

Leu Gly  Lys Gly Arg Asp Asp  Leu Val Ala Gly Leu  Ala Ser Leu
    1055                1060                1065

Ala Ser  Asp Gly Ser Ala Thr  Gly Val Val Ser Gly  Val Ala Arg
    1070                1075                1080

Gly Arg  Ala Arg Val Ala Phe  Gly Phe Ser Gly Gln  Gly Ala Gln
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    1085                1090                1095

Arg Val  Gly Met Gly Ala Glu  Leu Ala Ser Val Tyr  Pro Val Phe
    1100                1105                1110

Ala Glu  Ala Leu Ala Glu Val  Thr Gly Ala Leu Gly  Leu Asp Pro
    1115                1120                1125

Glu Val  Phe Gly Asp Val Asp  Arg Leu Gly Arg Thr  Glu Val Thr
    1130                1135                1140

Gln Ala  Ala Leu Phe Ala Phe  Glu Val Ala Val Val  Arg Leu Leu
    1145                1150                1155

Glu Ser  Phe Gly Val Arg Pro  Asp Val Leu Ile Gly  His Ser Ile
    1160                1165                1170

Gly Glu  Ile Ala Ala Ala Tyr  Val Ala Gly Val Phe  Ser Leu Gly
    1175                1180                1185

Asp Ala  Ala Ala Leu Val Gly  Ala Arg Gly Arg Leu  Met Gln Ala
    1190                1195                1200

Leu Pro  Ala Gly Gly Val Met  Val Ala Val Gln Ala  Gly Glu Ala
    1205                1210                1215

Glu Val  Val Ala Ala Leu Glu  Gly Phe Ala Asp Arg  Val Ser Leu
    1220                1225                1230

Ala Ala  Val Asn Gly Pro Ser  Ser Val Val Val Ser  Gly Glu Ala
    1235                1240                1245

Glu Ala  Val Glu Gln Val Val  Ala Arg Leu Gly Lys  Val Lys Ser
    1250                1255                1260

Lys Arg  Leu Arg Val Ser His  Ala Phe His Ser Pro  Leu Met Glu
    1265                1270                1275

Pro Met  Leu Ala Asp Phe Arg  Gln Val Ala Glu Gln  Ile Thr Tyr
    1280                1285                1290

Asn Glu  Pro Gln Leu Pro Val  Val Ser Asn Val Ser  Gly Arg Leu
    1295                1300                1305

Ala Glu  Pro Gly Glu Leu Thr  Thr Pro Asp Tyr Trp  Val Arg His
    1310                1315                1320

Val Arg  Glu Ala Val Arg Phe  Gly Asp Gly Val Arg  Ala Leu Ala
    1325                1330                1335

Ala Asp  Gly Val Gly Val Leu  Val Glu Val Gly Pro  Asp Ser Val
    1340                1345                1350

Leu Thr  Ala Leu Ala Arg Glu  Ser Leu Asp Gly Glu  Asp Gly Leu
    1355                1360                1365

Arg Ala  Val Pro Leu Leu Arg  Lys Asp Arg Pro Glu  Pro Glu Thr
    1370                1375                1380

Leu Leu  Thr Gly Val Ala Gln  Ala Phe Thr His Gly  Val Gln Val
    1385                1390                1395

Asp Trp  Pro Ala Leu Leu Pro  Gly Gly Arg Arg Val  Glu Leu Pro
    1400                1405                1410

Thr Tyr  Ala Phe Gln Arg Arg  Arg Tyr Trp Leu Glu  Asp Ala Asp
    1415                1420                1425

Pro Thr  Gly Gly Asp Pro Ala  Ala Leu Gly Leu Thr  Ala Ala Asp
    1430                1435                1440

His Pro  Leu Leu Gly Ala Ala  Val Pro Leu Ala Glu  Asp Gln Gly
    1445                1450                1455

Ile Val  Ile Thr Ser Arg Leu  Ser Leu Arg Thr His  Pro Trp Leu
    1460                1465                1470
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Ala Asp  His Glu Ile Gly Gly  Thr Val Leu Leu Pro  Gly Ala Gly
    1475                 1480                 1485

Leu Val  Glu Ile Ala Leu Arg  Ala Gly Asp Glu Val  Gly Cys Gly
    1490                 1495                 1500

Arg Val  Glu Glu Leu Thr Leu  Glu Ile Pro Leu Val  Val Pro Gln
    1505                 1510                 1515

Glu Gly  Gly Val Thr Val Gln  Ile Arg Val Gly Ala  Pro Asp Glu
    1520                 1525                 1530

Ser Gly  Trp Arg Pro Met Thr  Val His Ser Arg Thr  Asp Pro Glu
    1535                 1540                 1545

Glu Glu  Trp Thr Arg His Val  Ser Gly Val Leu Ser  Pro Asp Val
    1550                 1555                 1560

Pro Thr  Glu Arg Tyr Asp Leu  Gly Ala Trp Pro Pro  Ala Gly Ala
    1565                 1570                 1575

Thr Pro  Val Glu Leu Asp Gly  Phe Tyr Glu Ala Tyr  Ala Arg Leu
    1580                 1585                 1590

Gly Tyr  Ala Tyr Gly Pro Ser  Phe Gln Gly Leu Arg  Ala Ala Trp
    1595                 1600                 1605

Arg Arg  Gly Asp Glu Val Phe  Ala Glu Val Ser Leu  Pro Val Glu
    1610                 1615                 1620

Glu Gln  Glu Thr Ala Gly Arg  Phe Thr Leu His Pro  Ala Leu Leu
    1625                 1630                 1635

Asp Ala  Ala Leu Gln Ser Ala  Gly Ala Gly Ala Phe  Phe Asp Ser
    1640                 1645                 1650

Gly Gly  Ser Met Arg Leu Pro  Phe Ala Trp Ser Gly  Val Ser Val
    1655                 1660                 1665

Phe Ala  Ala Gly Ala Ser Thr  Val Arg Val Arg Leu  Ser Pro Ala
    1670                 1675                 1680

Gly Pro  Asp Ala Val Thr Val  Ala Leu Ala Asp Pro  Thr Gly Ala
    1685                 1690                 1695

Pro Val  Ala Leu Val Glu Arg  Leu Leu Ile Pro Glu  Met Ser Pro
    1700                 1705                 1710

Glu Gln  Leu Glu Arg Val Arg  Gly Glu Glu Lys Glu  Ala Pro Tyr
    1715                 1720                 1725

Val Leu  Asp Trp Val Pro Val  Glu Val Pro Ala Asp  Asp Leu Val
    1730                 1735                 1740

Arg Pro  Glu Arg Trp Thr Leu  Leu Gly Gly Ala Asp  Ala Gly Val
    1745                 1750                 1755

Gly Leu  Asp Val Ala Gly Ala  Phe Ala Ser Leu Glu  Pro Ser Asp
    1760                 1765                 1770

Gly Ala  Pro Glu Phe Val Val  Leu Pro Cys Val Pro  Pro Thr Ser
    1775                 1780                 1785

Pro Thr  Arg Ala Ala Asp Val  Arg Gln Ser Thr Leu  Gln Ala Leu
    1790                 1795                 1800

Thr Val  Leu Gln Asn Trp Val  Thr Asp Glu Arg His  Ala Asp Ser
    1805                 1810                 1815

Arg Leu  Val Leu Val Thr Arg  Arg Ala Val Gly Val  Gly Ala His
    1820                 1825                 1830

Asp Asp  Val Pro Asp Leu Thr  His Ala Ala Leu Trp  Gly Leu Val
    1835                 1840                 1845

Arg Ser  Ala Gln Thr Glu Asn  Pro Gly Arg Phe Leu  Leu Val Asp
    1850                 1855                 1860
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Leu Asp  Glu Gly Ala Glu Leu  Ala Glu Val Leu Pro  Gly Ala Leu
    1865                 1870                 1875

Gly Ser  Gly Glu Ser Gln Val  Ala Val Arg Ala Gly  Arg Val Leu
    1880                 1885                 1890

Ala Ala  Arg Leu Ala Arg Ser  Gly Ser Gly Gly Ala  Glu Leu Val
    1895                 1900                 1905

Pro Pro  Ala Gly Ala Pro Trp  Arg Leu Asp Thr Thr  Ser Pro Gly
    1910                 1915                 1920

Thr Leu  Glu Asn Leu Ala Leu  Val Pro Ser Ala Glu  Glu Pro Leu
    1925                 1930                 1935

Gly Pro  Leu Asp Val Arg Val  Ser Val Arg Ala Ala  Gly Leu Asn
    1940                 1945                 1950

Phe Arg  Asp Val Leu Ile Ala  Leu Gly Met Tyr Pro  Gly Asp Ala
    1955                 1960                 1965

Arg Met  Gly Gly Glu Gly Ala  Gly Val Val Thr Asp  Val Gly Ser
    1970                 1975                 1980

Glu Val  Thr Thr Leu Ala Pro  Gly Asp Arg Val Met  Gly Met Leu
    1985                 1990                 1995

Ser Ser  Ala Phe Gly Pro Thr  Ala Val Ser Asp His  Arg Ala Leu
    2000                 2005                 2010

Val Arg  Val Pro Asp Asp Trp  Ser Phe Glu Gln Ala  Ala Ser Val
    2015                 2020                 2025

Pro Thr  Val Phe Ala Thr Ala  Tyr Tyr Gly Leu Val  Asp Leu Ala
    2030                 2035                 2040

Glu Leu  Arg Ala Gly Gln Ser  Val Leu Val His Ala  Ala Ala Gly
    2045                 2050                 2055

Gly Val  Gly Met Ala Ala Val  Gln Leu Ala Arg His  Leu Gly Ala
    2060                 2065                 2070

Glu Val  Phe Gly Thr Ala Ser  Thr Gly Lys Trp Asp  Ser Leu Arg
    2075                 2080                 2085

Ala Gly  Gly Leu Asp Ala Glu  His Ile Ala Ser Ser  Arg Thr Val
    2090                 2095                 2100

Glu Phe  Glu Glu Thr Phe Leu  Ala Ala Thr Ala Gly  Arg Gly Val
    2105                 2110                 2115

Asp Val  Val Leu Asp Ser Leu  Ala Gly Glu Phe Val  Asp Ala Ser
    2120                 2125                 2130

Leu Arg  Leu Leu Pro Arg Gly  Gly Arg Phe Val Glu  Met Gly Lys
    2135                 2140                 2145

Ala Asp  Ile Arg Asp Ala Glu  Arg Val Ala Ala Asp  His Pro Gly
    2150                 2155                 2160

Val Thr  Tyr Arg Ser Phe Asp  Leu Leu Glu Ala Gly  Leu Asp Arg
    2165                 2170                 2175

Phe Gln  Glu Ile Leu Thr Glu  Val Val Arg Leu Phe  Glu Arg Gly
    2180                 2185                 2190

Val Leu  Arg His Leu Pro Val  Thr Ala Trp Asp Val  Arg Arg Ala
    2195                 2200                 2205

Ala Glu  Ala Phe Arg Phe Val  Ser Gln Ala Arg His  Val Gly Lys
    2210                 2215                 2220

Asn Val  Leu Val Met Pro Arg  Val Trp Asp Arg Asp  Gly Thr Val
    2225                 2230                 2235

Leu Ile  Thr Gly Gly Thr Gly  Ala Leu Gly Ala Leu  Val Ala Arg
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    2240                2245                2250

His Leu  Val Ala Glu His Gly  Met Arg Asn Val Leu  Leu Ala Gly
    2255                2260                2265

Arg Arg  Gly Val Asp Ala Pro  Gly Ala Arg Glu Leu  Leu Ala Glu
    2270                2275                2280

Leu Glu  Thr Ala Gly Ala Gln  Val Ser Val Val Ala  Cys Asp Val
    2285                2290                2295

Ala Asp  Arg Asp Ala Val Ala  Glu Leu Ile Ala Lys  Val Pro Val
    2300                2305                2310

Glu His  Pro Leu Thr Ala Val  Val His Thr Ala Gly  Val Val Ala
    2315                2320                2325

Asp Ala  Thr Leu Thr Ala Leu  Asp Ala Glu Arg Val  Asp Thr Val
    2330                2335                2340

Leu Arg  Ala Lys Val Asp Ala  Val Leu His Leu His  Glu Ala Thr
    2345                2350                2355

Arg Gly  Leu Asp Leu Ala Gly  Phe Val Leu Phe Ser  Ser Ala Ser
    2360                2365                2370

Gly Ile  Phe Gly Ser Pro Gly  Gln Gly Asn Tyr Ala  Ala Ala Asn
    2375                2380                2385

Ser Phe  Ile Asp Ala Phe Ala  His His Arg Arg Ala  Gln Gly Leu
    2390                2395                2400

Pro Ala  Leu Ser Leu Ala Trp  Gly Leu Trp Ala Arg  Thr Ser Gly
    2405                2410                2415

Met Ala  Gly Gln Leu Gly His  Asp Asp Val Ala Arg  Ile Ser Arg
    2420                2425                2430

Thr Gly  Leu Ala Pro Ile Thr  Asp Asp Gln Gly Met  Ala Leu Leu
    2435                2440                2445

Asp Ala  Ala Leu Gly Ala Gly  Arg Pro Leu Leu Val  Pro Val Arg
    2450                2455                2460

Leu Asp  Arg Ala Ala Leu Arg  Ser Gln Ala Thr Ala  Gly Thr Leu
    2465                2470                2475

Pro Pro  Ile Leu Arg Gly Leu  Val Arg Ala Thr Val  Arg Arg Ala
    2480                2485                2490

Ala Ser  Thr Ala Ala Ala Gln  Gly Pro Ser Leu Ala  Glu Arg Leu
    2495                2500                2505

Ala Gly  Leu Pro Val Thr Glu  His Glu Arg Ile Val  Val Glu Leu
    2510                2515                2520

Val Arg  Ala Asp Leu Ala Ala  Val Leu Gly His Ser  Ser Ser Ala
    2525                2530                2535

Gly Ile  Asp Pro Gly Arg Ala  Phe Gln Asp Met Gly  Ile Asp Ser
    2540                2545                2550

Leu Thr  Ala Val Glu Leu Arg  Asn Arg Leu Asn Gly  Ala Thr Gly
    2555                2560                2565

Leu Arg  Leu Ala Ala Ser Leu  Val Phe Asp Tyr Pro  Thr Pro Asn
    2570                2575                2580

Ala Leu  Ala Thr His Ile Leu  Asp Glu Leu Ala Leu  Asp Thr Ala
    2585                2590                2595

Gly Ala  Gly Ala Ala Gly Glu  Pro Asp Gly Pro Ala  Pro Ala Pro
    2600                2605                2610

Ala Asp  Glu Ala Arg Phe Arg  Arg Val Ile Asn Ser  Ile Pro Leu
    2615                2620                2625
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Asp Arg  Ile Arg Arg Ala Gly  Leu Leu Asp Ala Leu  Leu Gly Leu
    2630                 2635                 2640

Ala Gly  Thr Ser Ala Asp Thr  Ala Ala Ser Asp Asp  Phe Asp Gln
    2645                 2650                 2655

Glu Glu  Asp Gly Pro Ala Ile  Ala Ser Met Asp Val  Asp Asp Leu
    2660                 2665                 2670

Val Arg  Ile Ala Leu Gly Glu  Ser Asp Thr Thr Ala  Asp Ile Thr
    2675                 2680                 2685

Glu Gly  Thr Asp Arg Ser
    2690
```

<210> SEQ ID NO 3
<211> LENGTH: 2694
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: EryA1 loading module + KS1 and AT-ACP from IdmO

<400> SEQUENCE: 3

```
Met Ala Asp Leu Ser Lys Leu Ser Asp Ser Arg Thr Ala Gln Pro Gly
1               5                  10                  15

Arg Ile Val Arg Pro Trp Pro Leu Ser Gly Cys Asn Glu Ser Ala Leu
            20                  25                  30

Arg Ala Arg Ala Arg Gln Leu Arg Ala His Leu Asp Arg Phe Pro Asp
        35                  40                  45

Ala Gly Val Glu Gly Val Gly Ala Ala Leu Ala His Asp Glu Gln Ala
    50                  55                  60

Asp Ala Gly Pro His Arg Ala Val Val Val Ala Ser Ser Thr Ser Glu
65                  70                  75                  80

Leu Leu Asp Gly Leu Ala Ala Val Ala Asp Gly Arg Pro His Ala Ser
                85                  90                  95

Val Val Arg Gly Val Ala Arg Pro Ser Ala Pro Val Val Phe Val Phe
            100                 105                 110

Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala Gly Glu Leu Leu Gly
        115                 120                 125

Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala Cys Ala Arg Ala Phe
    130                 135                 140

Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val Leu Asp Ser Pro Glu
145                 150                 155                 160

Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala Leu Phe Ala Val Gln
                165                 170                 175

Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly Val Thr Pro Asp Ala
            180                 185                 190

Val Val Gly His Ser Ile Gly Glu Leu Ala Ala Ala His Val Cys Gly
        195                 200                 205

Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala Ala Leu Trp Ser Arg
    210                 215                 220

Glu Met Ile Pro Leu Val Gly Asn Gly Asp Met Ala Ala Val Ala Leu
225                 230                 235                 240

Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg Trp Asp Asp Asp Val
                245                 250                 255

Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu Leu Thr Gly Ser
            260                 265                 270

Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser Ala Glu Gly Val
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        275                 280                 285

Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His Ser Ala Gln Val
    290                 295                 300

Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala Trp Phe Ala Pro
305                 310                 315                 320

Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr Gly Gly Ala Val
                325                 330                 335

Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg Ser Phe Arg Leu
            340                 345                 350

Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu Glu Val Gly Pro
        355                 360                 365

Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Leu Ala Ala Ala Leu
    370                 375                 380

Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala Val Val Pro Thr
385                 390                 395                 400

Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu Leu Ala Ala Ala
                405                 410                 415

Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr Ala Ala Tyr Asp
            420                 425                 430

Asp Val Gly Ala Glu Pro Gly Ser Leu Pro Glu Phe Ala Pro Ala Glu
        435                 440                 445

Glu Glu Asp Glu Pro Ala Glu Ser Gly Val Asp Trp Asn Ala Pro Pro
    450                 455                 460

His Val Leu Arg Glu Arg Leu Leu Ala Val Val Asn Gly Glu Thr Ala
465                 470                 475                 480

Ala Leu Ala Gly Arg Glu Ala Asp Ala Glu Ala Thr Phe Arg Glu Leu
                485                 490                 495

Gly Leu Asp Ser Val Leu Ala Ala Gln Leu Arg Ala Lys Val Ser Ala
            500                 505                 510

Ala Ile Gly Arg Glu Val Asn Ile Ala Leu Leu Tyr Asp His Pro Thr
        515                 520                 525

Pro Arg Ala Leu Ala Glu Ala Leu Ala Ala Gly Thr Glu Val Ala Gln
    530                 535                 540

Arg Glu Thr Arg Ala Arg Thr Asn Glu Ala Ala Pro Gly Glu Pro Val
545                 550                 555                 560

Ala Val Val Ala Met Ala Cys Arg Leu Pro Gly Gly Val Ser Thr Pro
                565                 570                 575

Glu Glu Phe Trp Glu Leu Leu Ser Glu Gly Arg Asp Ala Val Ala Gly
            580                 585                 590

Leu Pro Thr Asp Arg Gly Trp Asp Leu Asp Ser Leu Phe His Pro Asp
        595                 600                 605

Pro Thr Arg Ser Gly Thr Ala His Gln Arg Gly Gly Gly Phe Leu Thr
    610                 615                 620

Glu Ala Thr Ala Phe Asp Pro Ala Phe Phe Gly Met Ser Pro Arg Glu
625                 630                 635                 640

Ala Leu Ala Val Asp Pro Gln Gln Arg Leu Met Leu Glu Leu Ser Trp
                645                 650                 655

Glu Val Leu Glu Arg Ala Gly Ile Pro Pro Thr Ser Leu Gln Ala Ser
            660                 665                 670

Pro Thr Gly Val Phe Val Gly Leu Ile Pro Gln Glu Tyr Gly Pro Arg
        675                 680                 685
```

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```
Leu Ala Glu Gly Gly Glu Gly Val Glu Gly Tyr Leu Met Thr Gly Thr
    690                 695                 700

Thr Thr Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Leu Glu
705                 710                 715                 720

Gly Pro Ala Ile Ser Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
                725                 730                 735

Val His Leu Ala Cys Gln Ser Leu Arg Arg Gly Glu Ser Ser Leu Ala
            740                 745                 750

Met Ala Gly Gly Val Thr Val Met Pro Thr Pro Gly Met Leu Val Asp
        755                 760                 765

Phe Ser Arg Met Asn Ser Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe
    770                 775                 780

Ser Ala Gly Ala Asn Gly Phe Gly Met Ala Glu Gly Ala Gly Met Leu
785                 790                 795                 800

Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Pro Val Leu
                805                 810                 815

Ala Val Leu Arg Gly Thr Ala Val Asn Ser Asp Gly Ala Ser Asn Gly
            820                 825                 830

Leu Ser Ala Pro Asn Gly Arg Ala Gln Val Arg Val Ile Gln Gln Ala
        835                 840                 845

Leu Ala Glu Ser Gly Leu Gly Pro Ala Asp Ile Asp Ala Val Glu Ala
    850                 855                 860

His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Arg Ala Leu
865                 870                 875                 880

Phe Glu Ala Tyr Gly Arg Asp Arg Glu Gln Pro Leu His Leu Gly Ser
                885                 890                 895

Val Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly
            900                 905                 910

Val Ile Lys Met Val Leu Ala Met Arg Ala Gly Thr Leu Pro Arg Thr
        915                 920                 925

Leu His Ala Ser Glu Arg Ser Lys Glu Ile Asp Trp Ser Ser Gly Ala
    930                 935                 940

Ile Ser Leu Leu Asp Glu Pro Glu Pro Trp Pro Ala Gly Ala Arg Pro
945                 950                 955                 960

Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser Gly Thr Asn Ala His
                965                 970                 975

Val Ile Val Glu Glu Ala Pro Glu Ser Ser Ala Asp Ala Val Ala Glu
            980                 985                 990

Ser Gly Val Arg Val Pro Val Pro  Val Val Pro Trp Val  Val Ser Ala
        995                 1000                1005

Arg Ser  Ala Glu Gly Leu Ala  Ala Gln Ala Glu Arg  Leu Ala Arg
    1010                1015                1020

Phe Val  Gly Glu Arg Ser Asp  Gln Asp Pro Val Asp  Ile Gly Phe
    1025                1030                1035

Ser Leu  Val Arg Ser Arg Ser  Leu Leu Glu His Arg  Ala Val Val
    1040                1045                1050

Leu Gly  Lys Gly Arg Asp Asp  Leu Val Ala Gly Leu  Ala Ser Leu
    1055                1060                1065

Ala Ser  Asp Gly Ser Ala Thr  Gly Val Val Ser Gly  Val Ala Arg
    1070                1075                1080

Gly Arg  Ala Arg Val Ala Phe  Gly Phe Ser Gly Gln  Gly Ala Gln
    1085                1090                1095
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```
Arg Val  Gly Met Gly Ala Glu  Leu Ala Ser Val Tyr  Pro Val Phe
    1100                1105                1110

Ala Glu  Ala Leu Ala Glu Val  Thr Gly Ala Leu Gly  Leu Asp Pro
    1115                1120                1125

Glu Val  Phe Gly Asp Val Asp  Arg Leu Gly Arg Thr  Glu Val Thr
    1130                1135                1140

Gln Ala  Ala Leu Phe Ala Phe  Glu Val Ala Val Val  Arg Leu Leu
    1145                1150                1155

Glu Ser  Phe Gly Val Arg Pro  Asp Val Leu Ile Gly  His Ser Ile
    1160                1165                1170

Gly Glu  Ile Ala Ala Ala Tyr  Val Ala Gly Val Phe  Ser Leu Gly
    1175                1180                1185

Asp Ala  Ala Ala Leu Val Gly  Ala Arg Gly Arg Leu  Met Gln Ala
    1190                1195                1200

Leu Pro  Ala Gly Gly Val Met  Val Ala Val Gln Ala  Gly Glu Ala
    1205                1210                1215

Glu Val  Val Ala Ala Leu Glu  Gly Phe Ala Asp Arg  Val Ser Leu
    1220                1225                1230

Ala Ala  Val Asn Gly Pro Ser  Ser Val Val Val Ser  Gly Glu Ala
    1235                1240                1245

Glu Ala  Val Glu Gln Val Val  Ala Arg Leu Gly Lys  Val Lys Ser
    1250                1255                1260

Lys Arg  Leu Arg Val Ser His  Ala Phe His Ser Pro  Leu Met Glu
    1265                1270                1275

Pro Met  Leu Ala Asp Phe Arg  Gln Val Ala Glu Gln  Ile Thr Tyr
    1280                1285                1290

Asn Glu  Pro Gln Leu Pro Val  Val Ser Asn Val Ser  Gly Arg Leu
    1295                1300                1305

Ala Glu  Pro Gly Glu Leu Thr  Thr Pro Asp Tyr Trp  Val Arg His
    1310                1315                1320

Val Arg  Glu Ala Val Arg Phe  Gly Asp Gly Val Arg  Ala Leu Ala
    1325                1330                1335

Ala Asp  Gly Val Gly Val Leu  Val Glu Val Gly Pro  Asp Ser Val
    1340                1345                1350

Leu Thr  Ala Leu Ala Arg Glu  Ser Leu Asp Gly Glu  Asp Gly Leu
    1355                1360                1365

Arg Ala  Val Pro Leu Leu Arg  Lys Asp Arg Pro Glu  Pro Glu Thr
    1370                1375                1380

Leu Leu  Thr Gly Val Ala Gln  Ala Phe Thr His Gly  Val Gln Val
    1385                1390                1395

Asp Trp  Pro Ala Leu Leu Pro  Gly Gly Arg Arg Val  Glu Leu Pro
    1400                1405                1410

Thr Tyr  Ala Phe Gln Arg Arg  Arg Tyr Trp Leu Glu  Asp Ala Asp
    1415                1420                1425

Pro Thr  Gly Gly Asp Pro Ala  Ala Leu Gly Leu Thr  Ala Ala Asp
    1430                1435                1440

His Pro  Leu Leu Gly Ala Ala  Val Pro Leu Ala Glu  Asp Gln Gly
    1445                1450                1455

Ile Val  Ile Thr Ser Arg Leu  Ser Leu Arg Thr His  Pro Trp Leu
    1460                1465                1470

Ala Asp  His Glu Ile Gly Gly  Thr Val Leu Leu Pro  Gly Ala Gly
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    1475                1480                1485

Leu Val  Glu Ile Ala Leu Arg  Ala Gly Asp Glu Val  Gly Cys Gly
    1490                1495                1500

Arg Val  Glu Glu Leu Thr Leu  Glu Ile Pro Leu Val  Val Pro Gln
    1505                1510                1515

Glu Gly  Gly Val Thr Val Gln  Ile Arg Val Gly Ala  Pro Asp Glu
    1520                1525                1530

Ser Gly  Trp Arg Pro Met Thr  Val His Ser Arg Thr  Asp Pro Glu
    1535                1540                1545

Glu Glu  Trp Thr Arg His Val  Ser Gly Val Leu Ser  Pro Asp Val
    1550                1555                1560

Pro Thr  Glu Arg Tyr Asp Leu  Gly Ala Trp Pro Pro  Ala Gly Ala
    1565                1570                1575

Thr Pro  Val Glu Leu Asp Gly  Phe Tyr Glu Ala Tyr  Ala Arg Leu
    1580                1585                1590

Gly Tyr  Ala Tyr Gly Pro Ser  Phe Gln Gly Leu Arg  Ala Ala Trp
    1595                1600                1605

Arg Arg  Gly Asp Glu Val Phe  Ala Glu Val Ser Leu  Pro Val Glu
    1610                1615                1620

Glu Gln  Glu Thr Ala Gly Arg  Phe Thr Leu His Pro  Ala Leu Leu
    1625                1630                1635

Asp Ala  Ala Leu Gln Ser Ala  Gly Ala Gly Ala Phe  Phe Asp Ser
    1640                1645                1650

Gly Gly  Ser Met Arg Leu Pro  Phe Ala Trp Ser Gly  Val Ser Val
    1655                1660                1665

Phe Ala  Ala Gly Ala Ser Thr  Val Arg Val Arg Leu  Ser Pro Ala
    1670                1675                1680

Gly Pro  Asp Ala Val Thr Val  Ala Leu Ala Asp Pro  Thr Gly Ala
    1685                1690                1695

Pro Val  Ala Leu Val Glu Arg  Leu Leu Ile Pro Glu  Met Ser Pro
    1700                1705                1710

Glu Gln  Leu Glu Arg Val Arg  Gly Glu Glu Lys Glu  Ala Pro Tyr
    1715                1720                1725

Val Leu  Asp Trp Val Pro Val  Glu Val Pro Ala Asp  Asp Leu Val
    1730                1735                1740

Arg Pro  Glu Arg Trp Thr Leu  Leu Gly Gly Ala Asp  Ala Gly Val
    1745                1750                1755

Gly Leu  Asp Val Ala Gly Ala  Phe Ala Ser Leu Glu  Pro Ser Asp
    1760                1765                1770

Gly Ala  Pro Glu Phe Val Val  Leu Pro Cys Val Pro  Pro Thr Ser
    1775                1780                1785

Pro Thr  Arg Ala Ala Asp Val  Arg Gln Ser Thr Leu  Gln Ala Leu
    1790                1795                1800

Thr Val  Leu Gln Asn Trp Val  Thr Asp Glu Arg His  Ala Asp Ser
    1805                1810                1815

Arg Leu  Val Leu Val Thr Arg  Arg Ala Val Gly Val  Gly Ala His
    1820                1825                1830

Asp Asp  Val Pro Asp Leu Thr  His Ala Ala Leu Trp  Gly Leu Val
    1835                1840                1845

Arg Ser  Ala Gln Thr Glu Asn  Pro Gly Arg Phe Leu  Leu Val Asp
    1850                1855                1860
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Leu Asp  Glu Gly Ala Glu Leu  Ala Glu Val Leu Pro  Gly Ala Leu
    1865                 1870                 1875

Gly Ser  Gly Glu Ser Gln Val  Ala Val Arg Ala Gly  Arg Val Leu
    1880                 1885                 1890

Ala Ala  Arg Leu Ala Arg Ser  Gly Ser Gly Gly Ala  Glu Leu Val
    1895                 1900                 1905

Pro Pro  Ala Gly Ala Pro Trp  Arg Leu Asp Thr Thr  Ser Pro Gly
    1910                 1915                 1920

Thr Leu  Glu Asn Leu Ala Leu  Val Pro Ser Ala Glu  Glu Pro Leu
    1925                 1930                 1935

Gly Pro  Leu Asp Val Arg Val  Ser Val Arg Ala Ala  Gly Leu Asn
    1940                 1945                 1950

Phe Arg  Asp Val Leu Ile Ala  Leu Gly Met Tyr Pro  Gly Asp Ala
    1955                 1960                 1965

Arg Met  Gly Gly Glu Gly Ala  Gly Val Val Thr Asp  Val Gly Ser
    1970                 1975                 1980

Glu Val  Thr Thr Leu Ala Pro  Gly Asp Arg Val Met  Gly Met Leu
    1985                 1990                 1995

Ser Ser  Ala Phe Gly Pro Thr  Ala Val Ser Asp His  Arg Ala Leu
    2000                 2005                 2010

Val Arg  Val Pro Asp Asp Trp  Ser Phe Glu Gln Ala  Ala Ser Val
    2015                 2020                 2025

Pro Thr  Val Phe Ala Thr Ala  Tyr Tyr Gly Leu Val  Asp Leu Ala
    2030                 2035                 2040

Glu Leu  Arg Ala Gly Gln Ser  Val Leu Val His Ala  Ala Ala Gly
    2045                 2050                 2055

Gly Val  Gly Met Ala Ala Val  Gln Leu Ala Arg His  Leu Gly Ala
    2060                 2065                 2070

Glu Val  Phe Gly Thr Ala Ser  Thr Gly Lys Trp Asp  Ser Leu Arg
    2075                 2080                 2085

Ala Gly  Gly Leu Asp Ala Glu  His Ile Ala Ser Ser  Arg Thr Val
    2090                 2095                 2100

Glu Phe  Glu Glu Thr Phe Leu  Ala Ala Thr Ala Gly  Arg Gly Val
    2105                 2110                 2115

Asp Val  Val Leu Asp Ser Leu  Ala Gly Glu Phe Val  Asp Ala Ser
    2120                 2125                 2130

Leu Arg  Leu Leu Pro Arg Gly  Gly Arg Phe Val Glu  Met Gly Lys
    2135                 2140                 2145

Ala Asp  Ile Arg Asp Ala Glu  Arg Val Ala Ala Asp  His Pro Gly
    2150                 2155                 2160

Val Thr  Tyr Arg Ser Phe Asp  Leu Leu Glu Ala Gly  Leu Asp Arg
    2165                 2170                 2175

Phe Gln  Glu Ile Leu Thr Glu  Val Val Arg Leu Phe  Glu Arg Gly
    2180                 2185                 2190

Val Leu  Arg His Leu Pro Val  Thr Ala Trp Asp Val  Arg Arg Ala
    2195                 2200                 2205

Ala Glu  Ala Phe Arg Phe Val  Ser Gln Ala Arg His  Val Gly Lys
    2210                 2215                 2220

Asn Val  Leu Val Met Pro Arg  Val Trp Asp Arg Asp  Gly Thr Val
    2225                 2230                 2235

Leu Ile  Thr Gly Gly Thr Gly  Ala Leu Gly Ala Leu  Val Ala Arg
    2240                 2245                 2250
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His Leu  Val Ala Glu His Gly  Met Arg Asn Val Leu  Leu Ala Gly
    2255                 2260                 2265

Arg Arg  Gly Val Asp Ala Pro  Gly Ala Arg Glu Leu  Leu Ala Glu
    2270                 2275                 2280

Leu Glu  Thr Ala Gly Ala Gln  Val Ser Val Val Ala  Cys Asp Val
    2285                 2290                 2295

Ala Asp  Arg Asp Ala Val Ala  Glu Leu Ile Ala Lys  Val Pro Val
    2300                 2305                 2310

Glu His  Pro Leu Thr Ala Val  Val His Thr Ala Gly  Val Val Ala
    2315                 2320                 2325

Asp Ala  Thr Leu Thr Ala Leu  Asp Ala Glu Arg Val  Asp Thr Val
    2330                 2335                 2340

Leu Arg  Ala Lys Val Asp Ala  Val Leu His Leu His  Glu Ala Thr
    2345                 2350                 2355

Arg Gly  Leu Asp Leu Ala Gly  Phe Val Leu Phe Ser  Ser Ala Ser
    2360                 2365                 2370

Gly Ile  Phe Gly Ser Pro Gly  Gln Gly Asn Tyr Ala  Ala Ala Asn
    2375                 2380                 2385

Ser Phe  Ile Asp Ala Phe Ala  His His Arg Arg Ala  Gln Gly Leu
    2390                 2395                 2400

Pro Ala  Leu Ser Leu Ala Trp  Gly Leu Trp Ala Arg  Thr Ser Gly
    2405                 2410                 2415

Met Ala  Gly Gln Leu Gly His  Asp Asp Val Ala Arg  Ile Ser Arg
    2420                 2425                 2430

Thr Gly  Leu Ala Pro Ile Thr  Asp Asp Gln Gly Met  Ala Leu Leu
    2435                 2440                 2445

Asp Ala  Ala Leu Gly Ala Gly  Arg Pro Leu Leu Val  Pro Val Arg
    2450                 2455                 2460

Leu Asp  Arg Ala Ala Leu Arg  Ser Gln Ala Thr Ala  Gly Thr Leu
    2465                 2470                 2475

Pro Pro  Ile Leu Arg Gly Leu  Val Arg Ala Thr Val  Arg Arg Ala
    2480                 2485                 2490

Ala Ser  Thr Ala Ala Ala Gln  Gly Pro Ser Leu Ala  Glu Arg Leu
    2495                 2500                 2505

Ala Gly  Leu Pro Val Thr Glu  His Glu Arg Ile Val  Val Glu Leu
    2510                 2515                 2520

Val Arg  Ala Asp Leu Ala Ala  Val Leu Gly His Ala  Ser Ala Glu
    2525                 2530                 2535

Arg Val  Pro Ala Asp Gln Ala  Phe Ala Glu Leu Gly  Val Asp Ser
    2540                 2545                 2550

Leu Thr  Ala Val Glu Leu Arg  Asn Arg Leu Asn Gly  Ala Thr Gly
    2555                 2560                 2565

Leu Arg  Leu Ala Ala Ser Leu  Val Phe Asp Tyr Pro  Thr Pro Asn
    2570                 2575                 2580

Ala Leu  Ala Thr His Ile Leu  Asp Glu Leu Ala Leu  Asp Thr Ala
    2585                 2590                 2595

Gly Ala  Gly Ala Ala Gly Glu  Pro Asp Gly Pro Ala  Pro Ala Pro
    2600                 2605                 2610

Ala Asp  Glu Ala Arg Phe Arg  Arg Val Ile Asn Ser  Ile Pro Leu
    2615                 2620                 2625

Asp Arg  Ile Arg Arg Ala Gly  Leu Leu Asp Ala Leu  Leu Gly Leu
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    2630                2635                2640

Ala Gly  Thr Ser Ala Asp Thr  Ala Ala Ser Asp Asp  Phe Asp Gln
    2645                2650                2655

Glu Glu  Asp Gly Pro Ala Ile  Ala Ser Met Asp Val  Asp Asp Leu
    2660                2665                2670

Val Arg  Ile Ala Leu Gly Glu  Ser Asp Thr Thr Ala  Asp Ile Thr
    2675                2680                2685

Glu Gly  Thr Asp Arg Ser
    2690
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<210> SEQ ID NO 4
<211> LENGTH: 2227
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: KS domain from IdmP and AT-TE domains from CurM

<400> SEQUENCE: 4

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Met Ser Ser Ala Ser Ser Glu Lys Ile Val Glu Ala Leu Arg Ala Ser
1               5                   10                  15

Leu Thr Glu Asn Glu Arg Leu Arg Arg Leu Asn Gln Glu Leu Ala Ala
            20                  25                  30

Ala Ala His Glu Pro Val Ala Ile Val Ser Met Ala Cys Arg Phe Pro
        35                  40                  45

Gly Gly Val Glu Ser Pro Glu Asp Phe Trp Asp Leu Ile Ser Glu Gly
    50                  55                  60

Arg Asp Ala Val Ser Gly Leu Pro Asp Asn Arg Gly Trp Asp Leu Asp
65                  70                  75                  80

Ala Leu Tyr Asp Pro Asp Pro Glu Ala Gln Gly Lys Thr Tyr Val Arg
                85                  90                  95

Glu Gly Ala Phe Leu Tyr Asp Ala Ala Glu Phe Asp Ala Glu Leu Phe
            100                 105                 110

Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu
        115                 120                 125

Leu Met Glu Thr Ser Trp Glu Val Leu Glu Arg Ala Gly Ile Arg Pro
    130                 135                 140

Asp Ser Leu Arg Gly Lys Pro Val Gly Val Phe Thr Gly Gly Ile Thr
145                 150                 155                 160

Ser Asp Tyr Val Thr Arg His Tyr Ala Ser Gly Thr Ala Pro Gln Leu
                165                 170                 175

Pro Ser Gly Val Glu Ser His Phe Met Thr Gly Ser Ala Gly Ser Val
            180                 185                 190

Phe Ser Gly Arg Ile Ala Tyr Thr Tyr Gly Phe Glu Gly Pro Ala Val
        195                 200                 205

Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Met Ala
    210                 215                 220

Ala Gln Ser Leu Arg Gln Gly Glu Cys Ser Leu Ala Phe Ala Gly Gly
225                 230                 235                 240

Val Ala Val Leu Pro Asn Pro Gly Thr Phe Val Gly Phe Ser Arg Gln
                245                 250                 255

Arg Ala Leu Ser Pro Asp Gly Arg Cys Lys Ala Phe Ser Ala Asp Ala
            260                 265                 270

Asp Gly Thr Gly Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Lys
        275                 280                 285
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Leu Ser Asp Ala Arg Arg Asn Gly His Pro Val Leu Ala Ile Leu Arg
    290                 295                 300

Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro
305                 310                 315                 320

Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Ala Ala Leu Ala Asn Ala
                325                 330                 335

Arg Leu Ser Pro Asp Asp Val Asp Val Val Glu Ala His Gly Thr Gly
            340                 345                 350

Thr Pro Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Gln Ala Thr Tyr
        355                 360                 365

Gly Arg Ser Arg Ser Ala Glu Arg Pro Leu Trp Leu Gly Ser Val Lys
    370                 375                 380

Ser Asn Val Ala His Ala Gln Ala Ala Ala Gly Val Ala Ser Val Ile
385                 390                 395                 400

Lys Val Val Met Ala Leu Arg His Arg Leu Leu Pro Lys Thr Leu His
                405                 410                 415

Ala Asp Glu Arg Ser Pro His Ile Asp Trp His Ser Gly Ala Val Glu
            420                 425                 430

Leu Leu Thr Glu Ala Arg Glu Trp Ser Arg Thr Glu Gly Arg Ala Arg
        435                 440                 445

Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val
    450                 455                 460

Ile Ile Glu Glu Ala Pro Glu Leu Ile Lys Gly Gln Lys Ala Lys Gly
465                 470                 475                 480

Lys Ser Glu Asn Asp Leu Glu Arg Pro Leu His Ile Leu Thr Leu Ser
                485                 490                 495

Thr Lys Thr Glu Lys Ala Leu Glu Glu Leu Val Ser Arg Tyr Gln Asn
            500                 505                 510

His Trp Glu Thr Tyr Pro Glu Leu Ala Ile Ser Asp Val Cys Tyr Thr
        515                 520                 525

Ala Asn Thr Gly Arg Ala Gln Phe Asn His Arg Leu Ala Val Ile Ala
    530                 535                 540

Ser Gly Ser Glu Glu Leu Thr Gln Lys Leu Arg Gln His Thr Ala Gly
545                 550                 555                 560

Glu Glu Val Val Gly Val Phe Ser Gly Lys Val Pro Asn Ser Gly Ser
                565                 570                 575

Glu Ser Lys Val Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln Tyr Leu
            580                 585                 590

Asn Met Gly Arg Gln Leu Tyr Glu Thr Gln Pro Thr Phe Arg Gln Ala
        595                 600                 605

Leu Asp Thr Cys Asp His Ile Leu Arg Pro Tyr Leu Asp Asn Pro Leu
    610                 615                 620

Leu Glu Ile Leu Tyr Pro Gln Asp Ala Gln Lys Ser Asn Asp Ser Pro
625                 630                 635                 640

Leu Asp Gln Thr Gly Tyr Thr Gln Pro Ala Leu Phe Ser Ile Glu Tyr
                645                 650                 655

Ala Leu Leu Lys Leu Trp Glu Ser Trp Gly Ile Lys Pro Asn Val Val
            660                 665                 670

Met Gly His Ser Val Gly Glu Tyr Val Ala Ala Thr Val Ala Gly Val
        675                 680                 685

Phe Ser Leu Glu Asp Gly Leu Lys Leu Ile Ala Ala Arg Gly Arg Leu
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    690                 695                 700

Met Gln Gly Leu Pro Ala Gly Gly Glu Met Val Ser Val Met Ala Ser
705                 710                 715                 720

Glu Ser Lys Val Leu Glu Thr Leu Lys Ala Met Ser Leu Glu Asp Lys
                725                 730                 735

Val Ala Ile Ala Ala Ile Asn Gly Pro Glu Ser Ile Val Ile Ser Gly
            740                 745                 750

Glu Ala Glu Ala Ile Arg Ala Met Ala Thr His Leu Glu Ser Val Gly
        755                 760                 765

Ile Lys Thr Lys Gln Leu Gln Val Ser His Ala Phe His Ser Pro Leu
    770                 775                 780

Met Glu Pro Met Leu Ala Glu Phe Glu Ala Val Ala Asn Gln Ile Thr
785                 790                 795                 800

Tyr His Gln Pro Arg Ile Pro Ile Ile Ser Asn Val Thr Gly Thr Lys
                805                 810                 815

Ala Asp Lys Ser Ile Ala Thr Ala Gln Tyr Trp Val Asn His Val Arg
            820                 825                 830

Gln Pro Val Arg Phe Ala Gln Gly Met Ala Thr Leu His Gln Gln Gly
        835                 840                 845

Tyr Glu Thr Phe Leu Glu Ile Gly Ala Lys Pro Ile Leu Leu Gly Met
    850                 855                 860

Gly Lys Gln Cys Leu Ser Pro Asp Val Gly Val Trp Leu Pro Ser Leu
865                 870                 875                 880

Arg His Gly Val Asp Glu Trp Gln Gln Ile Leu Ser Ser Leu Gly Gln
                885                 890                 895

Leu Tyr Val Gln Gly Ala Lys Val Asp Trp Ser Gly Phe Asp Arg Asp
            900                 905                 910

Tyr Ser Arg Glu Lys Val Val Leu Pro Thr Tyr Pro Phe Gln Arg Glu
        915                 920                 925

Arg Tyr Trp Val Glu Thr Ser Ile Asn Gln Gln Gln Val Val Cys Ser
    930                 935                 940

Gly Glu Pro Asn Leu Gln Gly Thr Pro Glu Gly Thr Ser Thr Thr Ile
945                 950                 955                 960

Val Lys Leu Leu Ser Gln Gly Asn Thr Lys Glu Leu Ala Glu Lys Val
                965                 970                 975

Glu Lys Thr Ser Asp Leu Pro Pro Glu Gln Leu Lys Leu Leu Pro Asp
            980                 985                 990

Leu Leu Ala Ser Leu Ser Gln Gln  His Gln Gln Glu Leu  Ala Arg Leu
        995                 1000                1005

Thr Thr  Lys Lys Trp Phe Tyr  Lys Val Gln Trp Ile  Ser Gln Ala
    1010                1015                1020

Ile Lys  Pro Gln Arg Asn Lys  Ser Asn Asn Gln Val  Cys His Trp
    1025                1030                1035

Leu Ile  Leu Thr Asp Ser Lys  Gly Leu Gly Lys Ser  Leu Ala Thr
    1040                1045                1050

His Leu  Gln Gln Leu Gly Asn  Glu Cys Ser Val Val  Tyr Gln Ala
    1055                1060                1065

Asp Asn  Tyr Gln Asn Tyr Glu  Pro Gly Ile Tyr His  Ile Asn Pro
    1070                1075                1080

Ser His  Pro Gln Glu Phe Glu  Gln Val Tyr Gln Thr  Ile Phe Glu
    1085                1090                1095
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Asn Gly  Lys Leu Pro Leu Gln  Lys Val Ile His Leu  Trp Ser Leu
    1100                 1105                 1110

Asp Thr  Ala Ser Glu Gln Asp  Leu Thr Thr Glu Thr  Leu Glu Gln
    1115                 1120                 1125

Ala Gln  Leu Trp Gly Cys Gly  Ser Thr Leu His Leu  Leu Gln Thr
    1130                 1135                 1140

Leu Val  Lys Asn Pro Asn Ser  Thr Pro Pro Lys Leu  Trp Met Ile
    1145                 1150                 1155

Thr Arg  Gly Thr Gln Pro Val  Leu Ser Pro Thr Glu  Lys Leu Thr
    1160                 1165                 1170

Val Ala  Thr Ser Pro Leu Trp  Gly Leu Gly Arg Thr  Ile Ala Ser
    1175                 1180                 1185

Glu His  Pro Gln Leu Trp Gly  Gly Leu Val Asp Leu  Asp Pro Gln
    1190                 1195                 1200

Gly Ser  Glu Asp Glu Val Glu  Val Leu Leu Gln Gln  Ile Ile Asp
    1205                 1210                 1215

Ser Gln  Lys Glu Asp His Leu  Ala Val Arg Asn Arg  Lys Ile Tyr
    1220                 1225                 1230

Val Ala  Arg Leu Leu Lys His  Ile Pro Gln Glu Ser  Gln Pro Leu
    1235                 1240                 1245

Ser Leu  Arg Ser Asp Ala Thr  Tyr Leu Ile Thr Gly  Gly Leu Gly
    1250                 1255                 1260

Ala Leu  Gly Leu Lys Thr Ala  Ala Trp Met Ala Glu  Lys Gly Ala
    1265                 1270                 1275

Arg Asn  Leu Val Leu Ile Ser  Arg Arg Gln Pro Ser  Glu Gln Ala
    1280                 1285                 1290

Gln Gln  Thr Ile Gln Ser Leu  Glu Glu Leu Gly Thr  Gln Val Lys
    1295                 1300                 1305

Val Leu  Ser Ala Asp Ile Ser  Val Glu Ser Asp Val  Ala Asn Ile
    1310                 1315                 1320

Leu Glu  Gln Ile Gln Thr Ser  Leu Pro Pro Leu Leu  Gly Val Ile
    1325                 1330                 1335

His Ala  Ala Gly Val Leu Asp  Asp Gly Leu Leu Gln  Gln Thr Asn
    1340                 1345                 1350

Trp Glu  Arg Phe Thr Lys Val  Met Ala Pro Lys Val  Asn Gly Thr
    1355                 1360                 1365

Trp Asn  Leu His Lys Leu Thr  Gln His Leu Ser Leu  Asp Phe Phe
    1370                 1375                 1380

Val Cys  Phe Ser Ser Met Ser  Ser Leu Leu Gly Ser  Pro Gly Gln
    1385                 1390                 1395

Gly Asn  Tyr Ala Ala Ala Asn  Ala Phe Met Asp Ala  Val Val His
    1400                 1405                 1410

Tyr Arg  Arg Glu Met Gly Leu  Pro Gly Leu Ser Ile  Asn Trp Gly
    1415                 1420                 1425

Gly Trp  Ser Glu Gly Gly Met  Ala Thr Arg Leu Ala  Ser Gln His
    1430                 1435                 1440

Gln Asn  Arg Met Gln Thr Ala  Gly Ile Ser Leu Ile  Ser Pro Glu
    1445                 1450                 1455

Gln Gly  Ile Gln Val Leu Glu  Glu Leu Val Arg Thr  Gln Ser Thr
    1460                 1465                 1470

Ala Gln  Val Gly Val Leu Pro  Val Asp Trp Ser Val  Leu Ala Lys
    1475                 1480                 1485
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Gln Phe  Ser Ser Ala Asn Pro  Ser Ser Leu Leu Leu  Glu Leu Leu
    1490                 1495                 1500

Gln Gln  Glu Thr Ser Ser Glu  Lys Thr Asp Glu Arg  Ile Leu Glu
    1505                 1510                 1515

Lys Leu  Gln Ala Ala Pro Ile  Thr Glu Arg Gln Asp  Ile Leu Lys
    1520                 1525                 1530

Asn Tyr  Ile Gln Leu Val Val  Ala Lys Thr Leu Gly  Ile Asn Pro
    1535                 1540                 1545

Ser Lys  Ile Ser Thr Asp Asp  Asn Phe Val Glu Leu  Gly Met Asp
    1550                 1555                 1560

Ser Leu  Met Gly Met Glu Val  Val Asn Lys Leu Ser  Gly Asp Leu
    1565                 1570                 1575

Asp Phe  Ile Ile Tyr Pro Arg  Glu Phe Tyr Glu Arg  Pro Thr Ile
    1580                 1585                 1590

Asp Ser  Leu Thr Gln Tyr Leu  Ser Ala Glu Leu Ser  Glu Asp Asn
    1595                 1600                 1605

Leu Ala  Thr Gln Pro Ser Pro  Thr Ser Leu Glu Ile  Phe Ala Thr
    1610                 1615                 1620

Lys Ser  Ser Pro Ser Gly Asn  Ser Ala Arg Pro Ala  Ser Val Ser
    1625                 1630                 1635

Ser Arg  Leu Pro Gly Ile Ile  Phe Ile Leu Ser Ser  Pro Arg Ser
    1640                 1645                 1650

Gly Ser  Thr Leu Leu Arg Val  Met Leu Ala Gly His  Ser Ser Leu
    1655                 1660                 1665

Phe Ser  Pro Pro Glu Leu His  Leu Leu Pro Phe Asn  Thr Met Lys
    1670                 1675                 1680

Glu Arg  Gln Glu Gln Leu Asn  Leu Ser Tyr Leu Gly  Glu Gly Leu
    1685                 1690                 1695

Gln Lys  Thr Phe Met Glu Val  Lys Asn Leu Asp Ala  Thr Ala Ser
    1700                 1705                 1710

Gln Ala  Leu Ile Lys Asp Leu  Glu Ser Gln Asn Leu  Ser Ile Gln
    1715                 1720                 1725

Gln Val  Tyr Gly Met Leu Gln  Glu Asn Ile Ala Pro  Arg Leu Leu
    1730                 1735                 1740

Val Asp  Lys Ser Pro Thr Tyr  Ala Met Glu Pro Thr  Ile Leu Glu
    1745                 1750                 1755

Arg Gly  Glu Ala Leu Phe Ala  Asn Ser Lys Tyr Ile  Tyr Leu Val
    1760                 1765                 1770

Arg His  Pro Tyr Ser Val Ile  Glu Ser Phe Val Arg  Met Arg Met
    1775                 1780                 1785

Gln Lys  Leu Val Gly Leu Gly  Glu Glu Asn Pro Tyr  Arg Val Ala
    1790                 1795                 1800

Glu Gln  Val Trp Ala Lys Ser  Asn Gln Asn Ile Leu  Asn Phe Leu
    1805                 1810                 1815

Ser Gln  Leu Glu Pro Glu Arg  Gln His Gln Ile Arg  Tyr Glu Asp
    1820                 1825                 1830

Leu Val  Lys Lys Pro Gln Gln  Val Leu Ser Gln Leu  Cys Asp Phe
    1835                 1840                 1845

Leu Asn  Val Pro Phe Glu Pro  Glu Leu Leu Gln Pro  Tyr Gln Gly
    1850                 1855                 1860

Asp Arg  Met Thr Gly Gly Val  His Gln Lys Ser Leu  Ser Ile Ser
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    1865                1870                1875

Asp Pro  Asn Phe Leu Lys His  Asn Thr Ile Asp Glu  Ser Leu Ala
    1880                1885                1890

Asp Lys  Trp Lys Thr Ile Gln  Leu Pro Tyr Pro Leu  Lys Ser Glu
    1895                1900                1905

Thr Gln  Arg Ile Ala Ser Gln  Leu Ser Tyr Glu Leu  Pro Asn Leu
    1910                1915                1920

Val Thr  Thr Pro Thr Asn Gln  Gln Pro Gln Val Ser  Thr Thr Pro
    1925                1930                1935

Ser Thr  Glu Gln Pro Ile Met  Glu Glu Lys Phe Leu  Glu Phe Gly
    1940                1945                1950

Gly Asn  Gln Ile Cys Leu Cys  Ser Trp Gly Ser Pro  Glu His Pro
    1955                1960                1965

Val Val  Leu Cys Ile His Gly  Ile Leu Glu Gln Gly  Leu Ala Trp
    1970                1975                1980

Gln Glu  Val Ala Leu Pro Leu  Ala Ala Gln Gly Tyr  Arg Val Val
    1985                1990                1995

Ala Pro  Asp Leu Phe Gly His  Gly Arg Ser Ser His  Leu Glu Met
    2000                2005                2010

Val Thr  Ser Tyr Ser Ser Leu  Thr Phe Leu Ala Gln  Ile Asp Arg
    2015                2020                2025

Val Ile  Gln Glu Leu Pro Asp  Gln Pro Leu Leu Leu  Val Gly His
    2030                2035                2040

Ser Met  Gly Ala Met Leu Ala  Thr Ala Ile Ala Ser  Val Arg Pro
    2045                2050                2055

Lys Lys  Ile Lys Glu Leu Ile  Leu Val Glu Leu Pro  Leu Pro Ala
    2060                2065                2070

Glu Glu  Ser Lys Lys Glu Ser  Ala Val Asn Gln Leu  Thr Thr Cys
    2075                2080                2085

Leu Asp  Tyr Leu Ser Ser Thr  Pro Gln His Pro Ile  Phe Pro Asp
    2090                2095                2100

Val Ala  Thr Ala Ala Ser Arg  Leu Arg Gln Ala Ile  Pro Ser Leu
    2105                2110                2115

Ser Glu  Glu Phe Ser Tyr Ile  Leu Ala Gln Arg Ile  Thr Gln Pro
    2120                2125                2130

Asn Gln  Gly Gly Val Arg Trp  Ser Trp Asp Ala Ile  Ile Arg Thr
    2135                2140                2145

Arg Ser  Ile Leu Gly Leu Asn  Asn Leu Pro Gly Gly  Arg Ser Gln
    2150                2155                2160

Tyr Leu  Glu Met Leu Lys Ser  Ile Gln Val Pro Thr  Thr Leu Val
    2165                2170                2175

Tyr Gly  Asp Ser Ser Lys Leu  Asn Arg Pro Glu Asp  Leu Gln Gln
    2180                2185                2190

Gln Lys  Met Thr Met Thr Gln  Ala Lys Arg Val Phe  Leu Ser Gly
    2195                2200                2205

Gly His  Asn Leu His Ile Asp  Ala Ala Ala Ala Leu  Ala Ser Leu
    2210                2215                2220

Ile Leu  Thr Ser
    2225
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<210> SEQ ID NO 5
<211> LENGTH: 2740

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<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Hybrid polyketide synthase capable of producing butene

<400> SEQUENCE: 5

Met Ala Asp Leu Ser Lys Leu Ser Asp Ser Arg Thr Ala Gln Pro Gly
1 5 10 15

Arg Ile Val Arg Pro Trp Pro Leu Ser Gly Cys Asn Glu Ser Ala Leu
20 25 30

Arg Ala Arg Ala Arg Gln Leu Arg Ala His Leu Asp Arg Phe Pro Asp
35 40 45

Ala Gly Val Glu Gly Val Gly Ala Ala Leu Ala His Asp Glu Gln Ala
50 55 60

Asp Ala Gly Pro His Arg Ala Val Val Val Ala Ser Ser Thr Ser Glu
65 70 75 80

Leu Leu Asp Gly Leu Ala Ala Val Ala Asp Gly Arg Pro His Ala Ser
85 90 95

Val Val Arg Gly Val Ala Arg Pro Ser Ala Pro Val Val Phe Val Phe
100 105 110

Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala Gly Glu Leu Leu Gly
115 120 125

Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala Cys Ala Arg Ala Phe
130 135 140

Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val Leu Asp Ser Pro Glu
145 150 155 160

Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala Leu Phe Ala Val Gln
165 170 175

Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly Val Thr Pro Asp Ala
180 185 190

Val Val Gly His Ser Ile Gly Glu Leu Ala Ala Ala His Val Cys Gly
195 200 205

Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala Ala Leu Trp Ser Arg
210 215 220

Glu Met Ile Pro Leu Val Gly Asn Gly Asp Met Ala Ala Val Ala Leu
225 230 235 240

Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg Trp Asp Asp Asp Val
245 250 255

Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu Leu Thr Gly Ser
260 265 270

Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser Ala Glu Gly Val
275 280 285

Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His Ser Ala Gln Val
290 295 300

Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala Trp Phe Ala Pro
305 310 315 320

Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr Gly Gly Ala Val
325 330 335

Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg Ser Phe Arg Leu
340 345 350

Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu Glu Val Gly Pro
355 360 365

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Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Leu Ala Ala Ala Leu
    370                 375                 380

Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala Val Val Pro Thr
385                 390                 395                 400

Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu Leu Ala Ala Ala
                405                 410                 415

Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr Ala Ala Tyr Asp
            420                 425                 430

Asp Val Gly Ala Glu Pro Gly Ser Leu Pro Glu Phe Ala Pro Ala Glu
        435                 440                 445

Glu Glu Asp Glu Pro Ala Glu Ser Gly Val Asp Trp Asn Ala Pro Pro
    450                 455                 460

His Val Leu Arg Glu Arg Leu Leu Ala Val Val Asn Gly Glu Thr Ala
465                 470                 475                 480

Ala Leu Ala Gly Arg Glu Ala Asp Ala Glu Ala Thr Phe Arg Glu Leu
                485                 490                 495

Gly Leu Asp Ser Val Leu Ala Ala Gln Leu Arg Ala Lys Val Ser Ala
            500                 505                 510

Ala Ile Gly Arg Glu Val Asn Ile Ala Leu Leu Tyr Asp His Pro Thr
        515                 520                 525

Pro Arg Ala Leu Ala Glu Ala Leu Ser Ser Gly Thr Glu Val Ala Gln
    530                 535                 540

Arg Glu Thr Arg Ala Arg Thr Asn Glu Ala Ala Pro Gly Glu Pro Ile
545                 550                 555                 560

Ala Val Val Ala Met Ala Cys Arg Leu Pro Gly Gly Val Ser Thr Pro
                565                 570                 575

Glu Glu Phe Trp Glu Leu Leu Ser Glu Gly Arg Asp Ala Val Ala Gly
            580                 585                 590

Leu Pro Thr Asp Arg Gly Trp Asp Leu Asp Ser Leu Phe His Pro Asp
        595                 600                 605

Pro Thr Arg Ser Gly Thr Ala His Gln Arg Gly Gly Gly Phe Leu Thr
    610                 615                 620

Glu Ala Thr Ala Phe Asp Pro Ala Phe Phe Gly Met Ser Pro Arg Glu
625                 630                 635                 640

Ala Leu Ala Val Asp Pro Gln Gln Arg Leu Met Leu Glu Leu Ser Trp
                645                 650                 655

Glu Val Leu Glu Arg Ala Gly Ile Pro Pro Thr Ser Leu Gln Ala Ser
            660                 665                 670

Pro Thr Gly Val Phe Val Gly Leu Ile Pro Gln Glu Tyr Gly Pro Arg
        675                 680                 685

Leu Ala Glu Gly Gly Glu Gly Val Glu Gly Tyr Leu Met Thr Gly Thr
    690                 695                 700

Thr Thr Ser Val Ala Ser Gly Arg Ile Ala Tyr Thr Leu Gly Leu Glu
705                 710                 715                 720

Gly Pro Ala Ile Ser Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
                725                 730                 735

Val His Leu Ala Cys Gln Ser Leu Arg Arg Gly Glu Ser Ser Leu Ala
            740                 745                 750

Met Ala Gly Gly Val Thr Val Met Pro Thr Pro Gly Met Leu Val Asp
        755                 760                 765

Phe Ser Arg Met Asn Ser Leu Ala Pro Asp Gly Arg Cys Lys Ala Phe
    770                 775                 780
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Ser Ala Gly Ala Asn Gly Phe Gly Met Ala Glu Gly Ala Gly Met Leu
785                 790                 795                 800

Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Pro Val Leu
                805                 810                 815

Ala Val Leu Arg Gly Thr Ala Val Asn Ser Asp Gly Ala Ser Asn Gly
            820                 825                 830

Leu Ser Ala Pro Asn Gly Arg Ala Gln Val Arg Val Ile Gln Gln Ala
        835                 840                 845

Leu Ala Glu Ser Gly Leu Gly Pro Ala Asp Ile Asp Ala Val Glu Ala
    850                 855                 860

His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Arg Ala Leu
865                 870                 875                 880

Phe Glu Ala Tyr Gly Arg Asp Arg Glu Gln Pro Leu His Leu Gly Ser
                885                 890                 895

Val Lys Ser Asn Leu Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly
            900                 905                 910

Val Ile Lys Met Val Leu Ala Met Arg Ala Gly Thr Leu Pro Arg Thr
        915                 920                 925

Leu His Ala Ser Glu Arg Ser Lys Glu Ile Asp Trp Ser Ser Gly Ala
    930                 935                 940

Ile Ser Leu Leu Asp Glu Pro Glu Pro Trp Pro Ala Gly Ala Arg Pro
945                 950                 955                 960

Arg Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His
                965                 970                 975

Ala Ile Ile Glu Glu Ala Pro Glu Leu Ile Lys Gly Gln Lys Ala Lys
            980                 985                 990

Gly Lys Ser Glu Asn Asp Leu Glu  Arg Pro Leu His Ile  Leu Thr Leu
        995                 1000                1005

Ser Thr  Lys Thr Glu Lys Ala  Leu Glu Glu Leu Val  Ser Arg Tyr
    1010                1015                1020

Gln Asn  His Trp Glu Thr Tyr  Pro Glu Leu Ala Ile  Ser Asp Val
    1025                1030                1035

Cys Tyr  Thr Ala Asn Thr Gly  Arg Ala Gln Phe Asn  His Arg Leu
    1040                1045                1050

Ala Val  Ile Ala Ser Gly Ser  Glu Glu Leu Thr Gln  Lys Leu Arg
    1055                1060                1065

Gln His  Thr Ala Gly Glu Glu  Val Val Gly Val Phe  Ser Gly Lys
    1070                1075                1080

Val Pro  Asn Ser Gly Ser Glu  Ser Lys Val Ala Phe  Leu Phe Thr
    1085                1090                1095

Gly Gln  Gly Ser Gln Tyr Leu  Asn Met Gly Arg Gln  Leu Tyr Glu
    1100                1105                1110

Thr Gln  Pro Thr Phe Arg Gln  Ala Leu Asp Thr Cys  Asp His Ile
    1115                1120                1125

Leu Arg  Pro Tyr Leu Asp Asn  Pro Leu Leu Glu Ile  Leu Tyr Pro
    1130                1135                1140

Gln Asp  Ala Gln Lys Ser Asn  Asp Ser Pro Leu Asp  Gln Thr Gly
    1145                1150                1155

Tyr Thr  Gln Pro Ala Leu Phe  Ser Ile Glu Tyr Ala  Leu Leu Lys
    1160                1165                1170

Leu Trp  Glu Ser Trp Gly Ile  Lys Pro Asn Val Val  Met Gly His
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    1175                1180                1185

Ser Val  Gly Glu Tyr Val Ala  Ala Thr Val Ala Gly  Val Phe Ser
    1190                1195                1200

Leu Glu  Asp Gly Leu Lys Leu  Ile Ala Ala Arg Gly  Arg Leu Met
    1205                1210                1215

Gln Gly  Leu Pro Ala Gly Gly  Glu Met Val Ser Val  Met Ala Ser
    1220                1225                1230

Glu Ser  Lys Val Leu Glu Thr  Leu Lys Ala Met Ser  Leu Glu Asp
    1235                1240                1245

Lys Val  Ala Ile Ala Ala Ile  Asn Gly Pro Glu Ser  Ile Val Ile
    1250                1255                1260

Ser Gly  Glu Ala Glu Ala Ile  Arg Ala Met Ala Thr  His Leu Glu
    1265                1270                1275

Ser Val  Gly Ile Lys Thr Lys  Gln Leu Gln Val Ser  His Ala Phe
    1280                1285                1290

His Ser  Pro Leu Met Glu Pro  Met Leu Ala Glu Phe  Glu Ala Val
    1295                1300                1305

Ala Asn  Gln Ile Thr Tyr His  Gln Pro Arg Ile Pro  Ile Ile Ser
    1310                1315                1320

Asn Val  Thr Gly Thr Lys Ala  Asp Lys Ser Ile Ala  Thr Ala Gln
    1325                1330                1335

Tyr Trp  Val Asn His Val Arg  Gln Pro Val Arg Phe  Ala Gln Gly
    1340                1345                1350

Met Ala  Thr Leu His Gln Gln  Gly Tyr Glu Thr Phe  Leu Glu Ile
    1355                1360                1365

Gly Ala  Lys Pro Ile Leu Leu  Gly Met Gly Lys Gln  Cys Leu Ser
    1370                1375                1380

Pro Asp  Val Gly Val Trp Leu  Pro Ser Leu Arg His  Gly Val Asp
    1385                1390                1395

Glu Trp  Gln Gln Ile Leu Ser  Ser Leu Gly Gln Leu  Tyr Val Gln
    1400                1405                1410

Gly Ala  Lys Val Asp Trp Ser  Gly Phe Asp Arg Asp  Tyr Ser Arg
    1415                1420                1425

Glu Lys  Val Val Leu Pro Thr  Tyr Pro Phe Gln Arg  Glu Arg Tyr
    1430                1435                1440

Trp Val  Glu Thr Ser Ile Asn  Gln Gln Gln Val Val  Cys Ser Gly
    1445                1450                1455

Glu Pro  Asn Leu Gln Gly Thr  Pro Glu Gly Thr Ser  Thr Thr Ile
    1460                1465                1470

Val Lys  Leu Leu Ser Gln Gly  Asn Thr Lys Glu Leu  Ala Glu Lys
    1475                1480                1485

Val Glu  Lys Thr Ser Asp Leu  Pro Pro Glu Gln Leu  Lys Leu Leu
    1490                1495                1500

Pro Asp  Leu Leu Ala Ser Leu  Ser Gln Gln His Gln  Gln Glu Leu
    1505                1510                1515

Ala Arg  Leu Thr Thr Lys Lys  Trp Phe Tyr Lys Val  Gln Trp Ile
    1520                1525                1530

Ser Gln  Ala Ile Lys Pro Gln  Arg Asn Lys Ser Asn  Asn Gln Val
    1535                1540                1545

Cys His  Trp Leu Ile Leu Thr  Asp Ser Lys Gly Leu  Gly Lys Ser
    1550                1555                1560
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Leu Ala  Thr His Leu Gln Gln  Leu Gly Asn Glu Cys  Ser Val Val
    1565                 1570                 1575

Tyr Gln  Ala Asp Asn Tyr Gln  Asn Tyr Glu Pro Gly  Ile Tyr His
    1580                 1585                 1590

Ile Asn  Pro Ser His Pro Gln  Glu Phe Glu Gln Val  Tyr Gln Thr
    1595                 1600                 1605

Ile Phe  Glu Asn Gly Lys Leu  Pro Leu Gln Lys Val  Ile His Leu
    1610                 1615                 1620

Trp Ser  Leu Asp Thr Ala Ser  Glu Gln Asp Leu Thr  Thr Glu Thr
    1625                 1630                 1635

Leu Glu  Gln Ala Gln Leu Trp  Gly Cys Gly Ser Thr  Leu His Leu
    1640                 1645                 1650

Leu Gln  Thr Leu Val Lys Asn  Pro Asn Ser Thr Pro  Pro Lys Leu
    1655                 1660                 1665

Trp Met  Ile Thr Arg Gly Thr  Gln Pro Val Leu Ser  Pro Thr Glu
    1670                 1675                 1680

Lys Leu  Thr Val Ala Thr Ser  Pro Leu Trp Gly Leu  Gly Arg Thr
    1685                 1690                 1695

Ile Ala  Ser Glu His Pro Gln  Leu Trp Gly Gly Leu  Val Asp Leu
    1700                 1705                 1710

Asp Pro  Gln Gly Ser Glu Asp  Glu Val Glu Val Leu  Leu Gln Gln
    1715                 1720                 1725

Ile Ile  Asp Ser Gln Lys Glu  Asp His Leu Ala Val  Arg Asn Arg
    1730                 1735                 1740

Lys Ile  Tyr Val Ala Arg Leu  Leu Lys His Ile Pro  Gln Glu Ser
    1745                 1750                 1755

Gln Pro  Leu Ser Leu Arg Ser  Asp Ala Thr Tyr Leu  Ile Thr Gly
    1760                 1765                 1770

Gly Leu  Gly Ala Leu Gly Leu  Lys Thr Ala Ala Trp  Met Ala Glu
    1775                 1780                 1785

Lys Gly  Ala Arg Asn Leu Val  Leu Ile Ser Arg Arg  Gln Pro Ser
    1790                 1795                 1800

Glu Gln  Ala Gln Gln Thr Ile  Gln Ser Leu Glu Glu  Leu Gly Thr
    1805                 1810                 1815

Gln Val  Lys Val Leu Ser Ala  Asp Ile Ser Val Glu  Ser Asp Val
    1820                 1825                 1830

Ala Asn  Ile Leu Glu Gln Ile  Gln Thr Ser Leu Pro  Pro Leu Leu
    1835                 1840                 1845

Gly Val  Ile His Ala Ala Gly  Val Leu Asp Asp Gly  Leu Leu Gln
    1850                 1855                 1860

Gln Thr  Asn Trp Glu Arg Phe  Thr Lys Val Met Ala  Pro Lys Val
    1865                 1870                 1875

Asn Gly  Thr Trp Asn Leu His  Lys Leu Thr Gln His  Leu Ser Leu
    1880                 1885                 1890

Asp Phe  Phe Val Cys Phe Ser  Ser Met Ser Ser Leu  Leu Gly Ser
    1895                 1900                 1905

Pro Gly  Gln Gly Asn Tyr Ala  Ala Ala Asn Ala Phe  Met Asp Ala
    1910                 1915                 1920

Val Val  His Tyr Arg Arg Glu  Met Gly Leu Pro Gly  Leu Ser Ile
    1925                 1930                 1935

Asn Trp  Gly Gly Trp Ser Glu  Gly Gly Met Ala Thr  Arg Leu Ala
    1940                 1945                 1950
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Ser Gln  His Gln Asn Arg Met  Gln Thr Ala Gly Ile  Ser Leu Ile
    1955                 1960                 1965

Ser Pro  Glu Gln Gly Ile Gln  Val Leu Glu Glu Leu  Val Arg Thr
    1970                 1975                 1980

Gln Ser  Thr Ala Gln Val Gly  Val Leu Pro Val Asp  Trp Ser Val
    1985                 1990                 1995

Leu Ala  Lys Gln Phe Ser Ser  Ala Asn Pro Ser Ser  Leu Leu Leu
    2000                 2005                 2010

Glu Leu  Leu Gln Gln Glu Thr  Ser Ser Glu Lys Thr  Asp Glu Arg
    2015                 2020                 2025

Ile Leu  Glu Lys Leu Gln Ala  Ala Pro Ile Thr Glu  Arg Gln Asp
    2030                 2035                 2040

Ile Leu  Lys Asn Tyr Ile Gln  Leu Val Val Ala Lys  Thr Leu Gly
    2045                 2050                 2055

Ile Asn  Pro Ser Lys Ile Ser  Thr Asp Asp Asn Phe  Val Glu Leu
    2060                 2065                 2070

Gly Met  Asp Ser Leu Met Gly  Met Glu Val Val Asn  Lys Leu Ser
    2075                 2080                 2085

Gly Asp  Leu Asp Phe Ile Ile  Tyr Pro Arg Glu Phe  Tyr Glu Arg
    2090                 2095                 2100

Pro Thr  Ile Asp Ser Leu Thr  Gln Tyr Leu Ser Ala  Glu Leu Ser
    2105                 2110                 2115

Glu Asp  Asn Leu Ala Thr Gln  Pro Ser Pro Thr Ser  Leu Glu Ile
    2120                 2125                 2130

Phe Ala  Thr Lys Ser Ser Pro  Ser Gly Asn Ser Ala  Arg Pro Ala
    2135                 2140                 2145

Ser Val  Ser Ser Arg Leu Pro  Gly Ile Ile Phe Ile  Leu Ser Ser
    2150                 2155                 2160

Pro Arg  Ser Gly Ser Thr Leu  Leu Arg Val Met Leu  Ala Gly His
    2165                 2170                 2175

Ser Ser  Leu Phe Ser Pro Pro  Glu Leu His Leu Leu  Pro Phe Asn
    2180                 2185                 2190

Thr Met  Lys Glu Arg Gln Glu  Gln Leu Asn Leu Ser  Tyr Leu Gly
    2195                 2200                 2205

Glu Gly  Leu Gln Lys Thr Phe  Met Glu Val Lys Asn  Leu Asp Ala
    2210                 2215                 2220

Thr Ala  Ser Gln Ala Leu Ile  Lys Asp Leu Glu Ser  Gln Asn Leu
    2225                 2230                 2235

Ser Ile  Gln Gln Val Tyr Gly  Met Leu Gln Glu Asn  Ile Ala Pro
    2240                 2245                 2250

Arg Leu  Leu Val Asp Lys Ser  Pro Thr Tyr Ala Met  Glu Pro Thr
    2255                 2260                 2265

Ile Leu  Glu Arg Gly Glu Ala  Leu Phe Ala Asn Ser  Lys Tyr Ile
    2270                 2275                 2280

Tyr Leu  Val Arg His Pro Tyr  Ser Val Ile Glu Ser  Phe Val Arg
    2285                 2290                 2295

Met Arg  Met Gln Lys Leu Val  Gly Leu Gly Glu Glu  Asn Pro Tyr
    2300                 2305                 2310

Arg Val  Ala Glu Gln Val Trp  Ala Lys Ser Asn Gln  Asn Ile Leu
    2315                 2320                 2325

Asn Phe  Leu Ser Gln Leu Glu  Pro Glu Arg Gln His  Gln Ile Arg
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    2330                2335                2340

Tyr Glu  Asp Leu Val Lys Lys  Pro Gln Gln Val Leu  Ser Gln Leu
    2345                2350                2355

Cys Asp  Phe Leu Asn Val Pro  Phe Glu Pro Glu Leu  Leu Gln Pro
    2360                2365                2370

Tyr Gln  Gly Asp Arg Met Thr  Gly Gly Val His Gln  Lys Ser Leu
    2375                2380                2385

Ser Ile  Ser Asp Pro Asn Phe  Leu Lys His Asn Thr  Ile Asp Glu
    2390                2395                2400

Ser Leu  Ala Asp Lys Trp Lys  Thr Ile Gln Leu Pro  Tyr Pro Leu
    2405                2410                2415

Lys Ser  Glu Thr Gln Arg Ile  Ala Ser Gln Leu Ser  Tyr Glu Leu
    2420                2425                2430

Pro Asn  Leu Val Thr Thr Pro  Thr Asn Gln Gln Pro  Gln Val Ser
    2435                2440                2445

Thr Thr  Pro Ser Thr Glu Gln  Pro Ile Met Glu Glu  Lys Phe Leu
    2450                2455                2460

Glu Phe  Gly Gly Asn Gln Ile  Cys Leu Cys Ser Trp  Gly Ser Pro
    2465                2470                2475

Glu His  Pro Val Val Leu Cys  Ile His Gly Ile Leu  Glu Gln Gly
    2480                2485                2490

Leu Ala  Trp Gln Glu Val Ala  Leu Pro Leu Ala Ala  Gln Gly Tyr
    2495                2500                2505

Arg Val  Val Ala Pro Asp Leu  Phe Gly His Gly Arg  Ser Ser His
    2510                2515                2520

Leu Glu  Met Val Thr Ser Tyr  Ser Ser Leu Thr Phe  Leu Ala Gln
    2525                2530                2535

Ile Asp  Arg Val Ile Gln Glu  Leu Pro Asp Gln Pro  Leu Leu Leu
    2540                2545                2550

Val Gly  His Ser Met Gly Ala  Met Leu Ala Thr Ala  Ile Ala Ser
    2555                2560                2565

Val Arg  Pro Lys Lys Ile Lys  Glu Leu Ile Leu Val  Glu Leu Pro
    2570                2575                2580

Leu Pro  Ala Glu Glu Ser Lys  Lys Glu Ser Ala Val  Asn Gln Leu
    2585                2590                2595

Thr Thr  Cys Leu Asp Tyr Leu  Ser Ser Thr Pro Gln  His Pro Ile
    2600                2605                2610

Phe Pro  Asp Val Ala Thr Ala  Ala Ser Arg Leu Arg  Gln Ala Ile
    2615                2620                2625

Pro Ser  Leu Ser Glu Glu Phe  Ser Tyr Ile Leu Ala  Gln Arg Ile
    2630                2635                2640

Thr Gln  Pro Asn Gln Gly Gly  Val Arg Trp Ser Trp  Asp Ala Ile
    2645                2650                2655

Ile Arg  Thr Arg Ser Ile Leu  Gly Leu Asn Asn Leu  Pro Gly Gly
    2660                2665                2670

Arg Ser  Gln Tyr Leu Glu Met  Leu Lys Ser Ile Gln  Val Pro Thr
    2675                2680                2685

Thr Leu  Val Tyr Gly Asp Ser  Ser Lys Leu Asn Arg  Pro Glu Asp
    2690                2695                2700

Leu Gln  Gln Gln Lys Met Thr  Met Thr Gln Ala Lys  Arg Val Phe
    2705                2710                2715
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Leu Ser  Gly Gly His Asn Leu  His Ile Asp Ala Ala  Ala Ala Leu
    2720                 2725                 2730

Ala Ser  Leu Ile Leu Thr Ser
    2735                 2740


<210> SEQ ID NO 6
<211> LENGTH: 3191
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Hybrid polyketide synthase capable of producing
      propene

<400> SEQUENCE: 6

Met Ala Gly His Gly Asp Ala Thr Ala Gln Lys Ala Gln Asp Ala Glu
1               5                  10                  15

Lys Ser Glu Asp Gly Ser Asp Ala Ile Ala Val Ile Gly Met Ser Cys
            20                  25                  30

Arg Phe Pro Gly Ala Pro Gly Thr Ala Glu Phe Trp Gln Leu Leu Ser
        35                  40                  45

Ser Gly Ala Asp Ala Val Val Thr Ala Ala Asp Gly Arg Arg Arg Gly
    50                  55                  60

Thr Ile Asp Ala Pro Ala Asp Phe Asp Ala Ala Phe Phe Gly Met Ser
65                  70                  75                  80

Pro Arg Glu Ala Ala Ala Thr Asp Pro Gln Gln Arg Leu Val Leu Glu
                85                  90                  95

Leu Gly Trp Glu Ala Leu Glu Asp Ala Gly Ile Val Pro Glu Ser Leu
            100                 105                 110

Arg Gly Glu Ala Ala Ser Val Phe Val Gly Ala Met Asn Asp Asp Tyr
        115                 120                 125

Ala Thr Leu Leu His Arg Ala Gly Ala Pro Thr Asp Thr Tyr Thr Ala
    130                 135                 140

Thr Gly Leu Gln His Ser Met Ile Ala Asn Arg Leu Ser Tyr Phe Leu
145                 150                 155                 160

Gly Leu Arg Gly Pro Ser Leu Val Val Asp Thr Gly Gln Ser Ser Ser
                165                 170                 175

Leu Val Ala Val Ala Leu Ala Val Glu Ser Leu Arg Gly Gly Thr Ser
            180                 185                 190

Gly Ile Ala Leu Ala Gly Gly Val Asn Leu Val Leu Ala Glu Glu Gly
        195                 200                 205

Ser Ala Ala Met Glu Arg Val Gly Ala Leu Ser Pro Asp Gly Arg Cys
    210                 215                 220

His Thr Phe Asp Ala Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly
225                 230                 235                 240

Ala Ile Val Val Leu Lys Pro Leu Ala Asp Ala Leu Ala Asp Gly Asp
                245                 250                 255

Arg Val Tyr Cys Val Val Arg Gly Val Ala Thr Gly Asn Asp Gly Gly
            260                 265                 270

Gly Pro Gly Leu Thr Val Pro Asp Arg Ala Gly Gln Glu Ala Val Leu
        275                 280                 285

Arg Ala Ala Cys Asp Gln Ala Gly Val Arg Pro Ala Asp Val Arg Phe
    290                 295                 300

Val Glu Leu His Gly Thr Gly Thr Pro Ala Gly Asp Pro Val Glu Ala
305                 310                 315                 320
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```
Glu Ala Leu Gly Ala Val Tyr Gly Thr Gly Arg Pro Ala Asn Glu Pro
                325                 330                 335

Leu Leu Val Gly Ser Val Lys Thr Asn Ile Gly His Leu Glu Gly Ala
            340                 345                 350

Ala Gly Ile Ala Gly Phe Val Lys Ala Ala Leu Cys Leu His Glu Arg
        355                 360                 365

Ala Leu Pro Ala Ser Leu Asn Phe Glu Thr Pro Asn Pro Ala Ile Pro
    370                 375                 380

Leu Glu Arg Leu Arg Leu Lys Val Gln Thr Ala His Ala Ala Leu Gln
385                 390                 395                 400

Pro Gly Thr Gly Gly Gly Pro Leu Leu Ala Gly Val Ser Ala Phe Gly
                405                 410                 415

Met Gly Gly Thr Asn Cys His Val Val Leu Glu Glu Thr Pro Gly Gly
            420                 425                 430

Arg Gln Pro Ala Glu Thr Gly Gln Ala Asp Ala Cys Leu Phe Ser Ala
        435                 440                 445

Ser Pro Met Leu Leu Leu Ser Ala Arg Ser Glu Gln Ala Leu Arg Ala
    450                 455                 460

Gln Ala Ala Arg Leu Arg Glu His Leu Glu Asp Ser Gly Ala Asp Pro
465                 470                 475                 480

Leu Asp Ile Ala Tyr Ser Leu Ala Thr Thr Arg Thr Arg Phe Glu His
                485                 490                 495

Arg Ala Ala Val Pro Cys Gly Asp Pro Asp Arg Leu Ser Ser Ala Leu
            500                 505                 510

Ala Ala Leu Ala Ala Gly Gln Thr Pro Arg Gly Val Arg Ile Gly Ser
        515                 520                 525

Thr Asp Ala Asp Gly Arg Leu Ala Leu Leu Phe Thr Gly Gln Gly Ala
    530                 535                 540

Gln His Pro Gly Met Gly Gln Glu Leu Tyr Thr Thr Asp Pro His Phe
545                 550                 555                 560

Ala Ala Ala Leu Asp Glu Val Cys Glu Glu Leu Gln Arg Cys Gly Thr
                565                 570                 575

Gln Asn Leu Arg Glu Val Met Phe Thr Pro Asp Gln Pro Asp Leu Leu
            580                 585                 590

Asp Arg Thr Glu Tyr Thr Gln Pro Ala Leu Phe Ala Leu Gln Thr Ala
        595                 600                 605

Leu Tyr Arg Thr Leu Thr Ala Arg Gly Thr Gln Ala His Leu Val Leu
    610                 615                 620

Gly His Ser Val Gly Glu Ile Thr Ala Ala His Ile Ala Gly Val Leu
625                 630                 635                 640

Asp Leu Pro Asp Ala Ala Arg Leu Ile Thr Ala Arg Ala His Val Met
                645                 650                 655

Gly Gln Leu Pro His Gly Gly Ala Met Leu Ser Val Gln Ala Ala Glu
            660                 665                 670

His Asp Leu Asp Gln Leu Ala His Thr His Gly Val Glu Ile Ala Ala
        675                 680                 685

Val Asn Gly Pro Thr His Cys Val Leu Ser Gly Pro Arg Thr Ala Leu
    690                 695                 700

Glu Glu Thr Ala Gln His Leu Arg Glu Gln Asn Val Arg His Thr Trp
705                 710                 715                 720

Leu Lys Val Ser His Ala Phe His Ser Ala Leu Met Asp Pro Met Leu
                725                 730                 735
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```
Gly Ala Phe Arg Asp Thr Leu Asn Thr Leu Asn Tyr Gln Pro Pro Thr
            740                 745                 750

Ile Pro Leu Ile Ser Asn Leu Thr Gly Gln Ile Ala Asp Pro Asn His
        755                 760                 765

Leu Cys Thr Pro Asp Tyr Trp Ile Asp His Ala Arg His Thr Val Arg
    770                 775                 780

Phe Ala Asp Ala Val Gln Thr Ala His His Gln Gly Thr Thr Thr Tyr
785                 790                 795                 800

Leu Glu Ile Gly Pro His Pro Thr Leu Thr Thr Leu Leu His His Thr
                805                 810                 815

Leu Asp Asn Pro Thr Thr Ile Pro Thr Leu His Arg Glu Arg Pro Glu
            820                 825                 830

Pro Glu Thr Leu Thr Gln Ala Ile Ala Ala Val Gly Val Arg Thr Asp
        835                 840                 845

Gly Ile Asp Trp Ala Val Leu Cys Gly Ala Ser Arg Pro Arg Arg Val
    850                 855                 860

Glu Leu Pro Thr Tyr Ala Phe Gln Arg Arg Thr His Trp Ala Pro Gly
865                 870                 875                 880

Leu Thr Pro Asn His Ala Pro Ala Asp Arg Pro Ala Ala Glu Pro Gln
                885                 890                 895

Arg Ala Met Ala Val Gly Pro Val Ser Arg Glu Ala Leu Val Arg Leu
            900                 905                 910

Val Gly Glu Thr Thr Ala Ser Val Leu Gly Leu Asp Gly Pro Asp Glu
        915                 920                 925

Val Ala Leu Asp Arg Pro Phe Thr Ser Gln Gly Leu Asp Ser Met Thr
    930                 935                 940

Ala Val Glu Leu Ala Gly Leu Leu Gly Thr Ala Ala Gly Val Ala Leu
945                 950                 955                 960

Asp Pro Thr Leu Val Tyr Glu Leu Pro Thr Pro Arg Ala Val Ala Asp
                965                 970                 975

His Leu Ala Lys Thr Leu Leu Gly Glu Ser Ala Ala Asp Ala Asp Gln
            980                 985                 990

Glu Val Asn Gly Arg Thr Gly Glu  Ala Glu Ala Lys Ala  Gly Asp Pro
        995                1000                1005

Ile Ala  Val Ile Gly Ile Gly  Cys Arg Phe Pro Gly  Gly Val Ala
    1010                1015                1020

Thr Pro  Asp Asp Leu Trp Glu  Leu Val Ala Ser Gly  Thr Asp Ala
    1025                1030                1035

Ile Ser  Thr Phe Pro Thr Asp  Arg Gly Trp Asp Leu  Asp Gly Leu
    1040                1045                1050

Tyr Asp  Pro Asp Pro Ser Thr  Pro Gly Lys Ser Tyr  Val Arg His
    1055                1060                1065

Gly Gly  Phe Leu His Asp Ala  Ala Gln Phe Asp Ala  Glu Phe Phe
    1070                1075                1080

Gly Ile  Ser Pro Arg Glu Ala  Thr Ala Met Asp Pro  Gln Gln Arg
    1085                1090                1095

Leu Leu  Leu Glu Thr Ser Trp  Glu Ala Leu Glu Arg  Ala Gly Val
    1100                1105                1110

Val Pro  Glu Ser Leu Arg Gly  Gly Arg Thr Gly Val  Phe Val Gly
    1115                1120                1125

Thr Thr  Ala Pro Glu Tyr Gly  Pro Arg Leu His Glu  Gly Thr Asp
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    1130                1135                1140

Gly Tyr  Glu Gly Phe Leu Leu  Thr Gly Thr Thr Ala  Ser Val Ala
    1145                1150                1155

Ser Gly  Arg Ile Ala Tyr Ala  Leu Gly Thr Arg Gly  Pro Ala Leu
    1160                1165                1170

Thr Val  Asp Thr Ala Cys Ser  Ser Ser Leu Val Ala  Leu His Leu
    1175                1180                1185

Ala Val  Gln Ser Leu Arg Arg  Gly Glu Cys Asp Leu  Ala Leu Ala
    1190                1195                1200

Gly Gly  Thr Thr Val Met Ser  Gly Pro Gly Met Phe  Val Glu Phe
    1205                1210                1215

Ser Arg  Gln Arg Gly Leu Ala  Pro Asp Gly Arg Cys  Lys Ala Phe
    1220                1225                1230

Ser Ala  Asp Ala Asp Gly Thr  Ala Trp Ala Glu Gly  Val Gly Met
    1235                1240                1245

Leu Leu  Val Glu Arg Leu Ser  Asp Ala Glu Arg Leu  Gly His Arg
    1250                1255                1260

Val Leu  Ala Val Val Arg Gly  Thr Ala Val Asn Gln  Asp Gly Ala
    1265                1270                1275

Ser Asn  Gly Leu Thr Ala Pro  Ser Gly Pro Ala Gln  Gln Gln Val
    1280                1285                1290

Ile Arg  Asp Ala Leu Ser Asp  Ala Gly Leu Ser Ala  Asp Asp Ile
    1295                1300                1305

Asp Ala  Val Glu Ala His Gly  Thr Gly Thr Ala Leu  Gly Asp Pro
    1310                1315                1320

Ile Glu  Ala Gly Ala Leu Leu  Ala Thr Tyr Gly His  Pro Lys Arg
    1325                1330                1335

Gln Thr  Pro Val Trp Leu Gly  Ser Leu Lys Ser Asn  Ile Gly His
    1340                1345                1350

Thr Gln  Ala Ala Ala Gly Ile  Ala Gly Ile Ile Lys  Met Val Gln
    1355                1360                1365

Ala Leu  Arg His Asp Thr Leu  Pro Arg Thr Leu His  Ala Asp His
    1370                1375                1380

Pro Ser  Ser Lys Val Asp Trp  Asp Ala Gly Pro Leu  Gln Leu Leu
    1385                1390                1395

Thr Asp  Ala Arg Pro Trp Pro  Ala Asp Pro Asp Arg  Pro Arg Arg
    1400                1405                1410

Ala Gly  Ile Ser Ala Phe Gly  Val Ser Gly Thr Asn  Ala His Val
    1415                1420                1425

Val Leu  Glu Glu Pro Pro Glu  Leu Ile Lys Gly Gln  Lys Ala Lys
    1430                1435                1440

Gly Lys  Ser Glu Asn Asp Leu  Glu Arg Pro Leu His  Ile Leu Thr
    1445                1450                1455

Leu Ser  Thr Lys Thr Glu Lys  Ala Leu Glu Glu Leu  Val Ser Arg
    1460                1465                1470

Tyr Gln  Asn His Trp Glu Thr  Tyr Pro Glu Leu Ala  Ile Ser Asp
    1475                1480                1485

Val Cys  Tyr Thr Ala Asn Thr  Gly Arg Ala Gln Phe  Asn His Arg
    1490                1495                1500

Leu Ala  Val Ile Ala Ser Gly  Ser Glu Glu Leu Thr  Gln Lys Leu
    1505                1510                1515
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Arg Gln  His Thr Ala Gly Glu  Glu Val Val Gly Val  Phe Ser Gly
    1520                  1525                  1530

Lys Val  Pro Asn Ser Gly Ser  Glu Ser Lys Val Ala  Phe Leu Phe
    1535                  1540                  1545

Thr Gly  Gln Gly Ser Gln Tyr  Leu Asn Met Gly Arg  Gln Leu Tyr
    1550                  1555                  1560

Glu Thr  Gln Pro Thr Phe Arg  Gln Ala Leu Asp Thr  Cys Asp His
    1565                  1570                  1575

Ile Leu  Arg Pro Tyr Leu Asp  Asn Pro Leu Leu Glu  Ile Leu Tyr
    1580                  1585                  1590

Pro Gln  Asp Ala Gln Lys Ser  Asn Asp Ser Pro Leu  Asp Gln Thr
    1595                  1600                  1605

Gly Tyr  Thr Gln Pro Ala Leu  Phe Ser Ile Glu Tyr  Ala Leu Leu
    1610                  1615                  1620

Lys Leu  Trp Glu Ser Trp Gly  Ile Lys Pro Asn Val  Val Met Gly
    1625                  1630                  1635

His Ser  Val Gly Glu Tyr Val  Ala Ala Thr Val Ala  Gly Val Phe
    1640                  1645                  1650

Ser Leu  Glu Asp Gly Leu Lys  Leu Ile Ala Ala Arg  Gly Arg Leu
    1655                  1660                  1665

Met Gln  Gly Leu Pro Ala Gly  Gly Glu Met Val Ser  Val Met Ala
    1670                  1675                  1680

Ser Glu  Ser Lys Val Leu Glu  Thr Leu Lys Ala Met  Ser Leu Glu
    1685                  1690                  1695

Asp Lys  Val Ala Ile Ala Ala  Ile Asn Gly Pro Glu  Ser Ile Val
    1700                  1705                  1710

Ile Ser  Gly Glu Ala Glu Ala  Ile Arg Ala Met Ala  Thr His Leu
    1715                  1720                  1725

Glu Ser  Val Gly Ile Lys Thr  Lys Gln Leu Gln Val  Ser His Ala
    1730                  1735                  1740

Phe His  Ser Pro Leu Met Glu  Pro Met Leu Ala Glu  Phe Glu Ala
    1745                  1750                  1755

Val Ala  Asn Gln Ile Thr Tyr  His Gln Pro Arg Ile  Pro Ile Ile
    1760                  1765                  1770

Ser Asn  Val Thr Gly Thr Lys  Ala Asp Lys Ser Ile  Ala Thr Ala
    1775                  1780                  1785

Gln Tyr  Trp Val Asn His Val  Arg Gln Pro Val Arg  Phe Ala Gln
    1790                  1795                  1800

Gly Met  Ala Thr Leu His Gln  Gln Gly Tyr Glu Thr  Phe Leu Glu
    1805                  1810                  1815

Ile Gly  Ala Lys Pro Ile Leu  Leu Gly Met Gly Lys  Gln Cys Leu
    1820                  1825                  1830

Ser Pro  Asp Val Gly Val Trp  Leu Pro Ser Leu Arg  His Gly Val
    1835                  1840                  1845

Asp Glu  Trp Gln Gln Ile Leu  Ser Ser Leu Gly Gln  Leu Tyr Val
    1850                  1855                  1860

Gln Gly  Ala Lys Val Asp Trp  Ser Gly Phe Asp Arg  Asp Tyr Ser
    1865                  1870                  1875

Arg Glu  Lys Val Val Leu Pro  Thr Tyr Pro Phe Gln  Arg Glu Arg
    1880                  1885                  1890

Tyr Trp  Val Glu Thr Ser Ile  Asn Gln Gln Gln Val  Val Cys Ser
    1895                  1900                  1905
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Gly Glu  Pro Asn Leu Gln Gly  Thr Pro Glu Gly Thr  Ser Thr Thr
    1910                 1915                 1920

Ile Val  Lys Leu Leu Ser Gln  Gly Asn Thr Lys Glu  Leu Ala Glu
    1925                 1930                 1935

Lys Val  Glu Lys Thr Ser Asp  Leu Pro Pro Glu Gln  Leu Lys Leu
    1940                 1945                 1950

Leu Pro  Asp Leu Leu Ala Ser  Leu Ser Gln Gln His  Gln Gln Glu
    1955                 1960                 1965

Leu Ala  Arg Leu Thr Thr Lys  Lys Trp Phe Tyr Lys  Val Gln Trp
    1970                 1975                 1980

Ile Ser  Gln Ala Ile Lys Pro  Gln Arg Asn Lys Ser  Asn Asn Gln
    1985                 1990                 1995

Val Cys  His Trp Leu Ile Leu  Thr Asp Ser Lys Gly  Leu Gly Lys
    2000                 2005                 2010

Ser Leu  Ala Thr His Leu Gln  Gln Leu Gly Asn Glu  Cys Ser Val
    2015                 2020                 2025

Val Tyr  Gln Ala Asp Asn Tyr  Gln Asn Tyr Glu Pro  Gly Ile Tyr
    2030                 2035                 2040

His Ile  Asn Pro Ser His Pro  Gln Glu Phe Glu Gln  Val Tyr Gln
    2045                 2050                 2055

Thr Ile  Phe Glu Asn Gly Lys  Leu Pro Leu Gln Lys  Val Ile His
    2060                 2065                 2070

Leu Trp  Ser Leu Asp Thr Ala  Ser Glu Gln Asp Leu  Thr Thr Glu
    2075                 2080                 2085

Thr Leu  Glu Gln Ala Gln Leu  Trp Gly Cys Gly Ser  Thr Leu His
    2090                 2095                 2100

Leu Leu  Gln Thr Leu Val Lys  Asn Pro Asn Ser Thr  Pro Pro Lys
    2105                 2110                 2115

Leu Trp  Met Ile Thr Arg Gly  Thr Gln Pro Val Leu  Ser Pro Thr
    2120                 2125                 2130

Glu Lys  Leu Thr Val Ala Thr  Ser Pro Leu Trp Gly  Leu Gly Arg
    2135                 2140                 2145

Thr Ile  Ala Ser Glu His Pro  Gln Leu Trp Gly Gly  Leu Val Asp
    2150                 2155                 2160

Leu Asp  Pro Gln Gly Ser Glu  Asp Glu Val Glu Val  Leu Leu Gln
    2165                 2170                 2175

Gln Ile  Ile Asp Ser Gln Lys  Glu Asp His Leu Ala  Val Arg Asn
    2180                 2185                 2190

Arg Lys  Ile Tyr Val Ala Arg  Leu Leu Lys His Ile  Pro Gln Glu
    2195                 2200                 2205

Ser Gln  Pro Leu Ser Leu Arg  Ser Asp Ala Thr Tyr  Leu Ile Thr
    2210                 2215                 2220

Gly Gly  Leu Gly Ala Leu Gly  Leu Lys Thr Ala Ala  Trp Met Ala
    2225                 2230                 2235

Glu Lys  Gly Ala Arg Asn Leu  Val Leu Ile Ser Arg  Arg Gln Pro
    2240                 2245                 2250

Ser Glu  Gln Ala Gln Gln Thr  Ile Gln Ser Leu Glu  Glu Leu Gly
    2255                 2260                 2265

Thr Gln  Val Lys Val Leu Ser  Ala Asp Ile Ser Val  Glu Ser Asp
    2270                 2275                 2280

Val Ala  Asn Ile Leu Glu Gln  Ile Gln Thr Ser Leu  Pro Pro Leu
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    2285                2290                2295

Leu Gly  Val Ile His Ala Ala  Gly Val Leu Asp Asp  Gly Leu Leu
    2300                2305                2310

Gln Gln  Thr Asn Trp Glu Arg  Phe Thr Lys Val Met  Ala Pro Lys
    2315                2320                2325

Val Asn  Gly Thr Trp Asn Leu  His Lys Leu Thr Gln  His Leu Ser
    2330                2335                2340

Leu Asp  Phe Phe Val Cys Phe  Ser Ser Met Ser Ser  Leu Leu Gly
    2345                2350                2355

Ser Pro  Gly Gln Gly Asn Tyr  Ala Ala Ala Asn Ala  Phe Met Asp
    2360                2365                2370

Ala Val  Val His Tyr Arg Arg  Glu Met Gly Leu Pro  Gly Leu Ser
    2375                2380                2385

Ile Asn  Trp Gly Gly Trp Ser  Glu Gly Gly Met Ala  Thr Arg Leu
    2390                2395                2400

Ala Ser  Gln His Gln Asn Arg  Met Gln Thr Ala Gly  Ile Ser Leu
    2405                2410                2415

Ile Ser  Pro Glu Gln Gly Ile  Gln Val Leu Glu Glu  Leu Val Arg
    2420                2425                2430

Thr Gln  Ser Thr Ala Gln Val  Gly Val Leu Pro Val  Asp Trp Ser
    2435                2440                2445

Val Leu  Ala Lys Gln Phe Ser  Ser Ala Asn Pro Ser  Ser Leu Leu
    2450                2455                2460

Leu Glu  Leu Leu Gln Gln Glu  Thr Ser Ser Glu Lys  Thr Asp Glu
    2465                2470                2475

Arg Ile  Leu Glu Lys Leu Gln  Ala Ala Pro Ile Thr  Glu Arg Gln
    2480                2485                2490

Asp Ile  Leu Lys Asn Tyr Ile  Gln Leu Val Val Ala  Lys Thr Leu
    2495                2500                2505

Gly Ile  Asn Pro Ser Lys Ile  Ser Thr Asp Asp Asn  Phe Val Glu
    2510                2515                2520

Leu Gly  Met Asp Ser Leu Met  Gly Met Glu Val Val  Asn Lys Leu
    2525                2530                2535

Ser Gly  Asp Leu Asp Phe Ile  Ile Tyr Pro Arg Glu  Phe Tyr Glu
    2540                2545                2550

Arg Pro  Thr Ile Asp Ser Leu  Thr Gln Tyr Leu Ser  Ala Glu Leu
    2555                2560                2565

Ser Glu  Asp Asn Leu Ala Thr  Gln Pro Ser Pro Thr  Ser Leu Glu
    2570                2575                2580

Ile Phe  Ala Thr Lys Ser Ser  Pro Ser Gly Asn Ser  Ala Arg Pro
    2585                2590                2595

Ala Ser  Val Ser Ser Arg Leu  Pro Gly Ile Ile Phe  Ile Leu Ser
    2600                2605                2610

Ser Pro  Arg Ser Gly Ser Thr  Leu Leu Arg Val Met  Leu Ala Gly
    2615                2620                2625

His Ser  Ser Leu Phe Ser Pro  Pro Glu Leu His Leu  Leu Pro Phe
    2630                2635                2640

Asn Thr  Met Lys Glu Arg Gln  Glu Gln Leu Asn Leu  Ser Tyr Leu
    2645                2650                2655

Gly Glu  Gly Leu Gln Lys Thr  Phe Met Glu Val Lys  Asn Leu Asp
    2660                2665                2670
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Ala Thr  Ala Ser Gln Ala Leu  Ile Lys Asp Leu Glu  Ser Gln Asn
    2675                 2680                 2685

Leu Ser  Ile Gln Gln Val Tyr  Gly Met Leu Gln Glu  Asn Ile Ala
    2690                 2695                 2700

Pro Arg  Leu Leu Val Asp Lys  Ser Pro Thr Tyr Ala  Met Glu Pro
    2705                 2710                 2715

Thr Ile  Leu Glu Arg Gly Glu  Ala Leu Phe Ala Asn  Ser Lys Tyr
    2720                 2725                 2730

Ile Tyr  Leu Val Arg His Pro  Tyr Ser Val Ile Glu  Ser Phe Val
    2735                 2740                 2745

Arg Met  Arg Met Gln Lys Leu  Val Gly Leu Gly Glu  Glu Asn Pro
    2750                 2755                 2760

Tyr Arg  Val Ala Glu Gln Val  Trp Ala Lys Ser Asn  Gln Asn Ile
    2765                 2770                 2775

Leu Asn  Phe Leu Ser Gln Leu  Glu Pro Glu Arg Gln  His Gln Ile
    2780                 2785                 2790

Arg Tyr  Glu Asp Leu Val Lys  Lys Pro Gln Gln Val  Leu Ser Gln
    2795                 2800                 2805

Leu Cys  Asp Phe Leu Asn Val  Pro Phe Glu Pro Glu  Leu Leu Gln
    2810                 2815                 2820

Pro Tyr  Gln Gly Asp Arg Met  Thr Gly Gly Val His  Gln Lys Ser
    2825                 2830                 2835

Leu Ser  Ile Ser Asp Pro Asn  Phe Leu Lys His Asn  Thr Ile Asp
    2840                 2845                 2850

Glu Ser  Leu Ala Asp Lys Trp  Lys Thr Ile Gln Leu  Pro Tyr Pro
    2855                 2860                 2865

Leu Lys  Ser Glu Thr Gln Arg  Ile Ala Ser Gln Leu  Ser Tyr Glu
    2870                 2875                 2880

Leu Pro  Asn Leu Val Thr Thr  Pro Thr Asn Gln Gln  Pro Gln Val
    2885                 2890                 2895

Ser Thr  Thr Pro Ser Thr Glu  Gln Pro Ile Met Glu  Glu Lys Phe
    2900                 2905                 2910

Leu Glu  Phe Gly Gly Asn Gln  Ile Cys Leu Cys Ser  Trp Gly Ser
    2915                 2920                 2925

Pro Glu  His Pro Val Val Leu  Cys Ile His Gly Ile  Leu Glu Gln
    2930                 2935                 2940

Gly Leu  Ala Trp Gln Glu Val  Ala Leu Pro Leu Ala  Ala Gln Gly
    2945                 2950                 2955

Tyr Arg  Val Val Ala Pro Asp  Leu Phe Gly His Gly  Arg Ser Ser
    2960                 2965                 2970

His Leu  Glu Met Val Thr Ser  Tyr Ser Ser Leu Thr  Phe Leu Ala
    2975                 2980                 2985

Gln Ile  Asp Arg Val Ile Gln  Glu Leu Pro Asp Gln  Pro Leu Leu
    2990                 2995                 3000

Leu Val  Gly His Ser Met Gly  Ala Met Leu Ala Thr  Ala Ile Ala
    3005                 3010                 3015

Ser Val  Arg Pro Lys Lys Ile  Lys Glu Leu Ile Leu  Val Glu Leu
    3020                 3025                 3030

Pro Leu  Pro Ala Glu Glu Ser  Lys Lys Glu Ser Ala  Val Asn Gln
    3035                 3040                 3045

Leu Thr  Thr Cys Leu Asp Tyr  Leu Ser Ser Thr Pro  Gln His Pro
    3050                 3055                 3060
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Ile Phe Pro Asp Val Ala Thr Ala Ala Ser Arg Leu Arg Gln Ala
3065 3070 3075

Ile Pro Ser Leu Ser Glu Glu Phe Ser Tyr Ile Leu Ala Gln Arg
3080 3085 3090

Ile Thr Gln Pro Asn Gln Gly Gly Val Arg Trp Ser Trp Asp Ala
3095 3100 3105

Ile Ile Arg Thr Arg Ser Ile Leu Gly Leu Asn Asn Leu Pro Gly
3110 3115 3120

Gly Arg Ser Gln Tyr Leu Glu Met Leu Lys Ser Ile Gln Val Pro
3125 3130 3135

Thr Thr Leu Val Tyr Gly Asp Ser Ser Lys Leu Asn Arg Pro Glu
3140 3145 3150

Asp Leu Gln Gln Gln Lys Met Thr Met Thr Gln Ala Lys Arg Val
3155 3160 3165

Phe Leu Ser Gly Gly His Asn Leu His Ile Asp Ala Ala Ala Ala
3170 3175 3180

Leu Ala Ser Leu Ile Leu Thr Ser
3185 3190

<210> SEQ ID NO 7
<211> LENGTH: 2688
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Hybrid polyketide synthase capable of producing styrene

<400> SEQUENCE: 7

Met Thr Lys Glu Tyr Thr Arg Pro Gln Ser Ala Pro Leu Thr Glu Gly
1 5 10 15

Asp Leu Leu Thr Leu Ile Val Ala His Leu Ala Glu Arg Leu Arg Met
20 25 30

Asp Ala Arg Phe Ile Asp Val His Glu Pro Phe Ser Arg His Gly Leu
35 40 45

Asp Ser Arg Gly Ala Val Asp Leu Val Val Asp Leu Arg Thr Ala Leu
50 55 60

Gly Arg Pro Leu Ser Pro Val Val Val Trp Gln His Pro Thr Pro Asp
65 70 75 80

Ala Leu Ala Arg His Leu Ala Gly Gly Ala Asp Ala Arg Glu Gly Gln
85 90 95

Ala Arg Ala Asp Ser Ala Tyr Glu Arg Pro Gly Ala Pro Asn Glu Pro
100 105 110

Ile Ala Ile Val Gly Met Ala Cys Arg Phe Pro Gly Ala Pro Asp Val
115 120 125

Asp Ser Tyr Trp Arg Leu Leu Ser Gly Gly Val Asp Ala Val Thr Glu
130 135 140

Val Pro Ala Gly Arg Trp Asp Met Asp Ala Phe Tyr Asp Arg Asp Pro
145 150 155 160

Arg Ser Leu Gly Asp Val Ser Thr Leu Arg Gly Gly Phe Ile Asp Asp
165 170 175

Val Asp Arg Phe Asp Ala Met Phe Phe Gly Ile Ser Pro Arg Glu Ala
180 185 190

Val Ser Met Asp Pro Gln Gln Arg Leu Met Leu Glu Leu Ala Trp Glu
195 200 205

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Ala Leu Glu Asp Ala Gly Ile Val Ala Glu Arg Leu Lys Glu Ser Leu
    210                 215                 220

Thr Gly Val Phe Phe Gly Cys Ile Trp Asp Asp Tyr Val Thr Leu Ile
225                 230                 235                 240

His Gln Arg Gly Arg Gly Ala Ile Ala Gln His Thr Val Thr Gly Asn
                245                 250                 255

His Arg Ser Ile Ile Ala Asn Arg Val Ser Tyr Thr Leu Asp Leu Arg
            260                 265                 270

Gly Pro Ser Met Thr Val Asp Ser Ala Cys Ser Ser Ala Leu Val Thr
        275                 280                 285

Ile His Met Ala Cys Glu Ser Leu Arg Ser Gly Glu Ser Thr Leu Ala
    290                 295                 300

Leu Ala Gly Gly Val Asn Leu Asn Ile Ala Pro Glu Ser Thr Ile Gly
305                 310                 315                 320

Val His Lys Phe Gly Gly Leu Ser Pro Asp Gly Arg Cys Phe Thr Phe
                325                 330                 335

Asp Ala Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Gly Val Val
            340                 345                 350

Val Leu Lys Arg Leu Ser Ser Ala Ile Ala Asp Gly Asp Pro Ile Ile
        355                 360                 365

Cys Val Ile Arg Gly Ser Ala Val Asn Asn Asp Gly Ala Ser Asn Gly
    370                 375                 380

Leu Thr Gly Pro Asn Pro Leu Ala Gln Glu Ala Val Leu Arg Thr Ala
385                 390                 395                 400

Tyr Glu Arg Ala Gly Val Asn Pro Ala Asp Val Gln Tyr Val Glu Leu
                405                 410                 415

His Gly Thr Gly Thr Gln Leu Gly Asp Pro Val Glu Ala Ser Ala Leu
            420                 425                 430

Gly Ala Val Leu Gly Lys Arg Arg Pro Ala Glu Arg Pro Leu Leu Val
        435                 440                 445

Gly Ser Ala Lys Thr Asn Val Gly His Leu Glu Gly Ala Ala Gly Ile
    450                 455                 460

Val Gly Leu Leu Lys Ala Ala Leu Cys Leu Lys His Lys Gln Leu Ala
465                 470                 475                 480

Pro Asn Leu Asn Phe Glu Thr Pro Asn Pro His Ile Pro Phe Ala Glu
                485                 490                 495

Leu Asn Leu Lys Val Gln Gly Ala Leu Gly Pro Trp Pro Asp Met Asp
            500                 505                 510

Arg Pro Leu Val Cys Gly Val Ser Ser Phe Gly Leu Gly Gly Thr Asn
        515                 520                 525

Ala His Val Val Leu Ser Glu Trp Ala Ser Leu Glu Ala Glu Leu His
    530                 535                 540

Pro Leu Ala Ala Glu Ser Pro Glu Ala Leu Arg Glu Glu Val Gln Arg
545                 550                 555                 560

Arg Leu Leu Thr Met Thr Ser Leu Val Gly Arg Ala Pro Leu Ser Phe
                565                 570                 575

Leu Cys Gly Arg Ser Ala Ala Gln Arg Ser Ala Lys Glu His Arg Leu
            580                 585                 590

Ala Val Thr Ala Arg Ser Phe Glu Glu Leu Lys Gln Arg Leu Leu Gly
        595                 600                 605

Phe Leu Glu His Glu Lys His Val Ser Val Ser Ala Gly Arg Val Asp
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    610                 615                 620

Leu Gly Ala Ala Pro Lys Val Val Phe Val Phe Ala Gly Gln Gly Ala
625                 630                 635                 640

Gln Trp Phe Gly Met Gly Arg Ala Leu Leu Gln Arg Glu Pro Val Phe
                645                 650                 655

Arg Thr Thr Ile Glu Gln Cys Ser Ser Phe Ile Gln Gln Asn Leu Gly
            660                 665                 670

Trp Ser Leu Leu Asp Glu Leu Met Thr Asp Arg Glu Ser Ser Arg Leu
        675                 680                 685

Asp Glu Ile Asp Val Ser Leu Pro Ala Ile Ile Ser Ile Glu Ile Ala
    690                 695                 700

Leu Ala Ala Gln Trp Arg Ala Trp Gly Val Glu Pro Ala Phe Val Val
705                 710                 715                 720

Gly His Ser Thr Gly Glu Ile Ala Ala Ala His Val Ala Gly Val Leu
                725                 730                 735

Ser Ile Glu Asp Ala Met Arg Thr Ile Cys Ala Tyr Gly Arg Ile Ile
            740                 745                 750

Arg Lys Leu Arg Gly Lys Gly Gly Met Gly Leu Val Ala Leu Ser Trp
        755                 760                 765

Glu Asp Ala Gly Lys Glu Leu Thr Gly Tyr Glu Gly Arg Leu Phe Arg
    770                 775                 780

Ala Ile Glu His Ser Ala Asp Ser Thr Val Leu Ala Gly Glu Pro Asp
785                 790                 795                 800

Ala Leu Asp Ala Leu Leu Gln Ala Leu Glu Arg Lys Asn Val Phe Cys
                805                 810                 815

Arg Arg Val Ala Met Asp Val Ala Pro His Cys Pro Gln Val Asp Cys
            820                 825                 830

Leu Arg Asp Glu Leu Phe Asp Ala Leu Arg Glu Val Arg Pro Asn Lys
        835                 840                 845

Ala Gln Ile Pro Ile Val Ser Glu Val Thr Gly Thr Ala Leu Asp Gly
    850                 855                 860

Glu Arg Phe Asp Ala Ser His Trp Val Arg Asn Phe Gly Asp Pro Ala
865                 870                 875                 880

Leu Phe Ser Thr Ala Ile Asp His Leu Leu Gln Glu Gly Phe Asp Ile
                885                 890                 895

Phe Leu Glu Leu Thr Pro His Pro Leu Ala Leu Pro Ala Ile Glu Ser
            900                 905                 910

Asn Leu Arg Arg Ser Gly Arg Arg Gly Val Val Leu Pro Ser Leu Arg
        915                 920                 925

Arg Asn Glu Asp Glu Arg Gly Val Met Leu Asp Thr Leu Gly Val Leu
    930                 935                 940

Tyr Val Arg Gly Ala Pro Val Arg Trp Asp Asn Val Tyr Pro Ala Ala
945                 950                 955                 960

Phe Glu Ser Met Pro Leu Pro Ser Thr Ala Gly Gly Gly Lys Pro Leu
                965                 970                 975

Pro Pro Met Pro Leu Leu Ile Ser Ala Arg Thr Asp Ala Ala Leu Ala
            980                 985                 990

Ala Gln Ala Ala Arg Leu Arg Ala  His Leu Asp Ser His  Leu Asp Leu
        995                 1000                1005

Glu Leu  Val Asp Val Ala Tyr  Ser Leu Ala Ala Thr  Arg Thr His
    1010                1015                1020
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Phe Glu  Arg Arg Ala Val Val  Val Ala Arg Asp Arg  Ala Gly Ile
    1025                 1030                 1035

Leu Asp  Gly Leu Asp Ala Leu  Ala His Gly Gly Ser  Ala Ala Leu
    1040                 1045                 1050

Leu Gly  Arg Ser Ala Ala His  Gly Lys Leu Ala Ile  Leu Phe Thr
    1055                 1060                 1065

Gly Gln  Gly Ser Gln Arg Pro  Thr Met Gly Arg Ala  Leu Tyr Asp
    1070                 1075                 1080

Ala Phe  Pro Val Phe Arg Gly  Ala Leu Asp Ala Ala  Ala Ala His
    1085                 1090                 1095

Leu Asp  Arg Asp Leu Asp Arg  Pro Leu Arg Asp Val  Leu Phe Ala
    1100                 1105                 1110

Pro Asp  Gly Ser Glu Gln Ala  Ala Arg Leu Asp Gln  Thr Ala Phe
    1115                 1120                 1125

Thr Gln  Pro Ala Leu Phe Ala  Leu Glu Val Ala Leu  Phe Glu Leu
    1130                 1135                 1140

Leu Gln  Ser Phe Gly Leu Lys  Pro Ala Leu Leu Leu  Gly His Ser
    1145                 1150                 1155

Ile Gly  Glu Leu Val Ala Ala  His Val Ala Gly Val  Leu Ser Leu
    1160                 1165                 1170

Gln Asp  Ala Cys Thr Leu Val  Ala Ala Arg Ala Lys  Leu Met Gln
    1175                 1180                 1185

Ala Leu  Pro Gln Gly Gly Ala  Met Val Thr Leu Gln  Ala Ser Glu
    1190                 1195                 1200

Gln Glu  Ala Arg Asp Leu Leu  Gln Ala Ala Glu Gly  Arg Val Ser
    1205                 1210                 1215

Leu Ala  Ala Val Asn Gly His  Leu Ser Thr Val Val  Ala Gly Asp
    1220                 1225                 1230

Glu Asp  Ala Val Leu Lys Ile  Ala Arg Gln Val Glu  Ala Leu Gly
    1235                 1240                 1245

Arg Lys  Ala Thr Arg Leu Arg  Val Ser His Ala Phe  His Ser Pro
    1250                 1255                 1260

His Met  Asp Gly Met Leu Asp  Asp Phe Arg Arg Val  Ala Gln Gly
    1265                 1270                 1275

Leu Thr  Phe His Pro Ala Arg  Ile Pro Ile Ile Ser  Asn Val Thr
    1280                 1285                 1290

Gly Ala  Arg Ala Thr Asp Gln  Glu Leu Ala Ser Pro  Glu Thr Trp
    1295                 1300                 1305

Val Arg  His Val Arg Asp Thr  Val Arg Phe Leu Asp  Gly Val Arg
    1310                 1315                 1320

Thr Leu  His Ala Glu Gly Ala  Arg Ala Phe Leu Glu  Leu Gly Pro
    1325                 1330                 1335

His Pro  Val Leu Ser Ala Leu  Ala Gln Asp Ala Leu  Gly His Asp
    1340                 1345                 1350

Glu Gly  Pro Ser Pro Cys Ala  Phe Leu Pro Thr Leu  Arg Lys Gly
    1355                 1360                 1365

Arg Asp  Asp Ala Glu Ala Phe  Thr Ala Ala Leu Gly  Ala Leu His
    1370                 1375                 1380

Ala Ala  Gly Leu Thr Pro Asp  Trp Asn Ala Phe Phe  Ala Pro Phe
    1385                 1390                 1395

Ala Pro  Cys Lys Val Pro Leu  Pro Thr Tyr Thr Phe  Gln Arg Glu
    1400                 1405                 1410
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Arg Phe  Trp Leu Asp Ala Ser  Thr Ala His Ala Ala  Ser Ala Thr
    1415                 1420                 1425

Pro Ala  Ala Ala Leu Glu Gly  Arg Phe Trp Gln Ala  Val Glu Ser
    1430                 1435                 1440

Gly Asp  Ile Asp Thr Leu Ser  Ser Glu Leu His Val  Asp Gly Asp
    1445                 1450                 1455

Glu Gln  Arg Ala Ala Leu Ala  Leu Val Leu Pro Thr  Leu Ser Ser
    1460                 1465                 1470

Phe Arg  His Lys Arg Gln Glu  Gln Ser Thr Val Asp  Ala Trp Arg
    1475                 1480                 1485

Tyr Arg  Val Thr Trp Lys Pro  Leu Thr Thr Ala Ala  Thr Pro Ala
    1490                 1495                 1500

Asp Leu  Ala Gly Thr Trp Leu  Leu Val Val Pro Ser  Ala Leu Gly
    1505                 1510                 1515

Asp Asp  Ala Leu Leu Ala Thr  Leu Thr Glu Ala Leu  Thr Arg Arg
    1520                 1525                 1530

Gly Ala  Arg Val Leu Ala Leu  Arg Val Ser Asp Ile  His Ile Gly
    1535                 1540                 1545

Arg Ser  Ala Leu Val Glu His  Leu Arg Glu Ala Leu  Ala Glu Thr
    1550                 1555                 1560

Ala Pro  Leu Arg Gly Val Leu  Ser Leu Leu Ala Leu  Asp Glu His
    1565                 1570                 1575

Arg Leu  Ala Asp Arg Ser Ala  Leu Pro Ala Gly Leu  Ala Leu Ser
    1580                 1585                 1590

Leu Ala  Leu Val Gln Gly Leu  Asp Asp Leu Ala Ile  Glu Ala Pro
    1595                 1600                 1605

Leu Trp  Leu Phe Thr Arg Gly  Ala Val Ser Ile Gly  His Ser Asp
    1610                 1615                 1620

Pro Ile  Thr His Pro Thr Gln  Ala Met Ile Trp Gly  Leu Gly Arg
    1625                 1630                 1635

Val Val  Gly Leu Glu His Pro  Glu Arg Trp Gly Gly  Leu Val Asp
    1640                 1645                 1650

Val Ser  Ala Gly Val Asp Glu  Ser Ala Val Gly Arg  Leu Leu Pro
    1655                 1660                 1665

Ala Leu  Ala Gln Arg His Asp  Glu Asp Gln Leu Ala  Leu Arg Pro
    1670                 1675                 1680

Ala Gly  Leu Tyr Ala Arg Arg  Ile Val Arg Ala Pro  Leu Gly Asp
    1685                 1690                 1695

Ala Pro  Pro Ala Arg Glu Phe  Arg Pro Arg Gly Thr  Ile Leu Ile
    1700                 1705                 1710

Thr Gly  Gly Thr Gly Ala Leu  Gly Ala His Val Ala  Arg Trp Leu
    1715                 1720                 1725

Ala Arg  Gln Gly Ala Glu His  Leu Ile Leu Ile Ser  Arg Arg Gly
    1730                 1735                 1740

Ala Glu  Ala Pro Gly Ala Ser  Glu Leu His Ala Glu  Leu Asn Ala
    1745                 1750                 1755

Leu Gly  Val Arg Thr Thr Leu  Ala Ala Cys Asp Val  Ala Asp Arg
    1760                 1765                 1770

Ser Ala  Leu Gln Ala Leu Leu  Asp Ser Ile Pro Ser  Asp Cys Pro
    1775                 1780                 1785

Leu Thr  Ala Val Phe His Thr  Ala Gly Ala Arg Asp  Asp Gly Leu
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    1790                1795                1800

Ile Gly  Asp Met Thr Pro Glu  Arg Ile Glu Arg Val  Leu Ala Pro
    1805                1810                1815

Lys Leu  Asp Ser Ala Leu His  Leu His Glu Leu Thr  Lys Asn Ser
    1820                1825                1830

Ala Leu  Asp Ala Phe Val Leu  Tyr Ala Ser Leu Ser  Gly Val Leu
    1835                1840                1845

Gly Asn  Pro Gly Gln Ala Asn  Tyr Ala Ala Ala Asn  Ala Phe Leu
    1850                1855                1860

Asp Ala  Leu Ala Glu His Arg  Arg Ser Leu Gly Leu  Thr Ala Thr
    1865                1870                1875

Ser Val  Ala Trp Gly Gly Trp  Gly Gly Gly Gly Met  Ala Thr Glu
    1880                1885                1890

Arg Val  Ala Ala Gln Leu Gln  Gln Arg Gly Leu Leu  Gln Met Ala
    1895                1900                1905

Pro Ser  Leu Ala Leu Ala Ala  Leu Ala Gln Ala Leu  Gln Gln Asp
    1910                1915                1920

Glu Thr  Thr Ile Thr Val Ala  Asp Ile Asp Trp Ser  Arg Phe Ala
    1925                1930                1935

Pro Ala  Phe Ser Val Ala Arg  Gln Arg Pro Leu Leu  Arg Asp Leu
    1940                1945                1950

Pro Glu  Ala Gln Arg Ala Leu  Gln Ala Ser Glu Gly  Ala Ser Ser
    1955                1960                1965

Glu His  Gly Pro Ala Thr Gly  Leu Leu Asp Glu Leu  Arg Ser Arg
    1970                1975                1980

Ser Glu  Ser Glu Gln Leu Asp  Leu Leu Ala Thr Leu  Val Arg Gly
    1985                1990                1995

Glu Thr  Ala Thr Val Leu Gly  His Ala Glu Ala Ser  His Val Asp
    2000                2005                2010

Pro Asp  Lys Gly Phe Met Asp  Leu Gly Leu Asp Ser  Leu Met Thr
    2015                2020                2025

Val Glu  Leu Arg Arg Arg Leu  Gln Lys Ala Thr Gly  Val Lys Leu
    2030                2035                2040

Pro Pro  Thr Leu Ala Phe Asp  His Pro Ser Pro His  Arg Val Ala
    2045                2050                2055

Phe Phe  Leu Arg Asp Ser Leu  Ser Glu Asp Asn Leu  Ala Thr Gln
    2060                2065                2070

Pro Ser  Pro Thr Ser Leu Glu  Ile Phe Ala Thr Lys  Ser Ser Pro
    2075                2080                2085

Ser Gly  Asn Ser Ala Arg Pro  Ala Ser Val Ser Ser  Arg Leu Pro
    2090                2095                2100

Gly Ile  Ile Phe Ile Leu Ser  Ser Pro Arg Ser Gly  Ser Thr Leu
    2105                2110                2115

Leu Arg  Val Met Leu Ala Gly  His Ser Ser Leu Phe  Ser Pro Pro
    2120                2125                2130

Glu Leu  His Leu Leu Pro Phe  Asn Thr Met Lys Glu  Arg Gln Glu
    2135                2140                2145

Gln Leu  Asn Leu Ser Tyr Leu  Gly Glu Gly Leu Gln  Lys Thr Phe
    2150                2155                2160

Met Glu  Val Lys Asn Leu Asp  Ala Thr Ala Ser Gln  Ala Leu Ile
    2165                2170                2175
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Lys Asp  Leu Glu Ser Gln Asn  Leu Ser Ile Gln Gln  Val Tyr Gly
    2180                 2185                 2190

Met Leu  Gln Glu Asn Ile Ala  Pro Arg Leu Leu Val  Asp Lys Ser
    2195                 2200                 2205

Pro Thr  Tyr Ala Met Glu Pro  Thr Ile Leu Glu Arg  Gly Glu Ala
    2210                 2215                 2220

Leu Phe  Ala Asn Ser Lys Tyr  Ile Tyr Leu Val Arg  His Pro Tyr
    2225                 2230                 2235

Ser Val  Ile Glu Ser Phe Val  Arg Met Arg Met Gln  Lys Leu Val
    2240                 2245                 2250

Gly Leu  Gly Glu Glu Asn Pro  Tyr Arg Val Ala Glu  Gln Val Trp
    2255                 2260                 2265

Ala Lys  Ser Asn Gln Asn Ile  Leu Asn Phe Leu Ser  Gln Leu Glu
    2270                 2275                 2280

Pro Glu  Arg Gln His Gln Ile  Arg Tyr Glu Asp Leu  Val Lys Lys
    2285                 2290                 2295

Pro Gln  Gln Val Leu Ser Gln  Leu Cys Asp Phe Leu  Asn Val Pro
    2300                 2305                 2310

Phe Glu  Pro Glu Leu Leu Gln  Pro Tyr Gln Gly Asp  Arg Met Thr
    2315                 2320                 2325

Gly Gly  Val His Gln Lys Ser  Leu Ser Ile Ser Asp  Pro Asn Phe
    2330                 2335                 2340

Leu Lys  His Asn Thr Ile Asp  Glu Ser Leu Ala Asp  Lys Trp Lys
    2345                 2350                 2355

Thr Ile  Gln Leu Pro Tyr Pro  Leu Lys Ser Glu Thr  Gln Arg Ile
    2360                 2365                 2370

Ala Ser  Gln Leu Ser Tyr Glu  Leu Pro Asn Leu Val  Thr Thr Pro
    2375                 2380                 2385

Thr Asn  Gln Gln Pro Gln Val  Ser Thr Thr Pro Ser  Thr Glu Gln
    2390                 2395                 2400

Pro Ile  Met Glu Glu Lys Phe  Leu Glu Phe Gly Gly  Asn Gln Ile
    2405                 2410                 2415

Cys Leu  Cys Ser Trp Gly Ser  Pro Glu His Pro Val  Val Leu Cys
    2420                 2425                 2430

Ile His  Gly Ile Leu Glu Gln  Gly Leu Ala Trp Gln  Glu Val Ala
    2435                 2440                 2445

Leu Pro  Leu Ala Ala Gln Gly  Tyr Arg Val Val Ala  Pro Asp Leu
    2450                 2455                 2460

Phe Gly  His Gly Arg Ser Ser  His Leu Glu Met Val  Thr Ser Tyr
    2465                 2470                 2475

Ser Ser  Leu Thr Phe Leu Ala  Gln Ile Asp Arg Val  Ile Gln Glu
    2480                 2485                 2490

Leu Pro  Asp Gln Pro Leu Leu  Leu Val Gly His Ser  Met Gly Ala
    2495                 2500                 2505

Met Leu  Ala Thr Ala Ile Ala  Ser Val Arg Pro Lys  Lys Ile Lys
    2510                 2515                 2520

Glu Leu  Ile Leu Val Glu Leu  Pro Leu Pro Ala Glu  Glu Ser Lys
    2525                 2530                 2535

Lys Glu  Ser Ala Val Asn Gln  Leu Thr Thr Cys Leu  Asp Tyr Leu
    2540                 2545                 2550

Ser Ser  Thr Pro Gln His Pro  Ile Phe Pro Asp Val  Ala Thr Ala
    2555                 2560                 2565
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Ala Ser  Arg Leu Arg Gln Ala  Ile Pro Ser Leu Ser  Glu Glu Phe
    2570                 2575                 2580

Ser Tyr  Ile Leu Ala Gln Arg  Ile Thr Gln Pro Asn  Gln Gly Gly
    2585                 2590                 2595

Val Arg  Trp Ser Trp Asp Ala  Ile Ile Arg Thr Arg  Ser Ile Leu
    2600                 2605                 2610

Gly Leu  Asn Asn Leu Pro Gly  Gly Arg Ser Gln Tyr  Leu Glu Met
    2615                 2620                 2625

Leu Lys  Ser Ile Gln Val Pro  Thr Thr Leu Val Tyr  Gly Asp Ser
    2630                 2635                 2640

Ser Lys  Leu Asn Arg Pro Glu  Asp Leu Gln Gln Gln  Lys Met Thr
    2645                 2650                 2655

Met Thr  Gln Ala Lys Arg Val  Phe Leu Ser Gly Gly  His Asn Leu
    2660                 2665                 2670

His Ile  Asp Ala Ala Ala Ala  Leu Ala Ser Leu Ile  Leu Thr Ser
    2675                 2680                 2685


<210> SEQ ID NO 8
<211> LENGTH: 3177
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Hybrid polyketide synthase capable of producing
      pentene

<400> SEQUENCE: 8

Met Arg Ala Pro Tyr Gly Asn Arg Gln Val Asn Arg Arg Phe Leu Arg
1               5                  10                  15

Glu Phe Arg Ala Lys Arg Pro His Cys Val Ser Pro Leu His Phe Leu
            20                  25                  30

Ala Glu Phe Ser Glu Ser Arg Gln Thr Thr Gly Ser Ala Gly Val Thr
        35                  40                  45

Ala Pro Ile Asp Arg Pro Gly Val Ser Met Ala Pro Lys Ser Gly Ala
    50                  55                  60

Gln Arg Ser Ser Asp Ile Ala Val Val Gly Met Ser Cys Arg Leu Pro
65                  70                  75                  80

Gly Ala Pro Gly Ile Asp Glu Phe Trp His Leu Leu Thr Thr Gly Gly
                85                  90                  95

Ser Ala Ile Glu Arg Arg Ala Asp Gly Thr Trp Arg Gly Ser Leu Asp
            100                 105                 110

Gly Ala Ala Asp Phe Asp Ala Ala Phe Phe Asp Met Thr Pro Arg Gln
        115                 120                 125

Ala Ala Ala Ala Asp Pro Gln Gln Arg Leu Met Leu Glu Leu Gly Trp
    130                 135                 140

Thr Ala Leu Glu Asn Ala Gly Ile Val Pro Gly Ser Leu Ala Gly Thr
145                 150                 155                 160

Asp Thr Gly Val Phe Val Gly Ile Ala Ala Asp Asp Tyr Ala Ala Leu
                165                 170                 175

Leu His Arg Ser Ala Thr Pro Val Ser Gly His Thr Ala Thr Gly Leu
            180                 185                 190

Ser Arg Gly Met Ala Ala Asn Arg Leu Ser Tyr Leu Leu Gly Leu Arg
        195                 200                 205

Gly Pro Ser Leu Ala Val Asp Ser Ala Gln Ser Ser Ser Leu Val Ala
    210                 215                 220
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Val His Leu Ala Cys Glu Ser Leu Arg Arg Gly Glu Ser Asp Leu Ala
225                 230                 235                 240

Ile Val Gly Gly Val Ser Leu Ile Leu Ala Glu Asp Ser Thr Ala Gly
                245                 250                 255

Met Glu Leu Met Gly Ala Leu Ser Pro Asp Gly Arg Cys His Thr Phe
            260                 265                 270

Asp Ala Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Ala Cys Val
        275                 280                 285

Val Leu Lys Pro Leu Glu Arg Ala Leu Ala Asp Gly Asp Arg Val His
    290                 295                 300

Cys Val Val Arg Gly Ser Ala Val Asn Asn Asp Gly Gly Gly Ser Thr
305                 310                 315                 320

Leu Thr Thr Pro His Arg Glu Ala Gln Ala Ala Val Leu Arg Ala Ala
                325                 330                 335

Tyr Glu Arg Ala Gly Val Gly Pro Asp Gln Val Ser Tyr Val Glu Leu
            340                 345                 350

His Gly Thr Gly Thr Pro Val Gly Asp Pro Val Glu Ala Ala Ala Leu
        355                 360                 365

Gly Ala Val Leu Gly Thr Ala His Gly Arg Asn Ala Pro Leu Ser Val
    370                 375                 380

Gly Ser Val Lys Thr Asn Val Gly His Leu Glu Ala Ala Ala Gly Leu
385                 390                 395                 400

Val Gly Phe Val Lys Ala Ala Leu Cys Val Arg Glu Gly Val Val Pro
                405                 410                 415

Pro Ser Leu Asn His Ala Thr Pro Asn Pro Ala Ile Pro Met Asp Arg
            420                 425                 430

Leu Asn Leu Arg Val Pro Thr Arg Leu Glu Pro Trp Pro His Pro Asp
        435                 440                 445

Asp Arg Ala Thr Gly Arg Leu Arg Leu Ala Gly Val Ser Ser Phe Gly
    450                 455                 460

Met Gly Gly Thr Asn Ala His Val Val Val Glu Glu Ala Pro Leu Pro
465                 470                 475                 480

Glu Ala Gly Glu Pro Val Gly Ala Gly Val Pro Leu Ala Val Val Pro
                485                 490                 495

Val Val Val Ser Gly Arg Ser Ala Gly Ala Val Ala Glu Leu Ala Ser
            500                 505                 510

Arg Leu Asn Glu Ser Val Arg Ser Asp Arg Leu Val Asp Val Gly Leu
        515                 520                 525

Ser Ser Val Val Ser Arg Ser Val Phe Glu His Arg Ser Val Val Leu
    530                 535                 540

Ala Gly Asp Ser Ala Glu Leu Ser Ala Gly Leu Asp Ala Leu Ala Ala
545                 550                 555                 560

Asp Gly Val Ser Pro Val Leu Val Ser Gly Val Ala Ser Val Gly Gly
                565                 570                 575

Gly Arg Ser Val Phe Val Phe Pro Gly Ala Gly Val Lys Trp Ala Gly
            580                 585                 590

Met Ala Leu Gly Leu Trp Ala Glu Ser Ala Val Phe Ala Glu Ser Met
        595                 600                 605

Ala Arg Cys Glu Ala Ala Phe Ala Gly Leu Val Glu Trp Arg Leu Ala
    610                 615                 620

Asp Val Leu Gly Asp Gly Ala Ala Leu Glu Arg Glu Asp Val Val Gln
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625                 630                 635                 640

Pro Ala Ser Phe Ala Val Met Val Ser Leu Ala Ala Leu Trp Arg Ser
                645                 650                 655

Leu Gly Val Val Pro Asp Ala Val Val Gly His Ser Gln Gly Glu Ile
            660                 665                 670

Ala Ala Ala Val Val Ala Gly Gly Leu Ser Leu Glu Asp Gly Ala Arg
        675                 680                 685

Val Val Val Leu Arg Ala Arg Val Ala Glu Glu Val Leu Ser Gly Gly
    690                 695                 700

Gly Ile Ala Ser Val Arg Leu Ser Arg Ala Glu Val Glu Glu Arg Leu
705                 710                 715                 720

Ala Gly Gly Gly Gly Gly Leu Ser Val Ala Val Val Asn Ala Pro Ser
                725                 730                 735

Ser Thr Val Val Ala Gly Glu Leu Gly Asp Leu Asp Arg Phe Val Ala
            740                 745                 750

Ala Cys Glu Ala Glu Gly Val Arg Ala Arg Arg Leu Glu Phe Gly Tyr
        755                 760                 765

Ala Ser His Ser Arg Phe Val Glu Pro Val Arg Glu Arg Leu Leu Glu
    770                 775                 780

Gly Leu Ala Asp Val Arg Pro Val Arg Gly Arg Ile Pro Phe Tyr Ser
785                 790                 795                 800

Thr Val Glu Ala Ala Glu Phe Asp Thr Ala Gly Leu Asp Ala Glu Tyr
                805                 810                 815

Trp Phe Gly Asn Leu Arg Arg Pro Val Arg Phe Gln Glu Thr Val Glu
            820                 825                 830

Arg Leu Leu Ala Asp Gly Phe Arg Val Phe Val Glu Cys Gly Ala His
        835                 840                 845

Pro Val Leu Thr Gly Ala Val Gln Glu Thr Ala Glu Thr Ala Gly Arg
    850                 855                 860

Glu Ile Cys Ser Val Gly Ser Leu Arg Arg Asp Glu Gly Gly Leu Arg
865                 870                 875                 880

Arg Phe Leu Thr Ser Ala Ala Glu Ala Phe Val Gln Gly Val Glu Val
                885                 890                 895

Ser Trp Pro Val Leu Phe Asp Gly Thr Gly Ala Arg Thr Val Asp Leu
            900                 905                 910

Pro Thr Tyr Pro Phe Gln Arg Arg His His Trp Ala Pro Asp Gly Ser
        915                 920                 925

Ala Ser Ala Ala Pro Thr Arg Asp Ile Arg Pro Asp Glu Thr Ala Ala
    930                 935                 940

Val Pro Ala Asp Thr Met Asp Leu Ala Gly Gln Leu Arg Ala Asp Val
945                 950                 955                 960

Ala Ser Leu Pro Thr Thr Glu Gln Ile Ala Arg Leu Leu Asp Gln Val
                965                 970                 975

Arg Asp Gly Val Ala Thr Val Leu Gly Leu Asp Ala Arg Asp Glu Val
            980                 985                 990

Arg Ala Glu Ala Thr Phe Lys Glu  Leu Gly Val Glu Ser  Leu Thr Gly
        995                 1000                1005

Val Glu  Leu Lys Asn His Leu  Arg Ala Arg Thr Gly  Leu His Val
    1010                1015                1020

Pro Thr  Ser Leu Ile Tyr Asp  Cys Pro Thr Pro Leu  Ala Ala Ala
    1025                1030                1035
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His Tyr  Leu Arg Asp Glu Leu  Leu Gly Arg Pro Ala  Glu Gln Ala
    1040                1045                1050

Val Val  Pro Ala Gly Ile Pro  Val Asp Glu Pro Ile  Ala Ile Val
    1055                1060                1065

Gly Met  Gly Cys Arg Leu Pro  Gly Gly Val Ser Ser  Pro Glu Gly
    1070                1075                1080

Leu Trp  Asp Leu Val Ala Ser  Gly Val Asp Ala Val  Ser Pro Phe
    1085                1090                1095

Pro Thr  Asp Arg Gly Trp Asp  Val Gly Gly Leu Phe  Asp Pro Glu
    1100                1105                1110

Pro Gly  Val Pro Gly Arg Ser  Tyr Val Arg Glu Gly  Gly Phe Leu
    1115                1120                1125

His Glu  Ala Gly Glu Phe Asp  Ala Gly Phe Phe Gly  Ile Ser Pro
    1130                1135                1140

Arg Glu  Ala Leu Ala Met Asp  Pro Gln Gln Arg Leu  Leu Leu Glu
    1145                1150                1155

Thr Ser  Trp Glu Ala Leu Glu  Arg Ala Gly Ile Asp  Pro His Thr
    1160                1165                1170

Leu Arg  Gly Ser Arg Thr Gly  Val Tyr Ala Gly Val  Met Ala Gln
    1175                1180                1185

Glu Tyr  Gly Pro Arg Leu His  Glu Gly Ala Asp Gly  Tyr Glu Gly
    1190                1195                1200

Tyr Leu  Leu Thr Gly Ser Ser  Ser Ser Val Ala Ser  Gly Arg Ile
    1205                1210                1215

Ser Tyr  Val Leu Gly Leu Glu  Gly Pro Ala Val Thr  Val Asp Thr
    1220                1225                1230

Ala Cys  Ser Ser Ser Leu Val  Ala Leu His Leu Ala  Val Arg Ala
    1235                1240                1245

Leu Arg  Ser Gly Glu Cys Asp  Leu Ala Leu Ala Gly  Gly Ala Thr
    1250                1255                1260

Val Met  Ala Glu Pro Gly Met  Phe Val Glu Phe Ser  Arg Gln Arg
    1265                1270                1275

Gly Leu  Ser Ala His Gly Arg  Cys Lys Ala Tyr Ser  Asp Ser Ala
    1280                1285                1290

Asp Gly  Thr Gly Trp Ala Glu  Gly Ala Gly Val Leu  Leu Val Glu
    1295                1300                1305

Arg Leu  Ser Asp Ala Val Arg  His Gly Arg Arg Val  Leu Ala Val
    1310                1315                1320

Val Arg  Gly Ser Ala Val Asn  Gln Asp Gly Ala Ser  Asn Gly Leu
    1325                1330                1335

Thr Ala  Pro Asn Gly Arg Ser  Gln Ser Arg Leu Ile  Arg Gln Ala
    1340                1345                1350

Leu Ala  Asp Ala Arg Leu Gly  Val Ala Asp Val Asp  Val Val Glu
    1355                1360                1365

Gly His  Gly Thr Gly Thr Arg  Leu Gly Asp Pro Ile  Glu Ala Gln
    1370                1375                1380

Ala Leu  Leu Ala Thr Tyr Gly  Gln Arg Asp Ala Gly  Arg Pro Leu
    1385                1390                1395

Arg Leu  Gly Ser Leu Lys Ser  Asn Val Gly His Thr  Gln Ala Ala
    1400                1405                1410

Ala Gly  Val Ala Gly Val Ile  Lys Met Val Met Ala  Met Arg His
    1415                1420                1425
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Gly Val  Leu Pro Lys Thr Leu  His Val Asp Glu Pro  Thr Ala Glu
    1430                 1435                 1440

Val Asp  Trp Ser Ala Gly Ala  Val Ser Leu Leu Arg  Glu Gln Glu
    1445                 1450                 1455

Ala Trp  Pro Arg Gly Glu Arg  Val Arg Arg Ala Gly  Val Ser Ser
    1460                 1465                 1470

Phe Gly  Val Ser Gly Thr Asn  Ala His Val Ile Leu  Glu Gln Pro
    1475                 1480                 1485

Pro Gly  Val Pro Ser Gln Ser  Ala Gly Pro Gly Ser  Gly Ser Val
    1490                 1495                 1500

Val Asp  Val Pro Val Val Pro  Trp Met Val Ser Gly  Lys Thr Pro
    1505                 1510                 1515

Glu Ala  Leu Ser Ala Gln Ala  Thr Ala Leu Met Thr  Tyr Leu Asp
    1520                 1525                 1530

Glu Arg  Pro Asp Val Ser Ser  Leu Asp Val Gly Tyr  Ser Leu Ala
    1535                 1540                 1545

Leu Thr  Arg Ser Ala Leu Asp  Glu Arg Ala Val Val  Leu Gly Ser
    1550                 1555                 1560

Asp Arg  Glu Thr Leu Leu Cys  Gly Val Lys Ala Leu  Ser Ala Gly
    1565                 1570                 1575

His Glu  Ala Ser Gly Leu Val  Thr Gly Ser Val Gly  Ala Gly Gly
    1580                 1585                 1590

Arg Ile  Gly Phe Val Phe Ser  Gly Gln Gly Gly Gln  Trp Leu Gly
    1595                 1600                 1605

Met Gly  Arg Gly Leu Tyr Arg  Ala Phe Pro Val Phe  Ala Ala Ala
    1610                 1615                 1620

Phe Asp  Glu Ala Cys Ala Glu  Leu Asp Ala His Leu  Gly Gln Glu
    1625                 1630                 1635

Ile Gly  Val Arg Glu Val Val  Ser Gly Ser Asp Ala  Gln Leu Leu
    1640                 1645                 1650

Asp Arg  Thr Leu Trp Ala Gln  Ser Gly Leu Phe Ala  Leu Gln Val
    1655                 1660                 1665

Gly Leu  Leu Lys Leu Leu Asp  Ser Trp Gly Val Arg  Pro Ser Val
    1670                 1675                 1680

Val Leu  Gly His Ser Val Gly  Glu Leu Ala Ala Ala  Phe Ala Ala
    1685                 1690                 1695

Gly Val  Val Ser Leu Ser Gly  Ala Ala Arg Leu Val  Ala Gly Arg
    1700                 1705                 1710

Ala Arg  Leu Met Gln Ala Leu  Pro Ser Gly Gly Gly  Met Leu Ala
    1715                 1720                 1725

Val Pro  Ala Gly Glu Glu Leu  Leu Trp Ser Leu Leu  Ala Asp Gln
    1730                 1735                 1740

Gly Asp  Arg Val Gly Ile Ala  Ala Val Asn Ala Ala  Gly Ser Val
    1745                 1750                 1755

Val Leu  Ser Gly Asp Arg Asp  Val Leu Asp Asp Leu  Ala Gly Arg
    1760                 1765                 1770

Leu Asp  Gly Gln Gly Ile Arg  Ser Arg Trp Leu Arg  Val Ser His
    1775                 1780                 1785

Ala Phe  His Ser Tyr Arg Met  Asp Pro Met Leu Ala  Glu Phe Ala
    1790                 1795                 1800

Glu Leu  Ala Arg Thr Val Asp  Tyr Arg Arg Cys Glu  Val Pro Ile
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    1805                1810                1815

Val Ser  Thr Leu Thr Gly Asp  Leu Asp Asp Ala Gly  Arg Met Ser
    1820                1825                1830

Gly Pro  Asp Tyr Trp Val Arg  Gln Val Arg Glu Pro  Val Arg Phe
    1835                1840                1845

Ala Asp  Gly Val Gln Ala Leu  Val Glu His Asp Val  Ala Thr Val
    1850                1855                1860

Val Glu  Leu Gly Pro Asp Gly  Ala Leu Ser Ala Leu  Ile Gln Glu
    1865                1870                1875

Cys Val  Ala Ala Ser Asp His  Ala Gly Arg Leu Ser  Ala Val Pro
    1880                1885                1890

Ala Met  Arg Arg Asn Gln Asp  Glu Ala Gln Lys Val  Met Thr Ala
    1895                1900                1905

Leu Ala  His Val His Val Arg  Gly Gly Ala Val Asp  Trp Arg Ser
    1910                1915                1920

Phe Phe  Ala Gly Thr Gly Ala  Lys Gln Ile Glu Leu  Pro Thr Tyr
    1925                1930                1935

Ala Phe  Gln Arg Gln Arg Tyr  Trp Leu Val Pro Ser  Asp Ser Gly
    1940                1945                1950

Asp Val  Thr Gly Ala Gly Leu  Ala Gly Ala Glu His  Pro Leu Leu
    1955                1960                1965

Gly Ala  Val Val Pro Val Ala  Gly Gly Asp Glu Val  Leu Leu Thr
    1970                1975                1980

Gly Arg  Ile Ser Val Arg Thr  His Pro Trp Leu Ala  Glu His Arg
    1985                1990                1995

Val Leu  Gly Glu Val Ile Val  Ala Gly Thr Ala Leu  Leu Glu Ile
    2000                2005                2010

Ala Leu  His Ala Gly Glu Arg  Leu Gly Cys Glu Arg  Val Glu Glu
    2015                2020                2025

Leu Thr  Leu Glu Ala Pro Leu  Val Leu Pro Glu Arg  Gly Ala Ile
    2030                2035                2040

Gln Val  Gln Leu Arg Val Gly  Ala Pro Glu Asn Ser  Gly Arg Arg
    2045                2050                2055

Pro Met  Ala Leu Tyr Ser Arg  Pro Glu Gly Ala Ala  Glu His Asp
    2060                2065                2070

Trp Thr  Arg His Ala Thr Gly  Arg Leu Ala Pro Gly  Arg Gly Glu
    2075                2080                2085

Ala Ala  Gly Asp Leu Ala Asp  Trp Pro Ala Pro Gly  Ala Leu Pro
    2090                2095                2100

Val Asp  Leu Asp Glu Phe Tyr  Arg Asp Leu Ala Glu  Leu Gly Leu
    2105                2110                2115

Glu Tyr  Gly Pro Ile Phe Gln  Gly Leu Lys Ala Ala  Trp Arg Gln
    2120                2125                2130

Gly Asp  Glu Val Tyr Ala Glu  Ala Ala Leu Pro Gly  Thr Glu Asp
    2135                2140                2145

Ser Gly  Phe Gly Val His Pro  Ala Leu Leu Asp Ala  Ala Leu His
    2150                2155                2160

Ala Thr  Ala Val Arg Asp Met  Asp Asp Ala Arg Leu  Pro Phe Gln
    2165                2170                2175

Trp Glu  Gly Val Ser Leu His  Ala Lys Ala Ala Pro  Ala Leu Arg
    2180                2185                2190
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Val Arg  Val Val Pro Ala Gly  Asp Asp Ala Lys Ser  Leu Leu Val
    2195                 2200                 2205

Cys Asp  Gly Thr Gly Arg Pro  Val Ile Ser Val Asp  Arg Leu Val
    2210                 2215                 2220

Leu Arg  Ser Ala Ala Ala Arg  Arg Thr Gly Ala Arg  Arg Gln Ala
    2225                 2230                 2235

His Gln  Ala Arg Leu Tyr Arg  Leu Ser Trp Pro Thr  Val Gln Leu
    2240                 2245                 2250

Pro Thr  Ser Ala Gln Pro Pro  Ser Cys Val Leu Leu  Gly Thr Ser
    2255                 2260                 2265

Glu Val  Ser Ala Asp Ile Gln  Val Tyr Pro Asp Leu  Arg Ser Leu
    2270                 2275                 2280

Thr Ala  Ala Leu Asp Ala Gly  Ala Glu Pro Pro Gly  Val Val Ile
    2285                 2290                 2295

Ala Pro  Thr Pro Pro Gly Gly  Gly Arg Thr Ala Asp  Val Arg Glu
    2300                 2305                 2310

Thr Thr  Arg His Ala Leu Asp  Leu Val Gln Gly Trp  Leu Ser Asp
    2315                 2320                 2325

Gln Arg  Leu Asn Glu Ser Arg  Leu Leu Leu Val Thr  Gln Gly Ala
    2330                 2335                 2340

Val Ala  Val Glu Pro Gly Glu  Pro Val Thr Asp Leu  Ala Gln Ala
    2345                 2350                 2355

Ala Leu  Trp Gly Leu Leu Arg  Ser Thr Gln Thr Glu  His Pro Asp
    2360                 2365                 2370

Arg Phe  Val Leu Val Asp Val  Pro Glu Pro Ala Gln  Leu Leu Pro
    2375                 2380                 2385

Ala Leu  Pro Gly Val Leu Ala  Cys Gly Glu Pro Gln  Leu Ala Leu
    2390                 2395                 2400

Arg Arg  Gly Gly Ala His Ala  Pro Arg Leu Ala Gly  Leu Gly Ser
    2405                 2410                 2415

Asp Asp  Val Leu Pro Val Pro  Asp Gly Thr Gly Trp  Arg Leu Glu
    2420                 2425                 2430

Ala Thr  Arg Pro Gly Ser Leu  Asp Gly Leu Ala Leu  Val Asp Glu
    2435                 2440                 2445

Pro Thr  Ala Thr Ala Pro Leu  Gly Asp Gly Glu Val  Arg Ile Ala
    2450                 2455                 2460

Met Arg  Ala Ala Gly Val Asn  Phe Arg Asp Ala Leu  Ile Ala Leu
    2465                 2470                 2475

Gly Met  Tyr Pro Gly Val Ala  Ser Leu Gly Ser Glu  Gly Ala Gly
    2480                 2485                 2490

Val Val  Val Glu Thr Gly Pro  Gly Val Thr Gly Leu  Ala Pro Gly
    2495                 2500                 2505

Asp Arg  Val Met Gly Met Ile  Pro Lys Ala Phe Gly  Pro Leu Ala
    2510                 2515                 2520

Val Ala  Asp His Arg Met Val  Thr Arg Ile Pro Ala  Gly Trp Ser
    2525                 2530                 2535

Phe Ala  Arg Ala Ala Ser Val  Pro Ile Val Phe Leu  Thr Ala Tyr
    2540                 2545                 2550

Tyr Ala  Leu Val Asp Leu Ala  Gly Leu Arg Pro Gly  Glu Ser Leu
    2555                 2560                 2565

Leu Val  His Ser Ala Ala Gly  Gly Val Gly Met Ala  Ala Ile Gln
    2570                 2575                 2580
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Leu Ala  Arg His Leu Gly Ala  Glu Val Tyr Ala Thr  Ala Ser Glu
    2585                 2590                 2595

Asp Lys  Trp Gln Ala Val Glu  Leu Ser Arg Glu His  Leu Ala Ser
    2600                 2605                 2610

Ser Arg  Thr Cys Asp Phe Glu  Gln Gln Phe Leu Gly  Ala Thr Gly
    2615                 2620                 2625

Gly Arg  Gly Val Asp Val Val  Leu Asn Ser Leu Ala  Gly Glu Phe
    2630                 2635                 2640

Ala Asp  Ala Ser Leu Arg Met  Leu Pro Arg Gly Gly  Arg Phe Leu
    2645                 2650                 2655

Glu Leu  Gly Lys Thr Asp Val  Arg Asp Pro Val Glu  Val Ala Asp
    2660                 2665                 2670

Ala His  Pro Gly Val Ser Tyr  Gln Ala Phe Asp Thr  Val Glu Ala
    2675                 2680                 2685

Gly Pro  Gln Arg Ile Gly Glu  Met Leu His Glu Leu  Val Glu Leu
    2690                 2695                 2700

Phe Glu  Gly Arg Val Leu Glu  Pro Leu Pro Val Thr  Ala Trp Asp
    2705                 2710                 2715

Val Arg  Gln Ala Pro Glu Ala  Leu Arg His Leu Ser  Gln Ala Arg
    2720                 2725                 2730

His Val  Gly Lys Leu Val Leu  Thr Met Pro Pro Val  Trp Asp Ala
    2735                 2740                 2745

Ala Gly  Thr Val Leu Val Thr  Gly Gly Thr Gly Ala  Leu Gly Ala
    2750                 2755                 2760

Glu Val  Ala Arg His Leu Val  Ile Glu Arg Gly Val  Arg Asn Leu
    2765                 2770                 2775

Val Leu  Val Ser Arg Arg Gly  Pro Ala Ala Ser Gly  Ala Ala Glu
    2780                 2785                 2790

Leu Val  Ala Gln Leu Thr Ala  Tyr Gly Ala Glu Val  Ser Leu Gln
    2795                 2800                 2805

Ala Cys  Asp Val Ala Asp Arg  Glu Thr Leu Ala Lys  Val Leu Ala
    2810                 2815                 2820

Ser Ile  Pro Asp Glu His Pro  Leu Thr Ala Val Val  His Ala Ala
    2825                 2830                 2835

Gly Val  Leu Asp Asp Gly Val  Ser Glu Ser Leu Thr  Val Glu Arg
    2840                 2845                 2850

Leu Asp  Gln Val Leu Arg Pro  Lys Val Asp Gly Ala  Arg Asn Leu
    2855                 2860                 2865

Leu Glu  Leu Ile Asp Pro Asp  Val Ala Leu Val Leu  Phe Ser Ser
    2870                 2875                 2880

Val Ser  Gly Val Leu Gly Ser  Gly Gly Gln Gly Asn  Tyr Ala Ala
    2885                 2890                 2895

Ala Asn  Ser Phe Leu Asp Ala  Leu Ala Gln Gln Arg  Gln Ser Arg
    2900                 2905                 2910

Gly Leu  Pro Thr Arg Ser Leu  Ala Trp Gly Pro Trp  Ala Glu His
    2915                 2920                 2925

Gly Met  Ala Ser Thr Leu Arg  Glu Ala Glu Gln Asp  Arg Leu Ala
    2930                 2935                 2940

Arg Ser  Gly Leu Leu Pro Ile  Ser Thr Glu Glu Gly  Leu Ser Gln
    2945                 2950                 2955

Phe Asp  Ala Ala Cys Gly Gly  Ala His Thr Val Val  Ala Pro Val
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    2960                2965                2970

Arg Phe  Ser Arg Leu Ser Asp  Gly Asn Ala Ile Lys  Phe Ser Val
    2975                2980                2985

Leu Gln  Gly Leu Val Gly Pro  His Arg Val Asn Lys  Ala Ala Thr
    2990                2995                3000

Ala Asp  Asp Ala Glu Ser Leu  Arg Lys Arg Leu Gly  Arg Leu Pro
    3005                3010                3015

Asp Ala  Glu Gln His Arg Ile  Leu Leu Asp Leu Val  Arg Met His
    3020                3025                3030

Val Ala  Ala Val Leu Gly Phe  Ala Gly Ser Gln Glu  Ile Thr Ala
    3035                3040                3045

Asp Gly  Thr Phe Lys Val Leu  Gly Phe Asp Ser Leu  Thr Val Val
    3050                3055                3060

Glu Leu  Arg Asn Arg Ile Asn  Gly Ala Thr Gly Leu  Arg Leu Pro
    3065                3070                3075

Ala Thr  Leu Val Phe Asn Tyr  Pro Thr Pro Asp Ala  Leu Ala Ala
    3080                3085                3090

His Leu  Val Thr Ala Leu Ser  Ala Asp Arg Leu Ala  Gly Thr Phe
    3095                3100                3105

Glu Glu  Leu Asp Arg Trp Ala  Ala Asn Leu Pro Thr  Leu Ala Arg
    3110                3115                3120

Asp Glu  Ala Thr Arg Ala Gln  Ile Thr Thr Arg Leu  Gln Ala Ile
    3125                3130                3135

Leu Gln  Ser Leu Ala Asp Val  Ser Gly Gly Thr Gly  Gly Gly Ser
    3140                3145                3150

Val Pro  Asp Arg Leu Arg Ser  Ala Thr Asp Asp Glu  Leu Phe Gln
    3155                3160                3165

Leu Leu  Asp Asn Asp Leu Glu  Leu Pro
    3170                3175


<210> SEQ ID NO 9
<211> LENGTH: 2081
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Hybrid polyketide synthase capable of producing
      pentene

<400> SEQUENCE: 9

Met Ser Asn Glu Glu Lys Leu Arg Glu Tyr Leu Arg Arg Ala Leu Val
1               5                   10                  15

Asp Leu His Gln Ala Arg Glu Arg Leu His Glu Ala Glu Ser Gly Glu
            20                  25                  30

Arg Glu Pro Ile Ala Ile Val Ala Met Gly Cys Arg Tyr Pro Gly Gly
        35                  40                  45

Val Gln Asp Pro Glu Gly Leu Trp Lys Leu Val Ala Ser Gly Gly Asp
    50                  55                  60

Ala Ile Gly Glu Phe Pro Ala Asp Arg Gly Trp His Leu Asp Glu Leu
65                  70                  75                  80

Tyr Asp Pro Asp Pro Asp Gln Pro Gly Thr Cys Tyr Thr Arg His Gly
                85                  90                  95

Gly Phe Leu His Asp Ala Gly Glu Phe Asp Ala Gly Phe Phe Asp Ile
            100                 105                 110

Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
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        115                 120                 125

Glu Ile Ser Trp Glu Thr Val Glu Ser Ala Gly Met Asp Pro Arg Ser
    130                 135                 140

Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met Tyr Glu Gly
145                 150                 155                 160

Tyr Asp Thr Gly Ala His Arg Ala Gly Glu Gly Val Glu Gly Tyr Leu
                165                 170                 175

Gly Thr Gly Asn Ala Gly Ser Val Ala Ser Gly Arg Val Ala Tyr Ala
            180                 185                 190

Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
        195                 200                 205

Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Gln Gly Glu
    210                 215                 220

Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ser Thr Pro Glu
225                 230                 235                 240

Arg Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg
                245                 250                 255

Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
            260                 265                 270

Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
        275                 280                 285

His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly
    290                 295                 300

Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Leu Ala Gln Glu Arg Val
305                 310                 315                 320

Ile Gln Gln Val Leu Thr Ser Ala Gly Leu Ser Ala Ser Asp Val Asp
                325                 330                 335

Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu
            340                 345                 350

Ala Gln Ala Leu Ile Ala Ala Tyr Gly Gln Asp Arg Asp Arg Asp Arg
        355                 360                 365

Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala
    370                 375                 380

Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met Ala Met Arg His
385                 390                 395                 400

Gly Glu Leu Pro Arg Thr Leu His Val Asp Glu Pro Asn Ser His Val
                405                 410                 415

Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Glu Asn Ile Arg Trp
            420                 425                 430

Pro Gly Thr Gly Thr Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser
        435                 440                 445

Gly Thr Asn Ala His Val Ile Val Gly Asp Tyr Ala Gln Gln Lys Ser
    450                 455                 460

Pro Leu Ala Pro Pro Ala Thr Gln Asp Arg Pro Trp His Leu Leu Thr
465                 470                 475                 480

Leu Ser Ala Lys Asn Ala Gln Ala Leu Asn Ala Leu Gln Lys Ser Tyr
                485                 490                 495

Gly Asp Tyr Leu Ala Gln His Pro Ser Val Asp Pro Arg Asp Leu Cys
            500                 505                 510

Leu Ser Ala Asn Thr Gly Arg Ser Pro Leu Lys Glu Arg Arg Phe Phe
        515                 520                 525
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Val Phe Lys Gln Val Ala Asp Leu Gln Gln Thr Leu Asn Gln Asp Phe
    530                 535                 540

Leu Ala Gln Pro Arg Leu Ser Ser Pro Ala Lys Ile Ala Phe Leu Phe
545                 550                 555                 560

Thr Gly Gln Gly Ser Gln Tyr Tyr Gly Met Gly Gln Gln Leu Tyr Gln
                565                 570                 575

Thr Ser Pro Val Phe Arg Gln Val Leu Asp Glu Cys Asp Arg Leu Trp
            580                 585                 590

Gln Thr Tyr Ser Pro Glu Ala Pro Ala Leu Thr Asp Leu Leu Tyr Gly
        595                 600                 605

Asn His Asn Pro Asp Leu Val His Glu Thr Val Tyr Thr Gln Pro Leu
    610                 615                 620

Leu Phe Ala Val Glu Tyr Ala Ile Ala Gln Leu Trp Leu Ser Trp Gly
625                 630                 635                 640

Val Thr Pro Asp Phe Cys Met Gly His Ser Val Gly Glu Tyr Val Ala
                645                 650                 655

Ala Cys Leu Ala Gly Val Phe Ser Leu Ala Asp Gly Met Lys Leu Ile
            660                 665                 670

Thr Ala Arg Gly Lys Leu Met His Ala Leu Pro Ser Asn Gly Ser Met
        675                 680                 685

Ala Ala Val Phe Ala Asp Lys Thr Val Ile Lys Pro Tyr Leu Ser Glu
    690                 695                 700

His Leu Thr Val Gly Ala Glu Asn Gly Ser His Leu Val Leu Ser Gly
705                 710                 715                 720

Lys Thr Pro Cys Leu Glu Ala Ser Ile His Lys Leu Gln Ser Gln Gly
                725                 730                 735

Ile Lys Thr Lys Pro Leu Lys Val Ser His Ala Phe His Ser Pro Leu
            740                 745                 750

Met Ala Pro Met Leu Ala Glu Phe Arg Glu Ile Ala Glu Gln Ile Thr
        755                 760                 765

Phe His Pro Pro Arg Ile Pro Leu Ile Ser Asn Val Thr Gly Gly Gln
    770                 775                 780

Ile Glu Ala Glu Ile Ala Gln Ala Asp Tyr Trp Val Lys His Val Ser
785                 790                 795                 800

Gln Pro Val Lys Phe Val Gln Ser Ile Gln Thr Leu Ala Gln Ala Gly
                805                 810                 815

Val Asn Val Tyr Leu Glu Ile Gly Val Lys Pro Val Leu Leu Ser Met
            820                 825                 830

Gly Arg His Cys Leu Ala Glu Gln Glu Ala Val Trp Leu Pro Ser Leu
        835                 840                 845

Arg Pro His Ser Glu Pro Trp Pro Glu Ile Leu Thr Ser Leu Gly Lys
    850                 855                 860

Leu Tyr Glu Gln Gly Leu Asn Ile Asp Trp Gln Thr Val Glu Ala Gly
865                 870                 875                 880

Asp Arg Arg Arg Lys Leu Ile Leu Pro Thr Tyr Pro Phe Gln Arg Gln
                885                 890                 895

Arg Tyr Trp Phe Asn Gln Gly Ser Trp Gln Thr Val Glu Thr Glu Ser
            900                 905                 910

Val Asn Pro Gly Pro Asp Asp Leu Asn Asp Trp Leu Tyr Gln Val Ala
        915                 920                 925

Trp Thr Pro Leu Asp Thr Leu Pro Pro Ala Pro Glu Pro Ser Ala Lys
    930                 935                 940
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Leu Trp Leu Ile Leu Gly Asp Arg His Asp His Gln Pro Ile Glu Ala
945                 950                 955                 960

Gln Phe Lys Asn Ala Gln Arg Val Tyr Leu Gly Gln Ser Asn His Phe
                965                 970                 975

Pro Thr Asn Ala Pro Trp Glu Val Ser Ala Asp Ala Leu Asp Asn Leu
            980                 985                 990

Phe Thr His Val Gly Ser Gln Asn  Leu Ala Gly Ile Leu  Tyr Leu Cys
        995                 1000                1005

Pro Pro  Gly Glu Asp Pro Glu  Asp Leu Asp Glu Ile  Gln Lys Gln
    1010                1015                1020

Thr Ser  Gly Phe Ala Leu Gln  Leu Ile Gln Thr Leu  Tyr Gln Gln
    1025                1030                1035

Lys Ile  Ala Val Pro Cys Trp  Phe Val Thr His Gln  Ser Gln Arg
    1040                1045                1050

Val Leu  Glu Thr Asp Ala Val  Thr Gly Phe Ala Gln  Gly Gly Leu
    1055                1060                1065

Trp Gly  Leu Ala Gln Ala Ile  Ala Leu Glu His Pro  Glu Leu Trp
    1070                1075                1080

Gly Gly  Ile Ile Asp Val Asp  Asp Ser Leu Pro Asn  Phe Ala Gln
    1085                1090                1095

Ile Cys  Gln Gln Arg Gln Val  Gln Gln Leu Ala Val  Arg His Gln
    1100                1105                1110

Lys Leu  Tyr Gly Ala Gln Leu  Lys Lys Gln Pro Ser  Leu Pro Gln
    1115                1120                1125

Lys Asn  Leu Gln Ile Gln Pro  Gln Gln Thr Tyr Leu  Val Thr Gly
    1130                1135                1140

Gly Leu  Gly Ala Ile Gly Arg  Lys Ile Ala Gln Trp  Leu Ala Ala
    1145                1150                1155

Ala Gly  Ala Glu Lys Val Ile  Leu Val Ser Arg Arg  Ala Pro Ala
    1160                1165                1170

Ala Asp  Gln Gln Thr Leu Pro  Thr Asn Ala Val Val  Tyr Pro Cys
    1175                1180                1185

Asp Leu  Ala Asp Ala Ala Gln  Val Ala Lys Leu Phe  Gln Thr Tyr
    1190                1195                1200

Pro His  Ile Lys Gly Ile Phe  His Ala Ala Gly Thr  Leu Ala Asp
    1205                1210                1215

Gly Leu  Leu Gln Gln Gln Thr  Trp Gln Lys Phe Gln  Thr Val Ala
    1220                1225                1230

Ala Ala  Lys Met Lys Gly Thr  Trp His Leu His Arg  His Ser Gln
    1235                1240                1245

Lys Leu  Asp Leu Asp Phe Phe  Val Leu Phe Ser Ser  Val Ala Gly
    1250                1255                1260

Val Leu  Gly Ser Pro Gly Gln  Gly Asn Tyr Ala Ala  Ala Asn Arg
    1265                1270                1275

Gly Met  Ala Ala Ile Ala Gln  Tyr Arg Gln Ala Gln  Gly Leu Pro
    1280                1285                1290

Ala Leu  Ala Ile His Trp Gly  Pro Trp Ala Glu Gly  Gly Met Ala
    1295                1300                1305

Asn Ser  Leu Ser Asn Gln Asn  Leu Ala Trp Leu Pro  Pro Pro Gln
    1310                1315                1320

Gly Leu  Thr Ile Leu Glu Lys  Val Leu Gly Ala Gln  Gly Glu Met
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    1325                1330                1335

Gly Val  Phe Lys Pro Asp Trp  Gln Asn Leu Ala Lys  Gln Phe Pro
    1340                1345                1350

Glu Phe  Ala Lys Thr His Tyr  Phe Ala Ala Val Ile  Pro Ser Ala
    1355                1360                1365

Glu Ala  Val Pro Pro Thr Ala  Ser Ile Phe Asp Lys  Leu Ile Asn
    1370                1375                1380

Leu Glu  Ala Ser Gln Arg Ala  Asp Tyr Leu Leu Asp  Tyr Leu Arg
    1385                1390                1395

Arg Ser  Val Ala Gln Ile Leu  Lys Leu Glu Ile Glu  Gln Ile Gln
    1400                1405                1410

Ser His  Asp Ser Leu Leu Asp  Leu Gly Met Asp Ser  Leu Met Ile
    1415                1420                1425

Met Glu  Ala Ile Ala Ser Leu  Lys Gln Asp Leu Gln  Leu Met Leu
    1430                1435                1440

Tyr Pro  Arg Glu Ile Tyr Glu  Arg Pro Arg Leu Asp  Val Leu Thr
    1445                1450                1455

Ala Tyr  Leu Ala Ala Glu Phe  Thr Lys Ala His Asp  Ser Glu Ala
    1460                1465                1470

Ala Thr  Ala Ala Ala Ala Ile  Pro Ser Gln Ser Leu  Ser Val Lys
    1475                1480                1485

Thr Lys  Lys Gln Trp Gln Lys  Pro Asp His Lys Asn  Pro Asn Pro
    1490                1495                1500

Ile Ala  Phe Ile Leu Ser Ser  Pro Arg Ser Gly Ser  Thr Leu Leu
    1505                1510                1515

Arg Val  Met Leu Ala Gly His  Pro Gly Leu Tyr Ser  Pro Pro Glu
    1520                1525                1530

Leu His  Leu Leu Pro Phe Glu  Thr Met Gly Asp Arg  His Gln Glu
    1535                1540                1545

Leu Gly  Leu Ser His Leu Gly  Glu Gly Leu Gln Arg  Ala Leu Met
    1550                1555                1560

Asp Leu  Glu Asn Leu Thr Pro  Glu Ala Ser Gln Ala  Lys Val Asn
    1565                1570                1575

Gln Trp  Val Lys Ala Asn Thr  Pro Ile Ala Asp Ile  Tyr Ala Tyr
    1580                1585                1590

Leu Gln  Arg Gln Ala Glu Gln  Arg Leu Leu Ile Asp  Lys Ser Pro
    1595                1600                1605

Ser Tyr  Gly Ser Asp Arg His  Ile Leu Asp His Ser  Glu Ile Leu
    1610                1615                1620

Phe Asp  Gln Ala Lys Tyr Ile  His Leu Val Arg His  Pro Tyr Ala
    1625                1630                1635

Val Ile  Glu Ser Phe Thr Arg  Leu Arg Met Asp Lys  Leu Leu Gly
    1640                1645                1650

Ala Glu  Gln Gln Asn Pro Tyr  Ala Leu Ala Glu Ser  Ile Trp Arg
    1655                1660                1665

Thr Ser  Asn Arg Asn Ile Leu  Asp Leu Gly Arg Thr  Val Gly Ala
    1670                1675                1680

Asp Arg  Tyr Leu Gln Val Ile  Tyr Glu Asp Leu Val  Arg Asp Pro
    1685                1690                1695

Arg Lys  Val Leu Thr Asn Ile  Cys Asp Phe Leu Gly  Val Asp Phe
    1700                1705                1710
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Asp Glu  Ala Leu Leu Asn Pro  Tyr Ser Gly Asp Arg  Leu Thr Asp
    1715                 1720                 1725

Gly Leu  His Gln Gln Ser Met  Gly Val Gly Asp Pro  Asn Phe Leu
    1730                 1735                 1740

Gln His  Lys Thr Ile Asp Pro  Ala Leu Ala Asp Lys  Trp Arg Ser
    1745                 1750                 1755

Ile Thr  Leu Pro Ala Ala Leu  Gln Leu Asp Thr Ile  Gln Leu Ala
    1760                 1765                 1770

Glu Thr  Phe Ala Tyr Asp Leu  Pro Gln Glu Pro Gln  Leu Thr Pro
    1775                 1780                 1785

Gln Thr  Gln Ser Leu Pro Ser  Met Val Glu Arg Phe  Val Thr Val
    1790                 1795                 1800

Arg Gly  Leu Glu Thr Cys Leu  Cys Glu Trp Gly Asp  Arg His Gln
    1805                 1810                 1815

Pro Leu  Val Leu Leu Leu His  Gly Ile Leu Glu Gln  Gly Ala Ser
    1820                 1825                 1830

Trp Gln  Leu Ile Ala Pro Gln  Leu Ala Ala Gln Gly  Tyr Trp Val
    1835                 1840                 1845

Val Ala  Pro Asp Leu Arg Gly  His Gly Lys Ser Ala  His Ala Gln
    1850                 1855                 1860

Ser Tyr  Ser Met Leu Asp Phe  Leu Ala Asp Val Asp  Ala Leu Ala
    1865                 1870                 1875

Lys Gln  Leu Gly Asp Arg Pro  Phe Thr Leu Val Gly  His Ser Met
    1880                 1885                 1890

Gly Ser  Ile Ile Gly Ala Met  Tyr Ala Gly Ile Arg  Gln Thr Gln
    1895                 1900                 1905

Val Glu  Lys Leu Ile Leu Val  Glu Thr Ile Val Pro  Asn Asp Ile
    1910                 1915                 1920

Asp Asp  Ala Glu Thr Gly Asn  His Leu Thr Thr His  Leu Asp Tyr
    1925                 1930                 1935

Leu Ala  Ala Pro Pro Gln His  Pro Ile Phe Pro Ser  Leu Glu Val
    1940                 1945                 1950

Ala Ala  Arg Arg Leu Arg Gln  Ala Thr Pro Gln Leu  Pro Lys Asp
    1955                 1960                 1965

Leu Ser  Ala Phe Leu Thr Gln  Arg Ser Thr Lys Ser  Val Glu Lys
    1970                 1975                 1980

Gly Val  Gln Trp Arg Trp Asp  Ala Phe Leu Arg Thr  Arg Ala Gly
    1985                 1990                 1995

Ile Glu  Phe Asn Gly Ile Ser  Arg Arg Arg Tyr Leu  Ala Leu Leu
    2000                 2005                 2010

Lys Asp  Ile Gln Ala Pro Ile  Thr Leu Ile Tyr Gly  Asp Gln Ser
    2015                 2020                 2025

Glu Phe  Asn Arg Pro Ala Asp  Leu Gln Ala Ile Gln  Ala Ala Leu
    2030                 2035                 2040

Pro Gln  Ala Gln Arg Leu Thr  Val Ala Gly Gly His  Asn Leu His
    2045                 2050                 2055

Phe Glu  Asn Pro Gln Ala Ile  Ala Gln Ile Val Tyr  Gln Gln Leu
    2060                 2065                 2070

Gln Thr  Pro Val Pro Lys Thr  Gln
    2075                 2080
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<210> SEQ ID NO 10

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<211> LENGTH: 582
<212> TYPE: PRT
<213> ORGANISM: Lyngbya majuscula

<400> SEQUENCE: 10

Phe Ile Leu Ser Ser Pro Arg Ser Gly Ser Thr Leu Leu Arg Val Met
1 5 10 15

Leu Ala Gly His Ser Ser Leu Phe Ser Pro Pro Glu Leu His Leu Leu
20 25 30

Pro Phe Asn Thr Met Lys Glu Arg Gln Glu Gln Leu Asn Leu Ser Tyr
35 40 45

Leu Gly Glu Gly Leu Gln Lys Thr Phe Met Glu Val Lys Asn Leu Asp
50 55 60

Ala Thr Ala Ser Gln Ala Leu Ile Lys Asp Leu Glu Ser Gln Asn Leu
65 70 75 80

Ser Ile Gln Gln Val Tyr Gly Met Leu Gln Glu Asn Ile Ala Pro Arg
85 90 95

Leu Leu Val Asp Lys Ser Pro Thr Tyr Ala Met Glu Pro Thr Ile Leu
100 105 110

Glu Arg Gly Glu Ala Leu Phe Ala Asn Ser Lys Tyr Ile Tyr Leu Val
115 120 125

Arg His Pro Tyr Ser Val Ile Glu Ser Phe Val Arg Met Arg Met Gln
130 135 140

Lys Leu Val Gly Leu Gly Glu Glu Asn Pro Tyr Arg Val Ala Glu Gln
145 150 155 160

Val Trp Ala Lys Ser Asn Gln Asn Ile Leu Asn Phe Leu Ser Gln Leu
165 170 175

Glu Pro Glu Arg Gln His Gln Ile Arg Tyr Glu Asp Leu Val Lys Lys
180 185 190

Pro Gln Gln Val Leu Ser Gln Leu Cys Asp Phe Leu Asn Val Pro Phe
195 200 205

Glu Pro Glu Leu Leu Gln Pro Tyr Gln Gly Asp Arg Met Thr Gly Gly
210 215 220

Val His Gln Lys Ser Leu Ser Ile Ser Asp Pro Asn Phe Leu Lys His
225 230 235 240

Asn Thr Ile Asp Glu Ser Leu Ala Asp Lys Trp Lys Thr Ile Gln Leu
245 250 255

Pro Tyr Pro Leu Lys Ser Glu Thr Gln Arg Ile Ala Ser Gln Leu Ser
260 265 270

Tyr Glu Leu Pro Asn Leu Val Thr Thr Pro Thr Asn Gln Gln Pro Gln
275 280 285

Val Ser Thr Thr Pro Ser Thr Glu Gln Pro Ile Met Glu Glu Lys Phe
290 295 300

Leu Glu Phe Gly Gly Asn Gln Ile Cys Leu Cys Ser Trp Gly Ser Pro
305 310 315 320

Glu His Pro Val Val Leu Cys Ile His Gly Ile Leu Glu Gln Gly Leu
325 330 335

Ala Trp Gln Glu Val Ala Leu Pro Leu Ala Ala Gln Gly Tyr Arg Val
340 345 350

Val Ala Pro Asp Leu Phe Gly His Gly Arg Ser Ser His Leu Glu Met
355 360 365

Val Thr Ser Tyr Ser Ser Leu Thr Phe Leu Ala Gln Ile Asp Arg Val
370 375 380

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Ile Gln Glu Leu Pro Asp Gln Pro Leu Leu Leu Val Gly His Ser Met
385                 390                 395                 400

Gly Ala Met Leu Ala Thr Ala Ile Ala Ser Val Arg Pro Lys Lys Ile
                405                 410                 415

Lys Glu Leu Ile Leu Val Glu Leu Pro Leu Pro Ala Glu Glu Ser Lys
            420                 425                 430

Lys Glu Ser Ala Val Asn Gln Leu Thr Thr Cys Leu Asp Tyr Leu Ser
        435                 440                 445

Ser Thr Pro Gln His Pro Ile Phe Pro Asp Val Ala Thr Ala Ala Ser
    450                 455                 460

Arg Leu Arg Gln Ala Ile Pro Ser Leu Ser Glu Glu Phe Ser Tyr Ile
465                 470                 475                 480

Leu Ala Gln Arg Ile Thr Gln Pro Asn Gln Gly Gly Val Arg Trp Ser
                485                 490                 495

Trp Asp Ala Ile Ile Arg Thr Arg Ser Ile Leu Gly Leu Asn Asn Leu
            500                 505                 510

Pro Gly Gly Arg Ser Gln Tyr Leu Glu Met Leu Lys Ser Ile Gln Val
        515                 520                 525

Pro Thr Thr Leu Val Tyr Gly Asp Ser Ser Lys Leu Asn Arg Pro Glu
    530                 535                 540

Asp Leu Gln Gln Gln Lys Met Thr Met Thr Gln Ala Lys Arg Val Phe
545                 550                 555                 560

Leu Ser Gly Gly His Asn Leu His Ile Asp Ala Ala Ala Ala Leu Ala
                565                 570                 575

Ser Leu Ile Leu Thr Ser
            580


<210> SEQ ID NO 11
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Lyngbya majuscula

<400> SEQUENCE: 11

Phe Ile Leu Ser Ser Pro Arg Ser Gly Ser Thr Leu Leu Arg Val Met
1               5                   10                  15

Leu Ala Gly His Ser Ser Leu Phe Ser Pro Pro Glu Leu His Leu Leu
            20                  25                  30

Pro Phe Asn Thr Met Lys Glu Arg Gln Glu Gln Leu Asn Leu Ser Tyr
        35                  40                  45

Leu Gly Glu Gly Leu Gln Lys Thr Phe Met Glu Val Lys Asn Leu Asp
    50                  55                  60

Ala Thr Ala Ser Gln Ala Leu Ile Lys Asp Leu Glu Ser Gln Asn Leu
65                  70                  75                  80

Ser Ile Gln Gln Val Tyr Gly Met Leu Gln Glu Asn Ile Ala Pro Arg
                85                  90                  95

Leu Leu Val Asp Lys Ser Pro Thr Tyr Ala Met Glu Pro Thr Ile Leu
            100                 105                 110

Glu Arg Gly Glu Ala Leu Phe Ala Asn Ser Lys Tyr Ile Tyr Leu Val
        115                 120                 125

Arg His Pro Tyr Ser Val Ile Glu Ser Phe Val Arg Met Arg Met Gln
    130                 135                 140

Lys Leu Val Gly Leu Gly Glu Glu Asn Pro Tyr Arg Val Ala Glu Gln
145                 150                 155                 160
```

-continued

```
Val Trp Ala Lys Ser Asn Gln Asn Ile Leu Asn Phe Leu Ser Gln Leu
                165                 170                 175

Glu Pro Glu Arg Gln His Gln Ile Arg Tyr Glu Asp Leu Val Lys Lys
            180                 185                 190

Pro Gln Gln Val Leu Ser Gln Leu Cys Asp Phe Leu Asn Val Pro Phe
        195                 200                 205

Glu Pro Glu Leu Leu Gln Pro Tyr Gln Gly Asp Arg Met Thr Gly Gly
    210                 215                 220

Val His Gln Lys Ser Leu Ser Ile Ser Asp Pro Asn Phe Leu Lys His
225                 230                 235                 240

Asn Thr Ile Asp Glu Ser Leu Ala Asp Lys Trp Lys Thr Ile Gln Leu
                245                 250                 255

Pro Tyr Pro Leu Lys
            260


<210> SEQ ID NO 12
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Lyngbya majuscula

<400> SEQUENCE: 12

Glu Lys Phe Leu Glu Phe Gly Gly Asn Gln Ile Cys Leu Cys Ser Trp
1               5                   10                  15

Gly Ser Pro Glu His Pro Val Val Leu Cys Ile His Gly Ile Leu Glu
            20                  25                  30

Gln Gly Leu Ala Trp Gln Glu Val Ala Leu Pro Leu Ala Ala Gln Gly
        35                  40                  45

Tyr Arg Val Val Ala Pro Asp Leu Phe Gly His Gly Arg Ser Ser His
    50                  55                  60

Leu Glu Met Val Thr Ser Tyr Ser Ser Leu Thr Phe Leu Ala Gln Ile
65                  70                  75                  80

Asp Arg Val Ile Gln Glu Leu Pro Asp Gln Pro Leu Leu Leu Val Gly
                85                  90                  95

His Ser Met Gly Ala Met Leu Ala Thr Ala Ile Ala Ser Val Arg Pro
            100                 105                 110

Lys Lys Ile Lys Glu Leu Ile Leu Val Glu Leu Pro Leu Pro Ala Glu
        115                 120                 125

Glu Ser Lys Lys Glu Ser Ala Val Asn Gln Leu Thr Thr Cys Leu Asp
    130                 135                 140

Tyr Leu Ser Ser Thr Pro Gln His Pro Ile Phe Pro Asp Val Ala Thr
145                 150                 155                 160

Ala Ala Ser Arg Leu Arg Gln Ala Ile Pro Ser Leu Ser Glu Glu Phe
                165                 170                 175

Ser Tyr Ile Leu Ala Gln Arg Ile Thr Gln Pro Asn Gln Gly Gly Val
            180                 185                 190

Arg Trp Ser Trp Asp Ala Ile Ile Arg Thr Arg Ser Ile Leu Gly Leu
        195                 200                 205

Asn Asn Leu Pro Gly Gly Arg Ser Gln Tyr Leu Glu Met Leu Lys Ser
    210                 215                 220

Ile Gln Val Pro Thr Thr Leu Val Tyr Gly Asp Ser Ser Lys Leu Asn
225                 230                 235                 240

Arg Pro Glu Asp Leu Gln Gln Gln Lys Met Thr Met Thr Gln Ala Lys
                245                 250                 255
```

-continued

Arg Val Phe Leu Ser Gly Gly His Asn Leu His Ile Asp Ala Ala Ala
260 265 270

Ala Leu Ala Ser Leu Ile Leu Thr Ser
275 280

<210> SEQ ID NO 13
<211> LENGTH: 626
<212> TYPE: PRT
<213> ORGANISM: Salmonella typhimurium

<400> SEQUENCE: 13

Met Ser Phe Ser Glu Phe Tyr Gln Arg Ser Ile Asn Glu Pro Glu Ala
1 5 10 15

Phe Trp Ala Glu Gln Ala Arg Arg Ile Asp Trp Arg Gln Pro Phe Thr
20 25 30

Gln Thr Leu Asp His Ser Arg Pro Pro Phe Ala Arg Trp Phe Cys Gly
35 40 45

Gly Thr Thr Asn Leu Cys His Asn Ala Val Asp Arg Trp Arg Asp Lys
50 55 60

Gln Pro Glu Ala Leu Ala Leu Ile Ala Val Ser Ser Glu Thr Asp Glu
65 70 75 80

Glu Arg Thr Phe Thr Phe Ser Gln Leu His Asp Glu Val Asn Ile Val
85 90 95

Ala Ala Met Leu Leu Ser Leu Gly Val Gln Arg Gly Asp Arg Val Leu
100 105 110

Val Tyr Met Pro Met Ile Ala Glu Ala Gln Ile Thr Leu Leu Ala Cys
115 120 125

Ala Arg Ile Gly Ala Ile His Ser Val Val Phe Gly Gly Phe Ala Ser
130 135 140

His Ser Val Ala Ala Arg Ile Asp Asp Ala Arg Pro Ala Leu Ile Val
145 150 155 160

Ser Ala Asp Ala Gly Ala Arg Gly Gly Lys Ile Leu Pro Tyr Lys Lys
165 170 175

Leu Leu Asp Asp Ala Ile Ala Gln Ala Gln His Gln Pro Lys His Val
180 185 190

Leu Leu Val Asp Arg Gly Leu Ala Lys Met Ala Trp Val Asp Gly Arg
195 200 205

Asp Leu Asp Phe Ala Thr Leu Arg Gln Gln His Leu Gly Ala Ser Val
210 215 220

Pro Val Ala Trp Leu Glu Ser Asn Glu Thr Ser Cys Ile Leu Tyr Thr
225 230 235 240

Ser Gly Thr Thr Gly Lys Pro Lys Gly Val Gln Arg Asp Val Gly Gly
245 250 255

Tyr Ala Val Ala Leu Ala Thr Ser Met Asp Thr Ile Phe Gly Gly Lys
260 265 270

Ala Gly Gly Val Phe Phe Cys Ala Ser Asp Ile Gly Trp Val Val Gly
275 280 285

His Ser Tyr Ile Val Tyr Ala Pro Leu Leu Ala Gly Met Ala Thr Ile
290 295 300

Val Tyr Glu Gly Leu Pro Thr Tyr Pro Asp Cys Gly Val Trp Trp Lys
305 310 315 320

Ile Val Glu Lys Tyr Gln Val Asn Arg Met Phe Ser Ala Pro Thr Ala
325 330 335

-continued

```
Ile Arg Val Leu Lys Lys Phe Pro Thr Ala Gln Ile Arg Asn His Asp
            340                 345                 350

Leu Ser Ser Leu Glu Ala Leu Tyr Leu Ala Gly Glu Pro Leu Asp Glu
        355                 360                 365

Pro Thr Ala Ser Trp Val Thr Glu Thr Leu Gly Val Pro Val Ile Asp
    370                 375                 380

Asn Tyr Trp Gln Thr Glu Ser Gly Trp Pro Ile Met Ala Leu Ala Arg
385                 390                 395                 400

Ala Leu Asp Asp Arg Pro Ser Arg Leu Gly Ser Pro Gly Val Pro Met
                405                 410                 415

Tyr Gly Tyr Asn Val Gln Leu Leu Asn Glu Val Thr Gly Glu Pro Cys
            420                 425                 430

Gly Ile Asn Glu Lys Gly Met Leu Val Ile Glu Gly Pro Leu Pro Pro
        435                 440                 445

Gly Cys Ile Gln Thr Ile Trp Gly Asp Asp Ala Arg Phe Val Lys Thr
    450                 455                 460

Tyr Trp Ser Leu Phe Asn Arg Gln Val Tyr Ala Thr Phe Asp Trp Gly
465                 470                 475                 480

Ile Arg Asp Ala Glu Gly Tyr Tyr Phe Ile Leu Gly Arg Thr Asp Asp
                485                 490                 495

Val Ile Asn Ile Ala Gly His Arg Leu Gly Thr Arg Glu Ile Glu Glu
            500                 505                 510

Ser Ile Ser Ser Tyr Pro Asn Val Ala Glu Val Ala Val Val Gly Ile
        515                 520                 525

Lys Asp Ala Leu Lys Gly Gln Val Ala Val Ala Phe Val Ile Pro Lys
    530                 535                 540

Gln Ser Asp Thr Leu Ala Asp Arg Glu Ala Ala Arg Asp Glu Glu Asn
545                 550                 555                 560

Ala Ile Met Ala Leu Val Asp Asn Gln Ile Gly His Phe Gly Arg Pro
                565                 570                 575

Ala His Val Trp Phe Val Ser Gln Leu Pro Lys Thr Arg Ser Gly Lys
            580                 585                 590

Met Leu Arg Arg Thr Ile Gln Ala Glu Gly Arg Asp Pro Gly Asp Leu
        595                 600                 605

Thr Thr Ile Asp Asp Pro Ala Ser Leu Gln Gln Ile Arg Gln Ala Ile
    610                 615                 620

Glu Glu
625
```

<210> SEQ ID NO 14
<211> LENGTH: 410
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 14

```
Met Ala Ala Ala Leu Leu Ala Arg Ala Arg Gly Pro Leu Arg Arg Ala
1               5                   10                  15

Leu Gly Val Arg Asp Trp Arg Arg Leu His Thr Val Tyr Gln Ser Val
            20                  25                  30

Glu Leu Pro Glu Thr His Gln Met Leu Arg Gln Thr Cys Arg Asp Phe
        35                  40                  45

Ala Glu Lys Glu Leu Val Pro Ile Ala Ala Gln Leu Asp Arg Glu His
    50                  55                  60
```

-continued

```
Leu Phe Pro Thr Ala Gln Val Lys Lys Met Gly Glu Leu Gly Leu Leu
65                  70                  75                  80

Ala Met Asp Val Pro Glu Glu Leu Ser Gly Ala Gly Leu Gly Tyr Leu
                85                  90                  95

Ala Tyr Ser Ile Ala Leu Glu Glu Ile Ser Arg Ala Cys Ala Ser Thr
            100                 105                 110

Gly Val Ile Met Ser Val Asn Asn Ser Leu Tyr Leu Gly Pro Ile Leu
        115                 120                 125

Lys Phe Gly Ser Ala Gln Gln Lys Gln Gln Trp Ile Thr Pro Phe Thr
    130                 135                 140

Asn Gly Asp Lys Ile Gly Cys Phe Ala Leu Ser Glu Pro Gly Asn Gly
145                 150                 155                 160

Ser Asp Ala Gly Ala Ala Ser Thr Thr Ala Arg Glu Glu Gly Asp Ser
                165                 170                 175

Trp Val Leu Asn Gly Thr Lys Ala Trp Ile Thr Asn Ser Trp Glu Ala
            180                 185                 190

Ser Ala Thr Val Val Phe Ala Ser Thr Asp Arg Ser Arg Gln Asn Lys
        195                 200                 205

Gly Ile Ser Ala Phe Leu Val Pro Met Pro Thr Pro Gly Leu Thr Leu
    210                 215                 220

Gly Lys Lys Glu Asp Lys Leu Gly Ile Arg Ala Ser Ser Thr Ala Asn
225                 230                 235                 240

Leu Ile Phe Glu Asp Cys Arg Ile Pro Lys Glu Asn Leu Leu Gly Glu
                245                 250                 255

Pro Gly Met Gly Phe Lys Ile Ala Met Gln Thr Leu Asp Met Gly Arg
            260                 265                 270

Ile Gly Ile Ala Ser Gln Ala Leu Gly Ile Ala Gln Ala Ser Leu Asp
        275                 280                 285

Cys Ala Val Lys Tyr Ala Glu Asn Arg Asn Ala Phe Gly Ala Pro Leu
    290                 295                 300

Thr Lys Leu Gln Asn Ile Gln Phe Lys Leu Ala Asp Met Ala Leu Ala
305                 310                 315                 320

Leu Glu Ser Ala Arg Leu Leu Thr Trp Arg Ala Ala Met Leu Lys Asp
                325                 330                 335

Asn Lys Lys Pro Phe Thr Lys Glu Ser Ala Met Arg Lys Leu Ala Ala
            340                 345                 350

Ser Glu Ala Ala Thr Ala Ile Ser Ala Ile Gln Ile Leu Gly Ser Met
        355                 360                 365

Gly Tyr Val Thr Glu Met Pro Ala Glu Arg Tyr Tyr Arg Asp Ala Arg
    370                 375                 380

Ile Thr Glu Ile Tyr Glu Gly Thr Ser Glu Ile Gln Arg Leu Val Ile
385                 390                 395                 400

Ala Gly His Leu Leu Arg Ser Tyr Arg Ser
                405                 410
```

<210> SEQ ID NO 15
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 15

```
Thr Ala Lys Thr Ala Asn Gly Cys Glu Ala Val Cys Ile Phe Val Asn
1               5                   10                  15
```

-continued

```
Asp Asp Gly Ser Arg Pro Val Leu Glu Glu Leu Lys Lys His Gly Val
            20                  25                  30

Lys Tyr Ile Ala Leu Arg Cys Ala Gly Phe Asn Asn Val Asp Leu Asp
        35                  40                  45

Ala Ala Lys Glu Leu Gly Leu Lys Val Val Arg Val Pro Ala Tyr Asp
    50                  55                  60

Pro Glu Ala Val Ala Glu His Ala Ile Gly Met Met Met Thr Leu Asn
65                  70                  75                  80

Arg Arg Ile His Arg Ala Tyr Gln Arg Thr Arg Asp Ala Asn Phe Ser
                85                  90                  95

Leu Glu Gly Leu Thr Gly Phe Thr Met Tyr Gly Lys Thr Ala Gly Val
            100                 105                 110

Ile Gly Thr Gly Lys Ile Gly Val Ala Met Leu Arg Ile Leu Lys Gly
        115                 120                 125

Phe Gly Met Arg Leu Leu Ala Phe Asp Pro Tyr Pro Ser Ala Ala Ala
    130                 135                 140

Leu Glu Leu Gly Val Glu Tyr Val Asp Leu Pro Thr Leu Phe Ser Glu
145                 150                 155                 160

Ser Asp Val Ile Ser Leu His Cys Pro Leu Thr Pro Glu Asn Tyr His
                165                 170                 175

Leu Leu Asn Glu Ala Ala Phe Asp Gln Met Lys Asn Gly Val Met Ile
            180                 185                 190

Val Asn Thr Ser Arg Gly Ala Leu Ile Asp Ser Gln Ala Ala Ile Glu
        195                 200                 205

Ala Leu Lys Asn Gln Lys Ile Gly Ser Leu Gly Met Asp Val Tyr Glu
    210                 215                 220

Asn Glu Arg Asp Leu Phe Phe Glu Asp Lys Ser Asn Asp Val Ile Gln
225                 230                 235                 240

Asp Asp Val Phe Arg Arg Leu Ser Ala Cys His Asn Val Leu Phe Thr
                245                 250                 255

Gly His Gln Ala Phe Leu Thr Ala Glu Ala Leu Thr Ser Ile Ser Gln
            260                 265                 270

Thr Thr Leu Gln Asn Leu Ser Asn Leu Glu Lys Gly Glu Thr Cys Pro
        275                 280                 285

Asn Glu Leu Val
    290


<210> SEQ ID NO 16
<211> LENGTH: 522
<212> TYPE: PRT
<213> ORGANISM: Clostridium proponicum

<400> SEQUENCE: 16

Met Arg Lys Val Pro Ile Ile Thr Ala Asp Glu Ala Ala Lys Leu Ile
1               5                   10                  15

Lys Asp Gly Asp Thr Val Thr Thr Ser Gly Phe Val Gly Asn Ala Ile
            20                  25                  30

Pro Glu Ala Leu Asp Arg Ala Val Glu Lys Arg Phe Leu Glu Thr Gly
        35                  40                  45

Glu Pro Lys Asn Ile Thr Tyr Val Tyr Cys Gly Ser Gln Gly Asn Arg
    50                  55                  60

Asp Gly Arg Gly Ala Glu His Phe Ala His Glu Gly Leu Leu Lys Arg
65                  70                  75                  80
```

-continued

```
Tyr Ile Ala Gly His Trp Ala Thr Val Pro Ala Leu Gly Lys Met Ala
                85                  90                  95

Met Glu Asn Lys Met Glu Ala Tyr Asn Val Ser Gln Gly Ala Leu Cys
            100                 105                 110

His Leu Phe Arg Asp Ile Ala Ser His Lys Pro Gly Val Phe Thr Lys
        115                 120                 125

Val Gly Ile Gly Thr Phe Ile Asp Pro Arg Asn Gly Gly Gly Lys Val
    130                 135                 140

Asn Asp Ile Thr Lys Glu Asp Ile Val Glu Leu Val Glu Ile Lys Gly
145                 150                 155                 160

Gln Glu Tyr Leu Phe Tyr Pro Ala Phe Pro Ile His Val Ala Leu Ile
                165                 170                 175

Arg Gly Thr Tyr Ala Asp Glu Ser Gly Asn Ile Thr Phe Glu Lys Glu
            180                 185                 190

Val Ala Pro Leu Glu Gly Thr Ser Val Cys Gln Ala Val Lys Asn Ser
        195                 200                 205

Gly Gly Ile Val Val Val Gln Val Glu Arg Val Val Lys Ala Gly Thr
    210                 215                 220

Leu Asp Pro Arg His Val Lys Val Pro Gly Ile Tyr Val Asp Tyr Val
225                 230                 235                 240

Val Val Ala Asp Pro Glu Asp His Gln Gln Ser Leu Asp Cys Glu Tyr
                245                 250                 255

Asp Pro Ala Leu Ser Gly Glu His Arg Arg Pro Glu Val Val Gly Glu
            260                 265                 270

Pro Leu Pro Leu Ser Ala Lys Lys Val Ile Gly Arg Arg Gly Ala Ile
        275                 280                 285

Glu Leu Glu Lys Asp Val Ala Val Asn Leu Gly Val Gly Ala Pro Glu
    290                 295                 300

Tyr Val Ala Ser Val Ala Asp Glu Glu Gly Ile Val Asp Phe Met Thr
305                 310                 315                 320

Leu Thr Ala Glu Ser Gly Ala Ile Gly Gly Val Pro Ala Gly Gly Val
                325                 330                 335

Arg Phe Gly Ala Ser Tyr Asn Ala Asp Ala Leu Ile Asp Gln Gly Tyr
            340                 345                 350

Gln Phe Asp Tyr Tyr Asp Gly Gly Gly Leu Asp Leu Cys Tyr Leu Gly
        355                 360                 365

Leu Ala Glu Cys Asp Glu Lys Gly Asn Ile Asn Val Ser Arg Phe Gly
    370                 375                 380

Pro Arg Ile Ala Gly Cys Gly Gly Phe Ile Asn Ile Thr Gln Asn Thr
385                 390                 395                 400

Pro Lys Val Phe Phe Cys Gly Thr Phe Thr Ala Gly Gly Leu Lys Val
                405                 410                 415

Lys Ile Glu Asp Gly Lys Val Ile Ile Val Gln Glu Gly Lys Gln Lys
            420                 425                 430
```

-continued

Lys Phe Leu Lys Ala Val Glu Gln Ile Thr Phe Asn Gly Asp Val Ala
435 440 445

Leu Ala Asn Lys Gln Gln Val Thr Tyr Ile Thr Glu Arg Cys Val Phe
450 455 460

Leu Leu Lys Glu Asp Gly Leu His Leu Ser Glu Ile Ala Pro Gly Ile
465 470 475 480

Gln Thr Gln Ile Leu Asp Val Met Asp Phe Ala Pro Ile Ile Asp Arg
485 490 495

Asp Ala Asn Gly Gln Ile Lys Leu Met Asp Ala Ala Leu Phe Ala Glu
500 505 510

Gly Leu Met Gly Leu Lys Glu Met Lys Ser
515 520

<210> SEQ ID NO 17
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Clostridium proponicum

<400> SEQUENCE: 17

Glu Phe Lys Ile Ala Ile Val Asp Asp Asp Leu Ala Gln Glu Ser Arg
1 5 10 15

Gln Ile Arg Val Asp Val Leu Asp Gly Glu Gly Gly Pro Leu Tyr Arg
20 25 30

Met Ala Lys Ala Trp Gln Gln Met Tyr Gly Cys Ser Leu Ala Thr Asp
35 40 45

Thr Lys Lys Gly Arg Gly Arg Met Leu Ile Asn Lys Thr Ile Gln Thr
50 55 60

Gly Ala Asp Ala Ile Val Val Ala Met Met Lys Phe Cys Asp Pro Glu
65 70 75 80

Glu Trp Asp Tyr Pro Val Met Tyr Arg Glu Phe Glu Glu Lys Gly Val
85 90 95

Lys Ser Leu Met Ile Glu Val Asp Gln Glu Val Ser Ser Phe Glu Gln
100 105 110

Ile Lys Thr Arg Leu Gln Ser Phe Val Glu Met Leu
115 120

<210> SEQ ID NO 18
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Streptomyces antibioticus

<400> SEQUENCE: 18

Ser Ser Ser Ala Gly Ile Asp Pro Gly Arg Ala Phe Gln Asp Met Gly
1 5 10 15

Ile

<210> SEQ ID NO 19
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Saccharopolyspora erythraea

<400> SEQUENCE: 19

Ala Ser Ala Glu Arg Val Pro Ala Asp Gln Ala Phe Ala Glu Leu Gly
1 5 10 15

Val

1. A non-naturally occurring polyketide synthase (PKS), or functional variant thereof, capable of synthesizing an α-olefin.

2. The PKS of claim **1**, wherein the α-olefin is not a compound synthesized by a naturally occurring PKS.

3. The PKS of claim **1**, wherein the PKS is a hybrid PKS comprising modules, domains, and/or portions thereof, or functional variant thereof, from two or more PKSs.

4. The PKS of claim **3**, wherein the PKS comprises a terminal module comprising ST, and TE, or functional variant thereof, of *Lyngbya majuscula* CurM.

5. The PKS of claim **4**, wherein the PKS comprises a terminal module comprising KR, ACP, ST, and TE, or functional variant thereof, of *Lyngbya majuscula* CurM.

6. The PKS of claim **5**, wherein the PKS comprises a terminal module comprising AT, KR, ACP, ST, and TE, or functional variant thereof, of *Lyngbya majuscula* CurM.

7. The PKS of claim **3**, wherein the PKS comprises at least one terminal module comprising a ST and a TE, or functional variant thereof, described in Tables 2-4.

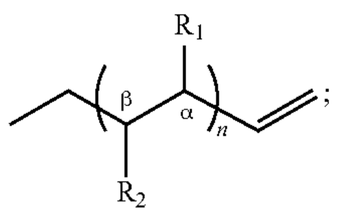
8. The PKS of claim **3**, wherein the PKS comprises a loading module which incorporates acrylyl-CoA.

9. The PKS of claim **3**, wherein the PKS comprises the loading module is a DEBS proprionyl-CoA specific loading domain modified to accept acrylyl-CoA.

10. The PKS of claim **9**, wherein the PKS comprises a module in which a terminal carbon is incorporated as a methyl group which is later oxidized.

11. The PKS of claim **1**, wherein the α-olefin has the following chemical structure:

(I)

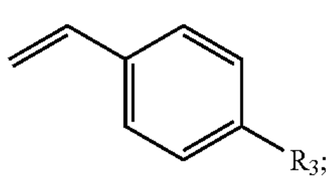


wherein each R_1 is independently —H or —CH_3, each R_2 is independently —H or —OH, n is an integer from 1 to 10, αβ is (1) a single bond or (2) a double bond, with the proviso that when an αβ is a double bond then the corresponding R_2 is H.

12. The PKS of claim **11**, wherein the α-olefin is 1-hexene, 1-decene, or (E)-deca-1,5-diene.

13. The PKS of claim **1**, wherein the α-olefin is an aromatic α-olefin having the following chemical structure:

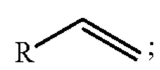
(III)



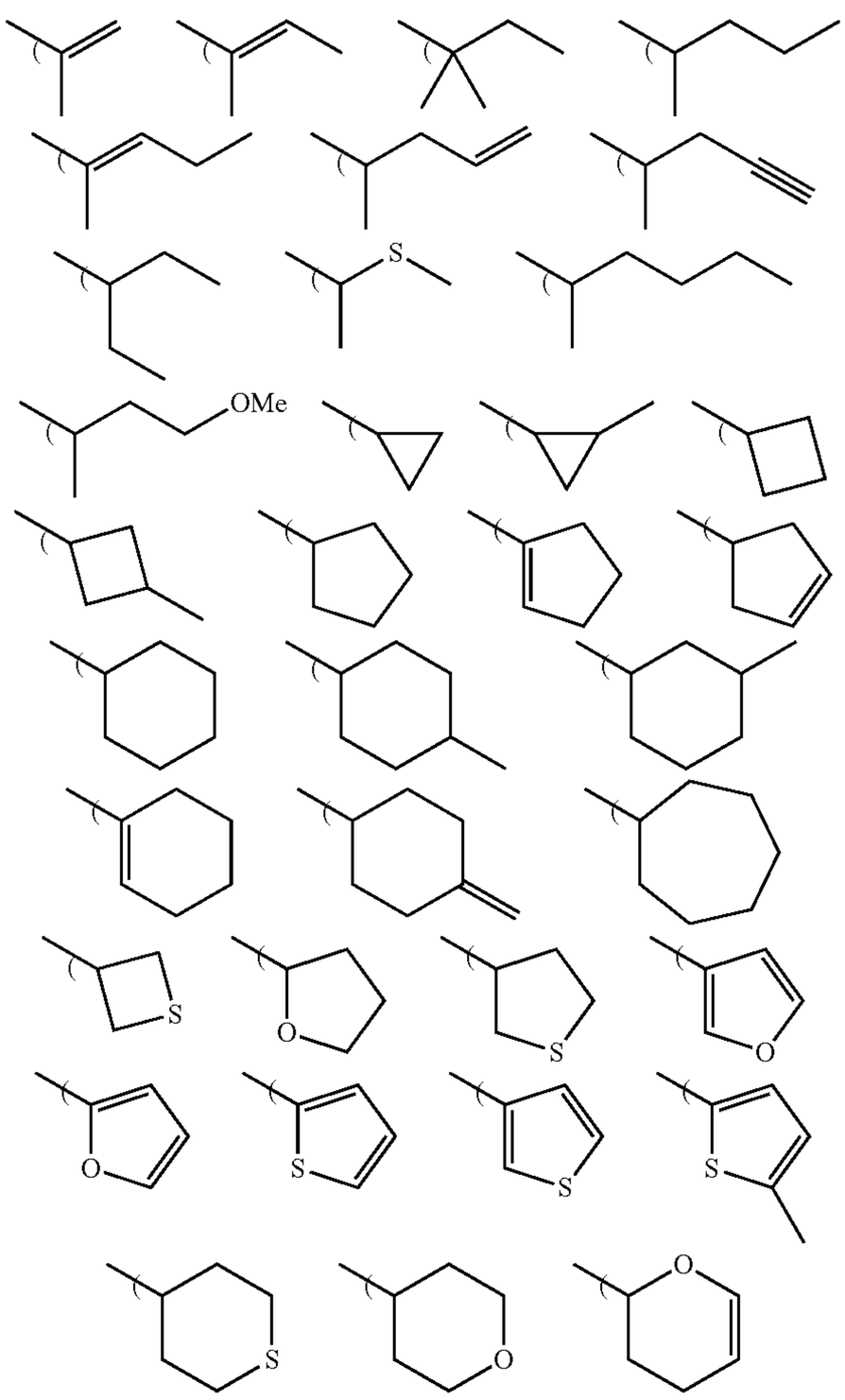
wherein R_3 is —H, —OH, —NH_3, or —NO_2.

14. The PKS of claim **1**, wherein the α-olefin has the following chemical structure:

(IV)



wherein R is one of the following structures



15. A recombinant nucleic acid encoding the polyketide synthase (PKS) of claim **1**.

16. A replicon comprising the recombinant nucleic acid 14, wherein the replicon is capable of stable maintenance in a host cell.

17. The replicon of claim **16**, wherein the replicon is a plasmid or vector.

18. The replicon of claim **17**, wherein the vector is an expression vector.

19. A host cell comprising the recombinant nucleic acid of claim **15**.

20. A host cell comprising the replicon of claim **16**.

21. The host cell of claim **19**, wherein the host cell when cultured produces the α-olefin.

22. The host cell of claim **21**, wherein the host cell comprises a PKS which produces butadiene comprising a loading module comprising an acrylyl-ACP starter, and further com-

prises one or more nucleic acids encoding propionyl-CoA ligase (synthetase) (EC 6.2.1.17) and acyl-CoA dehydrogenase (mammalian) (EC 1.3.99.3), or functional variants thereof, wherein when cultured and optionally provided with propionate the PKS is capable of synthesizing acrylyl-CoA and producing butadiene.

23. The host cell of claim **21**, wherein the host cell comprises a PKS which produces butadiene comprising a loading module comprising an acrylyl-ACP starter, and further comprises one or more nucleic acids encoding lactate dehydrogenase (EC 6.2.1.17), lactate CoA transferase (EC 2.8.3.1), propionyl-CoA ligase (synthetase) (EC 6.2.1.17), and lactoyl-CoA dehydratase (EC 4.2.164), or functional variants thereof, wherein when cultured and optionally provided with propionate and glucose the PKS is capable of synthesizing acrylyl-CoA and producing butadiene.

24. The host cell of claim **21**, wherein the host cell comprises a PKS which produces butadiene comprising a loading module comprising an acrylyl-ACP starter, and further comprises one or more nucleic acids encoding acetyl-CoA carboxylase (EC 6.4.1.2), malonyl-CoA reductase (EC 1.2.1.-), 3-hydroxypropionate:CoA ligase, and 3-hydroxypropionyl-CoA hydratase (EC 4.2.1.17), or functional variants thereof, wherein when cultured the PKS is capable of synthesizing acrylyl-CoA and producing butadiene

25. The host cell of claim **21**, wherein the host cell comprises a PKS which produces butadiene comprising a loading module comprising an acrylyl-ACP starter, and further comprises one or more nucleic acids encoding propionyl-CoA ligase (synthetase) (EC 6.2.1.17), the AccA/PccB gene products and lactoyl-CoA dehydratase (EC 4.2.164), and lactate dehydrogenase (EC 6.2.1.17), lactate CoA transferase (EC 2.8.3.1), propionyl-CoA ligase (synthetase) (EC 6.2.1.17), and lactoyl-CoA dehydratase (EC 4.2.164), or acyl-CoA dehydrogenase, or functional variants thereof, wherein when cultured and optionally provided with propionate the PKS is capable of synthesizing acrylyl-CoA and producing butadiene.

26. A method of producing an α-olefin, comprising: providing a host cell of claim **21**, and culturing said host cell in a suitable culture medium such that the α-olefin is produced.

27. The method of claim **26**, further comprising isolating the isolating the α-olefin.

28. The method of claim **27**, further comprising polymerizing the α-olefin to produce a polymer.

29. The method of claim **26**, wherein the α-olefin is a polyolefin.

30. The method of claim **29**, wherein the polyolefin is butadiene, isoprene, or (E)-deca-1,5-diene.

31. A composition comprising an α-olefin isolated from the host cell of claim **21**, and trace residues and/or contaminants of the host cell.

32. The composition of claim **31**, wherein the α-olefin is polyolefin.

33. The composition of claim **32**, wherein the polyolefin is butadiene, isoprene, or (E)-deca-1,5-diene.

* * * * *