US009896691B2

(12) **United States Patent**
Blazeck et al.

(10) **Patent No.: US 9,896,691 B2**
(45) **Date of Patent: Feb. 20, 2018**

(54) **COMPOSITIONS AND METHODS FOR LIPID PRODUCTION**

(71) Applicant: **Board of Regents, The University of Texas System**, Austin, TX (US)

(72) Inventors: **John Blazeck**, Austin, TX (US); **Andrew Hill**, Austin, TX (US); **Leqian Liu**, Austin, TX (US); **Hal Alper**, Austin, TX (US)

(73) Assignee: **Board of Regents, The University of Texas System**, Austin, TX (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 241 days.

(21) Appl. No.: **14/268,796**

(22) Filed: **May 2, 2014**

(65) **Prior Publication Data**

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Related U.S. Application Data

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(51) **Int. Cl.**

C12P 7/64	(2006.01)
C12N 15/81	(2006.01)
C07K 14/39	(2006.01)
C12N 1/16	(2006.01)
C12N 9/04	(2006.01)
C12N 9/02	(2006.01)

(Continued)

(52) **U.S. Cl.**

CPC ***C12N 15/815*** (2013.01); ***C07K 14/39*** (2013.01); ***C12N 1/16*** (2013.01); ***C12N 9/0006*** (2013.01); ***C12N 9/0008*** (2013.01); ***C12N 9/0042*** (2013.01); ***C12N 9/0077*** (2013.01); ***C12N 9/1007*** (2013.01); ***C12N 9/78*** (2013.01); ***C12N 9/88*** (2013.01); ***C12N 9/93*** (2013.01); ***C12N 15/01*** (2013.01); ***C12N 15/52*** (2013.01); ***C12P 7/64*** (2013.01); ***C12P 7/6409*** (2013.01); ***C12P 7/6463*** (2013.01); ***C12R 1/645*** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

8,367,395	B2 *	2/2013	Bailey	C11B 1/10 435/183
2009/0117253	A1	5/2009	Hong et al.	

(Continued)

FOREIGN PATENT DOCUMENTS

EP	0005277 A2	11/1979
WO	WO 2011/109548 A2	9/2011
WO	WO 2013/059649 A1	4/2013

OTHER PUBLICATIONS

Kamisaka et al. "DGA1 (diacylglycerol acyltransferase gene) overexpression and leucine biosynthesis significantly increase lipid accumulation in the delta-snf2 disruptant of *Saccharomyces cerevisiae*", Biochemical Journal, vol. 408, pp. 61-68, 2007.*

(Continued)

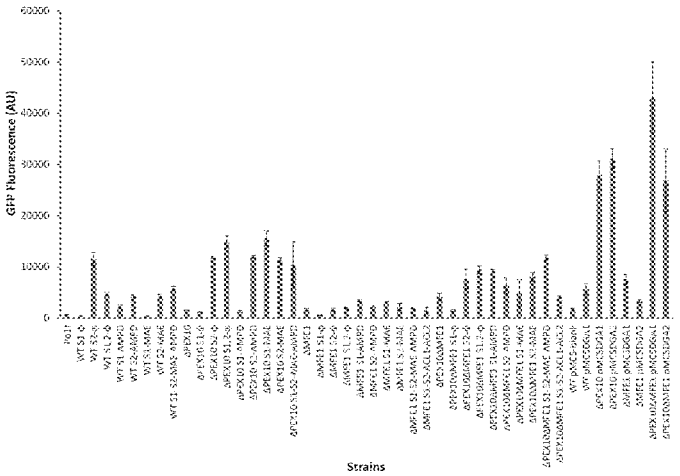
Primary Examiner — Richard Ekstrom

(74) *Attorney, Agent, or Firm* — Meunier Carlin & Curfman LLC

(57) **ABSTRACT**

Described herein, inter alia, are compositions, oleagnious organisms, and methods useful for producing lipids, lipid precursors, and/or oleochemicals.

10 Claims, 23 Drawing Sheets



(51) **Int. Cl.**

C12N 9/10	(2006.01)
C12N 9/78	(2006.01)
C12N 9/88	(2006.01)
C12N 9/00	(2006.01)
C12N 15/52	(2006.01)
C12N 15/01	(2006.01)
C12R 1/645	(2006.01)

(56) **References Cited**

U.S. PATENT DOCUMENTS

2011/0300595	A1*	12/2011	Lang	C12N 9/0006 435/145
2013/0143282	A1*	6/2013	Stephanopoulos	C12N 15/815 435/134
2013/0149754	A1*	6/2013	Dulermo	C12P 7/6409 435/134
2013/0230891	A1*	9/2013	Hong	C12N 9/0083 435/134
2013/0280793	A1*	10/2013	Brown	C12Y 102/01 435/257.2

OTHER PUBLICATIONS

Andre et al., "Biotechnological conversions of bio-diesel-derived crude glycerol by *Yarrowia lipolytica* strains", *Engineering in Life Sciences* 2009, 9(6):468-478.

Beopoulos et al., "Identification and characterization of DGA2, an acyltransferase of the DGAT1 acyl-CoA:diacylglycerol acyltransferase family in the oleaginous yeast *Yarrowia lipolytica*. New insights into the storage lipid metabolism of oleaginous yeasts", *Applied Microbiology and Biotechnology* 2012, 93(4):1523-1537.

Beopoulos et al., "Control of Lipid Accumulation in the Yeast *Yarrowia lipolytica", Applied and Environmental Microbiology* 2008, 74(24):7779-7789.

Blazeck et al., "Heterologous production of pentane in the oleaginous yeast *Yarrowia lipolytica.", Journal of Biotechnology* 2013, 165:184-194.

Blazeck et al., "Harnessing *Yarrowia lipolytica* lipogenesis to create a platform for lipid and biofuel production", *Nature Communications*, Jan. 2014, 5 Article 3131, 10 pages.

Chuang et al., "Co-expression of heterologous desaturase genes in *Yarrowia lipolytica.", New Biotechnology* 2010, 27(4):277-282.

Dulermo et al., "Involvement of the G3P shuttle and beta-oxidation pathway in the control of TAG synthesis and lipid accumulation in *Yarrowia lipolytica", Metabolic Engineering* 2011, 13(5):482-491.

Gebre et al., "Osh6 overexpression extends the lifespan of yeast by increasing vacuole fusion", *Cell Cycle* 2012, 11(11): 2176-2188.

Han et al., "Leucyl-tRNA Synthetase is an Intracellular Leucine Sensor for the mTORC1-Signaling Pathway", *Cell* 2012, 149(2):410-424.

Kamei et al., "GABA metabolism pathway genes, UGA1 and GAD1, regulate replicative lifespan in *Saccharomyces cerevisiae", Biochemical and Biophysical Research Communications* 2011, 407(1):185-190.

Kamisaka et al., "DGA1 (diacylglycerol acyltransferase gene) overexpression and leucine biosynthesis significantly increase lipid accumulation in the delta snf2 disruptant of *Saccharomyces cerevisiae", Biochemical Journal* 2007, 408:61-68.

Morin et al., "Transcriptomic Analyses during the Transition from Biomass Production to Lipid Accumulation in the Oleaginous Yeast *Yarrowia lipolytica", Plos One* 2011, 6(11):e27966, 13 pages.

Staschke et al., "Integration of General Amino Acid Control and Target of Rapamycin (TOR) Regulatory Pathways in Nitrogen Assimilation in Yeast", *Journal of Biological Chemistry* 2010, 285(22):16893-16911.

Tai et al, "Engineering the push and pull of lipid biosynthesis in oleaginous yeast *Yarrowia lipolytica* for biofuel production", *Metabolic Engineering* 2013, 15:1-9.

Xue et al., "Production of omega-3 eicosapentaenoic acid by metabolic engineering of *Yarrowia lipolytica", Nature Biotechnology* 2013, 31(8): 734-740.

Ageitos et al., "Oily yeasts as oleaginous cell factories", *Applied Microbiology and Biotechnology*, 2011, 90(4): 1219-1227.

Ratledge, C., "Regulation of lipid accumulation in oleaginous micro-organisms", *Biochemical Society Transactions*, 2002, 30(6):1047-1050.

Sitepu et al., "An improved high-throughput Nile red fluorescence assay for estimating intracellular lipids in a variety of yeast species", *Journal of Microbiological Methods*, 2012, 91(2):321-328.

Titorenko et al., "Four Distinct Secretory Pathways Serve Protein Secretion, Cell Surface Growth, and Peroxisome Biogenesis in the Yeast *Yarrowia lipolytica", Molecular and Cellulary Biology*, 1997, 17(9):5210-5226.

Invitation to Pay Additional Fees and Partial International Search Report dated Oct. 13, 2014 for International Application No. PCT/US2014/036663, 18 pages.

International Search Report and Written Opinion dated Dec. 15, 2014 for International Application No. PCT/US2014/036663, 38 pages.

* cited by examiner

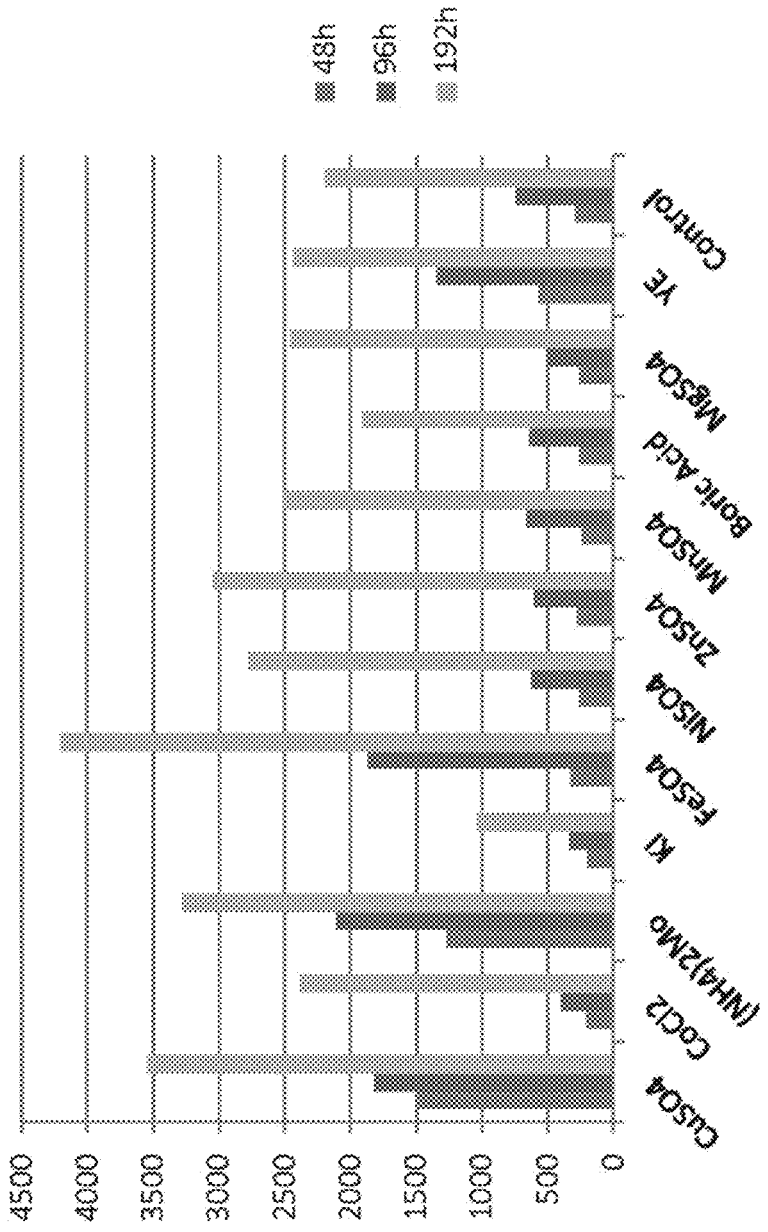

48h
96h
192h
4500
4000
3500
3000
2500
2000
1500
1000
500
0
CuSO4
CoCl2
(NH4)2MO
KI
FeSO4
NiSO4
ZnSO4
MnSO4
Boric Acid
MgSO4
VE
Control

FIG. 1

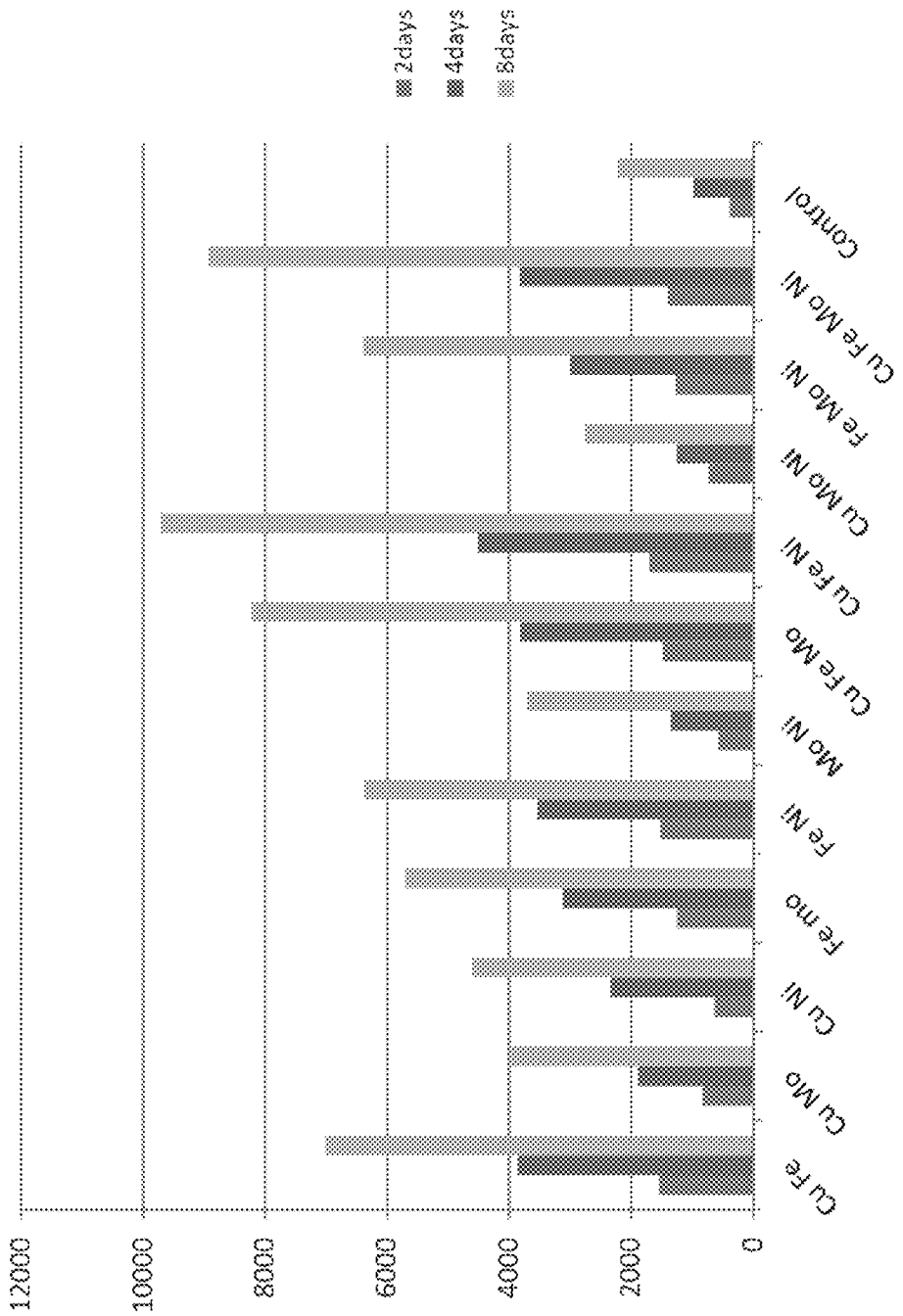

2days
4days
8days
12000
10000
8000
6000
4000
2000
0
Cu Fe
Cu Mo
Cu Ni
Fe mo
Fe Ni
Mo Ni
Cu Fe Mo
Cu Fe Ni
Cu Mo Ni
Fe Mo Ni
Cu Fe Mo Ni
Control

FIG. 2

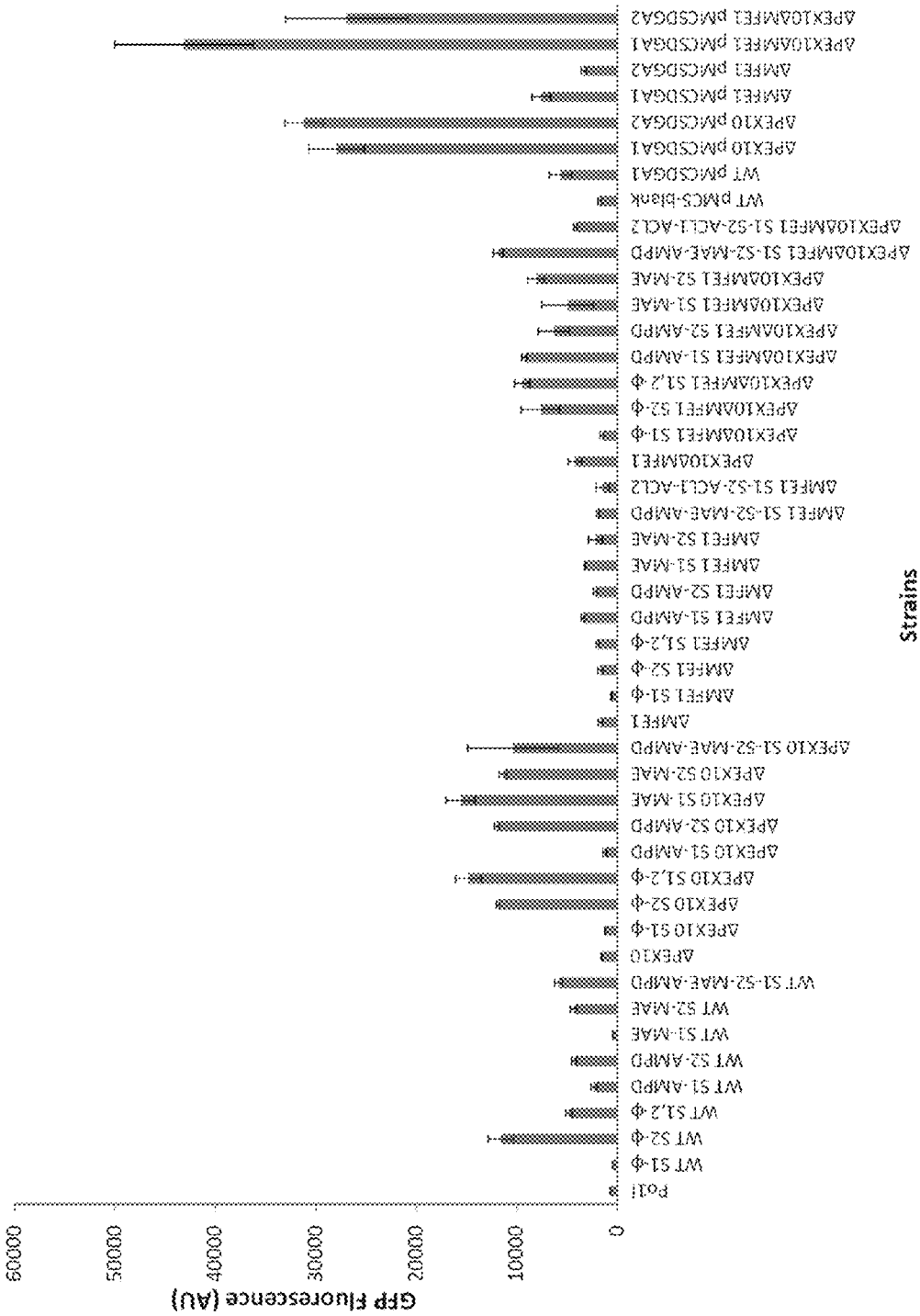

GFP fluorescence (AU)
0
100000
200000
300000
400000
500000
600000
Strains
ΔPEX10ΔMFE1 pMCSDGA2
ΔPEX10ΔMFE1 pMCSDGA1
ΔMFE1 pMCSDGA2
ΔMFE1 pMCSDGA1
ΔPEX10 pMCSDGA2
ΔPEX10 pMCSDGA1
WT pMCSDGA1
WT pMCS-blank
ΔPEX10ΔMFE1 S1-S2-ACL1-ACL2
ΔPEX10ΔMFE1 S1-S2-MAE-ANPD
ΔPEX10ΔMFE1 S2-MAE
ΔPEX10ΔMFE1 S1-MAE
ΔPEX10ΔMFE1 S2-ANPD
ΔPEX10ΔMFE1 S1-ANPD
ΔPEX10ΔMFE1 S1,2-Φ
ΔPEX10ΔMFE1 S2-Φ
ΔPEX10ΔMFE1 S1-Φ
ΔPEX10ΔMFE1
ΔMFE1 S1-S2-ACL1-ACL2
ΔMFE1 S1-S2-MAE-ANPD
ΔMFE1 S2-MAE
ΔMFE1 S1-MAE
ΔMFE1 S2-ANPD
ΔMFE1 S1-ANPD
ΔMFE1 S1,2-Φ
ΔMFE1 S2-Φ
ΔMFE1 S1-Φ
ΔMFE1
ΔPEX10 S1-S2-MAE-ANPD
ΔPEX10 S2-MAE
ΔPEX10 S1-MAE
ΔPEX10 S2-ANPD
ΔPEX10 S1-ANPD
ΔPEX10 S1,2-Φ
ΔPEX10 S2-Φ
ΔPEX10 S1-Φ
ΔPEX10
WT S1-S2-MAE-ANPD
WT S2-MAE
WT S1-MAE
WT S2-ANPD
WT S1-ANPD
WT S1,2-Φ
WT S2-Φ
WT S1-Φ
Pol1

FIG. 3

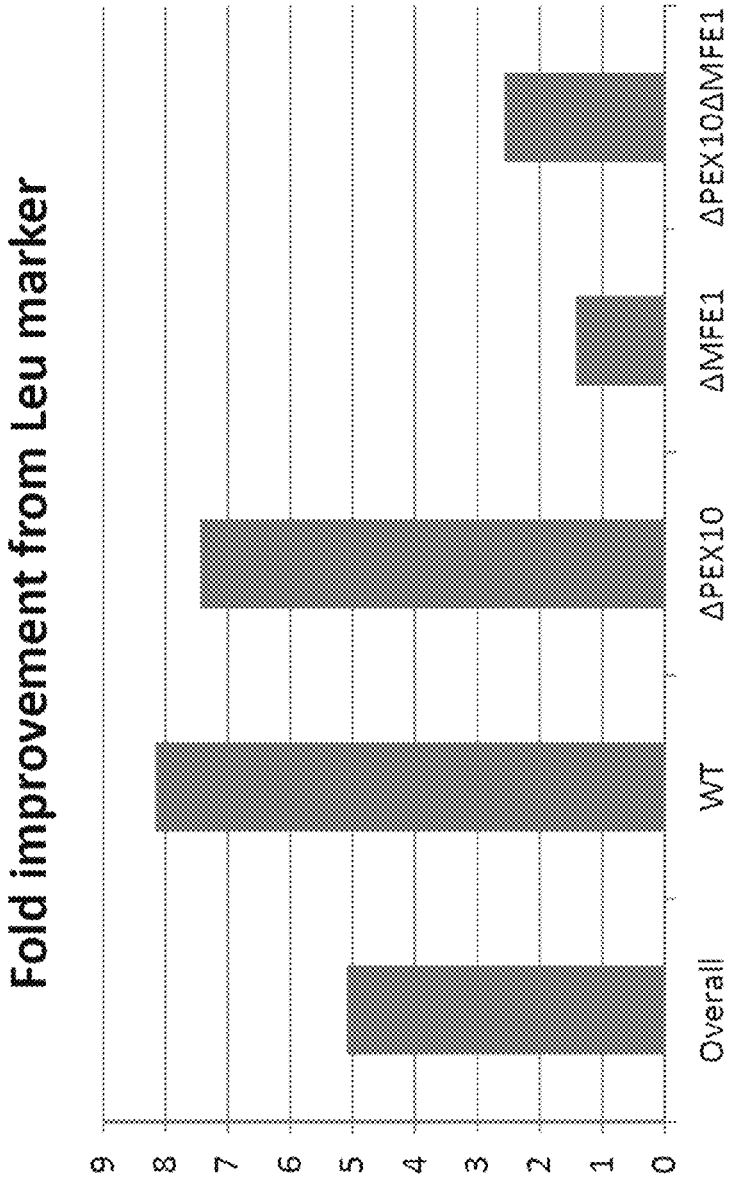

Fold improvement from Leu marker
9
8
7
6
5
4
3
2
1
0
Overall Average
WT
ΔPEX10
ΔMFE1
ΔPEX10ΔMFE1
Genotypic Background

FIG. 4

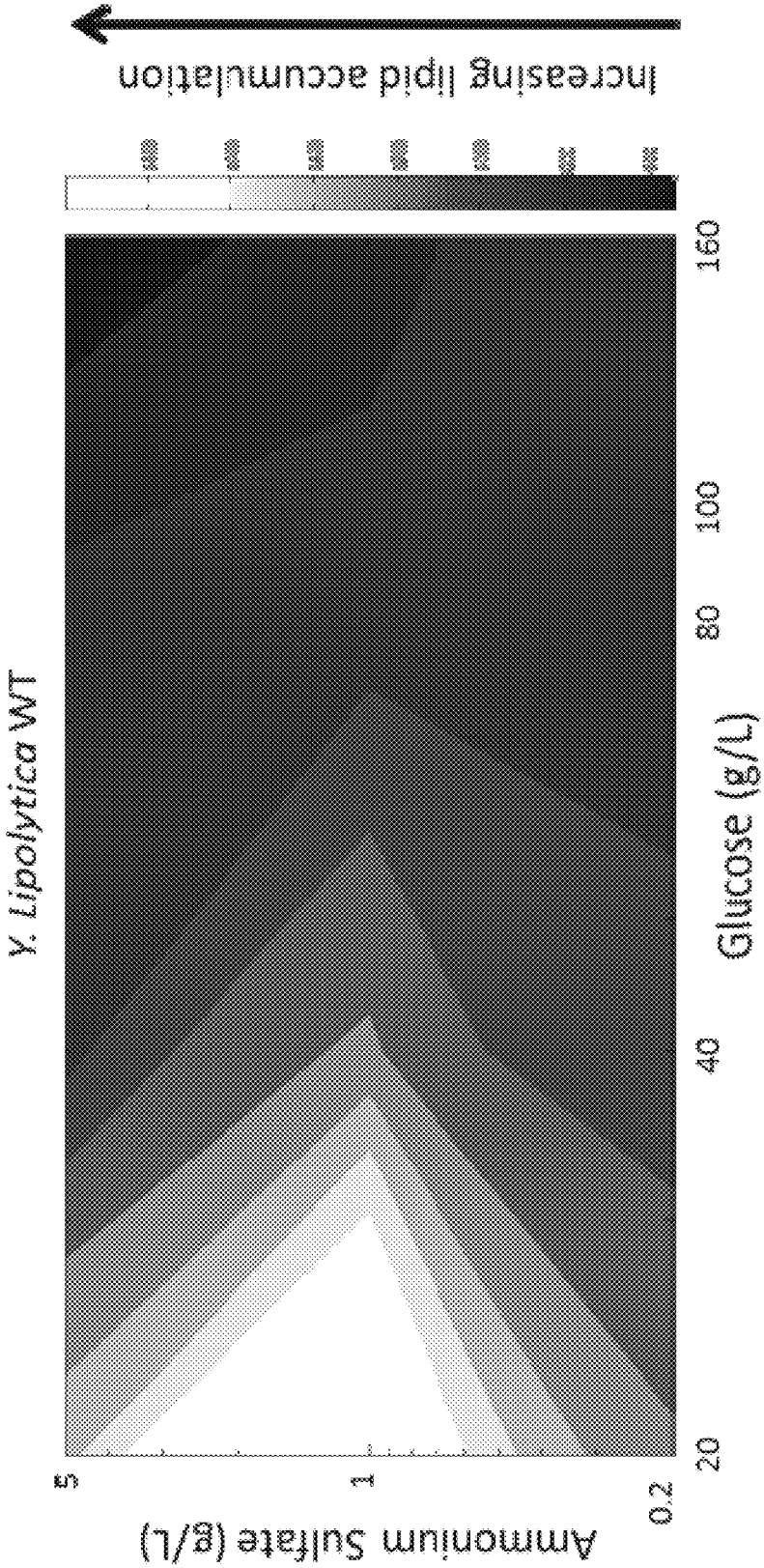

Increasing lipid accumulation
Y. Lipolytica WT
Glucose (g/L)
20
40
80
100
160
Ammonium Sulfate (g/L)
0.2
1
5

FIG. 5

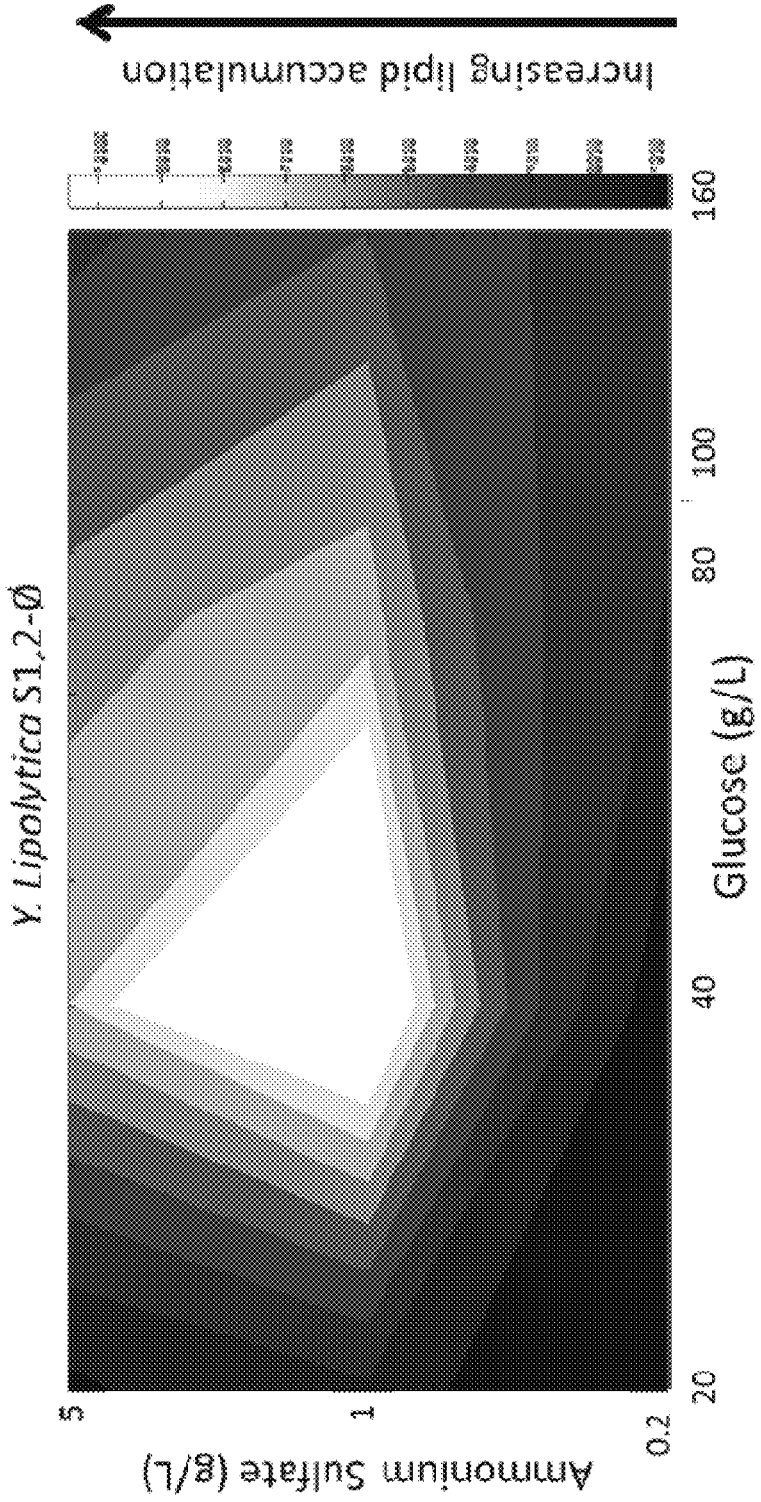

Increasing lipid accumulation
Y. Lipolytica S1,2-Ø
Ammonium Sulfate (g/L)
5
1
0.2
Glucose (g/L)
20
40
80
100
160

FIG. 6

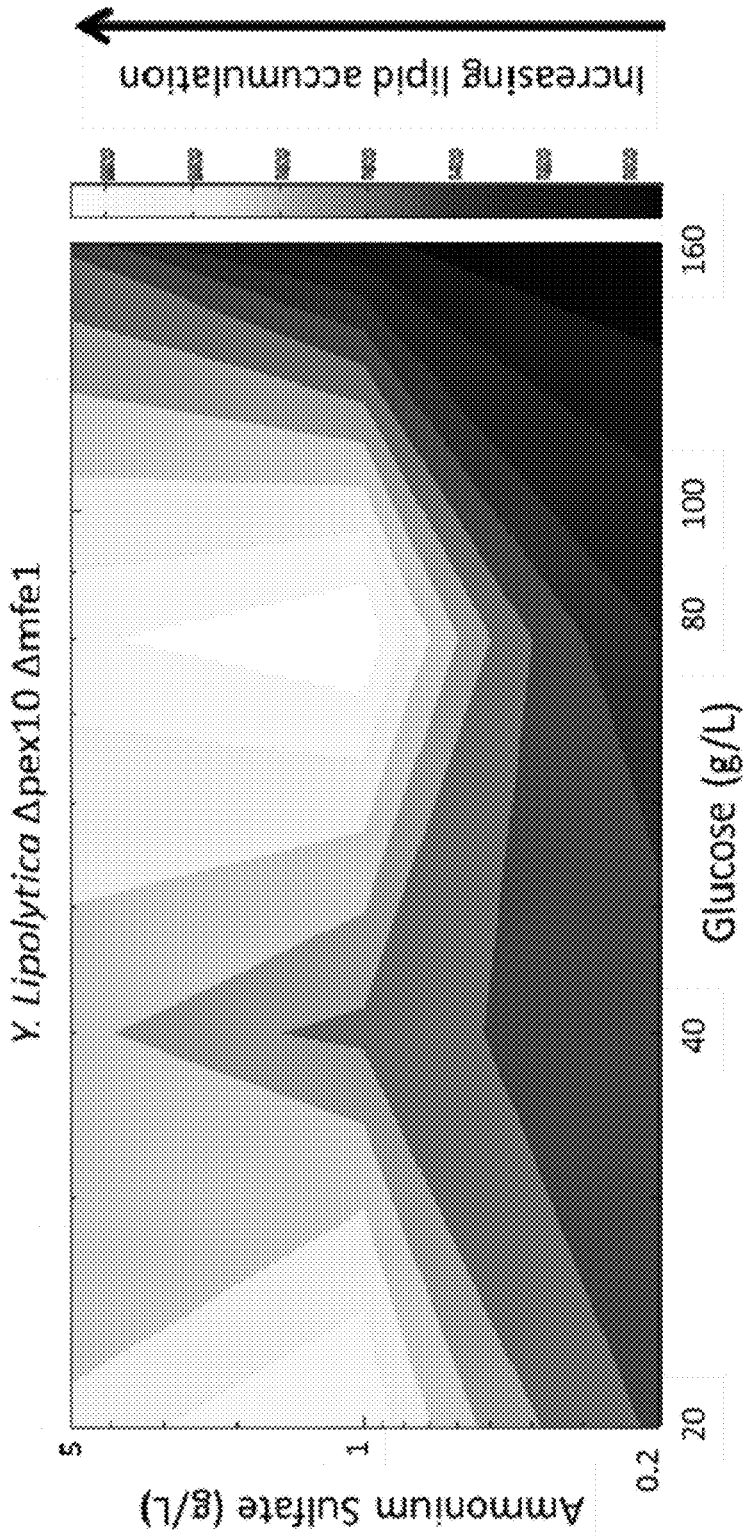

Increasing lipid accumulation
Y. Lipolytica Apex10 Δmfe1
Glucose (g/L)
20
40
80
100
160
Ammonium Sulfate (g/L)
0.2
1
5

FIG. 7

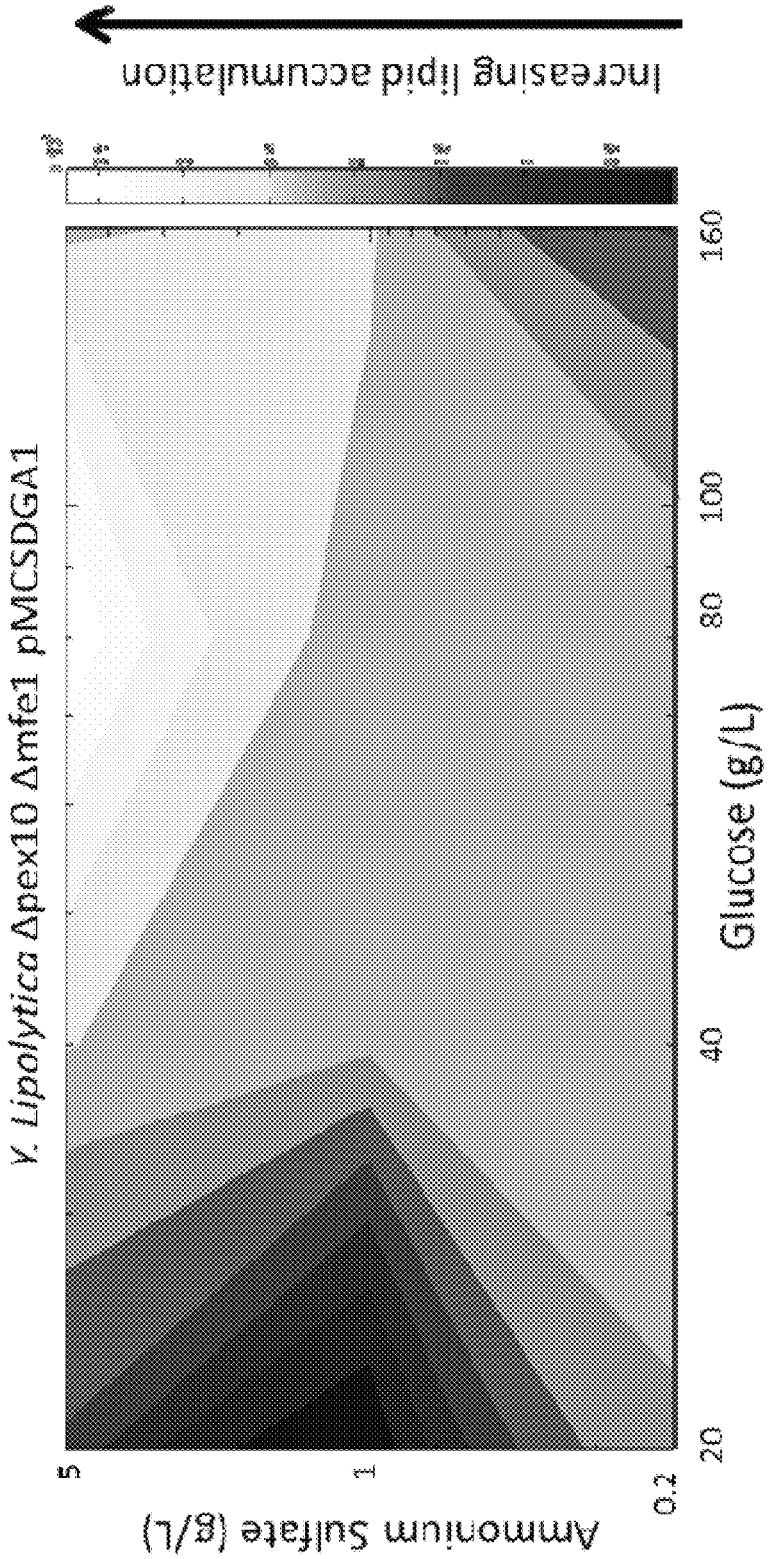

Increasing lipid accumulation
Y. Lipolytica Δpex10 Δmfe1 pMCSDGA1
Ammonium Sulfate (g/L)
5
1
0.2
20
40
80
100
160
Glucose (g/L)

FIG. 8

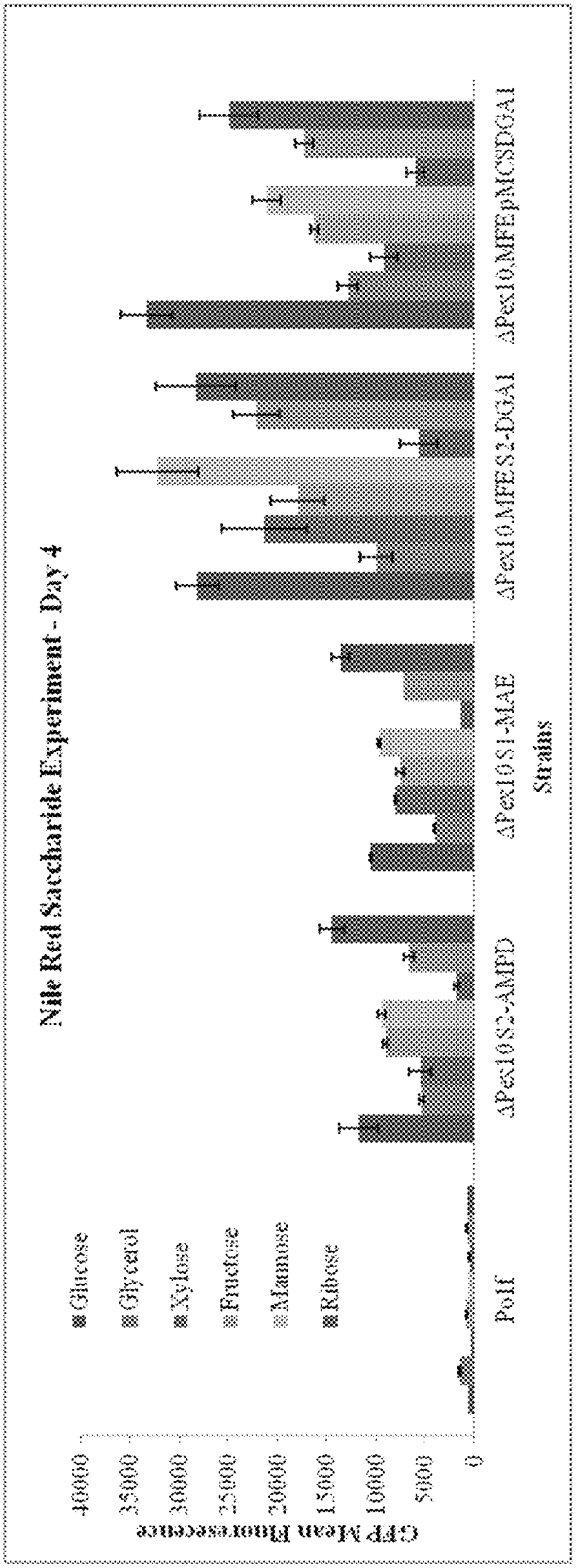

Nile Red Saccharide Experiment - Day 4
GFP Mean Fluorescence
40000
35000
30000
25000
20000
15000
10000
5000
0
Glucose
Glycerol
Xylose
Fructose
Mannose
Ribose
PoIf
ΔPex10S2-AMPD
ΔPex10S1-MAE
ΔPex10MFES2-DGA1
ΔPex10MFEpMCSDGA1
Strains

FIG. 9

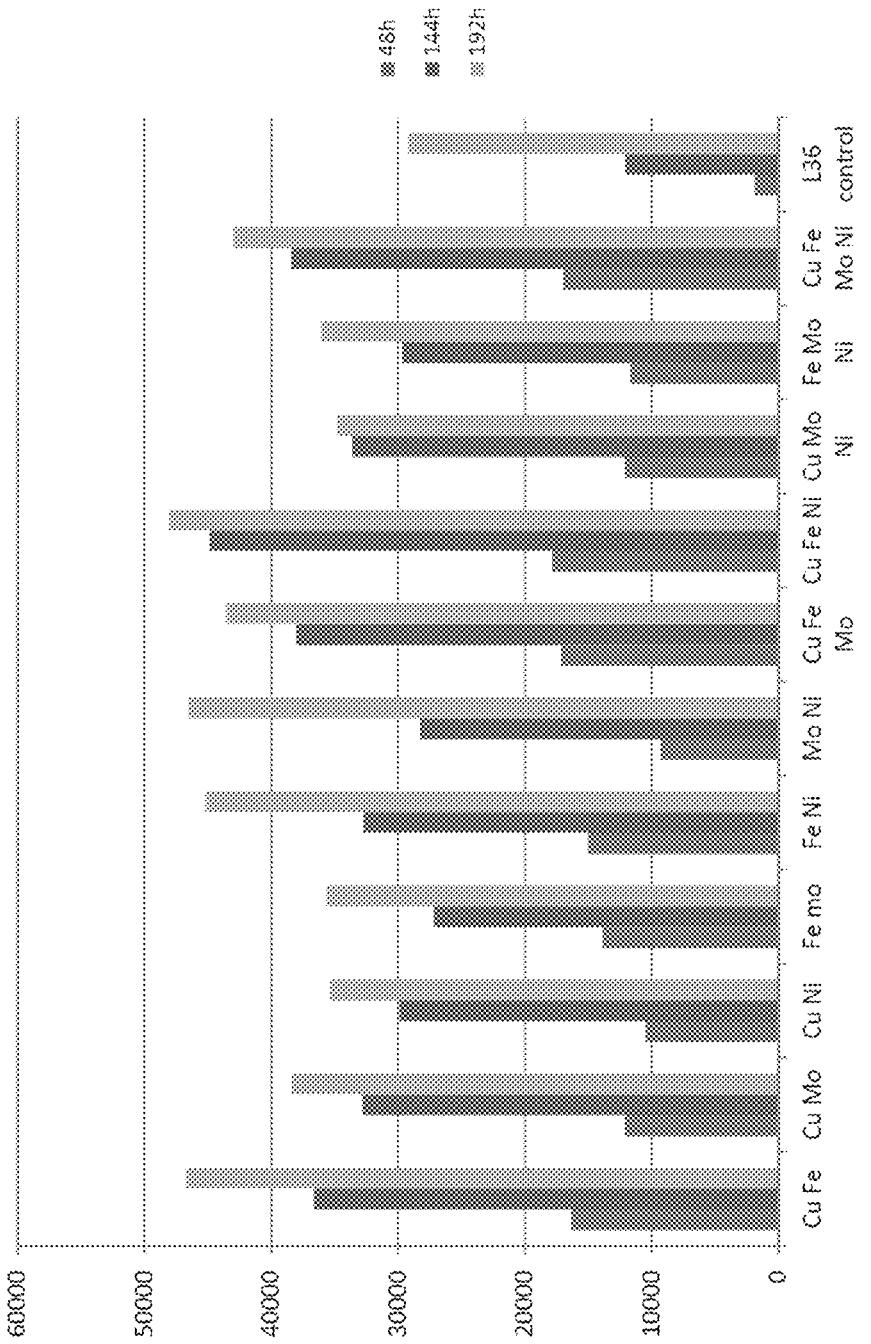

48h
144h
192h
60000
50000
40000
30000
20000
10000
0
Cu Fe
Cu Mo
Cu Ni
Fe mo
Fe Ni
Mo Ni
Cu Fe Mo
Cu Fe Ni Mo
Cu Mo Ni
Fe Mo Ni
Cu Fe Mo Ni
L36 control

FIG. 10

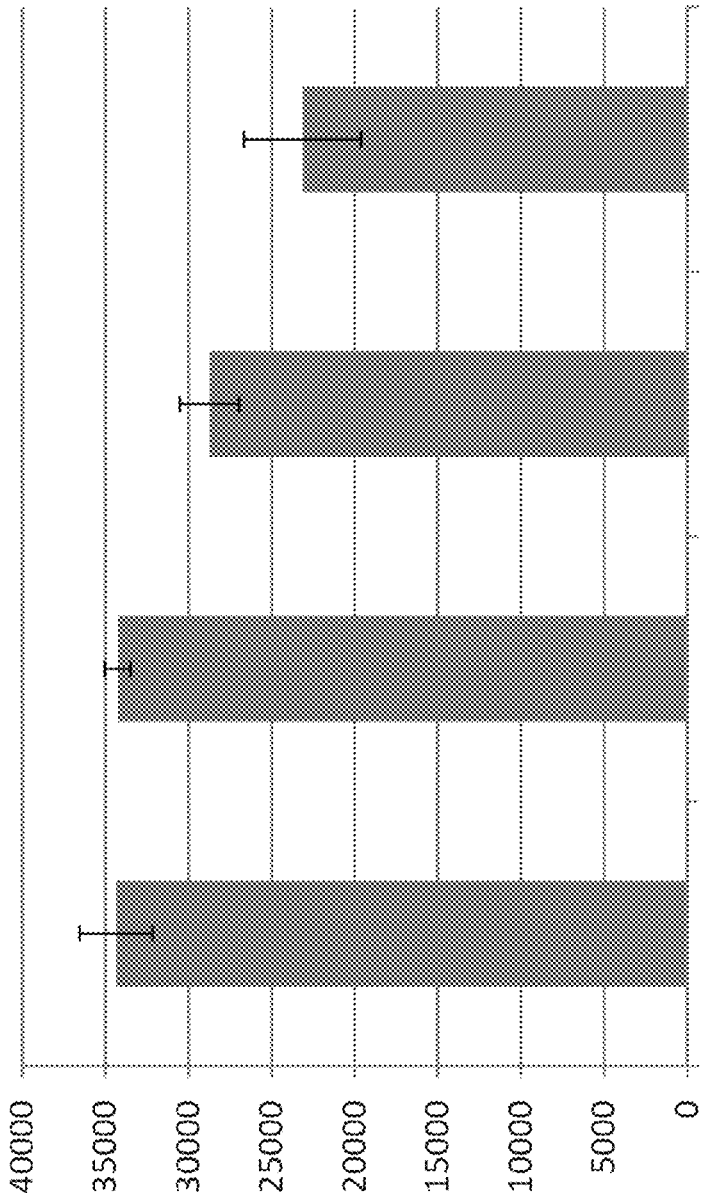

40000
35000
30000
25000
20000
15000
10000
5000
0
E1S6 4
E1S6 6
E1S6 8
CEN
L36 control on far right.
Left 3 - mutants

FIG. 11

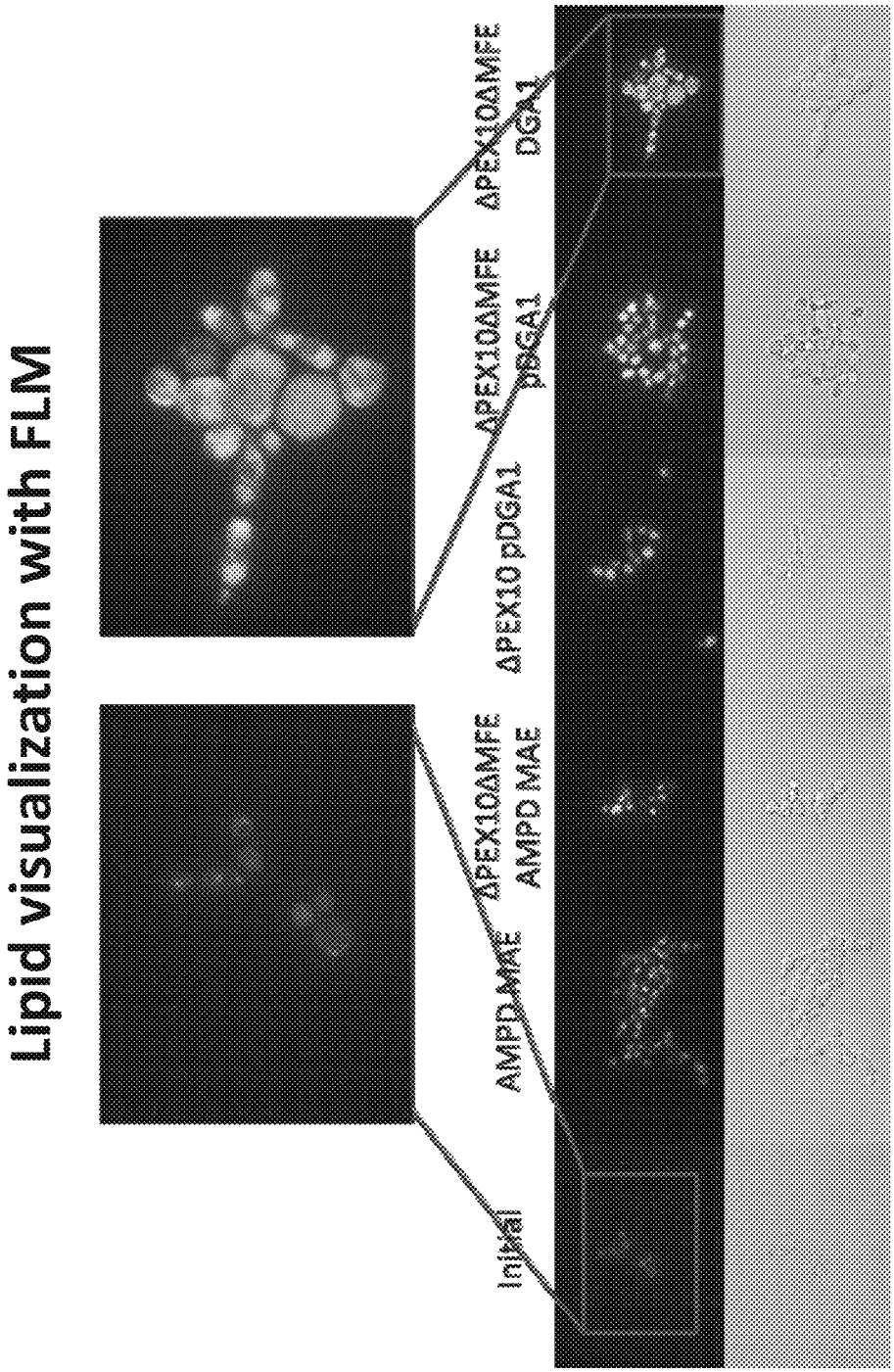

Lipid visualization with FLM
Initial
AMPDΔMAE
ΔPEX10ΔMFE AMPD MAE
ΔPEX10 pDGA1
ΔPEX10ΔMFE pDGA1
ΔPEX10ΔMFE DGA1

FIG. 12

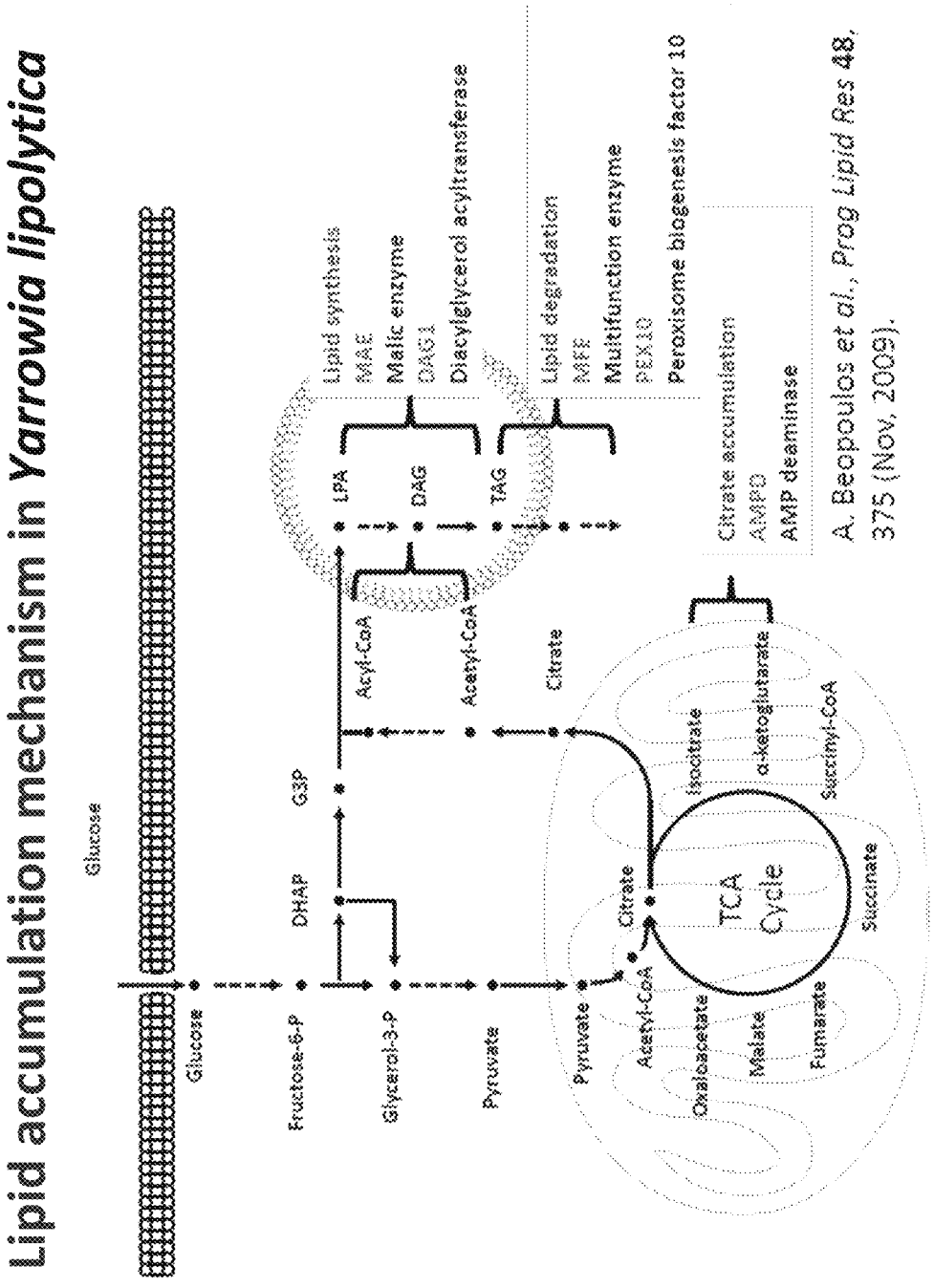

Lipid accumulation mechanism in Yarrowia lipolytica
Glucose
Glucose
Fructose-6-P
DHAP
G3P
Glycerol-3-P
Pyruvate
Pyruvate
Acetyl-CoA
Citrate
Oxaloacetate
Malate
Fumarate
Succinate
TCA Cycle
Isocitrate
α-ketoglutarate
Succinyl-CoA
Citrate
Acyl-CoA
Acetyl-CoA
LPA
DAG
TAG
Lipid synthesis
MAE
Malic enzyme
DAG1
Diacylglycerol acyltransferase
Lipid degradation
MFE
Multifunction enzyme
PEX10
Peroxisome biogenesis factor 10
Citrate accumulation
AMPD
AMP deaminase
A. Beopoulos et al., Prog Lipid Res 48, 375 (Nov, 2009).

FIG. 13

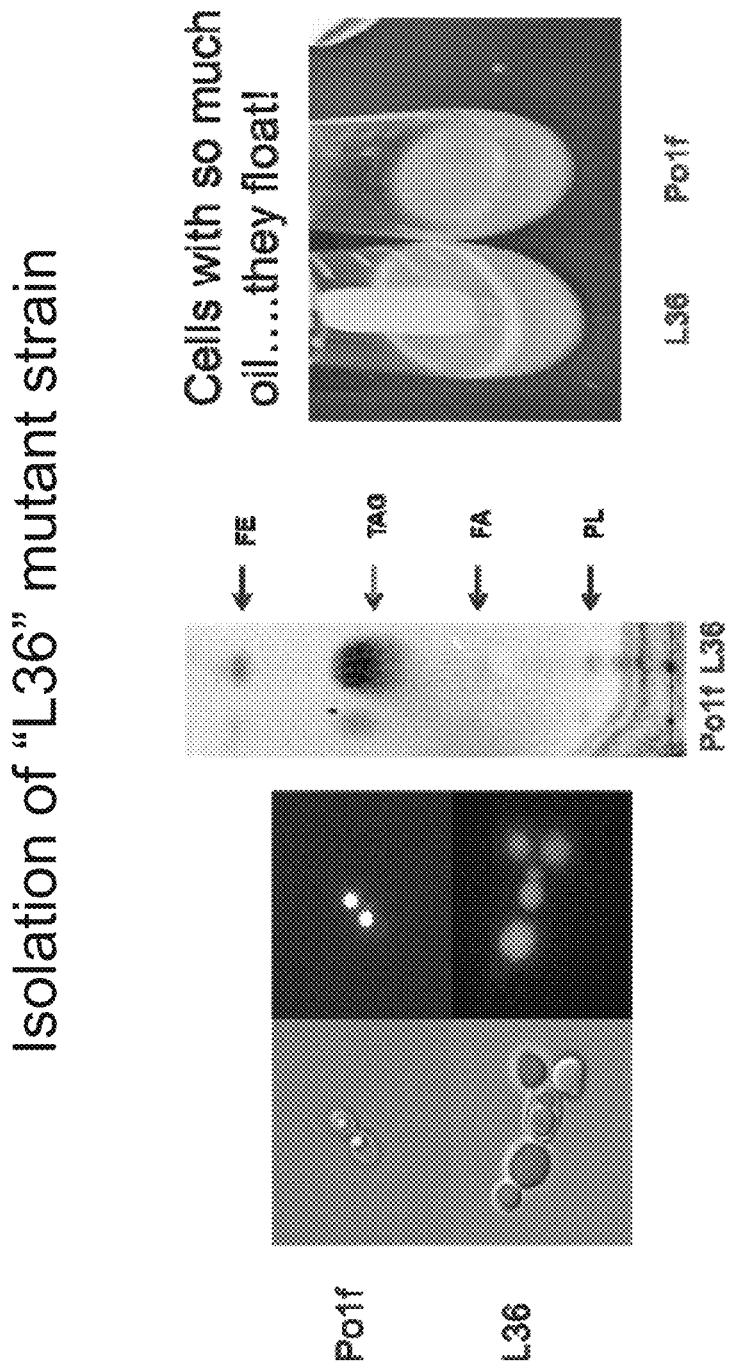

Isolation of "L36" mutant strain
Cells with so much oil....they float!
L36
Po1f
FE
TAG
FA
PL
Po1f L36
Po1f
L36

FIG. 14

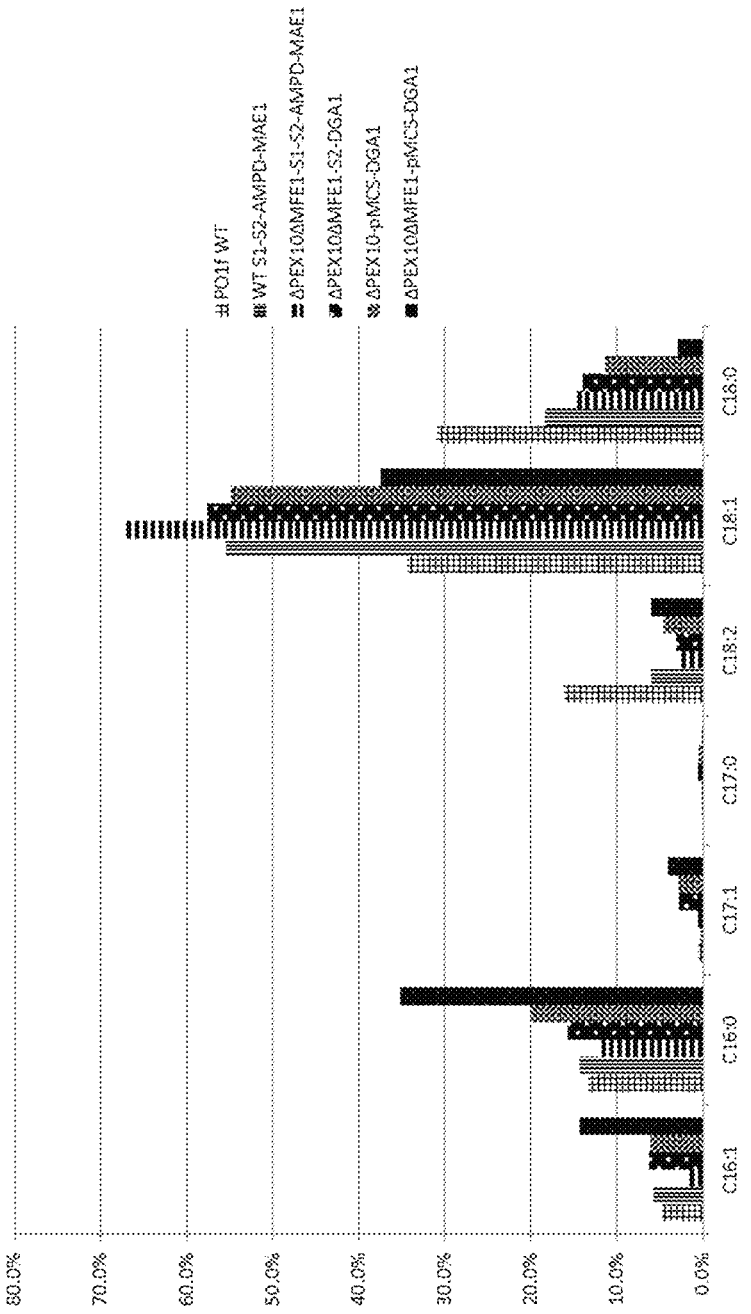

PO1f WT
WT S1-S2-AMPD-MAE1
ΔPEX10ΔMFE1-S1-S2-AMPD-MAE1
ΔPEX10ΔMFE1-S2-DGA1
ΔPEX10-pMCS-DGA1
ΔPEX10ΔMFE1-pMCS-DGA1
80.0%
70.0%
60.0%
50.0%
40.0%
30.0%
20.0%
10.0%
0.0%
C16:1
C16:0
C17:1
C17:0
C18:2
C18:1
C18:0

FIG. 15

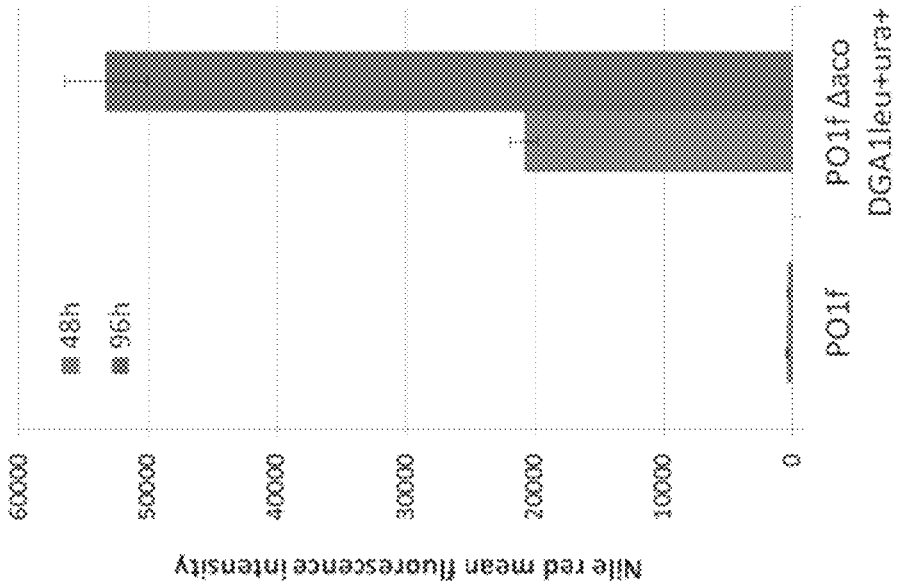

Nile red mean fluorescence intensity
60000
50000
40000
30000
20000
10000
0
48h
96h
PO1f
PO1f Δaco DGA1leu+ura+

FIG. 16

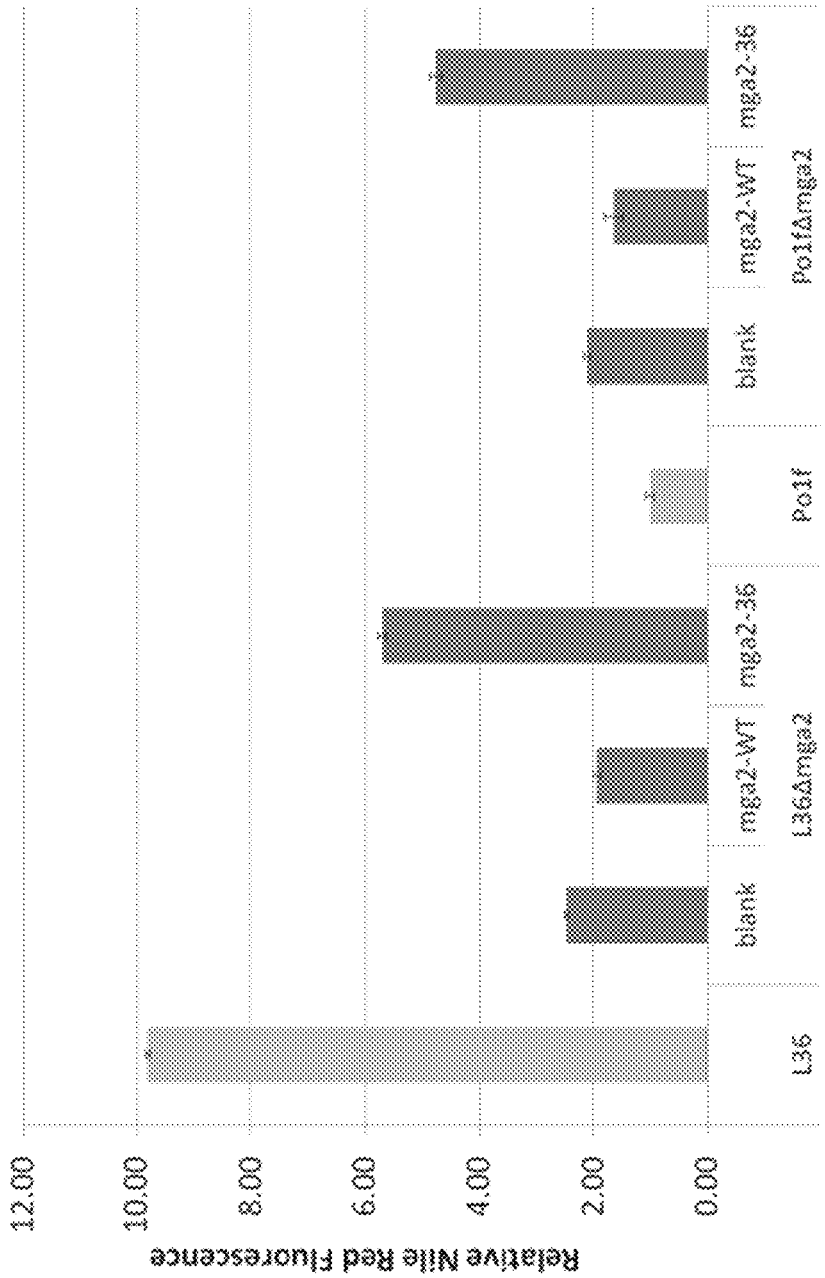

Relative Nile Red fluorescence
12.00
10.00
8.00
6.00
4.00
2.00
0.00
L36
blank
mga2-WT
L36Δmga2
mga2-36
Po1f
blank
mga2-WT
Po1fΔmga2
mga2-36

FIG. 17

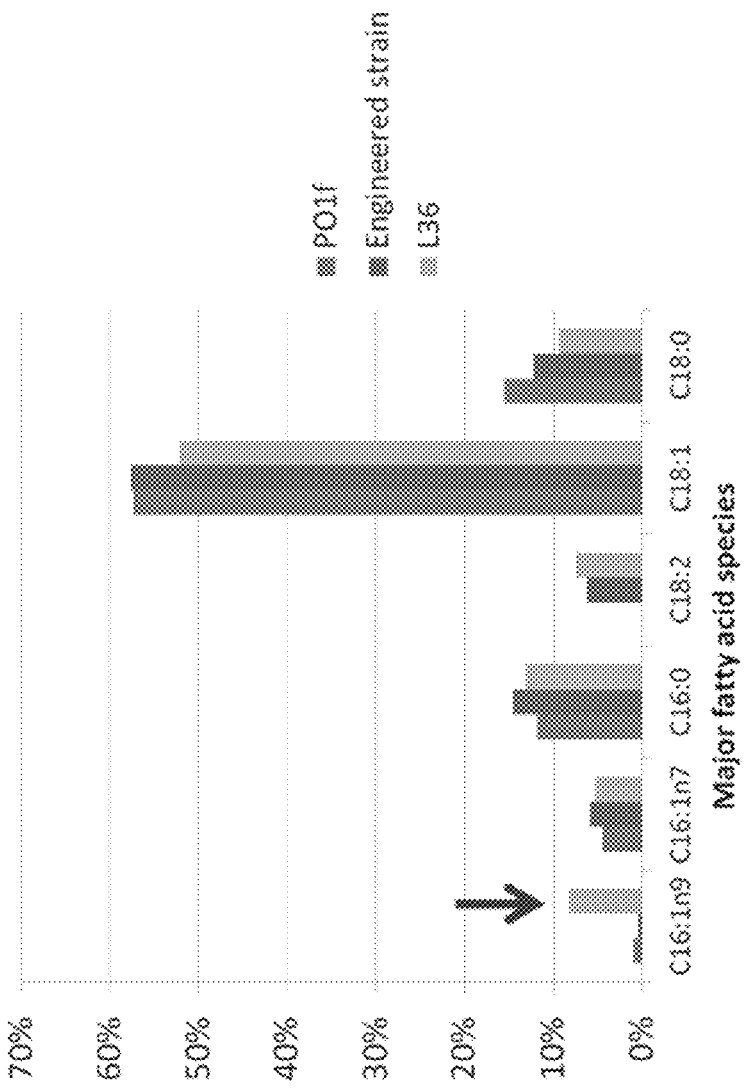

PO1f
Engineered strain
L36
70%
60%
50%
40%
30%
20%
10%
0%
C16:1n9
C16:1n7
C16:0
C18:2
C18:1
C18:0
Major fatty acid species

FIG. 18

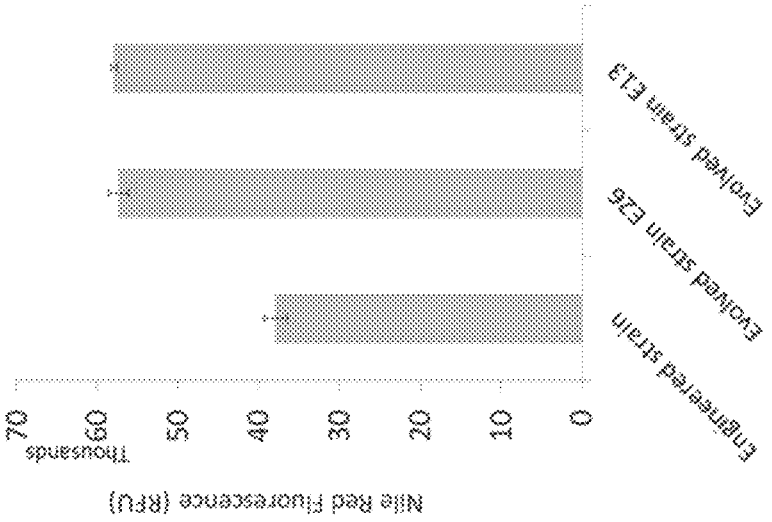

Nile Red Fluorescence (RFU)
Thousands
70
60
50
40
30
20
10
0
Engineered strain
Evolved strain E26
Evolved strain E13

FIG. 19

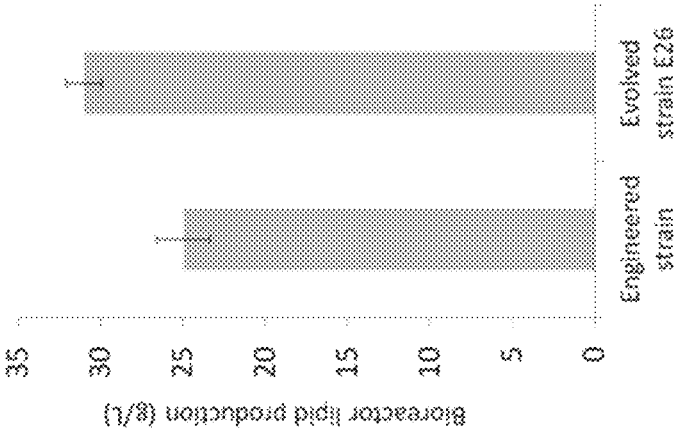

Bioreactor lipid production (g/L)
35
30
25
20
15
10
5
0
Engineered strain
Evolved strain E26

FIG. 20

YaliOA	297474	G	A	YALI0A02354g	similar to S. cerevisiae OSH6; member of an oxysterol-binding protein family
YaliOA	316425	CGGA	C	YALI0A02497g	no similarity
YaliOC	138994	T	C	YALI0C01001g	no similarity
YaliOC	139014	A	G	YALI0C01001g	no similarity
YaliOC	953493	G	A	YALI0C07150g	similar to S. cerevisiae IKI3/SKI8; E3 ubiquitin ligase and putative helicase
YaliOC	2966661	C	T	YALI0C22231g	weakly similar to Schizosaccharomyces pombe RNA polymerase III Transcription factor (TFIIIC subunit
YaliOC	3047264	G	A	YALI0C22726g	no similarity
YaliOD	1576990	G	A	YALI0D12628g	similar to Fusarium solani cutinase transcription factor 1 alpha
YaliOE	2038953	G	A	YALI0E17215g	some similarity to S. cerevisiae RME1
YaliOE	2038954	G	A	YALI0E17215g	some similarity to S. cerevisiae RME1
YaliOE	2424790	T	G	YALI0E20449g	weakly similar to S. cerevisiae YOX1
YaliOF	3369592	C	T	YALI0F26191g	similar to S. cerevisiae UGA3

FIG. 21

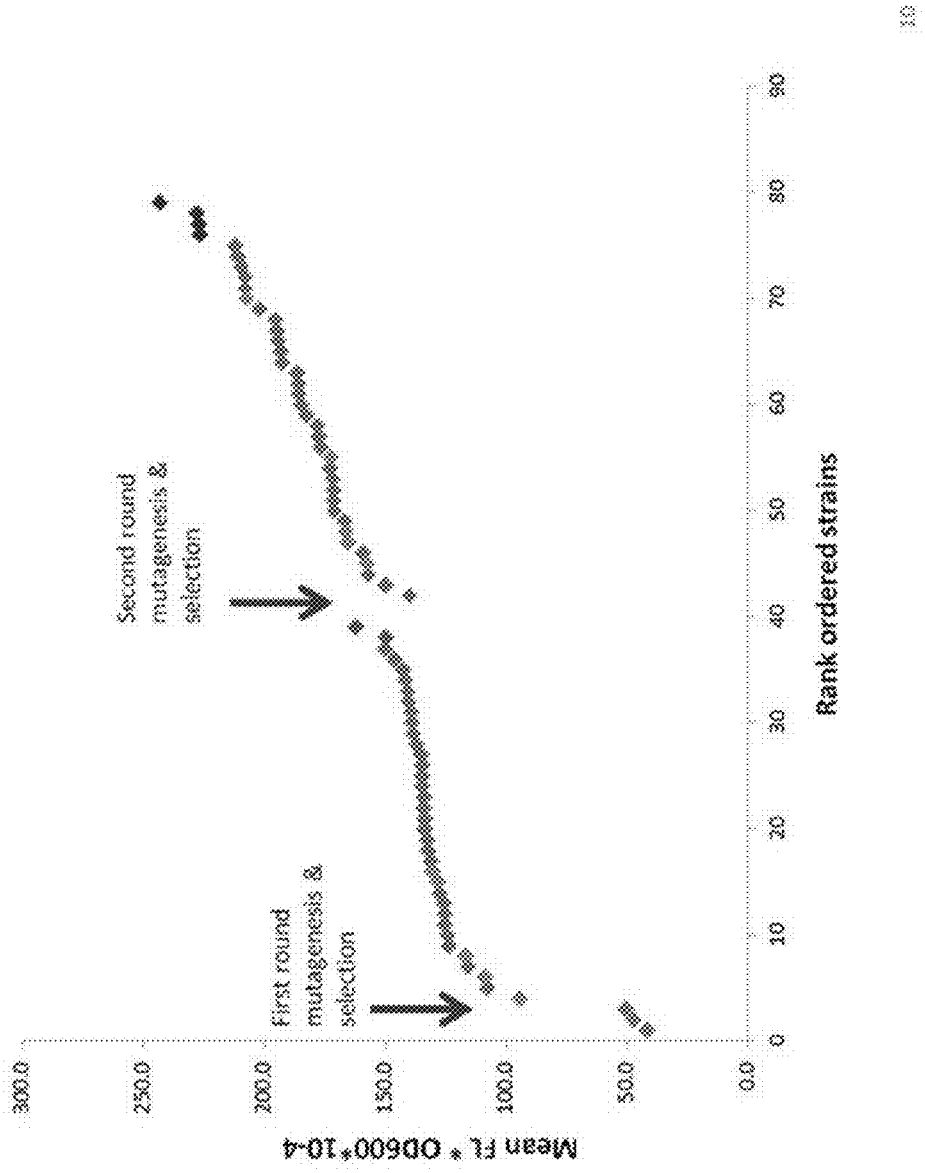

Mean FL * OD600*10-4
300.0
250.0
200.0
150.0
100.0
50.0
0.0
0
10
20
30
40
50
60
70
80
90
Rank ordered strains
First round mutagenesis & selection
Second round mutagenesis & selection

FIG. 22

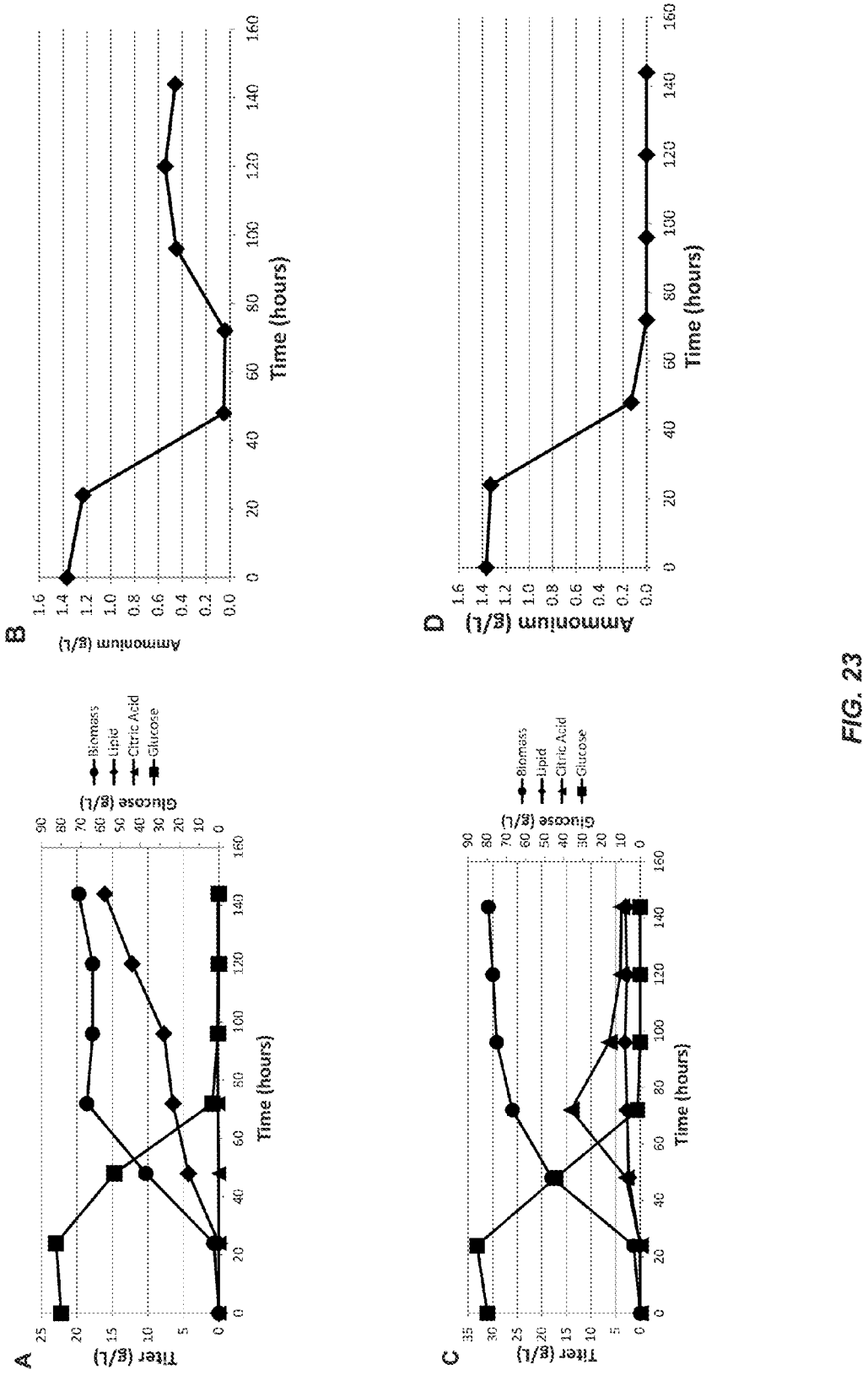

A
Titer (g/L)
Glucose (g/L)
Time (hours)
Biomass
Lipid
Citric Acid
Glucose
B
Ammonium (g/L)
Time (hours)
C
Titer (g/L)
Glucose (g/L)
Time (hours)
Biomass
Lipid
Citric Acid
Glucose
D
Ammonium (g/L)
Time (hours)

FIG. 23

COMPOSITIONS AND METHODS FOR LIPID PRODUCTION

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application No. 61/819,476, filed May 3, 2013, which is incorporated herein by reference in its entirety and for all purposes.

STATEMENT AS TO RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

This invention was made with government support under N000141110669 awarded by Office of Naval Research. The government has certain rights in the invention.

REFERENCE TO A "SEQUENCE LISTING," A TABLE, OR A COMPUTER PROGRAM LISTING APPENDIX SUBMITTED ON A COMPACT DISK

The Sequence Listing written in file 93331-003510US-907029_ST25.TXT, created on Apr. 29, 2014, 210,560 bytes, machine format IBM-PC, MS-Windows operating system, is hereby incorporated herein by reference in its entirety and for all purposes.

BACKGROUND

Increasing oil consumption makes continued dependence on petroleum reserves untenable. Microbial production of renewable alternatives can reduce petroleum footprints through the in vivo synthesis of ethanol, biodiesel, and industrial precursors (Curran et al. 2013; Elshahed 2010; Li et al. 2008; Xu et al. 2013; Yim et al. 2011). Economic viability is highly dependent upon microbial choice, and an ideal host efficiently generates high titers independent of fermentation condition, through native or imported biosynthetic metabolism (Alper and Stephanopoulos 2009). In this regard, *Yarrowia lipolytica*'s genetic tractability, efficient utilization of many energy sources, and native capacity to accumulate lipids make it an ideal platform for oleo-chemical synthesis (Barth and Gaillardin 1996; Beopoulos et al. 2009a; Papanikolaou and Aggelis 2002).

Here we have employed a large-scale combinatorial approach to maximize lipid production in *Y. lipolytica* through both genomic engineering and combinatorial and inverse metabolic engineering multiplexed with phenotypic induction.

Y. lipolytica has a fully defined metabolic engineering toolbox that enables intracellular flux control through genomic manipulation (Blazeck et al. 2013b; Dujon et al. 2004; Fickers et al. 2003; Juretzek et al. 2001; Matsuoka et al. 1993). *Y. lipolytica* is commonly utilized for heterologous protein excretion and to examine and manipulate lipid and fatty acid metabolism (Beopoulos et al. 2009b; Beopoulos et al. 2008; Dulermo and Nicaud 2011; Madzak et al. 2004; Thevenieau et al. 2009), and has proven amenable to downstream manipulation of its fatty acid content to alter desaturation levels (Chuang et al. 2010) or to synthesize novel oleo-chemicals (Blazeck et al. 2013a). Thus, *Y. lipolytica* lipid reserves are ideal for in vivo catalysis to alkanes (Schirmer et al. 2010), fatty acid esters (Shi et al. 2012) or for standard transesterification-based conversion and use as biodiesel. In particular, biodiesel production grants a high net energy gain compared to other alternative fuels with minimal environmental impact, and harvesting lipid reserves from a microbial source such as *Y. lipolytica* enables easily scaled-up production without compromising food supply (Christophe et al. 2012; Hill et al. 2006; Kirstine and Galbally 2012; Subramaniam et al. 2010). *Y. lipolytica*'s natural lipid content consists of predominantly C16:0, C16:1, C18:0, C18:1, and C18:2 fatty acids (Beopoulos et al. 2008; Blazeck et al. 2013a; Tai and Stephanopoulos 2013), very similar to the fatty acid content of biodiesel derived from soybeans and rapeseed (Gruzdiene and Anelauskaite 2011; Hammond et al. 2005). Economic viability can be greatly improved by fully utilizing all sugars from lignocellulosic biomass or by using carbon from industrial waste streams. In this regard, *Y. lipolytica* can efficient utilize hydrophobic and waste carbon sources, such as crude glycerol (Andre et al. 2009; Fickers et al. 2005; Makri et al. 2010; Rywinska et al. 2013), and has shown excellent heterologous gene expression when utilizing glucose, sucrose, glycerol, or oleic acid as a carbon source (Blazeck et al. 2013b). Finally, *Y. lipolytica* is regarded as a "safe-to-use" organism (Groenewald et al. 2013).

Lipid accumulation in *Y. lipolytica* can be induced by nitrogen starvation and has been associated with the activity of four enzymes: AMP Deaminase (AMPDp), ATP-Citrate Lyase (ACLp), Malic Enzyme (MAEp) and Acetyl-CoA Carboxylase (ACCp) (Beopoulos et al. 2009a; Dulermo and Nicaud 2011). AMPDp cleaves AMP into NH_4^+ and inosine 5'-monophosphate to replenish intracellular nitrogen levels; AMP deficiency inhibits the citric acid cycle resulting in citric acid accumulation. ACLp cleaves citric acid into oxaloacetate and acetyl-CoA, and ACCp carboxylates acetyl-CoA into malonyl-CoA fatty acid building blocks. Fatty acid synthesis is further encouraged by a MEAp-mediated increase in NADPH levels (Beopoulos et al. 2009a). Fatty acids can be directly stored in intracellular lipid bodies or further incorporated in triacylglycerides before storage (Beopoulos et al. 2008). Triacylglyceride synthesis follows the Kennedy Pathway to fuse three fatty acids to a glycerol-3-phosphate (G3P) backbone (Kennedy 1961). The ultimate step is catalyzed by the DGA1 or DGA2 acyl-CoA:diacylglycerol acyltransferases (Beopoulos et al. 2009a; Beopoulos et al. 2012). G3P backbone is synthesized from dihydroxyacetone phosphate (DHAP) by the cytosolic, NAD^+-dependent glycerol-3-phosphate dehydrogenase (GPD1) and recycled into glycolysis by the mitochondrial, FAD^+-dependent glycerol-3-phosphate dehydrogenase isoform (GUT2) (Dulermo and Nicaud 2011). TAG hydrolysis mobilizes free fatty acids for peroxisomal degradation through the four step β-oxidation cycle (Beopoulos et al. 2011)—oxidation by one of six acyl-CoA oxidases (POX1-6), hydration and dehydrogenation by the multifunctional enzyme (MFE1), and thiolysis by a 3-ketoacyl-CoA-thiolase (POT1 or PAT1) (Beopoulos et al. 2009a). The PEX10p transcription factor has been implicated in peroxisomal biogenesis and Δpex10 mutants display increased triacylglyceride content (Blazeck et al. 2013a; Hong et al. 2012; Zhu et al. 2012).

Genomic modifications to *Y. lipolytica* 's fatty acid, lipid, and central carbon metabolism have shown promise towards increasing lipid accumulation capacity. Deletion of the six POX genes increased ex novo incorporation of oleic acid in *Y. lipolytica*, while deletion of the single MFE1 gene had a similar effect (Beopoulos et al. 2008; Dulermo and Nicaud 2011). Increasing G3P backbone levels by combining GUT2p deletion and GPD1p overexpression in these β-oxi-

dation deficient backgrounds further increased ex novo lipid accumulation to 65-75% triacylglyceride content (Dulermo and Nicaud 2011). Overexpression of DGA1p increased de novo triacylglyceride accumulation fourfold over control levels to 33.8% triacylglyceride content, and co-overexpression of ACC1p further increased triacylglyceride accumulation to a final yield of 41% triacylglyceride content (Tai and Stephanopoulos 2013). To date, no study has attempted to combine the beneficial effects of engineering *Y. lipolytica*'s fatty acid, lipid and central metabolism in a single strain. Additionally, *Y. lipolytica*'s dependence on media formulation for lipid accumulation has not been adequately explored, nor has its ability to randomly accumulate mutations that enhance lipid accumulation. Furthermore, no attempt has been made to utilize mutation-based evolutionary selection to identify novel lipogenic genotypes. Thus, the ultimate capacity of *Y. lipolytica* to accumulate lipids and other oleochemicals has not been unlocked. To this end, we have employed a large scale combinatorial approach to maximize lipid production while accounting for unexpected interactions between genotype and environmentally-induced phenotype. The present invention provides solutions to these and other problems in the art.

BRIEF SUMMARY

In a first aspect is provided a genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) wherein the dry weight of said yeast cell includes greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals.

In a second aspect is provided a method of producing a lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) including: 1) culturing a yeast cell as described herein (including embodiments or as described in the examples, tables, figures, and/or claims) in a growth medium; and 2) isolating the lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) (e.g. from the medium or yeast cell).

In a third aspect is provided a method of isolating a genetically modified yeast cell from a plurality of yeast cells, including greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals in dry weight, including allowing a genetically modified yeast cell to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium thereby isolating the genetically modified yeast cell, wherein the population of yeast cells includes a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals than said genetically modified yeast cell.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1**. Nile Red assay quantifying lipid content of PO1f WT strain in C160N0.2 media supplemented with individual micronutrients after 2, 4, and 8 days of cultivation.

FIG. **2**. Nile Red assay quantifying lipid content of PO1f WT strain in C160N0.2 media supplemented with multiple micronutrients after 2, 4, and 8 days of cultivation.

FIG. **3**. Nile Red assay quantify lipid content of 46 rationally constructed genetically modified PO1f derivatives.

FIG. **4**. Fold improvement of lipid accumulation (from Nile Red assay signal (RFU)) by enabling the capacity to synthesis leucine through incorporation of the LEU2 marker to different genotypic background. LEU2 expression can be from an episomal or an integrated sequence.

FIG. **5**. Heat map of lipid content based on Nile Red signal of PO1f WT cultured in media formulations with different carbon to nitrogen ratios after 4 days.

FIG. **6**. Heat map of lipid content based on Nile Red signal of PO1f-S1-S2-ϕ cultured in media formulations with different carbon to nitrogen ratios after 4 days.

FIG. **7**. Heat map of lipid content based on Nile Red signal of ΔPEX10ΔMFE1 cultured in media formulations with different carbon to nitrogen ratios after 4 days.

FIG. **8**. Heat map of lipid content based on Nile Red signal of ΔPEX10ΔMFE1-pMCS-DGA1 cultured in media formulations with different carbon to nitrogen ratios after 4 days.

FIG. **9**. Nile Red assay quantify lipid content on Day 4 with different strains growing on different saccharides as carbon sources. Saccharide initial concentration was set at 80 g/L with 5 g/L ammonium sulfate.

FIG. **10**. Nile Red assay quantify lipid content of isolated L36 strain cultured in C160N0.2 media supplemented with multiple micronutrients after 2, 4, and 8 days of cultivation.

FIG. **11**. Nile Red assay quantify lipid content with EMS mutagenesis in evolved L36 strains and L36.

FIG. **12**. Fluorescence light microscopy pictures of lipid accumulation in selected strains. Lipids were stained with Nile Red as usual. Strain ΔPEX10ΔMFE1-pMCS-DGA1 shows almost total lipid content while PO1f WT has very little.

FIG. **13**. General lipid metabolism in yeast and a portion of selected targets to engineering lipid metabolism.

FIG. **14**. The isolation and characterization of superior lipid production strain L36.

FIG. **15**. Fatty acid profiles for different strains.

FIG. **16**. Lipid accumulation in strain PO1f and PO1fΔaco1 DGA1 leu+ ura+ characterized with flow cytometry using cells stained with Nile Red on 48 hour and 96 hour time point. The starting OD of the culture is 2.5 and the cells were cultivated in yeast synthetic medium with 80 g/L glucose.

FIG. **17**. Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 192 h time point. The starting OD of the culture is 5 and the cells were cultivated in yeast synthetic medium with 160 g/L glucose and 0.2 g/L ammonium sulfate. Illustrated in the bar graph, L36Δmga2 presented a significantly reduced lipid level comparing to L36 and L36Δmga2 MGA2-36 presented an elevated level of lipid accumulation comparing to L36Δmga2, indicating that mga2-36 is the reason of the high lipid accumulation phenotype in L36 strain. Combining the data with Δmga2 and Δmga2 MGA2-36 in PO1f, this set of data proves that Δmga2 can lead to improved lipid accumulation and further introduce the mutant transcriptional factor MGA2-36 can further elevate the level of lipid accumulation. (All strains in the set contain an episomal plasmid with LEU2). Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 192 h time point with yeast synthetic medium containing 160 g/L glucose and 0.2 g/L ammonium sulfate and 96 h time point with yeast synthetic medium containing 80 g/L glucose and 5 g/L ammonium sulfate. Introducing MGA2-36 to the engineered strain leads to elevated level of lipid accumulation, suggesting MGA2-36 can be used a lipid enhancer in the rationally engineered lipid production strain. Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 192 h time point with yeast synthetic medium containing 160 g/L glucose and 0.2 g/L ammonium sulfate. PO1fΔmga2 leu+ showed improved level of lipid accumulation comparing to PO1f leu+ indicating mga2 knockout

could improve lipid accumulation. Introducing a transmembrane domain truncated MGA2-36 in PO1f could elevate the lipid level inside the cell.

FIG. **18**. Gas chromatography characterization of major fatty acid species profile in PO1f, Engineered strain and L36. L36 overproduced C16:1n9 fatty acid which could be linked with the mutant of MGA2 gene, which plays an important function on activating/regulating delta9 desaturase expression.

FIG. **19**. Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 96 h time point with yeast synthetic medium containing 80 g/L glucose and 5 g/L ammonium sulfate. 1^{st} round EMS mutagenesis and floating cell transfer method selected strain E26 and E13 using final engineered strain PO1f Δpex10,mfe DGA1 leu+ ura+ presented a higher lipid accumulation level comparing to the engineered strain.

FIG. **20**. Lipid production (g/L) in bioreaction with 160 g/L glucose and 13.4 g/L YNB with ammonium sulfate without amino acid (set control DO at 50% and pH=3.5) with engineered strain and evolved strain E26.

FIG. **21**. List of consensus mutations in strain E26 and E13 identified in open reading frame through next generation sequencing analysis. Among them, YLOSH6; YLIRC20; YLRME1; YLYOX1; YLUGA2 contains missense mutations in annotated protein.

FIG. **22**. Summary illustration of 1^{st} and 2^{nd} round of EMS mutagenesis and floating cells transfer selection with final engineered strain PO1f Δpex10,mfe DGA1 leu+ ura+ as starting strain for evolving and selecting high lipid production strain. Green indicating the final engineering strain, blue indicating the non-EMS treated control stains and red indicating the selected high lipid production strains. Strains were rank ordered based on the value cultured OD600*Nile Red mean fluorescence intensity*10−4.

FIG. **23**. Fermentation profiles of pex10 mfe1 leucine$^+$ uracil$^+$ DGA1 and PO1f leucine$^+$ uracil$^+$. Time courses of the 1.5 L scale batch fermentation of the pex10 mfe1 leucine$^+$ uracil$^+$ DGA1 (a,b) and PO1f leucine$^+$ uracil$^+$ (c,d) strains in 80 g/L glucose, 6.7 g/L YNB (no amino acids, 1.365 g/L ammonium) are shown, including production of biomass, lipids, and citric acid (left axis a,c), consumption of glucose (right axis a,c), and ammonium level (b,d). (a) During the pex10 mfe1 leucine$^+$ uracil$^+$ DGA1 fermentation, negligible citric acid was produced, and lipid product accumulated during and after biomass production phases. This fermentation was run three times in identical conditions, reaching final yields of 15.25 g/L lipids and 20.3 g/L biomass (75% lipid content), 14.96 g/L lipids and 20.6 g/L biomass (73% lipid content), and 16.9 g/L lipids and 19.21 g/L biomass (88% lipid content). Most time points show average values from the former two fermentations (75% and 73% final lipid content), while endpoints represent averages from all three final values. Glucose and ammonium substrate were fully consumed after 72 hours, but surprisingly, (b) ammonium level was replenished to a steady state level of ~0.5 g/L, almost 40% of the original starting level. (c) During the PO1f leucine$^+$ uracil$^+$ fermentation, citric acid accumulated to more than 14 g/L after 72 hours before quickly reducing to 4 g/L. Lipid production did not trend with biomass production, reaching a final yield of only 3 g/L lipids, compared to 30 g/L biomass, and glucose was again consumed within 72 hours. (d) Ammonium was fully consumed after 72 hours with no replenishment as observed in the mutant strain.

DETAILED DESCRIPTION

Our work described herein represents the largest scale engineering effort in an oleaginous organism to date. We analyzed the effect of nitrogen starvation and carbon level on a wildtype *Y. lipolytica* strain and a strain with two genomic modifications to increase lipid (e.g. triacylglyceride) accumulation. By testing twenty media formulations containing between 10 g/L and 320 g/L glucose and 0.04 g/L and 10 g/L ammonium sulfate, we demonstrated that increasing carbon to nitrogen ratio (C:N ratio) generally induces lipid (e.g. triacylglyceride) accumulation, that carbon level is more important than nitrogen level towards this induction, and that this optimum carbon level is dependent upon genomic background. We further determined that lipid (e.g. triacylglyceride) accumulation could be increased through the addition of certain metallic cofactors in the wildtype background as well as for some *Y. lipolytica* strains already engineered for increased lipid (e.g. triacylglyceride) content. In an effort to rationally engineer *Y. lipolytica* for increased lipid (e.g. triacylglyceride) accumulation while accounting for unpredictable cumulative effects arising from simultaneously altering fatty acid, lipid, and central carbon metabolism, we overexpressed multiple (e.g. five) enzymes implicated in lipid (e.g. triacylglyceride) accumulation in multiple (e.g. four) background strains differentially deficient in fatty acid degradation. These native enzymatic overexpressions were driven by high-strength constitutive promoters, occurred singly or in tandem with a second enzyme overexpression, and alleviated one of two auxotrophies (leucine and uracil). This combinatorial approach generated over 50 distinct genotypes that produced a large range in lipid (e.g. triacylglyceride) accumulation ability, culminating in upwards of 40-fold above control when using Nile-red based fluorescence and nearly 5-fold when using concentration (g/L) or percent lipid by cell mass (% dcw). In the process, we discovered a correlation between the auxotrophic marker used to select for protein overexpression and a strain's capacity to accumulate oleo-content. Specifically, the ability to endogenously produce the amino acid leucine, conferred by a selectable leucine auxotrophic marker, is beneficial (e.g. essential) to enable high lipid titer. We further examined a few (e.g. thirteen) of these strains to determine how C:N ratio and genotype interacted towards producing lipid (e.g. triacylglyceride) content on a larger scale. We observed a strong tendency towards high lipid (e.g. triacylglyceride) levels in most high producers at a single media formulation—cultivated in 80 g/L glucose and 5 g/L ammonium sulfate. We selected a MFE1, PEX10 double knockout strain with no auxotrophies overexpressing the DGA1p lipid synthesis as our final rationally engineered strain, and demonstrated its triacylglyceride accumulation ability on a variety of carbon sources, demonstrating its robust capacity to accumulate triacylglycerides regardless of media composition.

Through our time working with *Y. lipolytica*, we became aware of its surprising capacity to randomly (or forcibly through the use of an exogenous mutagen such as EMS) generate isolatable sub-strains that reproducibly displayed higher than wildtype triacylglyceride levels. In fact, one such strain, dubbed L36, displayed remarkable accumulation ability. Whole-genome sequencing of this strain pinpointed a mutation in the MGA2 transcriptional regulator as the most likely genomic explanation. Complementation assays of an MGA2p truncation mutant into wildtype background reached 50% of L36 lipid levels. We sought to harness this general capacity for beneficial mutation by subjecting wildtype, L36, and two of our highest producing rationally engineered strains to ethylmethanesulfonate (EMS) mutagenesis and positive selection. By combining large-scale investigations of phenotypic induction, genomic

engineering, and positive random mutations, this work establishes a framework for engineering oleaginous organisms for increased lipid production. In this regard, we have pinpointed specific media formulations, genomic modifications, and genomic mutations that positively effect lipid (e.g. triacylglyceride) biosynthesis. The resultant strains are ideal for direct biodiesel precursor synthesis, lipid synthesis, oleochemical synthesis, lipid precursor synthesis, or for in vivo catalysis of fatty acid reserves to value added chemicals. Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 192 h time point with yeast synthetic medium containing 160 g/L glucose and 0.2 g/L ammonium sulfate and 96 h time point with yeast synthetic medium containing 80 g/L glucose and 5 g/L ammonium sulfate. Introducing MGA2-36 to the engineered strain leads to elevated level of lipid accumulation, suggesting MGA2-36 can be used a lipid enhancer in the rationally engineered lipid production strain. Lipid accumulation characterized with flow cytometry using cells stained with Nile Red on 192 h time point with yeast synthetic medium containing 160 g/L glucose and 0.2 g/L ammonium sulfate. PO1fΔmga2 leu+ showed improved level of lipid accumulation comparing to PO1f leu+ indicating mga2 knockout could improve lipid accumulation. Introducing a transmembrane domain truncated MGA2-36 in PO1f could elevate the lipid level inside the cell.

I. DEFINITIONS

The term "oleaginous organism" means an organism (e.g. a cell such as a yeast cell) that is capable of producing a lipid, lipid precursor, oleochemical, or oil (or combinations thereof) at a level exceeding the amount required for normal cellular survival and propagation of the organism (e.g. cell, yeast cell), such as for example necessary for structural integrity (e.g. membrane formation and maintenance) and cellular maintenance. Examples of amounts exceeding the amount required for normal cellular survival and propagation include an amount of lipids, oils, lipid precursors, and oleochemicals greater than 20% wt/wt total dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99%). In embodiments, the oleaginous organism is an oleaginous yeast. In some embodiments, the oleaginous yeast is from a genus selected from the group consisting of *Apiotrichum, Candida, Cryptococcus, Debaromyces, Endomycopsis, Geotrichum, Hyphopichia, Lipomyces, Lypomyces, Pichia, Rodosporidium, Rhodotorula, Sporobolomyces, Starmerella, Torulaspora, Trichosporon, Wickerhamomyces, Yarrowia*, and *Zygoascus*. In embodiments, the oleaginous yeast is selected from the group consisting of *Apiotrichum curvatum, Candida apicola, Candida curvata, Candida revkaufi, Candida pulcherrima, Candida tropicalis, Candida utilis, Cryptococcus curvatus, Cryptococcus terricolus, Debaromyces hansenii, Endomycopsis vernalis, Geotrichum carabidarum, Geotrichum cucujoidarum, Geotrichum histeridarum, Geotrichum silvicola, Geotrichum vulgare, Hyphopichia burtonii, Lipomyces lipoferus, Lipomyces lipofer, Lypomyces orentalis, Lipomyces starkeyi, Lipomyces tetrasporous, Pichia mexicana, Rodosporidium sphaerocarpum, Rhodosporidium toruloides, Rhodotorula aurantiaca, Rhodotorula dairenensis, Rhodotorula diffluens, Rhodotorula glutinus, Rhodotorula glutinis* var. *glutinis, Rhodotorula gracilis, Rhodotorula graminis, Rhodotorula minuta, Rhodotorula mucilaginosa, Rhodotorula mucilaginosa Rhodotorula mucilaginosa, Rhodotorula terpenoidalis, Rhodotorula toruloides, Sporobolomyces alborubescens, Starmerella bombicola, Torulaspora delbruekii, Torulaspora pretoriensis, Trichosporon behrend, Trichosporon brassicae, Trichosporon cutaneum, Trichosporon domesticum, Trichosporon fermentans, Trichosporon laibachii, Trichosporon loubieri, Trichosporon loubieri* var. *loubieri, Trichosporon montevideense, Trichosporon pullulans, Wickerhamomyces canadensis, Yarrowia lipolytica*, and *Zygoascus meyerae*.

The term "buoyancy" is used according to its plain ordinary meaning and refers to the upward force exerted by a fluid, which opposes the weight of an immersed object (e.g. oleaginous organism or oleaginous yeast cell). Pressure increases with depth, resulting in a net force tending to accelerate object upward, wherein the magnitude of the force is proportional to the difference between the top and bottom of the fluid and is equivalent to the weight of the fluid that would otherwise occupy the space occupied by the object (i.e. the displace fluid). In embodiments, an oleaginous organism or yeast cell is considered "buoyant" when it does not settle (e.g. due to gravitation force alone, due to centrifugal force, due to an applied force, or due to a combination of forces such as centrifugation) to the bottom of a vessel holding a liquid (e.g. media) in which the oleaginous organism or yeast cell resides. For example, a cell may be buoyant if it floats above the bottom of the vessel, at an intermediate position between the bottom level and top level of the liquid, or on top of the upper surface of the liquid. An example of a measurement of the buoyancy of an object (e.g. cell) is the weight of the fluid the object would displace if the object were placed in the fluid. Another example of a measurement of the buoyancy of an object (e.g. cell) is a comparison of the average density of the object and the average density of the liquid to be displaced, taking into account the depth of the liquid in a column of the liquid. The term "buoyant density" is used according to its plain ordinary meaning and refers to a measure of the tendency of a substance to float in some other substance.

The term "carbon substrate" means a carbon source that a microorganism (e.g. oleaginous organism or oleaginous yeast) will metabolize to derive energy (e.g. monosaccharides, oligosaccharides, polysaccharides, alkanes, fatty acids, esters of fatty acids, monoglycerides, carbon dioxide, methanol, formaldehyde, formate or carbon-containing amines). The term "carbon source" refers to a carbon containing composition (e.g. compound, mixture of compounds) that an organism (e.g. oleaginous organism, yeast cell) may metabolize for use by the organism or that may be used for organism viability. A "majority carbon source" refers to a carbon containing composition that accounts for greater than 50% of the available carbon sources for an organism (e.g. in a media, in a growth media, in a defined media for growing yeast cells, or in a defined media for producing lipids by yeast cells) at a specified time (e.g. media when starting a yeast culture, media in a bioreactor when growing yeast, or media when producing lipids from yeast). In embodiments, an oleaginous yeast may be cultured using a medium comprising one or more carbon sources selected from the group consisting of glucose, fructose, sucrose, lactose, galactose, xylose, mannose, rhamnose, arabinose, glycerol, acetate, depolymerized sugar beet pulp, black liquor, corn starch, depolymerized cellulosic material, corn stover, sugar beet pulp, switchgrass, milk whey, molasses, potato, rice, sorghum, sugar cane, wheat, and mixtures thereof (e.g. mixtures of glycerol and glucose, mixtures of

glucose and xylose, mixtures of fructose and glucose, mixtures of sucrose and depolymerized sugar beet pulp, black liquor, corn starch, depolymerized cellulosic material, corn stover, sugar beet pulp, switchgrass, milk whey, molasses, potato, rice, sorghum, sugar cane, and/or wheat). In embodiments, an oleaginous yeast is cultured using a medium comprising one or more carbon sources selected from the group consisting of depolymerized sugar beet pulp, black liquor, corn starch, depolymerized cellulosic material, corn stover, sugar beet pulp, switchgrass, milk whey, molasses, potato, rice, sorghum, sugar cane, thick cane juice, sugar beet juice, and wheat. In embodiments, an oleaginous yeast is cultured using a medium comprising lignocellulosic biomass. In embodiments carbon sources may be monosaccharides (e.g., glucose, fructose), disaccharides (e.g., lactose, sucrose), oligosaccharides, polysaccharides (e.g., starch, cellulose or mixtures thereof), sugar alcohols (e.g., glycerol) or mixtures from renewable feedstocks (e.g., cheese whey permeate, cornsteep liquor, sugar beet molasses, or barley malt). Additionally, carbon sources may include alkanes, fatty acids, esters of fatty acids, monoglycerides, diglycerides, triglycerides, phospholipids, various commercial sources of fatty acids including vegetable oils (e.g., soybean oil) or animal fats.

Nitrogen may be supplied from an inorganic (e.g., $(NH_4)_2SO_4$) or organic source (e.g., urea, glutamate). The term "nitrogen source" refers to a nitrogen containing composition (e.g. compound, mixture of compounds, salt) that an organism (e.g. oleaginous organism, yeast cell) may metabolize for use by the organism or that may be used for organism viability. A "majority nitrogen source" refers to a nitrogen containing composition that accounts for greater than 50% of the available nitrogen sources for an organism (e.g. in a media, in a growth media, in a defined media for growing yeast cells, or in a defined media for producing lipids by yeast cells) at a specified time (e.g. media when starting a yeast culture, media in a bioreactor when growing yeast, or media when producing lipids from yeast).

The term "Biomass" refers to material produced by growth and/or propagation of cells. "Lignocellulosic biomass" is used according to it plain ordinary meaning and refers to plant dry matter comprising carbohydrate (e.g. cellulose or hemicellulose) and polymer (e.g. lignin). Lignocellulosic biomass may include agricultural residues (e.g. corn stover or sugarcane bagasse), energy crops (e.g. poplar trees, willow, *Miscanthus purpureum, Pennisetum purpureum*, elephant grass, maize, Sudan grass, millet, white sweet clover, rapeseed, giant *miscanthus*, switchgrass, jatropha, *Miscanthus giganteus*, or sugarcane), wood residues (e.g. sawmill or papermill discard), or municipal paper waste.

The term "Culture", "cultivate", and "ferment" are used interchangeably and refer to the intentional growth, propagation, proliferation, and/or enablement of metabolism, catabolism, and/or anabolism of one or more cells (e.g. oleaginous organism or oleaginous yeast). The combination of both growth and propagation may be termed proliferation. Examples include production by an organism of lipids, lipid precursors, and/or oleochemicals or production of a lipid, lipid precursor, and/or oleochemical of interest. Culture does not refer to the growth or propagation of microorganisms in nature or otherwise without human intervention.

The terms "dry weight" and "dry cell weight" are used interchangeably and refer to a weight determined in the relative absence of water. In embodiments, oleaginous yeast biomass comprising a fraction or percentage of a particular component by dry weight means that the fraction or percentage is calculated based on the weight of the biomass after substantially all water has been removed.

The term "growth" means an increase in cell size, total cellular contents, and/or cell mass or weight of a cell (e.g. oleaginous organism or oleaginous yeast).

The term "lipid" refers to a class of molecules that are soluble in nonpolar solvents (e.g. ether or chloroform), are relatively or completely insoluble in water, and include one or more hydrocarbon chains which are hydrophobic. In embodiments, a lipid may be a triacylglyeride (i.e. fat), fatty acid (e.g. saturated or unsaturated); glyceride or glycerolipid (e.g. monoglyceride, diglyceride, triglyceride, neutral fat, phosphoglyceride, or glycerophospholipid); sphingolipid; sterol lipid (e.g. cholesterol or a steroid hormone); prenol lipid (e.g. terpenoid); fatty alcohol; wax; polyketide; sugar-linked lipid, glycolipid, or protein-linked lipid.

The term "oil" means a triacylglyceride (or triglyceride oil), produced by an organism (e.g. oleaginous organism, oleaginous yeast, plant, and/or animal). An oil is generally liquid at normal ambient temperatures and pressures. In embodiments, oil may be vegetable or seed oils derived from plants (e.g. soy, rapeseed, canola, palm, palm kernel, coconut, corn, olive, sunflower, cotton seed, *cuphea*, peanut, camelina sativa, mustard seed, cashew nut, oats, lupine, kenaf, *calendula*, hemp, coffee, linseed, hazelnut, *euphorbia*, pumpkin seed, coriander, camellia, sesame, safflower, rice, tung oil tree, cocoa, copra, pium poppy, castor beans, pecan, jojoba, jatropha, *macadamia*, Brazil nuts, avocado, or combinations thereof). An oil may include a plurality of different triacylglycerides. For example, a vegetable or seed oil may include more than one triacylglyceride and use of the name of that vegetable or seed oil (e.g. soy, rapeseed, canola, palm, etc.) when referring to an oil generated by an oleaginous organism will be understood to mean an oil including most (e.g. all) of the triacylglycerides normally in the vegetable or seed oil (e.g. at different ratios relative to each other or the same or similar ratios relative to each other). In other embodiments, an oil may be a plurality of triacylglyceride and other lipid molecules produced by an oleaginous organism.

The term "propagation" refers to an increase in cell number via cell division.

The terms "V/V", "vol/vol", or "v/v", referring to proportions by volume, means the ratio of the volume of one substance in a composition to the volume of the total composition including the substance.

The term "W/W", "wt/wt", or "w/w", referring to proportions by weight, means the ratio of the weight of one substance in a composition to the weight of the total composition including the substance. For example, 5% w/w substance X means that 5% of the composition's weight is composed of substance X and the remainder of the weight of the composition (i.e. 95%) is composed of other substances.

The term "promoter" or "regulatory element" refers to a region or sequence determinants located upstream or downstream from the start of transcription and which are involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. Promoters need not be of yeast origin, for example, promoters derived from viruses or from other organisms can be used in the compositions or methods described herein.

A polynucleotide sequence is "heterologous to" a second polynucleotide sequence if it originates from a foreign species, or, if from the same species, is modified by human action from its original form. For example, a promoter operably linked to a heterologous coding sequence refers to a coding sequence from a species different from that from

which the promoter was derived, or, if from the same species, a coding sequence which is different from naturally occurring allelic variants.

The term "recombinant" refers to a human manipulated nucleic acid (e.g. polynucleotide) or a copy or complement of a human manipulated nucleic acid (e.g. polynucleotide), or if in reference to a protein (i.e, a "recombinant protein"), a protein encoded by a recombinant nucleic acid (e.g. polynucleotide). In embodiments, a recombinant expression cassette comprising a promoter operably linked to a second nucleic acid (e.g. polynucleotide) may include a promoter that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation (e.g., by methods described in Sambrook et al., *Molecular Cloning—A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1989) or Current Protocols in Molecular Biology Volumes 1-3, John Wiley & Sons, Inc. (1994-1998)). In another example, a recombinant expression cassette may comprise nucleic acids (e.g. polynucleotides) combined in such a way that the nucleic acids (e.g. polynucleotides) are extremely unlikely to be found in nature. For instance, human manipulated restriction sites or plasmid vector sequences may flank or separate the promoter from the second nucleic acid (e.g. polynucleotide). In embodiments, a recombinant nucleic acid is a nucleic acid in an oleaginous organism (e.g. oleaginous yeast) that has been manipulated by a human, for example a recombinant nucleic acid comprising a coding region for a protein that is overexpressed in an oleaginous organism relative to the absence of the recombinant nucleic acid or a recombinant nucleic acid that results in disruption of a coding region or promoter region of an oleaginous organism and reduces or eliminates expression of a protein relative the absence of the recombinant nucleic acid. One of skill will recognize that nucleic acids (e.g. polynucleotides) can be manipulated in many ways and are not limited to the examples above.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. The term "nucleic acid" includes single-, double-, or multiple-stranded DNA, RNA and analogs (derivatives) thereof. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. In certain embodiments, the nucleic acids herein contain phosphodiester bonds. In other embodiments, nucleic acid analogs are included that may have alternate backbones. The term encompasses nucleic acids containing known analogues of natural nucleotides which have similar or improved binding properties, for the purposes desired, as the reference nucleic acid. A particular nucleic acid sequence also encompasses "splice variants." Similarly, a particular protein encoded by a nucleic acid encompasses any protein encoded by a splice variant of that nucleic acid. "Splice variants," as the name suggests, are products of alternative splicing of a gene. After transcription, an initial nucleic acid transcript may be spliced such that different (alternate) nucleic acid splice products encode different polypeptides. Mechanisms for the production of splice variants vary, but include alternate splicing of exons. Alternate polypeptides derived from the same nucleic acid by read-through transcription are also encompassed by this definition. Any products of a splicing reaction, including recombinant forms of the splice products, are included in this definition. An example of potassium channel splice variants is discussed in Leicher, et al., *J. Biol. Chem.* 273(52):35095-35101 (1998).

The term "expression cassette" refers to a nucleic acid construct, which when introduced into a host cell, results in transcription and/or translation of a RNA or polypeptide, respectively.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher identity over a specified region when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 10 amino acids or 20 nucleotides in length, or more preferably over a region that is 10-50 amino acids or 20-50 nucleotides in length. As used herein, percent (%) amino acid sequence identity is defined as the percentage of amino acids in a candidate sequence that are identical to the amino acids in a reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared can be determined by known methods.

For sequence comparisons, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 10 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J.*

Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel et al., eds. 1995 supplement)).

One example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nuc. Acids Res.* 25:3389-3402, and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=−4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=−4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence with a higher affinity, e.g., under more stringent conditions, than to other nucleotide sequences (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5×SSC, and 1% SDS, incubating at 42° C., or, 5×SSC, 1% SDS, incubating at 65° C., with wash in 0.2×SSC, and 0.1% SDS at 65° C.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 1×SSC at 45° C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and *Current Protocols in Molecular Biology*, ed. Ausubel, et al. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Exemplary conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, aspartic acid-glutamic acid, and asparagine-glutamine.

The term "modulator" refers to a composition that increases or decreases the level of a target molecule or the level of activity or function of a target molecule or the physical state of the target of the molecule. In embodiments a modulator is a recombinant nucleic acid that is capable of increasing or decreasing the amount of a protein in a cell or the level of activity of a protein in a cell or transcription of a second nucleic acid in a cell. In embodiments, a modulator increases or decreases the level of activity of a protein or the amount of the protein in a cell. The term "modulate" is used in accordance with its plain ordinary meaning and refers to the act of changing or varying one or more properties. "Modulation" refers to the process of changing or varying one or more properties. For example, as applied to the effects of a modulator on a target protein, to modulate means to change by increasing or decreasing a property or function of the target molecule or the amount of the target molecule. In embodiments, a recombinant nucleic acid that modulates the level of activity of a protein may increase the activity or amount of the protein relative the absence of the recombinant nucleic acid. In embodiments, an increase in the activity or amount of a protein may include overexpression of the protein. "Overexpression" is used in accordance with its plain meaning and refers to an increased level of expression of a protein relative to a control (e.g. cell or expression system not including a recombinant nucleic acid that contributes to the overexpression of a protein). In embodiments, a decrease in the activity or amount of a protein may include a mutation (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid; all/any of which may be in the coding region for a protein or in an operably linked region (e.g. promoter)) of the protein. The term "increased" refers to a detectable increase compared to a control. In some embodiments, the increase is by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000%, or more compared to the control. In embodiments, the increase is by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000%, or more compared to the control. In embodiments, the increase is by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000%, compared to the control. Similarly, the term "decreased" refers to a measurable decrease compared to a control. In some embodiments, the decrease is by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100%, or more compared to the control. In embodiments, the decrease is by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100%, or more compared to the control. In embodiments, the decrease is by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100%, compared to the control. One of ordinary skill will be able to identify a relevant control.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are near each other, and, in the case of a secretory leader, contiguous and in reading phase. However, operably linked nucleic acids (e.g. enhancers and coding sequences) do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. In embodiments, a promoter is operably linked with a coding sequence when it is capable of affecting (e.g. modulating relative to the absence of the promoter) the expression of a protein from that coding sequence (i.e., the coding sequence is under the transcriptional control of the promoter).

"Transformation" refers to the transfer of a nucleic acid molecule into a host organism (e.g. oleaginous organism or oleaginous yeast). In embodiments, the nucleic acid molecule may be a plasmid that replicates autonomously or it may integrate into the genome of the host organism (e.g. oleaginous organism or oleaginous yeast). Host organisms containing the transformed nucleic acid molecule may be referred to as "transgenic" or "recombinant" or "transformed" organisms (e.g. oleaginous organism or oleaginous yeast). A "genetically modified" organism (e.g. genetically modified yeast cell) is an organism (e.g. yeast cell) that includes a nucleic acid that has been modified by human intervention. Examples of a nucleic acid that has been modified by human intervention include, but are not limited to, insertions, deletions, mutations, expression nucleic acid constructs (e.g. over-expression or expression from a non-natural promoter or control sequence or an operably linked

promoter and gene nucleic acid distinct from a naturally occurring promoter and gene nucleic acid in an organism), extra-chromosomal nucleic acids, and genomically contained modified nucleic acids. Genetically modified organisms may be made by rational modification of a nucleic acid or may be made by use of a mutagen or mutagenesis protocol that results in a mutation that was not identified (e.g. intended or targeted) prior to the use of the mutagen or mutagenesis protocol (e.g. UV exposure, EMS exposure, mutagen exposure, random genomic mutagenesis, transformation of a library of different nucleic acid constructs). Genetically modified organisms that include a modification (e.g. modification, insertion, deletion, mutation) not previously known or intended prior to making of the genetically modified organism may be identified through screening a plurality of organism including one or more genetically modified organisms by using a selection criteria that identifies the genetically modified organism of interest (e.g. an increased level of lipids, lipid precursors, and/or oleochemicals; floats above an organism not including the same genetic modification). In embodiments, a genetically modified organism includes a recombinant nucleic acid.

Methods for synthesizing sequences and bringing sequences together are well established and known to those of skill in the art. For example, in vitro mutagenesis and selection, site-directed mutagenesis, error prone PCR (Melnikov et al., Nucleic Acids Research, 27(4):1056-1062 (Feb. 15, 1999)), "gene shuffling" or other means can be employed to obtain mutations of naturally occurring genes.

Mutagenesis (e.g. chemical mutagenesis or site directed mutagenesis) may be used to modulate lipid production or storage in an oleaginous organism (e.g. oleaginous yeast). For example, a mutant construct or mutagen is transformed into an oleaginous yeast cell and the ability of the resulting transformed oleaginous yeast cell to produce or store one or more lipids is assayed and compared to the control cell. In some embodiments, it may be useful to disrupt or inactivate a host organism's native gene to modulate lipid production or storage. For example, a recombinant DNA fragment (e.g. a selectable marker gene) may be inserted into the gene to be disrupted in order to interrupt its coding sequence and the resulting recombinant nucleic acid then transformed into a host cell. Another example of a method of gene disruption is the use of transposable elements or transposons, which is well known to those of skill in the art.

In general, means for the purification of lipids, may include extraction with organic solvents, sonication, supercritical fluid extraction, saponification physical means such as presses, extraction, treatment with urea, fractional crystallization, HPLC, fractional distillation, silica gel chromatography, high-speed centrifugation or distillation, or combinations of these techniques.

In embodiments, the protein AMP Deaminase (AMPD) is a protein able to be translated from the nucleic acid corresponding to YALI0E11495 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene AMP Deaminase (AMPD) is the nucleic acid or gene corresponding to YALI0E11495 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, AMP Deaminase (AMPD) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E11495 of *Yarrowia lipolytica* as described above. In embodiments, AMP Deaminase (AMPD) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E11495 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Leucine Biosynthesis Gene (LEU2), also known as 3-isopropylmalate dehydrogenase, is a protein able to be translated from the nucleic acid corresponding to GenBank AF260230 or YALI0C00407 g of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Leucine Biosynthesis Gene (LEU2) is the nucleic acid or gene corresponding to GenBank AF260230 or YALI0C00407 g of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Leucine Biosynthesis Gene (LEU2) is a protein or nucleic acid/gene of a yeast strain corresponding to AF260230 of *Yarrowia lipolytica* as described above. In embodiments, Leucine Biosynthesis Gene (LEU2) is a protein or nucleic acid/gene of an oleaginous organism corresponding to AF260230 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Uracil Biosynthesis gene (URA3), also known as Orotidine 5'-phosphate decarboxylase, is a protein able to be translated from the nucleic acid corresponding to GenBank YLU40564 or YALI0E26741 g of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Uracil Biosynthesis gene (URA3) is the nucleic acid or gene corresponding to GenBank YLU40564 or YALI0E26741 g of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Uracil Biosynthesis gene (URA3) is a protein or nucleic acid/gene of a yeast strain corresponding to YLU40564 of *Yarrowia lipolytica* as described above. In embodiments, Uracil Biosynthesis gene (URA3) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YLU40564 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein ATP-Citrate Lyase (ACL) is a protein including the protein ACL1, also called ATP-Citrate Lyase 1, able to be translated from the nucleic acid corresponding to YALI0E34793 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene ATP-Citrate Lyase (ACL) includes the nucleic acid or gene ACL1 corresponding to YALI0E34793 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, the protein ATP-Citrate Lyase (ACL) is a protein including the protein ACL2, also called ATP-Citrate Lyase 2, able to be translated from the nucleic acid corresponding to YALI0D24431 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, the

nucleic acid or gene ATP-Citrate Lyase (ACL) includes the nucleic acid or gene ACL2 corresponding to YALI0D24431 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, ATP-Citrate Lyase (ACL) includes a protein or nucleic acid/gene of a yeast strain corresponding to YALI0D24431 of *Yarrowia lipolytica* as described above. In embodiments, ATP-Citrate Lyase (ACL) includes a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0D24431 of *Yarrowia lipolytica* as described above. In embodiments, the protein ATP-Citrate Lyase (ACL) is a protein including the protein ACL1 able to be translated from the nucleic acid corresponding to YALI0E34793 of the Genolevures database and the protein ACL2 able to be translated from the nucleic acid corresponding to YALI0D24431 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, the nucleic acid or gene ATP-Citrate Lyase (ACL) includes the nucleic acid or gene ACL1 corresponding to YALI0E34793 and the nucleic acid or gene ACL2 corresponding to YALI0D24431 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, ATP-Citrate Lyase (ACL) includes proteins or nucleic acids/genes of a yeast strain corresponding to YALI0E34793 and YALI0D24431 of *Yarrowia lipolytica* as described above. In embodiments, ATP-Citrate Lyase (ACL) includes proteins or nucleic acids/genes of an oleaginous organism corresponding to YALI0E34793 and YALI0D24431 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Malic Enzyme (MAE, MEA, MEA1) is a protein able to be translated from the nucleic acid corresponding to YALI0E18634 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C, D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Malic Enzyme (MAE, MEA, MEA1) is the nucleic acid or gene corresponding to YALI0E18634 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Malic Enzyme (MAE, MEA, MEA1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E18634 of *Yarrowia lipolytica* as described above. In embodiments, Malic Enzyme (MAE, MEA, MEA1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E18634 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein acyl-CoA: diacylglycerol acyltransferase (DGA1), also called acyl-CoA:diacylglycerol acyltransfer 1 is a protein able to be translated from the nucleic acid corresponding to YALI0E32769 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C, D,E,F specifies chromosome. In embodiments, the nucleic acid or gene acyl-CoA:diacylglycerol acyltransferase (DGA1) is the nucleic acid or gene corresponding to YALI0E32769 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, acyl-CoA: diacylglycerol acyltransferase (DGA1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E32769 of *Yarrowia lipolytica* as described above. In embodiments, acyl-CoA:diacylglycerol acyltransferase (DGA1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E32769 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein acyl-CoA: diacylglycerol acyltransferase (DGA2), also called acyl-CoA:diacylglycerol acyltransfer 2, is a protein able to be translated from the nucleic acid corresponding to YALI0D07986 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C, D,E,F specifies chromosome. In embodiments, the nucleic acid or gene acyl-CoA:diacylglycerol acyltransferases (DGA2) is the nucleic acid or gene corresponding to YALI0D07986 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, acyl-CoA: diacylglycerol acyltransferases (DGA2) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0D07986 of *Yarrowia lipolytica* as described above. In embodiments, acyl-CoA:diacylglycerol acyltransferases (DGA2) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0D07986 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Lipid synthesis regulator (MGA2) is a protein able to be translated from the nucleic acid corresponding to YALI0B12342 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C, D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Lipid synthesis regulator (MGA2) is the nucleic acid or gene corresponding to YALI0B12342 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Lipid synthesis regulator (MGA2) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0B12342 of *Yarrowia lipolytica* as described above. In embodiments, Lipid synthesis regulator (MGA2) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0B12342 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Chromatin assembly gene (RLF2 subunit p90) is a protein able to be translated from the nucleic acid corresponding to YALI0F21637 g of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Chromatin assembly gene (RLF2 subunit p90) is the nucleic acid or gene corresponding to YALI0F21637 g of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Chromatin assembly gene (RLF2 subunit p90) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0F21637

g of *Yarrowia lipolytica* as described above. In embodiments, Chromatin assembly gene (RLF2 subunit p90) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0F21637 g of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Mitochondrial 2' O-ribose methyltransferase (MRM2) is a protein able to be translated from the nucleic acid corresponding to YALI0E31933 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Mitochondrial 2' O-ribose methyltransferase (MRM2) is the nucleic acid or gene corresponding to YALI0E31933 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Mitochondrial 2' O-ribose methyltransferase (MRM2) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E31933 of *Yarrowia lipolytica* as described above. In embodiments, Mitochondrial 2' O-ribose methyltransferase (MRM2) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E31933 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Transcription Factor (PEX10) is a protein able to be translated from the nucleic acid corresponding to YALI0C01023 g of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Transcription Factor (PEX10) is the nucleic acid or gene corresponding to YALI0C01023 g of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Transcription Factor (PEX10) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0C01023 g of *Yarrowia lipolytica* as described above. In embodiments, Transcription Factor (PEX10) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0C01023 g of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein multifunctional enzyme (MFE1) is a protein able to be translated from the nucleic acid corresponding to YALI0E15378 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene multifunctional enzyme (MFE1) is the nucleic acid or gene corresponding to YALI0E15378 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, multifunctional enzyme (MFE1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E15378 of *Yarrowia lipolytica* as described above. In embodiments, multifunctional enzyme (MFE1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E15378 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein O-6-methylguanine-DNA methyltransferase (MGMT, O6M) is a protein able to be translated from the nucleic acid corresponding to YALI0C10010p of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene O-6-methylguanine-DNA methyltransferase (MGMT, O6M) is the nucleic acid or gene corresponding to YALI0C10010p of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, O-6-methylguanine-DNA methyltransferase (MGMT, O6M) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0C10010p of *Yarrowia lipolytica* as described above. In embodiments, O-6-methylguanine-DNA methyltransferase (MGMT, O6M) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0C10010p of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Aconitase (ACO1) is a protein able to be translated from the nucleic acid corresponding to YALI0D09361 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Aconitase (ACO1) is the nucleic acid or gene corresponding to YALI0D09361 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Aconitase (ACO1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0D09361 of *Yarrowia lipolytica* as described above. In embodiments, O Aconitase (ACO1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0D09361 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Citrate Synthase (CIT1) is a protein able to be translated from the nucleic acid corresponding to YALI0E02684 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Citrate Synthase (CIT1) is the nucleic acid or gene corresponding to YALI0E02684 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Citrate Synthase (CIT1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E02684 of *Yarrowia lipolytica* as described above. In embodiments, Citrate Synthase (CIT1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E02684 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic

acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein Acetyl-CoA Carboxylase (ACC) is a protein able to be translated from the nucleic acid corresponding to YALI0C11407 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene Acetyl-CoA Carboxylase (ACC) is the nucleic acid or gene corresponding to YALI0C11407 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, Acetyl-CoA Carboxylase (ACC) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0C11407 of *Yarrowia lipolytica* as described above. In embodiments, Acetyl-CoA Carboxylase (ACC) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0C11407 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein RME1 zinc-finger transcription factor (RME1) is a protein able to be translated from the nucleic acid corresponding to YALI0E17215 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene RME1 zinc-finger transcription factor (RME1) is the nucleic acid or gene corresponding to YALI0E17215 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, RME1 zinc-finger transcription factor (RME1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E17215 of *Yarrowia lipolytica* as described above. In embodiments, RME1 zinc-finger transcription factor (RME1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E17215 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein YOX1 homeodomain protein (YOX1) is a protein able to be translated from the nucleic acid corresponding to YALI0E20449 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene YOX1 homeodomain protein (YOX1) is the nucleic acid or gene corresponding to YALI0E20449 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, YOX1 homeodomain protein (YOX1) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0E20449 of *Yarrowia lipolytica* as described above. In embodiments, YOX1 homeodomain protein (YOX1) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0E20449 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein UGA2 succinate semialdehyde dehydrogenase (UGA2) is a protein able to be translated from the nucleic acid corresponding to YALI0F26191 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene UGA2 succinate semialdehyde dehydrogenase (UGA2) is the nucleic acid or gene corresponding to YALI0F26191 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, UGA2 succinate semialdehyde dehydrogenase (UGA2) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0F26191 of *Yarrowia lipolytica* as described above. In embodiments, UGA2 succinate semialdehyde dehydrogenase (UGA2) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0F26191 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein OSH6 oxysterol-binding protein homolog 6 (OSH6) is a protein able to be translated from the nucleic acid corresponding to YALI0A02354 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene OSH6 oxysterol-binding protein homolog 6 (OSH6) is the nucleic acid or gene corresponding to YALI0A02354 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, OSH6 oxysterol-binding protein homolog 6 (OSH6) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0A02354 of *Yarrowia lipolytica* as described above. In embodiments, OSH6 oxysterol-binding protein homolog 6 (OSH6) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0A02354 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

In embodiments, the protein IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) is a protein able to be translated from the nucleic acid corresponding to YALI0C07150 of the Genolevures database (i.e. found at http://www.genolevures.org/), wherein YALI0 stands for *Yarrowia lipolytica* and A,B,C,D,E,F specifies chromosome. In embodiments, the nucleic acid or gene IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) is the nucleic acid or gene corresponding to YALI0C07150 of the Genolevures database (i.e. found at http://www.genolevures.org/). In embodiments, IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) is a protein or nucleic acid/gene of a yeast strain corresponding to YALI0C07150 of *Yarrowia lipolytica* as described above. In embodiments, IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) is a protein or nucleic acid/gene of an oleaginous organism corresponding to YALI0C07150 of *Yarrowia lipolytica* as described above. In embodiments, the protein and/or nucleic acid is a wildtype version of the protein or nucleic acid. In embodiments, the protein and/or nucleic

acid is a mutant form of the protein and/or nucleic acid (e.g. point mutant, loss of function mutation, missense mutation, deletion, or insertion of heterologous nucleic acid).

As used to describe a protein or nucleic/acid of another organism in comparison to a protein or nucleic/acid of *Yarrowia lipolytica*, the term "corresponds" or "corresponding" is used according to its ordinary meaning and refers to a protein or nucleic acid/gene that includes similar or identical sequence of amino acid or nucleotides respectively and/or performs a similar or identical function and/or has a similar of identical activity as the protein or nucleic acid/gene in *Yarrowia lipolytica* as described above. In some embodiments, a protein or nucleic acid corresponding to a protein or nucleic acid from *Yarrowia lipolytica* is a homolog. In embodiments, the protein and/or nucleic acid of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) includes an amino acid and/or nucleotide sequence included in the protein and/or nucleic acid sequence for Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) respectively, described herein (e.g. Examples section and/or sequence listing). In embodiments, the protein and/or nucleic acid of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) is the amino acid and/or nucleotide sequence of the protein and/or nucleic acid sequence for Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) respectively, described herein (e.g. Examples section and/or sequence listing).

The term "wildtype" as used herein when referring to an oleaginous organism (e.g. yeast strain or *Yarrowia lipolytica* strain) means an organism that has not been genetically modified to improve production of a lipid (e.g. increase yield of a lipid, alter the structure of a lipid produced by the organism, reduce production of one lipid to improve production of a second lipid, or modulate the production of a lipid). In embodiments, a wildtype yeast strain may be auxotrophic for one or more compounds (e.g. leucine and/or uracil). In embodiments, a wildtype *Yarrowia lipolytica* strain is PO1f (ATCC #MYA-2613), a leucine and uracil auxotroph devoid of any secreted protease activity (Madzak et al., 2000).

The term "oleochemical" is used herein in accordance with its well known meaning and refers to chemicals or compounds derived from lipids or fats. In embodiments, an oleochemical is a lipid or fat derived from a different lipid or fat. In embodiments an oleochemical is a chemical or compound produced by an oleaginous organism. In embodiments, an oleochemical is a chemical or compound derived from a lipid or lipid precursor produced by an oleaginous organism (e.g., fatty acid esters such as methyl esters, ethyl esters, propyl esters, or butyl esters that are derived from a fatty acid produced by an oleaginous organism by transesterification). In embodiments, an oleochemical may include further in vivo or in vitro modification of a lipid or lipid precursor enabled by endogenous or heterologous modifying enzymes or chemical reactions.

The term "lipid precursor" is used in accordance with its well known meaning and refers to a pathway intermediate (e.g., acetyl-CoA or malonyl-CoA) in the biosynthesis of a lipid. In embodiments, a lipid precursor may be any molecule along the biosynthetic pathway making triglycerides including free citrate, acetyl-CoA, free fatty acids, pyruvate, citric acid cycle intermediates, diacylglycerides, and/or triacylglycerides.

The term "micronutrient" is used in accordance with its well known meaning and refers to nutrients used by an organism (e.g. oleaginous organisms, yeast, oleaginous yeast) for growth, proliferation, propagation, survival, one or more essential biological functions, production of a lipid, lipid precursor, or oleochemical, which are required for such functions in small quantities. Examples of micronutrients include, but are not limited to, minerals, vitamins, and elements (e.g. cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, and/or boron).

II. OLEAGINOUS ORGANISMS

In a first aspect is provided a genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell,

Yarrowia lipolytica, algae, or plant cell) wherein the dry weight of the oleaginous organism includes greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 30% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 40% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 50% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 70% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 80% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 90% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes about an average of 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 g/L culture (e.g. in a bioreactor) of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 g/L culture (e.g. in a bioreactor) of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 g/L culture (e.g. in a bioreactor) of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

In embodiments, the oleaginous organism is a yeast cell. In embodiments, the oleaginous organism is an oleaginous yeast cell. In embodiments, the yeast cell is selected from the group consisting of the genera *Yarrowia, Candida, Rhodotorula, Rhodosporidium, Cryptococcus, Trichosporon* and *Lipomyces*. In embodiments, the yeast cell is selected from the group consisting of *Rhodosporidium toruloides, Lipomyces starkeyii, Lipomyces lipoferus, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Candida revkaufi, Candida pulcherrima, Candida tropicalis, Candida utilis, Trichosporon pullans, Trichosporon cutaneum, Rhodotorula glutinus, Rhodotorula graminis* and *Yarrowia lipolytica*. In embodiments, the yeast cell is selected from the group consisting of *Lipomyces starkeyii, Rhodosporidium toruloides, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Rhodotorula glutinis*, and *Yarrowia lipolytica*. In embodiments, the yeast cell is *Yarrowia lipolytica*.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is buoyant in an aqueous medium. In embodiments, the yeast cell includes a greater buoyancy (i.e. greater tendency to float, lower density) than a yeast cell that includes less than about 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) by dry weight (e.g. less than about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight). In embodiments, the yeast cell includes a greater buoyancy (i.e. greater tendency to float, lower density) than a yeast cell that includes less than 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) by dry weight (e.g. less than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) does not sediment to the bottom of a column of liquid (e.g. water, buffer, growth media, minimal media) that is about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 mm tall due to gravitation force alone. The term "about" when used in connection with a defined amount refers to an amount up to and including greater than and/or less than 10% of the associated value and includes the associated value. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) does not sediment to the bottom of a column of liquid (e.g. water, buffer, growth media, minimal media) that is 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 mm tall due to gravitation force alone. In embodiments, the yeast cell includes a greater buoyancy (i.e. greater tendency to float, lower density) than a yeast cell that does not include the same recombinant nucleic acid or combination of recombinant nucleic acids as the buoyant yeast cell. In embodiments, the yeast cell is buoyant following centrifugation (e.g. at about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950. 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, or 10000×g).

In embodiments of the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) including more than about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. more than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight), included are lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) selected from the group consisting of a fatty acid, wax, sterol, vitamin, monoglyceride, diglyceride, triglyceride, phospholipid, glycerolipid, glycerophospholipid, sphingolipid, saccharolipid, polyketide, sterol lipid, triacylglyceride, wax ester, fatty acid ethyl ester, fatty acid methyl ester, component of biodiesel, saturated hydrocarbon, unsaturated hydrocarbon, branched hydrocarbon, and a prenol lipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a fatty acid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a wax. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a sterol. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a vitamin. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a monoglyceride. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a diglyceride. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a triglyceride. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a phospholipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a glycerolipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a glycerophospholipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a sphingolipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a saccharolipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a polyketide.

In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a sterol lipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a triacylglyceride. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a prenol lipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a wax ester. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a fatty acid ethyl ester. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a fatty acid methyl ester. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a component of biodiesel. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a saturated hydrocarbon. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is an unsaturated hydrocarbon. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a branched hydrocarbon. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a lipid. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a lipid precursor. In embodiments, the majority lipid, lipid precursor, or oleochemical in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is an oleochemical.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C5:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C5:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C5:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C5:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C6:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C6:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C6:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C6:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C7:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C7:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C7:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C7:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C8:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C8:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C8:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C8:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C9:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C9:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C9:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C9:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C10:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C10:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C10:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C10:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C11:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C11:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C11:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C11:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C12:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C12:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C12:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C12:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C13:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C13:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C13:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell,

Yarrowia lipolytica, algae, or plant cell) produces C13:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C14:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C14:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C14:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C14:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C15:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C15:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C15:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C15:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C16:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C16:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C16:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C16:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C17:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C17:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C17:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C17:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C18:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C18:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C18:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C18:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C19:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C19:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C19:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C19:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C20:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C20:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C20:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C20:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C21:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C21:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C21:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C21:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C22:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C22:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C22:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C22:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C23:0 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C23:1 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C23:2 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces C23:3 fatty acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces a fatty acid described herein above at a greater level (e.g. 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 100000, 1000000 fold) compared to the same oleaginous organism lacking the genetic modification. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces a lipid including a fatty acid selected from the group consisting of C5:0, C5:1, C5:2, C5:3, C6:0, C6:1, C6:2, C6:3, C7:0, C7:1, C7:2, C7:3, C8:0, C8:1, C8:2, C8:3, C9:0, C9:1, C9:2, C9:3, C10:0, C10:1, C10:2, C10:3, C11:0, C11:1, C11:2, C11:3, C12:0, C12:1, C12:2, C12:3, C13:0, C13:1, C13:2, C13:3, C14:0, C14:1, C14:2, C14:3, C15:0, C15:1, C15:2, C15:3, C16:0, C16:1, C16:2, C16:3, C17:0, C17:1, C17:2, C17:3, C18:0, C18:1, C18:2, C18:3, C19:0, C19:1, C19:2, C19:3, C20:0, C20:1, C20:2, C20:3, C21:0, C21:1, C21:2, C21:3, C22:0, C22:1, C22:2, C22:3, C23:0, C23:1, C23:2, and C23:3. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces a lipid derived from an endogenously produced fatty acid selected from the group consisting of C5:0, C5:1, C5:2, C5:3, C6:0, C6:1, C6:2, C6:3, C7:0, C7:1, C7:2, C7:3, C8:0, C8:1, C8:2, C8:3, C9:0, C9:1, C9:2, C9:3, C10:0, C10:1, C10:2, C10:3, C11:0, C11:1, C11:2, C11:3,

C12:0, C12:1, C12:2, C12:3, C13:0, C13:1, C13:2, C13:3, C14:0, C14:1, C14:2, C14:3, C15:0, C15:1, C15:2, C15:3, C16:0, C16:1, C16:2, C16:3, C17:0, C17:1, C17:2, C17:3, C18:0, C18:1, C18:2, C18:3, C19:0, C19:1, C19:2, C19:3, C20:0, C20:1, C20:2, C20:3, C21:0, C21:1, C21:2, C21:3, C22:0, C22:1, C22:2, C22:3, C23:0, C23:1, C23:2, and C23:3. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces a lipid, lipid precursor, or oleochemical (e.g. fatty acid) described herein at a greater level (e.g. 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 100000, 1000000 fold) compared to the same oleaginous organism lacking the genetic modification.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a recombinant nucleic acid, wherein the recombinant nucleic acid modulates the level of activity of a protein in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to the absence of the recombinant nucleic acid. In embodiments, the protein is selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA:diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), and IRC20 E3 ubiquitin-protein ligase and helicase (IRC20). In embodiments, the protein is Leucine Biosynthesis Gene (LEU2). In embodiments, the protein is Uracil Biosynthesis gene (URA3). In embodiments, the protein is multifunctional enzyme (MFE1). In embodiments, the protein is Transcription Factor (PEX10). In embodiments, the protein is AMP Deaminase (AMPD). In embodiments, the protein is ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2). In embodiments, the protein is Malic Enzyme (MAE). In embodiments, the protein is Acetyl-CoA Carboxylase (ACC). In embodiments, the protein is acyl-CoA: diacylglycerol acyltransferase (DGA1). In embodiments, the protein is acyl-CoA:diacylglycerol acyltransferases (DGA2). In embodiments, the protein is Mitochondrial 2' O-ribose methyltransferase (MRM2). In embodiments, the protein is Lipid synthesis regulator (MGA2). In embodiments, the protein is Chromatin assembly gene (RLF2 subunit p90). In embodiments, the protein is O-6-methylguanine-DNA methyltransferase (MGMT). In embodiments, the protein is Aconitase (ACO1). In embodiments, the protein is Citrate Synthase (CIT1). In embodiments, the protein is RME1 zinc-finger transcription factor (RME1). In embodiments, the protein is YOX1 homeodomain protein (YOX1). In embodiments, the protein is UGA2 succinate semialdehyde dehydrogenase (UGA2). In embodiments, the protein is OSH6 oxysterol-binding protein homolog 6 (OSH6). In embodiments, the protein is IRC20 E3 ubiquitin-protein ligase and helicase (IRC20). In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the function of the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the amount of the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the transcription of the mRNA encoding the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the translation of the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the coding sequence of the gene encoding the protein (e.g. mutating (e.g. point mutant or missense mutant), truncating, inserting into, or deleting). In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the regulatory elements (e.g. promoter) of the gene encoding the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the stability of the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is modulating the stability of the transcript encoding the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is reducing the level of activity of the protein. In embodiments, modulating the level of activity of a protein in an oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is increasing the level of activity of the protein.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein in the citric acid cycle in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in the Kennedy Pathway in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in fatty acid synthesis in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modifica-

tion (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in fatty acid storage (e.g. accumulation) in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that that modulates (e.g. reduces or increases) the level of activity of a protein involved in lipid synthesis in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in lipid storage (e.g. accumulation) in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in triacylglyceride storage (e.g. accumulation) in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in triacylglyceride synthesis in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in peroxisomal biogenesis in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in the beta-oxidation cycle in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in fatty acid degradation in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in lipid degradation in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in triacylglyceride degradation in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid). In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a genetic modification (e.g. recombinant nucleic acid) that modulates (e.g. reduces or increases) the level of activity of a protein involved in central carbon metabolism in the oleaginous organism relative to the absence of the genetic modification (e.g. recombinant nucleic acid).

In embodiments, the recombinant nucleic acid increases the level of activity of a protein in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the protein is selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), and IRC20 E3 ubiquitin-protein ligase and helicase (IRC20). In embodiments, the protein is selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), 0-6-methylguanine-DNA methyltransferase (MGMT), and Citrate Synthase (CIT1). In embodiments, the protein is Leucine Biosynthesis Gene (LEU2). In embodiments, the protein is Uracil Biosynthesis gene (URA3). In embodiments, the protein is AMP Deaminase (AMPD). In embodiments, the protein is ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2). In embodiments, the protein is Malic Enzyme (MAE). In embodiments, the protein is Acetyl-CoA Carboxylase (ACC). In embodiments, the protein is acyl-CoA:diacylglycerol acyltransferase (DGA1). In embodiments, the protein is acyl-CoA:diacylglycerol acyltransferases (DGA2). In embodiments, the protein is Mitochondrial 2' O-ribose methyltransferase (MRM2). In embodiments, the protein is Lipid synthesis regulator (MGA2). In embodiments, the protein is Chromatin assembly gene (RLF2 subunit p90). In embodiments, the protein is O-6-methylguanine-DNA methyltransferase (MGMT). In embodiments, the protein is Citrate Synthase (CIT1). In embodiments, the protein is RME1 zinc-finger transcription factor (RME1). In embodiments, the protein is YOX1 homeodomain protein (YOX1). In embodiments, the protein is UGA2 succinate semialdehyde dehydrogenase (UGA2). In embodiments, the protein is OSH6 oxysterol-binding protein homolog 6 (OSH6). In embodiments, the protein is IRC20 E3 ubiquitin-protein ligase and helicase (IRC20). In embodiments, the protein is selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), Malic Enzyme (MAE), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid

synthesis regulator (MGA2), and O-6-methylguanine-DNA methyltransferase (MGMT) or said nucleic acid decreases the level of activity of Lipid synthesis regulator (MGA2).

In embodiments, the genetic modification (e.g. recombinant nucleic acid) decreases the level of activity of a protein in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the protein is selected from the group consisting of multifunctional enzyme (MFE1), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), Transcription Factor (PEX10), and Aconitase (ACO1). In embodiments, the protein is multifunctional enzyme (MFE1). In embodiments, the protein is Lipid synthesis regulator (MGA2). In embodiments, the protein is Chromatin assembly gene (RLF2 subunit p90). In embodiments, the protein is Transcription Factor (PEX10). In embodiments, the protein is Aconitase (ACO1). In embodiments, the protein is RME1 zinc-finger transcription factor (RME1). In embodiments, the protein is YOX1 homeodomain protein (YOX1). In embodiments, the protein is UGA2 succinate semialdehyde dehydrogenase (UGA2). In embodiments, the protein is OSH6 oxysterol-binding protein homolog 6 (OSH6). In embodiments, the protein is IRC20 E3 ubiquitin-protein ligase and helicase (IRC20).

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a plurality of genetic modifications (e.g. recombinant nucleic acids) that collectively modulate one, two, three, four, five, six, seven, eight, nine, ten, or more of the group of proteins consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), and IRC20 E3 ubiquitin-protein ligase and helicase (IRC20).

In embodiments, the recombinant nucleic acid encodes a protein comprising a mutation relative to the wildtype protein. In embodiments, the mutation is a point mutation. In embodiments, the mutation is a deletion. In embodiments, the mutation is an insertion. In embodiments, the mutation is a fusion with a second protein. In embodiments, the recombinant nucleic acid encodes a mutant of a protein selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20).

In embodiments, the recombinant nucleic acid encodes a mutant of a protein selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), or IRC20 E3 ubiquitin-protein ligase and helicase (IRC20).

In embodiments, the recombinant nucleic acid is an AMP Deaminase (AMPD) having the nucleotide sequence of SEQ ID NO.:33. In embodiments, the recombinant nucleic acid is an AMP Deaminase (AMPD) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or the entire sequence) with SEQ ID NO.:33, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Leucine Biosynthesis Gene (LEU2) having the nucleotide sequence of SEQ ID NO.:35. In embodiments, the recombinant nucleic acid is a Leucine Biosynthesis Gene (LEU2) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, or the entire sequence) with SEQ ID NO.:35, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Uracil Biosynthesis gene (URA3) having the nucleotide sequence of SEQ ID NO.:37. In embodiments, the recombinant nucleic acid is a Uracil Biosynthesis gene (URA3) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, or the entire sequence) with SEQ ID NO.:37, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is an ATP-Citrate Lyase (ACL) (subunit 1) having the nucleotide sequence of SEQ ID NO.:39. In embodiments, the recombinant nucleic acid is an ATP-Citrate Lyase (ACL) (subunit 1) having at least 60% identity (e.g. at least 61%, 62%, 63%,

64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, or the entire sequence) with SEQ ID NO.:39, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is an ATP-Citrate Lyase (ACL) (subunit 2) having the nucleotide sequence of SEQ ID NO.:41. In embodiments, the recombinant nucleic acid is an ATP-Citrate Lyase (ACL) (subunit 2) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or the entire sequence) with SEQ ID NO.:41, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Malic Enzyme (MEA, MAE, MEA1) having the nucleotide sequence of SEQ ID NO.:43. In embodiments, the recombinant nucleic acid is a Malic Enzyme (MEA, MAE, MEA1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, or the entire sequence) with SEQ ID NO.:43, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a acyl-CoA:diacylglycerol acyltransferase (DGA1) having the nucleotide sequence of SEQ ID NO.:45. In embodiments, the recombinant nucleic acid is a acyl-CoA: diacylglycerol acyltransferase (DGA1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, or the entire sequence) with SEQ ID NO.:45, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a acyl-CoA:diacylglycerol acyltransferase (DGA2) having the nucleotide sequence of SEQ ID NO.:47. In embodiments, the recombinant nucleic acid is a acyl-CoA:diacylglycerol acyltransferase (DGA2) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, or the entire sequence) with SEQ ID NO.:47, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Lipid synthesis regulator (MGA2) having the nucleotide sequence of SEQ ID NO.:49. In embodiments, the recombinant nucleic acid is a Lipid synthesis regulator (MGA2) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100, 3200, 3300, 3400, 3500, 3600, 3700, 3800, or the entire sequence) with SEQ ID NO.:49, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a mutant Lipid synthesis regulator (MGA2-L36 mutant) having the nucleotide sequence of SEQ ID NO.:51. In embodiments, the recombinant nucleic acid is a mutant Lipid synthesis regulator (MGA2-L36 mutant) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100, 3200, 3300, 3400, 3500, 3600, 3700, 3800, or the entire sequence) with SEQ ID NO.:51, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a truncated Lipid synthesis regulator (MGA2-truncated) having the nucleotide sequence of SEQ ID NO.:53. In embodiments, the recombinant nucleic acid is a truncated Lipid synthesis regulator (MGA2-truncated) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100, 3200, 3300, 3400, 3500, 3600, 3700, 3800, or the entire sequence) with SEQ ID NO.:53, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Chromatin assembly gene (RLF2 subunit p90) having the nucleotide sequence of SEQ ID NO.:58. In embodiments, the recombinant nucleic acid is a Chromatin assembly gene (RLF2 subunit p90) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, or the entire sequence) with SEQ ID NO.:58, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Mitochondrial 2' O-ribose methyltransferase (MRM2) having the nucleotide sequence of SEQ ID NO.:63. In embodiments, the recombinant nucleic acid is a Mitochondrial 2' O-ribose methyltransferase (MRM2) having at least 60% identity

(e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, or the entire sequence) with SEQ ID NO.:63, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Citrate Synthase (CIT1) having the nucleotide sequence of SEQ ID NO.:67. In embodiments, the recombinant nucleic acid is a Citrate Synthase (CIT1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, or the entire sequence) with SEQ ID NO.:67, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Acetyl-CoA Carboxylase (ACC) having the nucleotide sequence of SEQ ID NO.:69. In embodiments, the recombinant nucleic acid is a Acetyl-CoA Carboxylase (ACC) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 3000, 4000, 5000, 6000, 7000, or the entire sequence) with SEQ ID NO.:69, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Transcription Factor (PEX10) having the nucleotide sequence of SEQ ID NO.:71. In embodiments, the recombinant nucleic acid is a Transcription Factor (PEX10) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, or the entire sequence) with SEQ ID NO.:71, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a multifunctional enzyme (MFE1) having the nucleotide sequence of SEQ ID NO.:73. In embodiments, the recombinant nucleic acid is a multifunctional enzyme (MFE1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, or the entire sequence) with SEQ ID NO.:73, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a Aconitase (ACO1) having the nucleotide sequence of SEQ ID NO.:75. In embodiments, the recombinant nucleic acid is a Aconitase (ACO1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, or the entire sequence) with SEQ ID NO.:75, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a YOX1 homeodomain protein (YOX1) having the nucleotide sequence of SEQ ID NO.:77. In embodiments, the recombinant nucleic acid is a YOX1 homeodomain protein (YOX1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or the entire sequence) with SEQ ID NO.:77, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a UGA2 succinate semialdehyde dehydrogenase (UGA2) having the nucleotide sequence of SEQ ID NO.:78. In embodiments, the recombinant nucleic acid is a UGA2 succinate semialdehyde dehydrogenase (UGA2) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or the entire sequence) with SEQ ID NO.:78, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a RME1 zinc-finger transcription factor (RME1) having the nucleotide sequence of SEQ ID NO.:79. In embodiments, the recombinant nucleic acid is a RME1 zinc-finger transcription factor (RME1) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, or the entire sequence) with SEQ ID NO.:79, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a OSH6 oxysterol-binding protein homolog 6 (OSH6) having the nucleotide sequence of SEQ ID NO.:80. In embodiments, the recombinant nucleic acid is a OSH6 oxysterol-binding protein homolog 6 (OSH6) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, or the entire sequence) with SEQ ID NO.:80, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) having the

nucleotide sequence of SEQ ID NO.:81. In embodiments, the recombinant nucleic acid is a IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 3000, 4000, 5000, or the entire sequence) with SEQ ID NO.:81, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the recombinant nucleic acid is a O-6-methylguanine-DNA methyltransferase (MGMT) having the nucleotide sequence of SEQ ID NO.:65. In embodiments, the recombinant nucleic acid is a O-6-methylguanine-DNA methyltransferase (MGMT) having at least 60% identity (e.g. at least 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity) over a region of at least 100 nucleotides (e.g. at least 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, or the entire sequence) with SEQ ID NO.:65, (e.g. using the same length of nucleotides for comparison or the entirety of both nucleic acids).

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a recombinant nucleic acid that decreases the level of activity of multifunctional enzyme (MFE1) protein and Transcription Factor (PEX10) protein, increases the level of activity of acyl-CoA: diacylglycerol acyltransferase (DGA1) protein, or increases the level of activity of Leucine Biosynthesis Gene (LEU2) protein relative to a oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that does not include the recombinant nucleic acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes recombinant nucleic acids that decrease the level of activity of multifunctional enzyme (MFE1) protein and Transcription Factor (PEX10) protein, increase the level of activity of acyl-CoA:diacylglycerol acyltransferase (DGA1) protein, and increase the level of activity of Leucine Biosynthesis Gene (LEU2) protein relative to a oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that does not include the recombinant nucleic acids. In embodiments, the level of activity is the level of expression of the protein.

In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes an extra-chromosomal recombinant nucleic acid. In embodiments, the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes a recombinant nucleic acid integrated into the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) genome. In embodiments, the extra-chromosomal recombinant nucleic acid includes a gene that is also included in the genome of the yeast cell oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) (e.g. Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA:diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Aconitase (ACO1), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6 oxysterol-binding protein homolog 6 (OSH6), IRC20 E3 ubiquitin-protein ligase and helicase (IRC20), a wildtype version thereof, or a mutant version thereof). In embodiments, the extra-chromosomal recombinant nucleic acid includes a gene that is also included in the genome of the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) (e.g. Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL) (e.g. ACL subunit 1, ACL subunit 2, or subunit 1 and 2), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), O-6-methylguanine-DNA methyltransferase (MGMT), Citrate Synthase (CIT1), RME1 zinc-finger transcription factor (RME1), YOX1 homeodomain protein (YOX1), UGA2 succinate semialdehyde dehydrogenase (UGA2), OSH6-oxysterol-binding protein homolog 6 (OSH6), IRC20 E3 ubiquitin-protein ligase and helicase (IRC20), a wildtype version thereof, or a mutant version thereof). In embodiments, a recombinant nucleic acid integrated into the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) genome replaces (e.g. partially or completely) a promoter included in the oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) genome pror to integration of the recombinant nucleic acid.

In embodiments, the yeast cell is a yeast cell including one or more genetic modifications (e.g. recombinant nucleic acids), as described herein (including in the Examples section below, the tables, the figures, and the claims herein). In embodiments, the yeast cell is a yeast cell described herein, including in an example, table, figure, or claim. In embodiments, the oleaginous yeast cell is L36 as described herein (e.g. examples, tables, and figures). In embodiments, the oleaginous yeast cell is derived from L36 as described herein (e.g. examples, tables, and figures). In embodiments, the oleaginous yeast cell is E26 as described herein (e.g. examples, tables, and figures). In embodiments, the oleaginous yeast cell is E13 as described herein (e.g. examples, tables, and figures). In embodiments, the oleaginous yeast cell is derived from E26 or E13.

In embodiments, the dry weight of the genetically modified yeast cell described herein includes greater than about 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., greater than about 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99%; greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88,

89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99%; of lipid; lipids; lipid precursors; lipid precursor, oleochemical, and/or oleochemicals).

In embodiments, the genetically modified yeast cell described herein includes a recombinant Leucine Biosynthesis Gene (LEU2). In embodiments, the genetic modification increases the level of activity of the Leucine Biosynthesis Gene (LEU2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein is capable of de novo synthesis of leucine (e.g. at sufficient levels to meet the leucine requirements of the yeast cell). In embodiments, the genetically modified yeast cell described herein is capable of de novo synthesis of leucine independent of the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Uracil Biosynthesis gene (URA3). In embodiments, the genetic modification increases the level of activity of the Uracil Biosynthesis gene (URA3) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein is capable of de novo synthesis of uracil (e.g. at sufficient levels to meet the uracil requirements of the yeast cell). In embodiments, the genetically modified yeast cell described herein is capable of de novo synthesis of uracil independent of the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified multifunctional enzyme (MFE1) gene. In embodiments, the genetic modification decreases the level of activity of the multifunctional enzyme (MFE1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified PEX10 Transcription Factor (PEX10) gene. In embodiments, the genetic modification decreases the level of activity of the PEX10 Transcription Factor (PEX10) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant AMP Deaminase (AMPD) protein. In embodiments, the genetic modification increases the level of activity of the AMP Deaminase (AMPD) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant ATP-Citrate Lyase 1 (ACL1) protein. In embodiments, the genetic modification increases the level of activity of the ATP-Citrate Lyase 1 (ACL1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant ATP-Citrate Lyase 2 (ACL2) protein. In embodiments, the genetic modification increases the level of activity of the ATP-Citrate Lyase 2 (ACL2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant ATP-Citrate Lyase 1 (ACL1) protein and ATP-Citrate Lyase 2 (ACL2) protein. In embodiments, the genetic modification increases the level of activity of the ATP-Citrate Lyase 1 (ACL1) protein and ATP-Citrate Lyase 2 (ACL2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Malic Enzyme (MAE) protein. In embodiments, the genetic modification increases the level of activity of the Malic Enzyme (MAE) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Acetyl-CoA Carboxylase (ACC) protein. In embodiments, the genetic modification increases the level of activity of the Acetyl-CoA Carboxylase (ACC) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant acyl-CoA:diacylglycerol acyltransferase 1 (DGA1) protein. In embodiments, the genetic modification increases the level of activity of the acyl-CoA:diacylglycerol acyltransferase 1 (DGA1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant acyl-CoA:diacylglycerol acyltransferase 2 (DGA2) protein. In embodiments, the genetic modification increases the level of activity of the acyl-CoA:diacylglycerol acyltransferase 2 (DGA2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Mitochondrial 2' O-ribose methyltransferase (MRM2) protein. In embodiments, the genetic modification increases the level of activity of the Mitochondrial 2' O-ribose methyltransferase (MRM2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Lipid synthesis regulator (MGA2) protein. In embodiments, the genetically modified yeast cell described herein includes a genetically modified Lipid synthesis regulator (MGA2) gene. In embodiments, the genetically modified yeast cell described herein includes at least one nucleotide deletion in the genomic Lipid synthesis regulator (MGA2) gene and expression of a Lipid synthesis regulator (MGA2) protein including a mutation corresponding to G643R in *Yarrowia lipolytica* Lipid synthesis regulator (MGA2) In embodiments, the genetic modification decreases the level of activity of the Lipid synthesis regulator (MGA2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified Chromatin assembly gene (RLF2 subunit p90) gene. In embodiments, the genetic modification decreases the level of activity of the Chromatin assembly gene (RLF2 subunit p90) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant O-6-methylguanine-DNA methyltransferase (MGMT) protein. In embodiments, the genetic modification increases the level of activity of the O-6-methylguanine-DNA methyltransferase (MGMT) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified Aconitase (ACO1) gene. In embodiments, the genetic modification decreases the level of activity of the Aconitase (ACO1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a recombinant Citrate Synthase (CIT1) gene. In embodiments, the genetic modification increases the level of activity of the Citrate Synthase (CIT1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified RME1 zinc-finger transcription factor (RME1) gene. In embodiments, the genetic modification decreases the level of activity of the RME1 zinc-finger transcription factor (RME1) protein relative to an otherwise

identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified YOX1 homeodomain protein (YOX1) gene. In embodiments, the genetic modification decreases the level of activity of the YOX1 homeodomain protein (YOX1) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified UGA2 succinate semialdehyde dehydrogenase (UGA2) gene. In embodiments, the genetic modification decreases the level of activity of the UGA2 succinate semialdehyde dehydrogenase (UGA2) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified OSH6 oxysterol-binding protein homolog 6 (OSH6) gene. In embodiments, the genetic modification decreases the level of activity of the OSH6 oxysterol-binding protein homolog 6 (OSH6) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the genetically modified yeast cell described herein includes a genetically modified IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) gene. In embodiments, the genetic modification decreases the level of activity of the IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) protein relative to an otherwise identical yeast cell lacking the genetic modification. In embodiments, the gene or protein described herein is a *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is a yeast gene or protein corresponding to the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is a gene or protein from an oleaginous organism corresponding to the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is the *Yarrowia lipolytica* gene or protein identified by sequence herein. In embodiments, the gene or protein is a mutant gene or protein of a wildtype gene or protein corresponding to the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is a mutant gene or protein of a wildtype yeast gene or protein corresponding to the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is a homolog of the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein is a homolog of the *Yarrowia lipolytica* gene or protein identified by sequence herein. In embodiments, the gene or protein is a mutant of the *Yarrowia lipolytica* gene or protein. In embodiments, the gene or protein described in this paragraph is LEU2, URA3, MFE1, PEX10, AMPD, ACL, ACL1, ACL2, MAE, ACC, DGA, DGA1, DGA2, MRM2, MGA2, RLF2 subunit p90, MGMT, ACO1, CIT1, RME1, YOX1, UGA2, OSH6, or IRC20). In embodiments, the gene or protein described in this paragraph is LEU2, URA3, MFE1, PEX10, AMPD, ACL, ACL1, ACL2, MAE, ACC, DGA, DGA1, DGA2, MRM2, MGA2, RLF2 subunit p90, MGMT, ACO1, CIT1, RME1, YOX1, UGA2, OSH6, or IRC20), having the sequence identified herein.

In embodiments, the genetic modification modulates the level of activity of a component of a lipid biosynthetic pathway. In embodiments, the genetic modification modulates the level of activity of a component of a lipid precursor biosynthetic pathway. In embodiments, the genetic modification modulates the level of activity of a component of an oleochemical biosynthetic pathway. In embodiments, the genetic modification modulates the level of activity of a component of a pathway incorporating Acetyl-CoA into a lipid, lipid precursor, or oleochemical. In embodiments, the genetic modification modulates the level of activity of a component of a pathway incorporating malonyl-CoA into a lipid, lipid precursor, or oleochemical. In embodiments, the genetic modification increases the level of activity of a component of a lipid biosynthetic pathway. In embodiments, the genetic modification increases the level of activity of a component of a lipid precursor biosynthetic pathway. In embodiments, the genetic modification increases the level of activity of a component of an oleochemical biosynthetic pathway. In embodiments, the genetic modification increases the level of activity of a component of a pathway incorporating acetyl-CoA into a lipid, lipid precursor, or oleochemical. In embodiments, the genetic modification increases the level of activity of a component of a pathway incorporating malonyl-CoA into a lipid, lipid precursor, or oleochemical. In embodiments, the genetic modification modulates the level of activity of a component of a lipid, or lipid precursor, metabolic pathway. In embodiments, the genetic modification decreases the level of activity of a component of a lipid, or lipid precursor, metabolic pathway. In embodiments, the genetic modification decreases the level of activity of a component of a lipid, or lipid precursor, metabolic pathway. In embodiments, the genetic modification increases the level of acetyl-CoA in the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification increases the level of malonyl-CoA in the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification increases the level of triglyceride production in the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification decreases the level of beta-oxidation activity in the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification decreases the level of fatty acid catabolism in the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification decreases the level of peroxisome biogenesis activity in the genetically modified

oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification produces a lipid, lipid precursor, or oleochemical at a higher level than by a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) produces a lipid, lipid precursor, or oleochemical at a higher level than by a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the genetic modification modulates the level of activity of a component of the citric acid cycle. In embodiments, the genetic modification modulates the level of activity of a component of the TCA cycle. In embodiments, the genetic modification modulates the level of activity of a component of the Kennedy pathway. In embodiments, the genetic modification reduces the level of activity of the TCA cycle. In embodiments, the genetic modification increases the level of activity of the Kennedy pathway.

In embodiments, the lipid, lipid precursor, or oleochemical produced at a higher level by the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) is a fatty acid, wax, sterol, vitamin, monoglyceride, diglyceride, triglyceride, phospholipid, glycerolipid, glycerophospholipid, sphingolipid, saccharolipid, polyketide, sterol lipid, triacylglyceride, prenol lipid, fatty acid ester, fatty acid methyl ester, fatty acid ethyl ester, fatty acid propyl ester, fatty acid butyl ester, fatty alcohol, fatty amine, glycerol, alcohol ethoxylate, alcohol sulfate, or alcohol ether sulfate. In embodiments, the genetic modification includes a mutation relative to the wild type gene. In embodiments, the genetic modification includes a deletion of a portion of a gene. In embodiments, the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) includes an increased level of a fatty acid selected from the group consisting of C5:0, C5:1, C5:2, C5:3, C6:0, C6:1, C6:2, C6:3, C7:0, C7:1, C7:2, C7:3, C8:0, C8:1, C8:2, C8:3, C9:0, C9:1, C9:2, C9:3, C10:0, C10:1, C10:2, C10:3, C11:0, C11:1, C11:2, C11:3, C12:0, C12:1, C12:2, C12:3, C13:0, C13:1, C13:2, C13:3, C14:0, C14:1, C14:2, C14:3, C15:0, C15:1, C15:2, C15:3, C16:0, C16:1, C16:2, C16:3, C17:0, C17:1, C17:2, C17:3, C18:0, C18:1, C18:2, C18:3, C19:0, C19:1, C19:2, C19:3, C20:0, C20:1, C20:2, C20:3, C21:0, C21:1, C21:2, C21:3, C22:0, C22:1, C22:2, C22:3, C23:0, C23:1, C23:2, and C23:3, relative to a genetically unmodified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell) that is otherwise identical (e.g. genetically) to the genetically modified oleaginous organism (e.g. yeast cell, oleaginous yeast cell, *Yarrowia lipolytica*, algae, or plant cell). In embodiments, the fatty acid is C17:0 C17:1. In embodiments, the fatty acid is C16:1n9.

In embodiments, the genetic modification is an engineered genetic modification. In embodiments, the engineered genetic modification includes modulated expression of a protein. In embodiments, the engineered genetic modification includes increased expression of a protein. In embodiments, the engineered genetic modification includes decreased expression of a protein. In embodiments, the genetic modification is associated with exposure to a mutagen. In embodiments, the genetic modification includes modulated expression of a protein in a lipid, or lipid precursor, or oleochemical biosynthetic pathway.

III. METHODS OF MAKING AND PURIFYING LIPIDS, LIPID PRECURSORS, AND/OR OLEOCHEMICALS

Lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) produced by cells of the invention can be harvested, or otherwise collected, by any convenient method (e.g. centrifugation of extracellular secreted lipids, exposure to solvent, whole cell extraction (e.g. cell disruption and collection), hydrophobic solvent extraction (e.g. hexane), liquefaction, supercritical carbon dioxide extraction, freeze drying, mechanical pulverization, secretion (e.g. by addition of effective exporter proteins), or combinations thereof).

In embodiments, reduced nitrogen conditions promote accumulation of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical). In embodiments, cells (e.g. oleaginous organisms or oleaginous yeast) are first cultured in standard conditions and then cultured in low nitrogen conditions where harvesting is desired. In embodiments, oleaginous yeast species are grown in a medium including a carbon substrate and/or nitrogen source, optionally in the absence of light, optionally in an aerobic environment. In embodiments, media for culturing oleaginous yeast may include a carbon substrate, a fixed nitrogen source, trace elements, a buffer for pH maintenance, phosphate, or a combination thereof.

In embodiments, the carbon substrate may be selected from the group consisting of monosaccharides, oligosaccharides, polysaccharides, alkanes, fatty acids, esters of fatty acids, monoglycerides, carbon dioxide, methanol, formaldehyde, formate, carbon-containing amines, glucose, fructose, sucrose, lactose, galactose, xylose, mannose, rhamnose, arabinose, glycerol, acetate, depolymerized sugar beet pulp, black liquor, corn starch, depolymerized cellulosic material, corn stover, sugar beet pulp, switchgrass, milk whey, molasses, potato, rice, sorghum, sugar cane, wheat, thick cane juice, sugar beet juice, wheat, lignocellulosic biomass, and combinations thereof.

Examples of cellulosic material that may be depolymerized and used as a carbon substrate (e.g. fixed carbon source) include sugarcane bagasse, rice hulls, corn fiber (including stalks, leaves, husks, and cobs), wheat straw, rice straw, sugar beet pulp, citrus pulp, citrus peels; hardwood and softwood thinnings; hardwood and softwood residues; saw mill wastes (wood chips, sawdust) and pulp mill waste; paper fractions of municipal solid waste; municipal grass clippings; wood construction waste; and cellulosic crops such as switchgrass, hybrid poplar wood, and *miscanthus*, fiber cane, and fiber sorghum.

Oleaginous yeast cultures may yield oleaginous yeast biomass in fermentation media. To extract lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical)

from the biomass, the biomass may be harvested, concentrated, dewatered (i.e. separation of the biomass from the liquid medium) (e.g. through centrifugation, filtration, use of mechanical pressure, simple sedimentation, or sedimentation), or combinations thereof. Centrifugation does not always remove significant amounts of intracellular water from the oleaginous yeast and so is often considered a dewatering, not a drying, step. The biomass can optionally be dried (oven dried, lyophilized, and the like) and conditioned prior to cell disruption (lysis).

In a second aspect is provided a method of producing a lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) including: 1) culturing a yeast cell as described herein (including embodiments or as described in the examples, tables, figures, and/or claims) in a growth medium; and 2) isolating the lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) (e.g. from the medium or yeast cell).

In embodiments, the lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) is isolated from the yeast cell. In embodiments, the lipid, lipid precursor, or oleochemical (e.g., lipid, lipid precursor, oleochemical) is isolated from the medium. In embodiments, the growth medium includes a majority carbon source selected from the group consisting of glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, and lignocellulosic biomass. In embodiments, the majority carbon source is glucose. In embodiments, the majority carbon source is glycerol. In embodiments, the majority carbon source is xylose. In embodiments, the majority carbon source is fructose. In embodiments, the majority carbon source is mannose. In embodiments, the majority carbon source is ribose. In embodiments, the majority carbon source is sucrose. In embodiments, the majority carbon source is lignocellulosic biomass. In embodiments, the carbon source is glucose. In embodiments, the carbon source is glycerol. In embodiments, the carbon source is xylose. In embodiments, the carbon source is fructose. In embodiments, the carbon source is mannose. In embodiments, the carbon source is ribose. In embodiments, the carbon source is sucrose. In embodiments, the carbon source is lignocellulosic biomass. In embodiments, the majority carbon source is not glucose. In embodiments, the majority nitrogen source is ammonium sulfate ($(NH_4)_2SO_4$).

In embodiments, the growth medium includes a carbon source and a nitrogen source wherein the carbon source is at a concentration at least 2-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 3-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 4-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 5-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 6-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 7-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 8-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 9-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 10-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 11-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 12-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 13-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 14-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 15-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 16-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 17-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 18-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 19-fold greater than the concentration of the nitrogen source. In embodiments, the carbon source is at a concentration at least 20-fold greater than the concentration of the nitrogen source. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is about 0.03125, 0.0625, 0.125, 0.25, 0.5, 1.0, 2.0, 4.0, 8.0, 16, 32, 64, 128, 256, 512, 1024, 1600, 2048, 4096, 8192, or 16284. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is about 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, or 10000. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, or 10000. In embodiments, the ratio of the carbon source to the nitrogen source (wt/wt) is at least 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, or 10000. In embodiments, the carbon source to nitrogen source ratio corresponds to a ratio calculated from one or more of the ratios described above when the ratios described above are for a carbon source of glucose (g/L) and a nitrogen source of ammonium sulfate (g/L) for a carbon source that may not be glucose and a nitrogen source that may not be ammonium sulfate. In embodiments, the ratio of the concentration of the carbon source to the concentration of the nitrogen source is as described herein, including in embodiments, examples, tables, figures, and claims. In embodiments, the amount and

ratio of the carbon source to the nitrogen source (wt/wt) is equivalent to 160:0.2 glucose:ammonium sulfate. In embodiments, the amount and ratio of the carbon source to the nitrogen source (wt/wt) is equivalent to 80:5 glucose: ammonium sulfate.

In embodiments, the carbon source is at a concentration (g/L) of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 100, 410, 420, 430, 440, 450, 460, 470, 480, 490, or 500. In embodiments, the carbon source is at a concentration (g/L) of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 100, 410, 420, 430, 440, 450, 460, 470, 480, 490, or 500. In embodiments, the carbon source, which is optionally not glucose, is at a concentration for the carbon source that would provide an equal amount of carbon as one of the amounts described above where the amount described above is for glucose.

In embodiments, the nitrogen source is at a concentration (g/L) of about 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100. In embodiments, the nitrogen source is at a concentration (g/L) of 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100. In embodiments, the nitrogen source, which is optionally not ammonium sulfate, is at a concentration for the nitrogen source that would provide an equal amount of nitrogen as one of the amounts described above where the amount described above is for ammonium sulfate.

In embodiments, the growth medium includes a micronutrient. In embodiments, the growth medium includes a plurality of micronutrients. In embodiments, the growth medium includes cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, and/or boron. In embodiments, the growth medium includes iron and copper or molybdenum. In embodiments, the growth medium includes copper and nickel. In embodiments, the growth medium includes copper, iron, and either molybdenum or nickel. In embodiments, the growth medium includes copper, iron, molybdenum, and nickel. In embodiments, the growth medium includes cobalt. In embodiments, the growth medium includes iron. In embodiments, the growth medium includes magnesium. In embodiments, the growth medium includes potassium. In embodiments, the growth medium includes zinc. In embodiments, the growth medium includes nickel. In embodiments, the growth medium includes molybdenum. In embodiments, the growth medium includes manganese. In embodiments, the growth medium includes copper. In embodiments, the growth medium includes boron. In embodiments, the growth medium is supplemented with cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, and/or boron. In embodiments, the growth medium is supplemented with iron and copper or molybdenum. In embodiments, the growth medium is supplemented with copper and nickel. In embodiments, the growth medium is supplemented with copper, iron, and either molybdenum or nickel. In embodiments, the growth medium is supplemented with copper, iron, molybdenum, and nickel. In embodiments, the growth medium is supplemented with cobalt. In embodiments, the growth medium is supplemented with iron. In embodiments, the growth medium is supplemented with magnesium. In embodiments, the growth medium is supplemented with potassium. In embodiments, the growth medium is supplemented with zinc. In embodiments, the growth medium is supplemented with nickel. In embodiments, the growth medium is supplemented with molybdenum. In embodiments, the growth medium is supplemented with manganese. In embodiments, the growth medium is supplemented with copper. In embodiments, the growth medium is supplemented with boron. In embodiments, the growth medium includes $CoCl_2$ at a concentration of about 15 mg/L. In embodiments, the growth medium includes $MgSO_4$ at a concentration of about 250 mg/L. In embodiments, the growth medium includes KI at a concentration of about 15 mg/L. In embodiments, the growth medium includes $ZnSO_4.7H_2O$ at a concentration of about 20 mg/L. In embodiments, the growth medium includes $MnSO_4.H_2O$ at a concentration of about 12.5 mg/L. In embodiments, the growth medium includes Boric acid at a concentration of about 12.5 mg/L. In embodiments, the growth medium includes $(NH_4)_2Mo.4H_2O$ at a concentration of about 15 mg/L. In embodiments, the growth medium includes $NiSO_4.6H_2O$ at a concentration of about 12.5 mg/L. In embodiments, the growth medium includes $FeSO_4.7H_2O$ at a concentration of about 20 mg/L. In embodiments, the growth medium includes $CuSO_4$ at a concentration of about 15 mg/L. In embodiments, the growth medium includes $CoCl_2$ at a concentration of 15 mg/L. In embodiments, the growth medium includes $MgSO_4$ at a concentration of 250 mg/L. In embodiments, the growth medium includes KI at a concentration of 15 mg/L. In embodiments, the growth medium includes $ZnSO_4.7H_2O$ at a concentration of 20 mg/L. In embodiments, the growth medium includes $MnSO_4.H_2O$ at a concentration of 12.5 mg/L. In embodiments, the growth medium includes Boric acid at a concentration of 12.5 mg/L. In embodiments, the growth medium includes $(NH_4)_2Mo.4H_2O$ at a concentration of 15 mg/L. In embodiments, the growth medium includes $NiSO_4.6H_2O$ at a concentration of 12.5 mg/L. In embodiments, the growth medium includes $FeSO_4.7H_2O$ at a concentration of 20 mg/L. In embodiments, the growth medium includes $CuSO_4$ at a concentration of 15 mg/L. In embodiments, the growth medium is supplemented with $CoCl_2$ at a concentration of about 15 mg/L. In embodiments, the growth medium is supplemented with $MgSO_4$ at a concentration of about 250 mg/L. In embodiments, the growth medium is supplemented

with KI at a concentration of about 15 mg/L. In embodiments, the growth medium is supplemented with $ZnSO_4.7H_2O$ at a concentration of about 20 mg/L. In embodiments, the growth medium is supplemented with $MnSO_4.H_2O$ at a concentration of about 12.5 mg/L. In embodiments, the growth medium is supplemented with Boric acid at a concentration of about 12.5 mg/L. In embodiments, the growth medium is supplemented with $(NH_4)_2Mo.4H_2O$ at a concentration of about 15 mg/L. In embodiments, the growth medium is supplemented with $NiSO_4.6H_2O$ at a concentration of about 12.5 mg/L. In embodiments, the growth medium is supplemented with $FeSO_4.7H_2O$ at a concentration of about 20 mg/L. In embodiments, the growth medium is supplemented with $CuSO_4$ at a concentration of about 15 mg/L. In embodiments, the growth medium is supplemented with $CoCl_2$ at a concentration of 15 mg/L. In embodiments, the growth medium is supplemented with $MgSO_4$ at a concentration of 250 mg/L. In embodiments, the growth medium is supplemented with KI at a concentration of 15 mg/L. In embodiments, the growth medium is supplemented with $ZnSO_4.7H_2O$ at a concentration of 20 mg/L. In embodiments, the growth medium is supplemented with $MnSO_4.H_2O$ at a concentration of 12.5 mg/L. In embodiments, the growth medium is supplemented with Boric acid at a concentration of 12.5 mg/L. In embodiments, the growth medium is supplemented with $(NH_4)_2Mo.4H_2O$ at a concentration of 15 mg/L. In embodiments, the growth medium is supplemented with $NiSO_4.6H_2O$ at a concentration of 12.5 mg/L. In embodiments, the growth medium is supplemented with $FeSO_4.7H_2O$ at a concentration of 20 mg/L. In embodiments, the growth medium is supplemented with $CuSO_4$ at a concentration of 15 mg/L. In embodiments, the growth medium includes $CoCl_2$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $MgSO_4$ at a concentration of about 125 to 375 mg/L. In embodiments, the growth medium includes KI at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $ZnSO_4.7H_2O$ at a concentration of about 10 to 30 mg/L. In embodiments, the growth medium includes $MnSO_4.H_2O$ at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium includes Boric acid at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium includes $(NH_4)_2Mo.4H_2O$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $NiSO_4.6H_2O$ at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium includes $FeSO_4.7H_2O$ at a concentration of about 10 to 30 mg/L. In embodiments, the growth medium includes $CuSO_4$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $CoCl_2$ at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $MgSO_4$ at a concentration of 125 to 375 mg/L. In embodiments, the growth medium includes KI at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $ZnSO_4.7H_2O$ at a concentration of 10 to 30 mg/L. In embodiments, the growth medium includes $MnSO_4.H_2O$ at a concentration of 6 to 18 mg/L. In embodiments, the growth medium includes Boric acid at a concentration of 6 to 18 mg/L. In embodiments, the growth medium includes $(NH_4)_2Mo.4H_2O$ at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium includes $NiSO_4.6H_2O$ at a concentration of 6 to 18 mg/L. In embodiments, the growth medium includes $FeSO_4.7H_2O$ at a concentration of 10 to 30 mg/L. In embodiments, the growth medium includes $CuSO_4$ at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $CoCl_2$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $MgSO_4$ at a concentration of about 125 to 375 mg/L. In embodiments, the growth medium is supplemented with KI at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $ZnSO_4.7H_2O$ at a concentration of about 10 to 30 mg/L. In embodiments, the growth medium is supplemented with $MnSO_4.H_2O$ at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium is supplemented with Boric acid at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium is supplemented with $(NH_4)_2Mo.4H_2O$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $NiSO_4.6H_2O$ at a concentration of about 6 to 18 mg/L. In embodiments, the growth medium is supplemented with $FeSO_4.7H_2O$ at a concentration of about 10 to 30 mg/L. In embodiments, the growth medium is supplemented with $CuSO_4$ at a concentration of about 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $CoCl_2$ at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $MgSO_4$ at a concentration of 125 to 375 mg/L. In embodiments, the growth medium is supplemented with KI at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $ZnSO_4.7H_2O$ at a concentration of 10 to 30 mg/L. In embodiments, the growth medium is supplemented with $MnSO_4.H_2O$ at a concentration of 6 to 18 mg/L. In embodiments, the growth medium is supplemented with Boric acid at a concentration of 6 to 18 mg/L. In embodiments, the growth medium is supplemented with $(NH_4)_2Mo.4H_2O$ at a concentration of 7.5 to 22.5 mg/L. In embodiments, the growth medium is supplemented with $NiSO_4.6H_2O$ at a concentration of 6 to 18 mg/L. In embodiments, the growth medium is supplemented with $FeSO_4.7H_2O$ at a concentration of 10 to 30 mg/L. In embodiments, the growth medium is supplemented with $CuSO_4$ at a concentration of 7.5 to 22.5 mg/L.

In embodiments, the method does not include nitrogen starvation of the oleaginous organism (e.g. oleaginous yeast cell).

In embodiments, the oleaginous yeast is cultured for about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, or 500 hours. In embodiments, the oleaginous yeast is cultured for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, or 500 hours. In embodiments, the oleaginous yeast is cultured for about 48, 96, 144, or 192 hours. In embodiments, the oleaginous yeast is cultured for 48, 96, 144, or 192 hours. In embodiments, the oleaginous yeast is cultured for about 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 days. In embodiments, the oleaginous yeast is cultured for 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 days.

In an aspect is provided a method of producing a lipid, lipid precursor, or oleochemical including culturing a yeast cell described herein in a growth medium; and isolating the lipid, lipid precursor, or oleochemical.

In embodiments, the lipid, lipid precursor, or oleochemical is isolated from the yeast cell. In embodiments, the lipid, lipid precursor, or oleochemical is isolated from the growth medium. In embodiments, the growth medium includes a majority carbon source selected from the group consisting of glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, and lignocellulosic biomass. In embodiments, the growth medium includes lignocellulosic biomass as the majority carbon source. In embodiments, the growth medium includes a carbon source and a nitrogen source wherein the carbon source is at a concentration at least 10-fold greater than the concentration of the nitrogen source (wt/wt). In embodiments, the growth medium includes a carbon source and a nitrogen source wherein the carbon source is at a concentration at least 16-fold greater than the concentration of the nitrogen source (wt/wt). In embodiments, the growth medium includes a carbon source and a nitrogen source wherein the carbon source is at a concentration at least 320-fold greater than the concentration of the nitrogen source (wt/wt).

In embodiments, the growth medium includes cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, or boron. In embodiments, the growth medium includes any combination of two or more of cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, or boron. In embodiments, the growth medium includes cobalt in an amount equivalent to 7.5 to 22.5 mg/L $CoCl_2$, magnesium in an amount equivalent to 125 to 375 mg/L $MgSO_4$, potassium in an amount equivalent to 7.5 to 22.5 mg/L KI, zinc in an amount equivalent to 10 to 30 mg/L $ZnSO_4.7H_2O$, manganese in an amount equivalent to 6 to 18 mg/L $MnSO_4.H_2O$, boron in an amount equivalent to 6 to 18 mg/L Boric acid, molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$. In embodiments, the growth medium includes about 5.77×10^{-5} M to 1.73×10^{-4}M cobalt, about 0.001 M to 0.003 M magnesium, about 4.52×10^{-5} M to 1.35×10^{-4} M potassium, about 4.05×10^{-5} M to 1.22×10^{-4} M zinc, about 3.55×10^{-5} to 1.06×10^{-4}M manganese, about 9.07×10^{-5} M to 2.91×10^{-4} M boron, about 3.76×10^{-5} M to 1.10×10^{-4}M molybdenum, about 2.28×10^{-5} M to 6.84×10^{-5} M nickel, about 3.60×10^{-5} M to 1.08×10^{-4}M iron, or about 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes 5.77×10^{-5} M to 1.73×10^{-4} M cobalt, 0.001 M to 0.003 M magnesium, 4.52×10^{-5} M to 1.35×10^{-4} M potassium, 4.05×10^{-5} M to 1.22×10^{-4} M zinc, 3.55×10^{-5} to 1.06×10^{-4} M manganese, 9.07×10^{-5} M to 2.91×10^{-4} M boron, 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 2.28×10^{-5} M to 6.84×10^{-5} M nickel, 3.60×10^{-5} M to 1.08×10^{-4} M iron, or 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes about 5.77×10^{-5} M to 1.73×10^{-4}M cobalt. In embodiments, the growth medium includes about 0.001 M to 0.003 M magnesium. In embodiments, the growth medium includes about 4.52×10^{-5} M to 1.35×10^{-4} M potassium. In embodiments, the growth medium includes about 4.05×10^{-5} M to 1.22×10^{-4} M zinc. In embodiments, the growth medium includes about 3.55×10^{-5} to 1.06×10^{-4} M manganese. In embodiments, the growth medium includes about 9.07×10^{-5} M to 2.91×10^{-4} M boron. In embodiments, the growth medium includes about 3.76×10^{-5} M to 1.10×10^{-4}M molybdenum. In embodiments, the growth medium includes about 2.28×10^{-5} M to 6.84×10^{-5} M nickel. In embodiments, the growth medium includes about 3.60×10^{-5} M to 1.08×10^{-4}M iron. In embodiments, the growth medium includes about 4.70×10^{-5} M to 1.41×10^{-4}M copper. In embodiments, the growth medium includes 5.77×10^{-5} M to 1.73×10^{-4} M cobalt. In embodiments, the growth medium includes 0.001 M to 0.003 M magnesium. In embodiments, the growth medium includes 4.52×10^{-5} M to 1.35×10^{-4} M potassium. In embodiments, the growth medium includes 4.05×10^{-5} M to 1.22×10^{-4} M zinc. In embodiments, the growth medium includes 3.55×10^{-5} to 1.06×10^{-4} M manganese. In embodiments, the growth medium includes 9.07×10^{-5} M to 2.91×10^{-4} M boron. In embodiments, the growth medium includes 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum. In embodiments, the growth medium includes 2.28×10^{-5} M to 6.84×10^{-5} M nickel. In embodiments, the growth medium includes 3.60×10^{-5} M to 1.08×10^{-4} M iron. In embodiments, the growth medium includes 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes iron, copper, and molybdenum. In embodiments, the growth medium includes molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$. In embodiments, the growth medium includes 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 3.60×10^{-5} M to 1.08×10^{-4} M iron, or 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes copper and nickel. In embodiments, the growth medium includes nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$ or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$. In embodiments, the growth medium includes 2.28×10^{-5} M to 6.84×10^{-5} M nickel or 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes copper, iron, and either molybdenum or nickel. In embodiments, the growth medium includes molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$. In embodiments, the growth medium includes 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 2.28×10^{-5} M to 6.84×10^{-5} M nickel, 3.60×10^{-5} M to 1.08×10^{-4} M iron, or 4.70×10^{-5} M to 1.41×10^{-4} M copper. In embodiments, the growth medium includes copper, iron, molybdenum, and nickel.

In another aspect is provided a method of isolating a yeast cell including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight from a plurality of yeast cells, including allowing a yeast cell including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium thereby isolating the yeast cell including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical), wherein the population of yeast cells includes a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors,

lipid precursor, oleochemicals, or oleochemical). In another aspect is provided a method of isolating a genetically modified yeast cell from a plurality of yeast cells including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a genetically modified yeast cell to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium thereby isolating the genetically modified yeast cell, wherein the population of yeast cells includes a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the genetically modified yeast cell.

In embodiments is a method of isolating a yeast cell (e.g. genetically modified yeast cell), including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, from a plurality of yeast cells, including allowing a yeast cell (e.g. genetically modified yeast cell) to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium thereby isolating the yeast cell (e.g. genetically modified yeast cell), wherein the population of yeast cells includes a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the genetically modified yeast cell.

In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 30% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 40% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 50% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 70% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 80% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) includes greater than 90% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) is floating on the top surface of the aqueous medium. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) is above the bottom of a vessel containing the aqueous medium. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) is floating above the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight by about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 mm in the aqueous medium. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) is floating above the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight by at least 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, or 99 mm in the aqueous medium. In embodiments, the genetically modified yeast cell including greater than 20% wt/wt lipids, lipid

precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) floating above the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight has a buoyant density greater than the buoyant density of the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight by about 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, g/mL. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight (e.g. greater than 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight) floating above the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight has a buoyant density greater than the buoyant density of the population of yeast cells including a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight by 0.001, 0.002, 0.003, 0.004, 0.005, 0.006, 0.007, 0.008, 0.009, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, g/mL. In embodiments, the yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical), includes a mutation created by natural genetic drift.

In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 0.5 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 1.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 2.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 2.5 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 3.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 4.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 0.5 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 1.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 2.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 2.5 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 3.0 vvm (volume per volume per minute). In embodiments of the method, the plurality of yeast cells are in a bioreactor with agitation and aeration rates of 4.0 vvm (volume per volume per minute).

In embodiments of the method, the aqueous medium includes a yeast growth medium, minimal media, complete supplement media, or greater than 50 g/L carbon source (e.g. glucose) and less than 5 g/L of a nitrogen source (e.g. ammonium sulfate). In embodiments of the method, the aqueous medium includes a yeast growth medium. In embodiments of the method, the aqueous medium includes a minimal media. In embodiments of the method, the aqueous medium includes a complete supplement media. In embodiments of the method, the aqueous medium includes greater than 50 g/L carbon source (e.g. glucose) and less than 5 g/L of a nitrogen source (e.g. ammonium sulfate). In embodiments of the method, the aqueous medium is a yeast growth medium. In embodiments of the method, the aqueous medium is a minimal media. In embodiments of the method, the aqueous medium is a complete supplement media.

In embodiments of the method of isolating a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium, the allowing is performed by centrifugation or simple sedimentation. In embodiments of the method of isolating a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid,

lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium, the allowing is performed by centrifugation. In embodiments of the method of isolating a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium, the allowing is performed by simple sedimentation. In embodiments of the method of isolating a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium, the allowing is performed by sedimentation. In embodiments of the method of isolating a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, including allowing a yeast cell (e.g. genetically modified yeast cell) including greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight to separate from a population of yeast cells within the plurality of yeast cells by floating above the population of yeast cells within an aqueous medium, the allowing is performed by sedimentation due to gravity.

In embodiments of the method, the genetically modified yeast cell is formed by transforming a yeast cell with a recombinant nucleic acid (e.g. as described herein, including in embodiments, examples, tables, figures, and/or claims). In embodiments, the genetically modified yeast cell is formed by mutagenizing a yeast cell. In embodiments, the yeast cell (e.g. genetically modified yeast cell includes a mutation created by natural genetic drift.

In embodiments, the method is a method described herein, including in embodiments, examples, tables, figures, and claims.

IV. ADDITIONAL EMBODIMENTS

1p. A genetically modified yeast cell wherein the dry weight of said yeast cell comprises greater than 20% wt/wt lipid.

2p. The yeast cell of embodiment 1p comprising greater than 30% wt/wt lipid.

3p. The yeast cell of embodiment 1p comprising greater than 40% wt/wt lipid.

4p. The yeast cell of embodiment 1p comprising greater than 50% wt/wt lipid.

5p. The yeast cell of embodiment 1p comprising greater than 60% wt/wt lipid.

6p. The yeast cell of embodiment 1p comprising greater than 70% wt/wt lipid.

7p. The yeast cell of embodiment 1p comprising greater than 80% wt/wt lipid.

8p. The yeast cell of embodiment 1p comprising greater than 90% wt/wt lipid.

9p. The yeast cell of any one of embodiments 1p to 8p, selected from the group consisting of the genera *Yarrowia, Candida, Rhodotorula, Rhodosporidium, Cryptococcus, Trichosporon* and *Lipomyces.*

10p. The yeast cell of any one of embodiments 1p to 8p, selected from the group consisting of *Rhodosporidium toruloides, Lipomyces starkeyii, Lipomyces lipoferus, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Candida revkaufi, Candida pulcherrima, Candida tropicalis, Candida utilis, Trichosporon pullans, Trichosporon cutaneum, Rhodotorula glutinus, Rhodotorula graminis* and *Yarrowia lipolytica.*

11p. The yeast cell of any one of embodiments 1p to 8p, selected from the group consisting of *Lipomyces starkeyii, Rhodosporidium toruloides, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Rhodotorula glutinis*, and *Yarrowia lipolytica.*

12p. The yeast cell of any one of embodiments 1p to 8p, wherein said yeast cell is *Yarrowia lipolytica.*

13p. The yeast cell of any one of embodiments 1p to 12p, wherein said yeast cell is buoyant in an aqueous medium.

14p. The yeast cell of any one of embodiments 1p to 13p, wherein said lipid is selected from the group consisting of a fatty acid, wax, sterol, vitamin, monoglyceride, diglyceride, triglyceride, phospholipid, glycerolipid, glycerophospholipid, sphingolipid, saccharolipid, polyketide, sterol lipid, triacylglyceride, and a prenol lipid.

15p. A yeast cell comprising a recombinant nucleic acid, wherein said recombinant nucleic acid modulates the level of activity of a protein in said yeast cell relative to the absence of the recombinant nucleic acid, and wherein said protein is selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), multifunctional enzyme (MFE1), Transcription Factor (PEX10), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA:diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), and O-6-methylguanine-DNA methyltransferase (MGMT).

16p. The yeast cell of embodiment 15p, wherein said recombinant nucleic acid increases the level of activity of a protein in said yeast cell selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), AMP Deaminase (AMPD), ATP-Citrate Lyase (ACL), Malic Enzyme (MAE), Acetyl-CoA Carboxylase (ACC), acyl-CoA: diacylglycerol acyltransferase (DGA1), acyl-CoA: diacylglycerol acyltransferases (DGA2), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), and O-6-methylguanine-DNA methyltransferase (MGMT).

17p. The yeast cell of any one of embodiments 15p to 16p, wherein said recombinant nucleic acid decreases the level of activity of a protein in said yeast cell selected from the group consisting of multifunctional enzyme (MFE1), Lipid synthesis regulator (MGA2), Chromatin assembly gene (RLF2 subunit p90), and Transcription Factor (PEX10).

18p. The yeast cell of any one of embodiments 15p to 17p, wherein said recombinant nucleic acid increases the level of activity of a protein in said yeast cell selected from the group consisting of Leucine Biosynthesis Gene (LEU2), Uracil Biosynthesis gene (URA3), Malic Enzyme (MAE), Mitochondrial 2' O-ribose methyltransferase (MRM2), Lipid synthesis regulator (MGA2), and O-6-methylguanine-DNA methyltransferase (MGMT) or said nucleic acid decrease the level of activity of Lipid synthesis regulator (MGA2).

19p. The yeast cell of any one of embodiments 15p to 18p, wherein said recombinant nucleic acid encodes a protein comprising a mutation relative to the wildtype protein.

20p. The yeast cell of any one of embodiments 15p to 18p, wherein said nucleic acid modulates the level of expression of a protein.

21p. The yeast cell of embodiment 15p, wherein said yeast cell comprises a recombinant nucleic acid that decreases the level of activity of multifunctional enzyme (MFE1) protein and Transcription Factor (PEX10) protein, increases the level of activity of acyl-CoA:diacylglycerol acyltransferase (DGA1) protein, or increases the level of activity of Leucine Biosynthesis Gene (LEU2) protein relative to a yeast cell that does not comprise said recombinant nucleic acids.

22p. The yeast cell of any one of embodiments 1p to 21p, wherein said yeast cell comprises a fatty acid selected from the group consisting of C5:0, C5:1, C5:2, C5:3, C6:0, C6:1, C6:2, C6:3, C7:0, C7:1, C7:2, C7:3, C8:0, C8:1, C8:2, C8:3, C9:0, C9:1, C9:2, C9:3, C10:0, C10:1, C10:2, C10:3, C11:0, C11:1, C11:2, C11:3, C12:0, C12:1, C12:2, C12:3, C13:0, C13:1, C13:2, C13:3, C14:0, C14:1, C14:2, C14:3, C15:0, C15:1, C15:2, C15:3, C16:0, C16:1, C16:2, C16:3, C17:0, C17:1, C17:2, C17:3, C18:0, C18:1, C18:2, C18:3, C19:0, C19:1, C19:2, C19:3, C20:0, C20:1, C20:2, C20:3, C21:0, C21:1, C21:2, C21:3, C22:0, C22:1, C22:2, C22:3, C23:0, C23:1, C23:2, and C23:3.

23p. The yeast cell of any one of embodiments 1p to 21p, wherein said yeast cell comprises a fatty acid selected from the group consisting of C17:0 and C17:1.

24p. A method of producing a lipid comprising:

1) culturing a yeast cell of any one of embodiments 1p to 23p in a growth medium;

2) isolating said lipid.

25p. The method of embodiment 24p, wherein said lipid is isolated from said yeast cell. 26p. The method of embodiment 24p, wherein said lipid is isolated from the medium.

27p. The method of any one of embodiments 24p to 26p, wherein said growth medium comprises a majority carbon source selected from the group consisting of glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, and lignocellulosic biomass.

28p. The method of any one of embodiments 24p to 26p, wherein said growth medium comprises lignocellulosic biomass as the majority carbon source.

29p. The method of any one of embodiments 24p to 28p, wherein said growth medium comprises a carbon source and a nitrogen source wherein said carbon source is at a concentration at least 10-fold greater than the concentration of the nitrogen source.

30p. The method of any one of embodiments 24p to 29p, wherein said growth medium comprises cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, or boron.

31p. The method of embodiment 30p, wherein the growth medium comprises iron, copper, and molybdenum.

32p. The method of embodiment 30p, wherein the growth medium comprises copper and nickel.

33p. The method of embodiment 30p, wherein the growth medium comprises copper, iron, and either molybdenum or nickel.

34p. The method of embodiment 30p, wherein the growth medium comprises copper, iron, molybdenum, and nickel.

35p. A method of isolating a genetically modified yeast cell from a plurality of yeast cells comprising greater than 20% wt/wt lipids in dry weight, comprising allowing a genetically modified yeast cell to separate from a population of yeast cells within said plurality of yeast cells by floating above said population of yeast cells within an aqueous medium thereby isolating said genetically modified yeast cell, wherein said population of yeast cells comprises a lower percentage wt/wt of lipids than said genetically modified yeast cell.

36p. The method of any embodiment 35p, wherein said genetically modified yeast cell comprises greater than 30% wt/wt lipids in dry weight.

37p. The method of embodiment 35p, wherein said genetically modified yeast cell comprises greater than 40% wt/wt lipids in dry weight.

38p. The method of embodiment 35p, wherein said genetically modified yeast cell comprises greater than 50% wt/wt lipids in dry weight.

39p. The method of embodiment 35p, wherein said genetically modified yeast cell comprises greater than 60% wt/wt lipids in dry weight.

40p. The method of any one of embodiments 35p to 39p, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 0.5 vvm (volume per volume per minute).

41p. The method of any one of embodiments 35p to 39p, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 1.0 vvm (volume per volume per minute).

42p. The method of any one of embodiments 35p to 39p, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 2.0 vvm (volume per volume per minute).

43p. The method of any one of embodiments 35p to 39p, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 3.0 vvm (volume per volume per minute).

44p. The method of any one of embodiments 35p to 39p, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 4.0 vvm (volume per volume per minute).

45p. The method of any one of embodiments 35p to 44p, wherein said aqueous medium comprises a yeast growth medium, minimal media, complete supplement media, or greater than 50 g/L glucose and less than 5 g/L of a nitrogen source.

46p. The method of any one of embodiments 35p to 45p, wherein said allowing is performed by centrifugation or simple sedimentation.

47p. The method of any one of embodiments 35p to 46p, wherein said genetically modified yeast cell was formed by transforming a yeast cell with a recombinant nucleic acid.

48p. The method of any one of embodiments 35p to 4'7p, wherein said genetically modified yeast cell was formed by mutagenizing a yeast cell.

1. A genetically modified yeast cell wherein the dry weight of said yeast cell comprises greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

2. The genetically modified yeast cell of embodiment 1 comprising greater than 30% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

3. The genetically modified yeast cell of embodiment 1 comprising greater than 40% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

4. The genetically modified yeast cell of embodiment 1 comprising greater than 50% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

5. The genetically modified yeast cell of embodiment 1 comprising greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

6. The genetically modified yeast cell of embodiment 1 comprising greater than 70% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

7. The genetically modified yeast cell of embodiment 1 comprising greater than 80% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

8. The genetically modified yeast cell of embodiment 1 comprising greater than 90% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

9. The genetically modified yeast cell of any one of embodiments 1 to 8, selected from the group consisting of the genera *Yarrowia, Candida, Rhodotorula, Rhodosporidium, Cryptococcus, Trichosporon* and *Lipomyces.*

10. The genetically modified yeast cell of any one of embodiments 1 to 8, selected from the group consisting of *Rhodosporidium toruloides, Lipomyces starkeyii, Lipomyces lipoferus, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Candida revkaufi, Candida pulcherrima, Candida tropicalis, Candida utilis, Trichosporon pullans, Trichosporon cutaneum, Rhodotorula glutinus, Rhodotorula graminis* and *Yarrowia lipolytica.*

11. The genetically modified yeast cell of any one of embodiments 1 to 8, selected from the group consisting of *Lipomyces starkeyii, Rhodosporidium toruloides, Apiotrichum curvatum, Candida curvata, Cryptococcus curvatus, Trichosporon fermentans, Rhodotorula glutinis*, and *Yarrowia lipolytica.*

12. The genetically modified yeast cell of any one of embodiments 1 to 8, wherein said yeast cell is *Yarrowia lipolytica.*

13. The genetically modified yeast cell of any one of embodiments 1 to 12, wherein said yeast cell is buoyant in an aqueous medium.

14. The genetically modified yeast cell of one of embodiments 1 to 13, comprising a recombinant Leucine Biosynthesis Gene (LEU2).

15. The genetically modified yeast cell of one of embodiments 1 to 13, wherein said genetic modification increases the level of activity of the Leucine Biosynthesis Gene (LEU2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

16. The genetically modified yeast cell of one of embodiments 1 to 15, comprising a recombinant Uracil Biosynthesis gene (URA3).

17. The genetically modified yeast cell of one of embodiments 1 to 15, wherein said genetic modification increases the level of activity of the Uracil Biosynthesis gene (URA3) protein relative to an otherwise identical yeast cell lacking said genetic modification.

18. The genetically modified yeast cell of one of embodiments 1 to 17, comprising a genetically modified multifunctional enzyme (MFE1) gene.

19. The genetically modified yeast cell of one of embodiments 1 to 17, wherein said genetic modification decreases the level of activity of the multifunctional enzyme (MFE1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

20. The genetically modified yeast cell of one of embodiments 1 to 19, comprising a genetically modified PEX10 Transcription Factor (PEX10) gene.

21. The genetically modified yeast cell of one of embodiments 1 to 19, wherein said genetic modification decreases the level of activity of the PEX10 Transcription Factor (PEX10) protein relative to an otherwise identical yeast cell lacking said genetic modification.

22. The genetically modified yeast cell of one of embodiments 1 to 21, comprising a recombinant AMP Deaminase (AMPD) protein.

23. The genetically modified yeast cell of one of embodiments 1 to 21, wherein said genetic modification increases the level of activity of the AMP Deaminase (AMPD) protein relative to an otherwise identical yeast cell lacking said genetic modification.

24. The genetically modified yeast cell of one of embodiments 1 to 23, comprising a recombinant ATP-Citrate Lyase (ACL1) protein.

25. The genetically modified yeast cell of one of embodiments 1 to 23, wherein said genetic modification increases the level of activity of the ATP-Citrate Lyase (ACL1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

26. The genetically modified yeast cell of one of embodiments 1 to 25, comprising a recombinant ATP-Citrate Lyase (ACL2) protein.

27. The genetically modified yeast cell of one of embodiments 1 to 25, wherein said genetic modification increases the level of activity of the ATP-Citrate Lyase (ACL2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

28. The genetically modified yeast cell of one of embodiments 1 to 27, comprising a recombinant Malic Enzyme (MAE) protein.

29. The genetically modified yeast cell of one of embodiments 1 to 27, wherein said genetic modification increases the level of activity of the Malic Enzyme (MAE) protein relative to an otherwise identical yeast cell lacking said genetic modification.

30. The genetically modified yeast cell of one of embodiments 1 to 29, comprising a recombinant Acetyl-CoA Carboxylase (ACC) protein.

31. The genetically modified yeast cell of one of embodiments 1 to 29, wherein said genetic modification increases the level of activity of the Acetyl-CoA Carboxylase (ACC) protein relative to an otherwise identical yeast cell lacking said genetic modification.

32. The genetically modified yeast cell of one of embodiments 1 to 31, comprising a recombinant acyl-CoA: diacylglycerol acyltransferase 1 (DGA1) protein.

33. The genetically modified yeast cell of one of embodiments 1 to 31, wherein said genetic modification increases the level of activity of the acyl-CoA:diacylglycerol acyltransferase 1 (DGA1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

34. The genetically modified yeast cell of one of embodiments 1 to 33, comprising a recombinant acyl-CoA: diacylglycerol acyltransferase 2 (DGA2) protein.

35. The genetically modified yeast cell of one of embodiments 1 to 33, wherein said genetic modification increases the level of activity of the acyl-CoA:diacylglycerol acyltransferase 2 (DGA2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

36. The genetically modified yeast cell of one of embodiments 1 to 35, comprising a recombinant Mitochondrial 2' O-ribose methyltransferase (MRM2) protein.

37. The genetically modified yeast cell of one of embodiments 1 to 35, wherein said genetic modification increases the level of activity of the Mitochondrial 2' O-ribose methyltransferase (MRM2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

38. The genetically modified yeast cell of one of embodiments 1 to 37, comprising a recombinant Lipid synthesis regulator (MGA2) protein.

39. The genetically modified yeast cell of one of embodiments 1 to 37, comprising a genetically modified Lipid synthesis regulator (MGA2) gene.

40. The genetically modified yeast cell of one of embodiments 1 to 37, comprising at least one nucleotide deletion in the genomic Lipid synthesis regulator (MGA2) gene and expression of a Lipid synthesis regulator (MGA2) protein comprising a mutation corresponding to G643R in *Yarrowia lipolytica*. Lipid synthesis regulator (MGA2)

41. The genetically modified yeast cell of one of embodiments 1 to 37, wherein said genetic modification decreases the level of activity of the Lipid synthesis regulator (MGA2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

42. The genetically modified yeast cell of one of embodiments 1 to 41, comprising a genetically modified Chromatin assembly gene (RLF2 subunit p90) gene.

43. The genetically modified yeast cell of one of embodiments 1 to 41, wherein said genetic modification decreases the level of activity of the Chromatin assembly gene (RLF2 subunit p90) protein relative to an otherwise identical yeast cell lacking said genetic modification.

44. The genetically modified yeast cell of one of embodiments 1 to 43, comprising a recombinant O-6-methylguanine-DNA methyltransferase (MGMT) protein.

45. The genetically modified yeast cell of one of embodiments 1 to 43, wherein said genetic modification increases the level of activity of the O-6-methylguanine-DNA methyltransferase (MGMT) protein relative to an otherwise identical yeast cell lacking said genetic modification.

46. The genetically modified yeast cell of one of embodiments 1 to 45, comprising a genetically modified Aconitase (ACO1) gene.

47. The genetically modified yeast cell of one of embodiments 1 to 45, wherein said genetic modification decreases the level of activity of the Aconitase (ACO1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

48. The genetically modified yeast cell of one of embodiments 1 to 47, comprising a recombinant Citrate Synthase (CIT1) gene.

49. The genetically modified yeast cell of one of embodiments 1 to 47, wherein said genetic modification increases the level of activity of the Citrate Synthase (CIT1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

50. The genetically modified yeast cell of one of embodiments 1 to 49, comprising a genetically modified RME1 zinc-finger transcription factor (RME1) gene.

51. The genetically modified yeast cell of one of embodiments 1 to 49, wherein said genetic modification decreases the level of activity of the RME1 zinc-finger transcription factor (RME1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

52. The genetically modified yeast cell of one of embodiments 1 to 51, comprising a genetically modified YOX1 homeodomain protein (YOX1) gene.

53. The genetically modified yeast cell of one of embodiments 1 to 51, wherein said genetic modification decreases the level of activity of the YOX1 homeodomain protein (YOX1) protein relative to an otherwise identical yeast cell lacking said genetic modification.

54. The genetically modified yeast cell of one of embodiments 1 to 53, comprising a genetically modified UGA2 succinate semialdehyde dehydrogenase (UGA2) gene.

55. The genetically modified yeast cell of one of embodiments 1 to 53, wherein said genetic modification decreases the level of activity of the UGA2 succinate semialdehyde dehydrogenase (UGA2) protein relative to an otherwise identical yeast cell lacking said genetic modification.

56. The genetically modified yeast cell of one of embodiments 1 to 55, comprising a genetically modified OSH6 oxysterol-binding protein homolog 6 (OSH6) gene.

57. The genetically modified yeast cell of one of embodiments 1 to 55, wherein said genetic modification decreases the level of activity of the OSH6 oxysterol-binding protein homolog 6 (OSH6) protein relative to an otherwise identical yeast cell lacking said genetic modification.

58. The genetically modified yeast cell of one of embodiments 1 to 57, comprising a genetically modified IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) gene.

59. The genetically modified yeast cell of one of embodiments 1 to 57, wherein said genetic modification decreases the level of activity of the IRC20 E3 ubiquitin-protein ligase and helicase (IRC20) protein relative to an otherwise identical yeast cell lacking said genetic modification.

60. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification modulates the level of activity of a component of a lipid biosynthetic pathway.

61. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification modulates the level of activity of a component of a pathway incorporating Acetyl-CoA into a lipid, lipid precursor, or oleochemical.

62. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification modulates the level of activity of a component of a pathway incorporating malonyl-CoA into a lipid, lipid precursor, or oleochemical.

63. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification increases the level of activity of a component of a lipid biosynthetic pathway.

64. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification increases the level of activity of a component of a pathway incorporating acetyl-CoA into a lipid, lipid precursor, or oleochemical.

65. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification

increases the level of activity of a component of a pathway incorporating malonyl-CoA into a lipid, lipid precursor, or oleochemical.

66. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification modulates the level of activity of a component of a lipid, lipid precursor, or oleochemical, metabolic pathway.

67. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification decreases the level of activity of a component of a lipid, lipid precursor, or oleochemical, metabolic pathway.

68. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification decreases the level of activity of a component of a lipid, lipid precursor, or oleochemical, metabolic pathway.

69. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification increases the level of acetyl-CoA in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

70. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification increases the level of malonyl-CoA in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

71. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification increases the level of triglyceride production in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

72. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification decreases the level of beta-oxidation activity in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

73. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification decreases the level of fatty acid catabolism in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

74. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification decreases the level of peroxisome biogenesis activity in the genetically modified yeast cell relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

75. The genetically modified yeast cell of any one of embodiments 1 to 59, wherein said genetic modification produces a lipid, lipid precursor, or oleochemical at a higher level than by a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

76. The genetically modified yeast cell of embodiment 75, wherein said lipid, lipid precursor, or oleochemical produced at a higher level by said genetically modified yeast cell is a fatty acid, wax, sterol, vitamin, monoglyceride, diglyceride, triglyceride, phospholipid, glycerolipid, glycerophospholipid, sphingolipid, saccharolipid, polyketide, sterol lipid, triacylglyceride, prenol lipid, fatty acid ester, fatty acid methyl ester, fatty acid ethyl ester, fatty acid propyl ester, fatty acid butyl ester, fatty alcohol, fatty amine, glycerol, alcohol ethoxylate, alcohol sulfate, or alcohol ether sulfate.

77. The genetically modified yeast cell of any one of embodiments 1 to 76, wherein said genetic modification comprises a mutation relative to the wild type gene.

78. The genetically modified yeast cell of any one of embodiments 1 to 76, wherein said genetic modification comprises a deletion of a portion of a gene.

79. The genetically modified yeast cell of one of embodiments 1 to 78, wherein said yeast cell comprises an increased level of a fatty acid selected from the group consisting of C5:0, C5:1, C5:2, C5:3, C6:0, C6:1, C6:2, C6:3, C7:0, C7:1, C7:2, C7:3, C8:0, C8:1, C8:2, C8:3, C9:0, C9:1, C9:2, C9:3, C10:0, C10:1, C10:2, C10:3, C11:0, C11:1, C11:2, C11:3, C12:0, C12:1, C12:2, C12:3, C13:0, C13:1, C13:2, C13:3, C14:0, C14:1, C14:2, C14:3, C15:0, C15:1, C15:2, C15:3, C16:0, C16:1, C16:2, C16:3, C17:0, C17:1, C17:2, C17:3, C18:0, C18:1, C18:2, C18:3, C19:0, C19:1, C19:2, C19:3, C20:0, C20:1, C20:2, C20:3, C21:0, C21:1, C21:2, C21:3, C22:0, C22:1, C22:2, C22:3, C23:0, C23:1, C23:2, and C23:3, relative to a genetically unmodified yeast cell that is otherwise identical to said genetically modified yeast cell.

80. The genetically modified yeast cell of embodiment 79, wherein said fatty acid is C17:0 C17:1.

81. The genetically modified yeast cell of embodiment 79, wherein said fatty acid is C16:1n9.

82. The genetically modified yeast cell of one of embodiments 1 to 81, wherein said genetic modification is an engineered genetic modification.

83. The genetically modified yeast cell of embodiment 82, wherein said engineered genetic modification comprises modulated expression of a protein.

84. The genetically modified yeast cell of embodiment 82, wherein said engineered genetic modification comprises increased expression of a protein.

85. The genetically modified yeast cell of embodiment 82, wherein said engineered genetic modification comprises decreased expression of a protein.

86. The genetically modified yeast cell of one of embodiments 1 to 81, wherein said genetic modification is associated with exposure to a mutagen.

87. The genetically modified yeast cell of one of embodiments 1 to 86, wherein said genetic modification comprises modulated expression of a protein in a lipid, or lipid precursor, biosynthetic pathway.

88. A method of producing a lipid, lipid precursor, or oleochemical comprising:

1) culturing a yeast cell of any one of embodiments 1 to 87 in a growth medium; and

2) isolating said lipid, lipid precursor, or oleochemical.

89. The method of embodiment 88, wherein said lipid, lipid precursor, or oleochemicalis isolated from said yeast cell.

90. The method of embodiment 88, wherein said lipid, lipid precursor, or oleochemical is isolated from the growth medium.

91. The method of any one of embodiments 88 to 90, wherein said growth medium comprises a majority carbon source selected from the group consisting of glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, and lignocellulosic biomass.

92. The method of any one of embodiments 88 to 90, wherein said growth medium comprises lignocellulosic biomass as the majority carbon source.

93. The method of any one of embodiments 88 to 92, wherein said growth medium comprises a carbon source and a nitrogen source wherein said carbon source is at a concentration at least 10-fold greater than the concentration of the nitrogen source (wt/wt).

94. The method of any one of embodiments 88 to 92, wherein said growth medium comprises a carbon source and a nitrogen source wherein said carbon source is at a concentration at least 16-fold greater than the concentration of the nitrogen source (wt/wt).

95. The method of any one of embodiments 88 to 92, wherein said growth medium comprises a carbon source and a nitrogen source wherein said carbon source is at a concentration at least 320-fold greater than the concentration of the nitrogen source (wt/wt).

96. The method of any one of embodiments 88 to 95, wherein said growth medium comprises micronutrients (e.g. cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, or boron).

97. The method of any one of embodiments 88 to 95, wherein said growth medium comprises cobalt in an amount equivalent to 7.5 to 22.5 mg/L $CoCl_2$, magnesium in an amount equivalent to 125 to 375 mg/L $MgSO_4$, potassium in an amount equivalent to 7.5 to 22.5 mg/L KI, zinc in an amount equivalent to 10 to 30 mg/L $ZnSO_4.7H_2O$, manganese in an amount equivalent to 6 to 18 mg/L $MnSO_4.H_2O$, boron in an amount equivalent to 6 to 18 mg/L Boric acid, molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$.

98. The method of any one of embodiments 88 to 95, wherein said growth medium comprises 5.77×10^{-5} M to 1.73×10^{-4} M cobalt, 0.001 M to 0.003 M magnesium, 4.52×10^{-5} M to 1.35×10^{-4} M potassium, 4.05×10^{-5} M to 1.22×10^{-4} M zinc, 3.55×10^{-5} M to 1.06×10^{-4} M manganese, 9.07×10^{-5} M to 2.91×10^{-4} M boron, 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 2.28×10^{-5} M to 6.84×10^{-5} M nickel, 3.60×10^{-5} M to 1.08×10^{-4} M iron, or 4.70×10^{-5} M to 1.41×10^{-4} M copper.

99. The method of any one of embodiments 88 to 95, wherein the growth medium comprises iron, copper, and molybdenum.

100. The method of any one of embodiments 88 to 95, wherein said growth medium comprises molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$.

101. The method of any one of embodiments 88 to 95, wherein said growth medium comprises 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 3.60×10^{-5} M to 1.08×10^{-4} M iron, or 4.70×10^{-5} M to 1.41×10^{-4} M copper.

102. The method of any one of embodiments 88 to 95, wherein the growth medium comprises copper and nickel.

103. The method of any one of embodiments 88 to 95, wherein said growth medium comprises nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$ or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$.

104. The method of any one of embodiments 88 to 95, wherein said growth medium comprises 2.28×10^{-5} M to 6.84×10^{-5} M nickel or 4.70×10^{-5} M to 1.41×10^{-4} M copper.

105. The method of any one of embodiments 88 to 95, wherein the growth medium comprises copper, iron, and either molybdenum or nickel.

106. The method of any one of embodiments 88 to 95, wherein said growth medium comprises molybdenum in an amount equivalent to 7.5 to 22.5 mg/L $(NH_4)_2Mo.4H_2O$, nickel in an amount equivalent to 6 to 18 mg/L $NiSO_4.6H_2O$, iron in an amount equivalent to 10 to 30 mg/L $FeSO_4.7H_2O$, or copper in an amount equivalent to 7.5 to 22.5 mg/L $CuSO_4$.

107. The method of any one of embodiments 88 to 95, wherein said growth medium comprises 3.76×10^{-5} M to 1.10×10^{-4} M molybdenum, 2.28×10^{-5} M to 6.84×10^{-5} M nickel, 3.60×10^{-5} M to 1.08×10^{-4}M iron, or 4.70×10^{-5} M to 1.41×10^{-4}M copper.

108. The method of any one of embodiments 88 to 95, wherein the growth medium comprises copper, iron, molybdenum, and nickel.

109. A method of isolating a genetically modified yeast cell from a plurality of yeast cells, comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight, comprising allowing a genetically modified yeast cell to separate from a population of yeast cells within said plurality of yeast cells by floating above said population of yeast cells within an aqueous medium thereby isolating said genetically modified yeast cell, wherein said population of yeast cells comprises a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than said genetically modified yeast cell.

110. The method of embodiment 109, wherein said genetically modified yeast cell comprises greater than 30% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

111. The method of embodiment 109, wherein said genetically modified yeast cell comprises greater than 40% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

112. The method of embodiment 109, wherein said genetically modified yeast cell comprises greater than 50% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

113. The method of embodiment 109, wherein said genetically modified yeast cell comprises greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

114. The method of any one of embodiments 109 to 113, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 0.5 vvm (volume per volume per minute).

115. The method of any one of embodiments 109 to 113, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 1.0 vvm (volume per volume per minute).

116. The method of any one of embodiments 109 to 113, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 2.0 vvm (volume per volume per minute).

117. The method of any one of embodiments 109 to 113, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 3.0 vvm (volume per volume per minute).

118. The method of any one of embodiments 109 to 113, wherein said plurality of yeast cells are in a bioreactor with agitation and aeration rates of about 4.0 vvm (volume per volume per minute).

119. The method of any one of embodiments 109 to 118, wherein said aqueous medium comprises a yeast growth

medium, minimal media, complete supplement media, or greater than 50 g/L glucose and less than 5 g/L of a nitrogen source.

120. The method of any one of embodiments 109 to 119, wherein said allowing is performed by centrifugation or simple sedimentation.

121. The method of any one of embodiments 109 to 120, wherein said genetically modified yeast cell was formed by transforming a yeast cell with a recombinant nucleic acid.

122. The method of any one of embodiments 109 to 120, wherein said genetically modified yeast cell was formed by mutagenizing a yeast cell.

123. The method of any one of embodiments 109 to 120, wherein said genetically modified yeast cell is created by first exposing a yeast cell to a mutagen (e.g. a chemical mutagen, radiation, UV, or a biological mutagen).

124. The method of any one of embodiments 109 to 120, wherein said genetically modified yeast cell was formed by mutagenizing a yeast cell.

125. A method of isolating a yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight from a plurality of yeast cells, comprising allowing a yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) to separate from a population of yeast cells within said plurality of yeast cells by floating above said population of yeast cells within an aqueous medium thereby isolating said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical), wherein said population of yeast cells comprises a lower percentage wt/wt of lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) than said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical).

126. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 30% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

127. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 40% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

128. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 50% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

129. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 60% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

130. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 70% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

131. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 80% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

132. The method of embodiment 125, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises greater than 90% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) in dry weight.

133. The method of one of embodiments 125 to 132, wherein said yeast cell comprising greater than 20% wt/wt lipids, lipid precursors, and/or oleochemicals (e.g., lipid, lipids, lipid precursors, lipid precursor, oleochemicals, or oleochemical) comprises a mutation created by natural genetic drift.

134. The method of any one of embodiments 88 to 95, wherein said growth medium comprises cobalt.

135. The method of any one of embodiments 88 to 95 and 134, wherein said growth medium comprises iron.

136. The method of any one of embodiments 88 to 95 and 134 to 135, wherein said growth medium comprises magnesium.

137. The method of any one of embodiments 88 to 95 and 134 to 136, wherein said growth medium comprises potassium.

138. The method of any one of embodiments 88 to 95 and 134 to 137, wherein said growth medium comprises zinc.

139. The method of any one of embodiments 88 to 95 and 134 to 138, wherein said growth medium comprises nickel.

140. The method of any one of embodiments 88 to 95 and 134 to 139, wherein said growth medium comprises molybdenum.

141. The method of any one of embodiments 88 to 95 and 134 to 140, wherein said growth medium comprises manganese.

142. The method of any one of embodiments 88 to 95 and 134 to 141, wherein said growth medium comprises copper.

143. The method of any one of embodiments 88 to 95 and 134 to 142, wherein said growth medium comprises boron.

V. EXAMPLES

The following examples are meant to illustrate certain embodiments of the invention and not to limit the scope of the invention described herein.

A. MATERIALS AND METHODS

Base Strains and Media.

E. coli strain DH10B was used for cloning and plasmid propagation. DH10B was grown at 37° C. with constant shaking in Luria-Bertani Broth (Teknova) supplemented with 50 μg/ml of ampicillin for plasmid propagation. *Yar-*

rowia lipolytica strain PO1f (ATCC #MYA-2613), a leucine and uracil auxotroph devoid of any secreted protease activity (Madzak et al., 2000), was used as the base strain for all studies. Table 1 contains a list of PO1f derivatives produced in this study. *Y. lipolytica* was cultivated at 30° C. with constant agitation. 2 mL cultures of *Y. lipolytica* used in large-scale screens were grown in a rotary drum (CT-7, New Brunswick Scientific) at speed seven, and larger culture volumes were shaken in flasks at 225 rpm.

YSC media consisted of 20 g/L glucose (Fisher Scientific), 0.79 g/L CSM supplement (MP Biomedicals), and 6.7 g/L Yeast Nitrogen Base w/o amino acids (Becton, Dickinson, and Company). YSC-URA, YSC-LEU, and YSC-LEU-URA media contained 0.77 g/L CSM-Uracil, 0.69 g/L CSM-Leucine, or 0.67 g/L CSM-Leucine-Uracil in place of CSM, respectively. YPD media contained 10 g/L yeast extract (Fisher Scientific), 20 g/L peptone (Fisher Scientific) and 20 g/L glucose, and was often supplemented with 300 μg/ml Hygromycin B (Invitrogen) for knockout selection. Lipid accumulation response towards media formulation was investigated by cultivation in varying concentrations of glucose and nitrogen. These media formulations contained 0.79 g/L CSM, 1.7 g/L Yeast Nitrogen Base w/o amino acid and w/o $(NH_4)_2SO_4$ (Becton, Dickinson, and Company), between 10 g/L and 320 g/L glucose, and between 0.04 g/L and 10 g/L ammonium sulfate—$(NH_4)_2SO_4$ (Fisher Scientific). These media are routinely referred to by their ratio of carbon content (glucose) to nitrogen content (ammonium sulfate). For instance, media containing 80 g/L glucose and 5 g/L ammonium sulfate is called C_{80}:N_5 media. When utilizing alternative carbon sources, glucose was replaced by 80 g/L arabinose, 80 g/L fructose, 80 g/L galactose, 80 g/L glycerol (Fisher Scientific), 80 g/L mannose, 80 g/L maltose 80 g/L ribose, 80 g/L sucrose (Acros Organics), 80 g/L Xylose, or 80 g/L of a saccharide mix resembling the composition of lignocellulosic biomass (57% Glucose, 32% Xylose, 5% Arabinose, 3% Mannose, and 3% Galactose by weight). Solid media for *E. coli* and *Yarrowia lipolytica* was prepared by adding 20 g/L agar (Teknova) to liquid media formulations.

When analyzing the effect of micronutrient supplementation, $CoCl_2$ (15 mg/L), $MgSO_4$ (250 mg/L), KI (15 mg/L), $ZnSO_4.7H_2O$ (20 mg/L), $MnSO_4.H_2O$ (12.5 mg/L), Boric acid (12.5 mg/L), $(NH_4)_2Mo.4H_2O$ (15 mg/L), $NiSO_4.6H_2O$ (12.5 mg/L), $FeSO_4.7H_2O$ (20 mg/L), or $CuSO_4$ (15 mg/L) were added to the stated media formulation. Concentrations given are the final concentrations of the metal ion.

Initial Optimization of Media Formulation for Wildtype and Engineered Strains.

Nitrogen starvation is the accepted impetus for effecting a state of lipid accumulation in oleaginous organisms (Ratledge 2002). As a preliminary analysis of this induction potential, we selected seven media variations wildly variant in their ratios' of carbon content (glucose) to nitrogen content (ammonium sulfate) to assay for their ability to induce lipid accumulation. These media formulations are routinely referred to by this carbon to nitrogen ratio (C:N ratio), i.e., media containing 160 g/L glucose and 0.2 g/L ammonium sulfate is called C_{160}:$N_{0.2}$ media. We cultivated wildtype *Y. lipolytica* strain PO1f in these seven media formulations and assayed for relative lipid (e.g. triacylglyceride) accumulation using nile red fluorescence flow cytometry after 2, 4, 6, and 8 days. We observed a strong correlation between increasing carbon to nitrogen ratio and increased lipid (e.g. triacylglyceride) accumulation that spanned a 10-fold range, and we were able to increase nile red fluorescence levels by three-fold compared to levels induced in standard minimal (YSC) media. Thus, we confirmed the beneficial effect of increasing C:N ratio towards lipid (e.g. triacylglyceride) accumulation in non-engineered *Y. lipolytica*, so we sought to further improve oleo-content with additional media supplementation. In particular, $FeSO_4$ supplementation has been implicated in enabling increased citric acid accumulation in *Y. lipolytica* (Kamzolova et al. 2003), specifically under oxygen limiting conditions. Citric acid and fatty acid accumulation are closely linked in *Y. lipolytica*, so we hypothesized that this iron-responsive citric acid accumulation could also increase downstream lipid (e.g. triacylglyceride) accumulation. To fully analyze the potential benefits of micronutrient addition towards lipid (e.g. triacylglyceride) accumulation (Song et al. 2012; Zhao et al. 2008), we cultivated PO1f in minimal media supplemented with cobalt, magnesium, potassium, zinc, manganese, boric acid, molybdenum, nickel, iron, and copper (FIG. **1**), and saw increased lipid (e.g. triacylglyceride) accumulation with iron, nickel, copper, molybdenum, and zinc. We performed a combinatorial screening of iron, nickel, copper, and molybdenum supplementation to detect cumulative beneficial effects towards increasing cellular lipid content. Triple supplementation with copper, nickel, and iron increased lipid accumulation levels to the highest observed at that time (FIG. **2**).

Thus, manipulating media formulation effectively increased lipid formulation in a wildtype strain, however, the relationship between strain genotype and this effect has yet to be explored. We sought to determine if a strain rationally engineered for increased lipid accumulation would benefit in the same manner from increasing C:N ratio. In our initial attempts to engineer a *Y. lipolytica* strain for increased lipid accumulation, we overexpressed the AMPDp in a ΔPEX10 background to create a strain with a 17-fold increase in nile red fluorescence levels. To determine if genomic modifications could affect differential responses towards media-induced lipid accumulation, we cultivated unmodified PO1f and our engineered high lipid producer in twenty media formulations that varied in carbon and nitrogen levels (Table 3) and analyzed for lipid content with nile red fluorescence flow cytometry after two days, four days, and eight days. Two days was insufficient time to induce lipid accumulation, while lipid accumulation is evident a majority of media formulation for the PO1f ΔPEX10 AMPDp overexpression strain after eight days. Heat graphs of relative fluorescent values illustrate that the PO1f ΔPEX10 AMPDp overexpression strain accumulates lipids efficiently at an optimum value of 80 g/L glucose after 4 days, while PO1f is only slight induced in any condition, most noticeably after six to eight days in $C_{160}N_{0.2}$ media. In general, the 320 g/L glucose condition is too high to induce lipid accumulation effectively, most likely because the high sugar content prevents cell growth. Likewise, formulations 0.04 and 0.2 g/L ammonium sulfate tend to poorly induce lipid accumulation, especially within four days or less. Finally, an optimum C:N ratio of ~10 to 40 can be observed when discounting these highest glucose and lowest ammonium sulfate.

B. CLONING AND TRANSFORMATION PROCEDURES

All restriction enzymes were purchased from New England Biolabs and all digestions were performed according to standard protocols. PCR reactions were set up with recommended conditions using Phusion high fidelity DNA polymerase (Finnzymes), or LongAmp Taq DNA polymerase (New England Biolabs). Ligation reactions were performed

overnight at room temperature using T4 DNA Ligase (Fermentas). Gel extractions were performed using the Fermentas GeneJET extraction kit purchased from Fisher Thermo-Scientific. *E. coli* minipreps were performed using the Zyppy Plasmid Miniprep Kit (Zymo Research Corporation). *E. coli* maxipreps were performed using the Qiagen HiSpeed Plasmid Maxi Kit. Transformation of *E. coli* strains was performed using standard electroporator protocols (Sambrook and Russell, 2001). Large amounts of linearized DNA (>20n), necessary for *Y. lipolytica* PO1f transformation were cleaned and precipitated using a standard phenol:chloroform extraction followed by an ethanol precipitation (Kirby, 1956).

Genomic DNA (gDNA) was extracted from *Y. lipolytica* using the Wizard Genomic DNA Purification kit (Promega). Transformation of *Y. lipolytica* with replicative plasmids was performed using the Zymogen Frozen EZ Yeast Transformation Kit II (Zymo Research Corporation), with plating on YSC-LEU plates. Transformation of *Y. lipolytica* PO1f with linearized cassettes was performed as described previously (Blazeck et al. 2013a), with selection on appropriate plates. All auxotrophic or antibiotic selection markers were flanked with LoxP sites to allow for retrieval of integrated markers the pMCS-UAS1B$_{16}$-TEF-Cre replicative vector (Blazeck et al. 2013a).

Plasmid Construction.

Primer sequences can be found in the Table 2. All *Y. lipolytica* episomal plasmids were centromeric, replicative vectors derived from plasmid pS116-Cen1-1(227) (Yamane et al. 2008) after it had been modified to include a multi-cloning site, a hrGFP green fluorescent reporter gene (pIRES-hrGFP, Agilent) driven by the strong UAS1B$_{16}$-TEF promoter (Blazeck et al. 2011), and a cycl terminator (Mumberg et al. 1995) to create plasmid pMCS-UAS1B$_{16}$-TEF-hrGFP. Integrative plasmids were derived from plasmids pUC-S1-UAS1B$_{16}$-Leum or pUC-S1-UAS1B$_{16}$-TEF (Blazeck et al. 2013a) that contained 5' and 3' rDNA integrative sequences surrounding the following elements—(from 5' to 3') a uracil section marker surrounded by LoxP sites for marker retrieval, the strong UAS1B$_{16}$-Leum or UAS1B$_{16}$-TEF promoter, AscI and Pad restriction enzyme sites for gene insertion, and a XPR2 minimal terminator. These integrative plasmids were also designed to contain two identical NotI restriction enzyme sites directly outside of the rDNA regions so that plasmid linearization would simultaneously remove *E. coli* pUC19-based DNA. All plasmids containing expression cassettes were sequenced confirmed before transformation into *Y. lipolytica*.

Construction of Episomal Expression Cassettes:

The following genes were PCR amplified from *Y. lipolytica* PO1f gDNA and inserted into vector pMCS-UAS1B$_{16}$-TEF-hrGFP in place of hrGFP with an AscI/PacI digest: AMPD, ACL subunit 1 (ACL1), ACL subunit 2 (ACL2), MEA1, DGA1, DGA2, the TupI general transcriptional repressor (Morin et al. 2011), and the HAC1 basic leucine zipper transcription factor involved in unfolded protein response (Morin et al. 2011) with primers, respectively. This formed plasmids pMCS-UAS1B$_{16}$-TEF-AMPD, pMCS-UAS1B$_{16}$-TEF-ACL1, pMCS-UAS1B$_{16}$-TEF-ACL2, pMCS-UAS1B$_{16}$-TEF-MEA, pMCS-UAS1B$_{16}$-TEF-DGA1, pMCS-UAS1B$_{16}$-TEF-DGA2, pMCS-UAS1B$_{16}$-TEF-TUP1, and pMCS-UAS1B$_{16}$-TEF-HAC1.

Construction of Integrative Expression Cassettes:

The following genes were gel extracted from the previously constructed episomal expression vectors and inserted into vector pUC-S1-UAS1B$_{16}$-TEF with an AscI/PacI digest: AMPD, ACL subunit 1 (ACL1), ACL subunit 2 (ACL2), MEA1, DGA1, and DGA2. This formed plasmids pUC-S1-UAS1B$_{16}$-TEF-AMPD, pUC-S1-UAS1B$_{16}$-TEF-ACL1, pUC-S1-UAS1B$_{16}$-TEF-ACL2, pUC-S1-UAS1B$_{16}$-TEF-MEA1, and pUC-S1-UAS1B$_{16}$-TEF-DGA1, and pUC-S1-UAS1B$_{16}$-TEF-DGA2. The loxP-surrounded uracil marker of these integrative plasmids was replaced with a loxP-surrounded leucine marker to enable integrative selection with leucine auxotrophy and co-expression of two enzymes without marker retrieval. These leucine marker integrative plasmids were dubbed plasmids pUC-S2-UAS1B$_{16}$-TEF-AMPD, pUC-S2-UAS1B$_{16}$-TEF-ACL1, pUC-S2-UAS1B$_{16}$-TEF-ACL2, pUC-S2-UAS1B$_{16}$-TEF-MEA1, and pUC-S2-UAS1B$_{16}$-TEF-DGA1, and pUC-S2-UAS1B$_{16}$-TEF-DGA2.

ACL1 and ACL2 were similarly inserted into pUC-S1-UAS1B$_{16}$-Leum with primers, respectively, to form plasmids pUC-S1-UAS1B$_{16}$-Leum-ACL1 and pUC-S1-UAS1B$_{16}$-Leum-ACL2.

Strain Construction.

All strains were confirmed through gDNA extraction and PCR confirmation and are listed in Table 1. We previously constructed two markerless single-gene deletion strains in the *Y. lipolytica* PO1f background, PO1f-Δmfe1 and PO1f-Δpex10, deficient in their β-oxidation and peroxisomal biogenesis capacity, respectively (Blazeck et al. 2013a). Following our previous protocol, the PEX10 gene was deleted from strain PO1f-Δmfe1 to form the markerless double mutant PO1f-Δmfe1-Δpex10. These four strains, PO1f, PO1f-Δmfe1, PO1f-Δpex10, and PO1f-Δmfe1-Δpex10 were utilized as backgrounds for single and double overexpression of the AMPD, ACL1, ACL2, MEA, DGA1, and DGA2 genes, including variation in selective marker utilized, i.e., leucine (S2 integrative cassette or pMCS episomal cassette) vs. uracil (S1 integrative cassette). S2 and S1 integrative cassettes were linearized, transformed into our four background strains, and selected for on appropriate dropout plates. Table 1 contains a list of rationally engineered strains derived in this manner. ORF-less plasmids pUC-S1-UAS1B$_{16}$-TEF and pUC-S1-UAS1B$_{16}$-TEF were utilized to create strains lacking leucine, uracil, or both leucine and uracil auxotrophies, dubbed S1-Ø, S2-Ø, and S1-S2-Ø (Table 1).

Combinatorial Genome Engineering.

Prior engineering efforts have successfully increased lipid accumulation in *Y. lipolytica* by manipulating fatty acid, lipid, or central carbon metabolism, but no attempt has been made to simultaneously alter these metabolic functionalities (Beopoulos et al. 2008; Dulermo and Nicaud 2011; Tai and Stephanopoulos 2013). We sought to concurrently control these aspects of lipid synthesis by overexpressing three enzymes that control metabolic flux from central carbon metabolism into fatty acid synthesis (AMPDp, ACLp, and MEA1p) or two isozymes that control lipid synthesis (DGA1p and DGA2p) in four genomic backgrounds with altered fatty acid catabolic ability. These four genomic backgrounds included the PO1f (WT) strain, a PO1f MFE1 deletion strain (ΔMFE1), a PO1f PEX10 deletion strain (ΔPEX10), and a MFE1 PEX10 double knockout strain (ΔPEX10ΔMFE1). The majority of enzymatic overexpressions were driven by the high strength UAS1B$_{16}$-TEF constitutive promoter (Blazeck et al. 2011), were integrated into *Y. lipolytica* 's genomic rDNA repeats (Blazeck et al. 2013a; Ledall et al. 1994), and alleviated either PO1f s uracil or leucine auxotrophy. In our previous work, we noticed that alleviation of the leucine auxotrophy tended to increase lipid (e.g. triacylglyceride) accumulation far more than alleviation of the uracil auxotrophy. Therefore, nearly identical

strains were routinely created differing only in the marker utilized to integrate an enzymatic overexpression cassette, enabling either uracil synthesis (S1) or leucine synthesis (S2). Initial overexpressions of the DGA1p and DGA2p enzymes occurred episomally with an identical $UAS1B_{16}$-TEF promoter on a leucine-marker containing plasmid, though final strain construction entailed integrating these cassettes. Strain names included background (WT, ΔMFE1, ΔPEX10, or ΔPEX10ΔMFE1), markers used (S1, S2, S1-S2, or pMCS), and enzymes overexpressed (AMPD, MEA, ACL1, ACL2, DGA1, DGA2) so a strain overexpressing the AMPDp enzyme with a leucine marker in the ΔPEX10ΔMFE1 background is called ΔPEX10ΔMFE1 S2-AMPD. S1-Ø, S2-Ø, and S1, 2-Ø refer to strains without protein overexpressions but with uracil, leucine, or uracil+ leucine auxotrophies alleviated. ACL1p and ACL2p form a heterodimer in vivo so were tested as concurrent overexpressions.

Our combinatorial approach generated over 46 distinct genotypes that were analyzed for lipid (e.g. triacylglyceride) accumulation with nile red fluorescence flow cytometry after four days growth in $C_{80}N_5$ media and produced a large range in lipid (e.g. triacylglyceride) accumulation ability, culminating in a 60-fold improvement over PO1f WT control (FIG. **3**). We saw that the deletion of the pex10 peroxisomal biogenesis transcription factor combined with overexpression of a acyl-CoA:diacylglycerol acyltransferase (DGA1 or DGA2) are essential for the highest lipid (e.g. triacylglyceride) production (FIG. **3**). When comparing ammonia depletion in PO1f WT and our highest lipid producer, ΔPEX10ΔMFE1 pMCSDGA1, we observed a pronounced reduction in steady state nitrogen concentration in the ΔPEX10ΔMFE1 pMCSDGA1 strain. We saw a very noticeable correlation between the ability to synthesize leucine and lipid (e.g. triacylglyceride) accumulation ability, with an average increase of five fold in lipid content between comparable strains with and without a leucine marker present (FIG. **4**). Deletion of mfe1 drastically reduced this increase in lipid (e.g. triacylglyceride) content. ΔMFE1 and ΔPEX10ΔMFE1 saw only a 1.42 fold and 2.58 fold increases in lipid (e.g. triacylglyceride) content granted from the capacity to synthesize leucine compared to 8.16 and 7.45 fold increases in WT and ΔPEX10 backgrounds (FIG. **4**). In three of our four backgrounds, DGA1p outperformed DGA2p (FIG. **3**); WT pMCSDGA2 was not included, but subsequent testing showed WT pMCSDGA1 to give higher lipid (e.g. triacylglyceride) levels than WT pMCSDGA2. Overall, fluorescence levels were highest in the ΔPEX10 and ΔPEX10ΔMFE1 backgrounds (~3-fold WT), and lowest in the ΔMFE1 background (~65% of WT), although mfe1 deletion has been shown to increase lipid (e.g. triacylglyceride) accumulation in media containing higher C:N ratio in eight day cultivation periods (Blazeck et al. 2013a). Because mfe1 deletion should further inhibit fatty acid degradation in the ΔPEX10ΔMFE1 background in long-scale fermentations, the DGA1p was integrated into the ΔPEX10ΔMFE1 background with S2 cassette and a S1-Ø to form our final fully heterotrophic rationally engineered strain. This ΔPEX10ΔMFE1 S1-S2-DGA1 strain displayed similar lipid (e.g. triacylglyceride) content to strains containing episomally expressed DGA1p and could accumulate lipids (e.g. triacylglyceride) effectively without any amino acid supplementation (Table 4) and yielded are highest % lipid (e.g. triacylglyceride) content of 32% dry cell weight for a total of 1.32 g/L. Furthermore, we saw no significant difference in LEU3 or DGA1 mRNA levels between these two strains. During bioreactor runs, these strains are able to produce significant amounts of lipids and cells exhibit 88% by dry cell weight lipids. Improved lipid production with one of the highest producing strains, ΔPEX10ΔMFE1-S1-S2-DGA1 in a bioreactor. Lipid levels have reached 22 g/L in media containing only 80 g/L glucose, 5 g/L ammonium sulfate, and 1.7 g/L Yeast Nitrogen Base (without amino acids or ammonium sulfate). Increasing dissolved oxygen content and maintaining pH at or above 5.0 enabled this yield. This represents ~86% of the theoretical yield. Furthermore, in these strains, we identify the presence of unique C17 fatty acids (FIG. **15**).

Complex control of cellular processes, like lipid accumulation, is coordinated by transcription factors that regulate gene networks. In particular, the TupI general transcriptional repressor and the Had leucine zipper transcription factor involved in unfolded protein response have been shown to be upregulated in lipid (e.g. triacylglyceride) accumulation cell states (Morin et al. 2011). However, overexpression of these two proteins decreased lipid (e.g. triacylglyceride) accumulation in the PO1f WT background.

Dissection of Genotype-Dependence Towards Media Induction.

We more fully examined how C:N ratio and genotype interacted towards enabling lipid (e.g. triacylglyceride) accumulate on a larger scale by examining the response of twelve strains grown in thirteen different C:N ratios (Table 5). We were pleased to observe a strong tendency towards high lipid (e.g. triacylglyceride) levels in most high producers at a single media formulation—$C_{80}N_5$ (FIG. **5-8**), allowing us to pinpoint a formulation for later use. Two trends stand out—(1) The 0.2 g/L ammonium sulfate formulations rarely enable lipid (e.g. triacylglyceride) accumulation, so that (2) the difference in induction from media containing 1 g/L and 5 g/L is slight, making glucose concentration seem more important towards increasing content than nitrogen content (after a certain threshold is reached).

Lipid Accumulation on Multiple Carbon Sources.

Viability of lipid (e.g. triacylglyceride) production depends on the capacity to fully convert all sugars from lignocellulosic biomass to lipids or to use carbon from industrial waste streams for lipid production. We analyzed the ability PO1f WT, ΔPEX10 S1-MEA, ΔPEX10 S2-AMPD, ΔPEX10ΔMFE1 S2-DGA1, and ΔPEX10ΔMFE pMCSDGA1 to generate lipids (e.g. triacylglyceride) when utilizing glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, or a lignocellulosic sugar blend as their carbon source (FIG. **9**). ΔPEX10ΔMFE1 S2-DGA1 and ΔPEX10ΔMFE1 pMCSDGA1 generated the highest lipid (e.g. triacylglyceride) content across the board under conditions tested, and all engineered strains demonstrated the capacity to utilize each carbon source for lipid (e.g. triacylglyceride) production. Glucose, mannose, and the lignocellulosic saccharide blend were utilized easiest while ribose utilizations generated the least lipid (e.g. triacylglyceride) content of the conditions tested. The PO1f WT and ΔPEX10ΔMFE1 S2-DGA1 strain were tested to determine if decreasing carbon content or increasing initial inoculum amount could increase xylose-generate lipid (e.g. triacylglyceride) accumulation. Increasing xylose concentration and decreasing inoculum amount increased lipid (e.g. triacylglyceride) content in the ΔPEX10ΔMFE1 S2-DGA1 strain, while little difference was noticeable in the PO1f WT strain. However, PO1f WT demonstrated a surprising capacity to utilize pure glycerol for lipid (e.g. triacylglyceride) generation.

Isolation of a Novel MGA2 Mutation with Whole Genome Sequencing.

During the screening of a gDNA overexpression library intended to increase *Y. lipolytica*'s lipid (e.g. triacylglyceride) production, we isolated a strain, dubbed L36, with incredible lipid (e.g. triacylglyceride) accumulation ability (FIG. **10**). L36's lipid (e.g. triacylglyceride) production could be enhanced with micronutrient supplementation (FIG. **10**). Complete sequencing of the L36 genome revealed a missense mutation in the MGA2 lipid synthesis regulator (MGA2G643R) as the most likely potential cause for L36's lipid (e.g. triacylglyceride) production capacity. Overexpression of a truncated MGA2p in a PO1f WT background reconstituted 58% of the observed L36 phenotype.

Directed Evolution with EMS Mutagenesis to Increase Lipid Accumulation

Direct evolution is commonly utilized to increase growth rate or to decrease sensitivity to a toxic metabolite. However, directed evolution has never been evaluated as a tool to increase lipid (e.g. triacylglyceride) production in oleaginous organisms. As evidenced by the isolation of strain L36, it is likely that *Y. lipolytica* is amenable to this approach. We subjected both L36 (FIG. **11**) and ΔPEX10ΔMFE1 S2-DGA1 to EMS mutagenesis followed by serial selection via subculturing and then nile red staining. Both backgrounds proved highly responsive towards the directed evolution approach, and an increase in fluorescence with a large increase in final cell concentration (Table 6).

Besides the minerals, during the experiments, we also observed a critical phenotype for lipid (e.g. triacylglyceride) production in *Yarrowia lipolytica*: the lipid (e.g. triacylglyceride) de novo lipid (e.g. triacylglyceride) accumulation is close related to leucine biosynthesis pathway. A 5 fold lipid (e.g. triacylglyceride) level increase was achieved with strain harboring complete LEU biosynthesis pathway comparing to the one without complete pathway. Although this phenotype has been reported with engineered *Saccharomyces cerevisiae* (Kamisaka et al. 2007), this is the first observation in oleaginous yeast to our best knowledge. Understanding of this phenotype could be essential to understand the basic differences between oleaginous microbes and normal ones. However, to the date, the fundamental reason is still missing. Two possible routes may contribute to this, one is through TOR pathway (Kim and Guan 2011; Laplante and Sabatini 2009) and the other one is through leucine degradation and ketone body generation (Endemann et al. 1982). Either pathway heavily interacts with the whole cell metabolism which requires deep analysis to reveal the true mechanism behind.

Engineering with Known: Biosynthesis pathways and basic regulations. Rational systematic engineering *Yarrowia lipolytica* for high lipid production. Engineering with Unknown: Pathway interactions and complex regulation networks. Engineering lipid production in *Yarrowia lipolytica* through Inverse combinatorial metabolic Engineering. Confirmed lipid enhancers include DGA1 (Diacylglycerol acyltransferase) 300% improvement, MRM2 (Mitochondrial 2' O-ribose methyltransferase) 25% improvement, MGMT (O-6-methylguanine-DNA methyltransferase) 15% improvement.

C. FATTY ACID CHARACTERIZATION BY NILE RED STAINING COUPLE WITH FLOW CYTOMETRY OR FLUORESCENCE MICROSCOPY

Nile Red is commonly utilized to stain oleaginous cellular material, and can be coupled with fluorescence flow cytometry to gauge relative lipid content (Greenspan et al. 1985). *Y. lipolytica* strains were routinely inoculated from glycerol stock in biological triplicate in appropriate media for 72 hours at 30° C. with shaking Cell concentrations were normalized to a specific OD_{600} for reinoculation in fresh media and further incubation. In general, 2 mL cultures were inoculated to an OD_{600}=2.5, and larger volume cultures were inoculated to an OD_{600}=0.1. Cultures were incubated for two to eight days at 30° C. with constant agitation. 2 mL cultures were incubated in a rotary drum (CT-7, New Brunswick Scientific) at speed seven and flasks were shaken at 225 rpm in a standing incubator. To harvest, one OD_{600} unit of each cultures was spun down at 1000 g for three minutes and resuspended in 500 μL Phosphate Buffered Saline solution (PBS) (Sigma Aldrich). 6 μL of 1 mM Nile Red (dissolved in DMSO) was added, and then cells were incubated in the dark at room temperature for 15 minutes. Cells were spun down at 1000 g for three minutes, resuspended in 800 μL ice cold water, spun down again, and resuspended again in 800 μL ice cold water. 300 μL of stained cells were added to 1 ml ice cold water and tested with a FACS Fortessa (BD Biosciences), a voltage of 350, a 10,000 cell count, a forward scatter of 125, a side scatter of 125, and the 535LP and 585/42BP filters for fluorescence detection using the GFP fluorochrome. Samples were kept on ice and in the dark during the test and the data was analyzed using FlowJo software (Tree Star Inc., Ashland, Oreg.) to compute mean fluorescence values. Day-to-day variability was mitigated by analyzing all comparable strains on the same day. An average fluorescence and standard deviation were calculated from the mean values of biological replicates. Stained cells were routinely examined with fluorescence microscopy under a 100× oil immersion objective using the FITC channel on an Axiovert 200M microscope (Zeiss).

D. LIPID QUANTIFICATION AND FATTY ACID PROFILE ANALYSIS

Lipids from ~20-30 OD_{600} equivalents were extracted following the procedure described by (Folch et al. 1957) and modified for yeast (Schneiter and Daum 2006). Dried lipids were transesterified with N-tert-Butyldimethylsilyl-N-methyltrifluoroacetamide (Sigma-Aldrich) following the procedure of (Paik et al., 2009), and 2 μL samples were injected into a GC-FID (Agilent Technologies 6890 Network GC System) equipped with an Agilent HP-5 column (5% phenyl-95% methylsiloxane—product number 19091J-413) to analyze fatty acid fractions. Briefly, the following settings were used: Detector Temp=300° C., He Flow=1.0 mL/min, Oven Temp=80° C. for 2 min, increased at 30° C./min to 200° C., increased at 2° C./min to 229° C., increased at 1° C./min to 232° C., increased at 50° C./min to 325° C. Fatty acid standards for C16:0 palmitic acid, C16:1(n-7) palmitoleic acid, C18:0 stearic acid, C18:1 (n-9) oleic acid, and C18:2 (n-6) linoleic acid were purchased from Sigma-Aldrich, transesterified, and analyzed by GC to identify fatty acid peaks.

E. CITRIC ACID QUANTIFICATION

A 2 mL culture sample was pelleted down for 5 minutes at 3000×g, and the supernatant was filtered using a 0.2 mm syringe filter (Corning Incorporated). Filtered supernatant was analyzed with a HPLC Ultimate 3000 (Dionex) and a Zorbax SB-Aq column (Agilent Technologies). A 2.0 μL injection volume was used in a mobile phase composed of a 99.5:0.5 ratio of 25 mM potassium phosphate buffer (pH=2.0) to acetonitrile with a flow rate of 1.25 mL/min.

The column temperature was maintained at 30° C. and UV-Vis absorption was measured at 210 nm. A citric acid standard (Sigma-Aldrich) was used to detect and quantify citric acid production.

F. EMS MUTAGENESIS AND ISOLATION OF HIGH LIPID PRODUCING STRAINS

10 OD units from cultures grown overnight were spun down in sterile microcentrifuge tubes at 5000 g for 10 seconds. Cell pellets were resuspended in 1 mL H_2O, repelleted, and resuspended in 1 mL PBS. Two samples were spun down from each culture, one for EMS mutagenesis (30 μl of EMS added) and one as a control to determine the prevalence of spontaneous beneficial mutation (no EMS added). Cells were incubated for 1 hr at 30° C., with agitation, pelleted and resuspended in 200 μl of 5% sodium thiosulfate, transferred to fresh microcentrifuge tubes, washed twice in 200 μl of 5% sodium thiosulfate, and resuspended in 1 mL H_2O. Cells were then grown to stationary phase in YSC media, and then reinoculated at an OD_{600}=2.5 in 1 mL $C_{80}N_5$ media and grown for four days. Three to six serial transfers of the cell cultures followed in which the 1 mL cultures were spun down at 1000 g for two minutes, and the top 200 μL of the supernatant was transferred to 1 mL of fresh YSC media and allowed to grow to stationary phase before again spinning down and transferring. Final cultures (top 200 μL after spin down) were plated on YSC plates containing 0.01 mM Nile Red. After four days, high lipid producers were selected by viewing plates under a blue fluorescent light and picking colonies with brighter pink fluorescent color. Lipid amount was determined by coupling Nile Red staining with flow cytometry as described above.

The EMS mutagenesis procedures were performed following the protocol described by Winston (Winston 2001). Briefly, an overnight culture was cultivated to OD about 10. Cells were then harvested, washed and resuspended with 0.1 M sodium phosphate buffer (pH 7). 30 μl of EMS were added and incubated with unmutagenized control for 1 hr at 30° C., with agitation. The cells were then washed with 5% sodium thiosulfate and ready for serial transfer experiments to enrich the high lipid population. The EMS treated cells and unmutagenized cells were first cultured YSC media for 72 hours and then cultured in high glucose media with starting OD at 2.5 for 96 hours. The cells were centrifuged down with 100 g, the unclear supernatant, which contains high lipid accumulation strains, was used as seed for another round of cultivation. After five rounds of transfer, the cells were plated on Nile Red YSC plate to facilitate the isolation of high lipid production strains. Individual colonies were picked from the EMS treated cells as well as unmutagenized cells for characterization.

Characterization of EMS mutagenesis and floating cell transfer selection procedure selected strain E13 and E26. Second generation sequencing platform illumina paired ended sequencing PE 2×100 were performed with genomic DNA extracted from strain E26, E13 as well as PO1f by Genomic Sequencing and Analysis Facility in The University of Texas at Austin. 6424381 reads for strain E26 and 6565093 reads for strain E13 were collected from illumina HiSeq, which lead to a coverage approximately 65×. The Illumina reads were mapped to the CLIB122 genome using BWA (Li and Durbin 2009) and analyzed with Samtools (Beopoulos, Cescut et al. 2009) and BEDTools (Quinlan and Hall 2010). The SNPs identified were then filtered with SnpSift with QUAL>=30 (Pablo, Viral et al. 2012) The SNPs identified from PO1f, EMS26 and EMS13 were compared to extract the authentic SNPs in EMS26 and EMS13. The identified SNPs were then visualized in the IGV genome visualization software to validate as well as study the location of the SNPs in the genome due to the high false error rate in SNP calling process (Liu, Guo et al. 2012).

Information on identified targets in E26 and E13 strains following mutagenesis. Succinate semialdehyde dehydrogenase (SSADH), which coverts succinate semialdehyde to succinate after UGA1,4-aminobutyrate aminotransferase, deaminates GABA to succinate (Ramos, El Guezzar et al. 1985). Higher levels of accumulation of α-ketoglutarate were found in uga2 mutants in *Saccharomyces cerevisiae* (Cao, Barbosa et al. 2013) (3VZ1; 3VZ3). In the same time, lower levels of succinic acid (more than 5 fold decrease) were also identified in the yeast (Kamei, Tamura et al. 2011). The identified mutation in UGA2 in sequenced strains of Proline 209 is a highly conserved residual and close to a hydrogen bond forming Serine (Yuan, Yin et al. 2013). GABA metabolism is closely related to nitrogen assimilation in yeast and nitrogen limitation has been studied as a key function for triggering lipogenesis in *Yarrowia lipolytica* (Beopoulos, Cescut et al. 2009). Nitrogen sources have also been proven as an important factor for lipid accumulation inside cells (Evans and Ratledge 1984). A relationship between GABA metabolism and the TOR pathway, an important signaling pathway for lipid accumulation (Blazeck, Hill et al. 2014), has also been suggested (Cardenas, Cutler et al. 1999; Staschke, Dey et al. 2010). YALI0E17215 g codes for a protein with similarity to *Saccharomyces cerevisiae* RME1, which is a zinc finger protein involved in the control of meiosis (Covitz, Herskowitz et al. 1991). A similar protein has shown significant levels of increase in mRNA levels in a lipid accumulation-improved snf1 mutant in *Yarrowia lipolytica* (Xue, Sharpe et al. 2013). YALI0E20449p shows limited similarity to known protein sequences except the homeodomain, a DNA binding domain involved in the transcriptional regulation of key eukaryotic developmental processes, which shows similarities. Mutation V289G in YALI0E20449p exists outside of the homeodomain. *S. cerevisiae* homeodomain protein yox1 is able to bind leucine-tRNA (Kaufmann 1993) and leucine-tRNA synthase plays an important role (Han, Jeong et al. 2012) in the TOR pathway. Leucine has been suggested to be a critical lipid production enhancer (Blazeck, Hill et al. 2014). Recently, IRC20 containing a Snf2/Swi2 family ATPase/helicase and a RING finger domain, has been shown to be an E3 ubiquitin ligase (Richardson, Gardner et al. 2013) as well as a putative helicase. OSH6 overexpression has shown lifespan extension effect on yeast by increasing vacuole fusion and may relate to TORC (Gebre, Connor et al. 2012).

G. REFERENCES

Alper H, Stephanopoulos G. 2009. Engineering for biofuels: exploiting innate microbial capacity or importing biosynthetic potential? Nature Reviews Microbiology 7(10): 715-723. Andre A, Chatzifragkou A, Diamantopoulou P, Sarris D, Philippoussis A, Galiotou-Panayotou M, Komaitis M, Papanikolaou S. 2009. Biotechnological conversions of bio-diesel-derived crude glycerol by *Yarrowia lipolytica* strains. Engineering in Life Sciences 9(6):468-478. Barth G, Gaillardin C. 1996. *Yarrowia lipolytica*. In: Wolf K, editor. Nonconventional Yeasts in Biotechnology: A Handbook: Springer. p 313-388. Beopoulos A, Cescut J, Haddouche R, Uribelarrea J L, Molina-Jouve C, Nicaud J M. 2009a.

Yarrowia lipolytica as a model for bio-oil production. Progress in Lipid Research 48(6):375-387. Beopoulos A, Chardot T, Nicaud J M. 2009b. *Yarrowia lipolytica*: A model and a tool to understand the mechanisms implicated in lipid accumulation. Biochimie 91(6):692-696. Beopoulos A, Haddouche R, Kabran P, Dulermo T, Chardot T, Nicaud J M. 2012. Identification and characterization of DGA2, an acyltransferase of the DGAT1 acyl-CoA:diacylglycerol acyltransferase family in the oleaginous yeast *Yarrowia lipolytica*. New insights into the storage lipid metabolism of oleaginous yeasts. Applied Microbiology and Biotechnology 93(4):1523-1537. Beopoulos A, Mrozova Z, Thevenieau F, Le Dall M T, Hapala I, Papanikolaou S, Chardot T, Nicaud J M. 2008. Control of Lipid Accumulation in the Yeast *Yarrowia lipolytica*. Applied and Environmental Microbiology 74(24):7779-7789. Beopoulos A, Nicaud J M, Gaillardin C. 2011. An overview of lipid metabolism in yeasts and its impact on biotechnological processes. Applied Microbiology and Biotechnology 90(4):1193-1206. Blazeck J, Liu L, Knight R, Alper H. 2013a. Heterologous production of pentane in the oleaginous yeast *Yarrowia lipolytica*. Journal of Biotechnology. Blazeck J, Liu L, Redden H, Alper H. 2011. Tuning Gene Expression in *Yarrowia lipolytica* by a Hybrid Promoter Approach. Applied and Environmental Microbiology 77(22):7905-7914 Blazeck J, Reed B, Garg R, Gerstner R, Pan A, Agarwala V, Alper H. 2013b. Generalizing a hybrid synthetic promoter approach in *Yarrowia lipolytica*. Appl Microbiol Biotechnol 97(7): 3037-3052. Christophe G, Kumar V, Nouaille R, Gaudet G, Fontanille P, Pandey A, Soccol C R, Larroche C. 2012. Recent Developments in Microbial Oils Production: a Possible Alternative to Vegetable Oils for Biodiesel Without Competition with Human Food? Brazilian Archives of Biology and Technology 55(1):29-46. Chuang L T, Chen D C, Nicaud J M, Madzak C, Chen Y H, Huang Y S. 2010. Co-expression of heterologous desaturase genes in *Yarrowia lipolytica*. New Biotechnology 27(4):277-282. Curran K A, Leavitt J, Karim A, Alper H S. 2013. Metabolic engineering of muconic acid production in *Saccharomyces cerevisiae*. Metabolic Engineering 15:55-66. Dujon B, Sherman D, Fischer G, Durrens P, Casaregola S, Lafontaine I, de Montigny J, Marck C, Neuveglise C, Talla E and others. 2004. Genome evolution in yeasts. Nature 430(6995):35-44. Dulermo T, Nicaud J M. 2011. Involvement of the G3P shuttle and beta-oxidation pathway in the control of TAG synthesis and lipid accumulation in *Yarrowia lipolytica*. Metabolic Engineering 13(5):482-491. Elshahed M S. 2010. Microbiological aspects of biofuel production: Current status and future directions. Journal of Advanced Research 1(103-111). Endemann G, Goetz P G, Edmond J, Brunengraber H. 1982. Lipogenesis from ketone bodies in the isolated perfused rat liver. Evidence for the cytosolic activation of acetoacetate. Journal of Biological Chemistry 257(7):3434-3440. Fickers P, Benetti P H, Wache Y, Marty A, Mauersberger S, Smit M S, Nicaud J M. 2005. Hydrophobic substrate utilisation by the yeast *Yarrowia lipolytica*, and its potential applications. Fems Yeast Research 5(6-7):527-543. Fickers P, Le Dall M T, Gaillardin C, Thonart P, Nicaud J M. 2003. New disruption cassettes for rapid gene disruption and marker rescue in the yeast *Yarrowia lipolytica*. Journal of Microbiological Methods 55(3):727-737. Folch J, Lees M, Stanley G H S. 1957. A simple method for the isolation and purification of total lipids from animal tissues. Journal of Biological Chemistry 226(1):497-509. Greenspan P, Mayer E P, Fowler S D. 1985. Nile red: a selective fluoroscent stain for intracelluluar lipid droplets. Journal of Cell Biology 100(3):965-973. Groenewald M, Boekhout T, Neuveglise C, Gaillardin C, van Dijck P W M, Wyss M. 2013. *Yarrowia lipolytica*: Safety assessment of an oleaginous yeast with a great industrial potential. Critical Reviews in Microbiology:1-20. Gruzdienė D, Anelauskaitė E. 2011. Chemical composition and stability of rapeseed oil produced from various cultivars grown in Lithuania. 1 lth International Congress on Engineering and Food (ICEF) Athens, Greece. Hammond E G, Johnson L A, Su C, Wang T, White P J. 2005. Soybean Oil. In: Shahidi F, editor. Bailey's Industrial Oil and Fat Products. 6 ed: John Wiley & Sons, Inc. p 577-653. Hill J, Nelson E, Tilman D, Polasky S, Tiffany D. 2006. Environmental, economic, and energetic costs and benefits of biodiesel and ethanol biofuels. Proceedings of the National Academy of Sciences of the United States of America 103(30):11206-11210. Hong S, Sharpe P, Xue Z, Yadav N, Zhu Q; E. I. du Pont de Nemours and Company (Wilmington, Del.), assignee. 2012. Peroxisome biogenesis factor protein (pex) disruptions for altering the content of polyunsaturated fatty acids and the total lipid content in oleaginous eukaryotic organisms. USA. Juretzek T, Le Dall M T, Mauersberger S, Gaillardin C, Barth G, Nicaud J M. 2001. Vectors for gene expression and amplification in the yeast *Yarrowia lipolytica*. Yeast 18(2):97-113. Kamisaka Y, Tomita N, Kimura K, Kainou K, Uemura H. 2007. DGA1 (diacylglycerol acyltransferase gene) overexpression and leucine biosynthesis significantly increase lipid accumulation in the delta snf2 disruptant of *Saccharomyces cerevisiae*. Biochemical Journal 408:61-68. Kamzolova S V, Shishkanova N V, Morgunov I G, Finogenova T V. 2003. Oxygen requirements for growth and citric acid production of *Yarrowia lipolytica*. Fems Yeast Research 3(2):217-222. Kennedy E P. 1961. Biosynthesis of Complex Lipids. Federation Proceedings 20(4):934-940. Kim J, Guan K L. 2011. Amino Acid Signaling in TOR Activation. In: Kornberg R D, Raetz C R H, Rothman J E, Thorner J W, editors Annual Review of Biochemistry, Vol 80. p 1001-1032. Kirstine W V, Galbally I E. 2012. Ethanol in the Environment: A Critical Review of Its Roles as a Natural Product, a Biofuel, and a Potential Environmental Pollutant. Critical Reviews in Environmental Science and Technology 42(16):1735-1779. Laplante M, Sabatini D M. 2009. An Emerging Role of mTOR in Lipid Biosynthesis. Current Biology 19(22):R1046-R1052. Ledall M T, Nicaud J M, Gaillardin C. 1994. Multiple-copy integration in the yeast *Yarrowia lipolytica*. Current Genetics 26(1):38-44. Li Q, Du W, Liu D H. 2008. Perspectives of microbial oils for biodiesel production. Applied Microbiology and Biotechnology 80(5):749-756. Madzak C, Gaillardin C, Beckerich J M. 2004. Heterologous protein expression and secretion in the non-conventional yeast *Yarrowia lipolytica*: a review. Journal of Biotechnology 109(1-2):63-81. Makri A, Fakas S, Aggelis G. 2010. Metabolic activities of biotechnological interest in *Yarrowia lipolytica* grown on glycerol in repeated batch cultures. Bioresource Technology 101(7):2351-2358. Matsuoka M, Matsubara M, Daidoh H, Imanaka T, Uchida K, Aiba S. 1993. Analysis of regions essential for the function of chromosomal replicator sequences from *Yarrowia lipolytica*. Molecular & General Genetics 237(3):327-333. Morin N, Cescut J, Beopoulos A, Lelandais G, Le Berre V, Uribelarrea J L, Molina-Jouve C, Nicaud J M. 2011. Transcriptomic Analyses during the Transition from Biomass Production to Lipid Accumulation in the Oleaginous Yeast *Yarrowia lipolytica*. Plos One 6(11): 13. Mumberg D, Muller R, Funk M. 1995. Yeast vectors for

the controlled expression of heterologous proteins in different genetic backgrounds. Gene 156(1):119-22. Papanikolaou S, Aggelis G. 2002. Lipid production by *Yarrowia lipolytica* growing on industrial glycerol in a single-stage continuous culture. Bioresource Technology 82(1):43-49. Ratledge C. 2002. Regulation of lipid accumulation in oleaginous micro-organisms. Biochemical Society Transactions 30:1047-1050. Rywinska A, Juszczyk P, Wojtatowicz M, Robak M, Lazar Z, Tomaszewska L, Rymowicz W. 2013. Glycerol as a promising substrate for *Yarrowia lipolytica* biotechnological applications. Biomass & Bioenergy 48:148-166. Rywinska A, Musial I, Rymowicz W, Zarowska B, Boruczkowski T. 2012. Effect of agitation and aeration on the citric acid production by *Yarrowia lipolytica* grown on glycerol. Preparative Biochemistry & Biotechnology 42(3): 279-291. Schirmer A, Rude M A, Li X Z, Popova E, del Cardayre S B. 2010. Microbial Biosynthesis of Alkanes. Science 329(5991):559-562. Schneiter R, Daum G. 2006. Extraction of yeast lipids. Methods in Molecular Biology 313:41-45. Shi S B, Valle-Rodriguez J O, Khoomrung S, Siewers V, Nielsen J. 2012. Functional expression and characterization of five wax ester synthases in *Saccharomyces cerevisiae* and their utility for biodiesel production. Biotechnology for Biofuels 5(7):1-10. Song L, Qin J G, Su S Q, Xu J H, Clarke S, Shan Y C. 2012. Micronutrient Requirements for Growth and Hydrocarbon Production in the Oil Producing Green Alga *Botryococcus braunii* (Chlorophyta). Plos One 7(7). Subramaniam R, Dufreche S, Zappi M, Bajpai R. 2010. Microbial lipids from renewable resources: production and characterization. Journal of Industrial Microbiology & Biotechnology 37(12):1271-1287. Tai M, Stephanopoulos G. 2013. Engineering the push and pull of lipid biosynthesis in oleaginous yeast *Yarrowia lipolytica* for biofuel production. Metabolic Engineering 15:1-9. Thevenieau F, Nicaud J M, Gaillardin C. 2009. Applications of the Non-Conventional Yeast *Yarrowia lipolytca*. In: Satyanarayana T, Kunze G, editors. Yeast biotechnology: diversity and applications. Dordrecht: Springer Science and Business Media. p 589-613. Xu J Y, Du W, Zhao X B, Zhang G L, Liu D H. 2013. Microbial oil production from various carbon sources and its use for biodiesel preparation. Biofuels Bioproducts & Biorefining-Biofpr 7(1):65-77. Yamane T, Sakai H, Nagahama K, Ogawa T, Matsuoka M. 2008. Dissection of centromeric DNA from yeast *Yarrowia lipolytica* and identification of protein-binding site required for plasmid transmission. J Biosci Bioeng 105(6):571-8. Yim H, Haselbeck R, Niu W, Pujol-Baxley C, Burgard A, Boldt J, Khandurina J, Trawick J D, Osterhout R E, Stephen R and others. 2011. Metabolic engineering of *Escherichia coli* for direct production of 1,4-butanediol. Nature Chemical Biology 7(7):445-452. Zhao X, Kong X L, Hua Y Y, Feng B, Zhao Z B. 2008. Medium optimization for lipid production through co-fermentation of glucose and xylose by the oleaginous yeast *Lipomyces starkeyi*. European Journal of Lipid Science and Technology 110(5):405-412. Zhu Q, Xue Z, Yadav N, Sharpe P, Fan X, Tyreus B, Short D, Xie D, Boonyaratanakornkit B, Dellomonaco C and others. 2012. Production of omega-3 fatty acids from *Yarrowia lipolytica*: factors affecting lipid accumulation SIMB Annual Meeting & Exhbition. Washington, D.C. Beopoulos, A., Haddouche, R., Kabran, P., Dulermo, T., Chardot, T., Nicaud, J. M., (2012) Identification and characterization of DGA2, an acyl transferase of the DGAT1 acyl-CoA: diacylglycerol acyltransferase family in the oleaginous yeast *Yarrowia lipolytica*. New insights into the storage lipid metabolism of oleaginous yeasts. Applied Microbiology and Biotechnology 93, 1523-1537. Mlicknva, K., Roux, E., Athenstaedt, K., d'Andrea, S., Daum, G., Chardot, T., Nicaud, J. M., (2004) Lipid accumulation, lipid body formation, and acyl coenzyme A oxidases of the yeast *Yarrowia lipolytica*. Appl Environ Microbiol 70, 3918-3924. Thierry, D., Nicaud, J. M., (2011) Involvement of the G3P shuttle and beta-oxidation pathway in the control of TAG synthesis and lipid accumulation in *Yarrowia lipolytica*. Metab. Eng. 13, 482-491. Wang, H. J. J., Le Dall, M. T., Wache, Y., Laroche, C., Belin, J. M., Gaillardin, C., Nicaud, J. M., (1999) Evaluation of acyl coenzyme A oxidase (Aox) isozyme function in the n-alkane-assimilating yeast *Yarrowia lipolytica*. Journal of Bacteriology 181, 5140-5148. Tai, Stephanopoulos (2013), Engineering the push and pull of lipid biosynthesis in oleaginous yeast *Yarrowia lipolytica* for biofuel production, Metabolic Engineering, doi: 10.1016/j.ymben.2012.08.007. Beopoulos, A., J. Cescut, et al. (2009). Progress in Lipid Research 48(6): 375-387. Beopoulos, A., J. Cescut, et al. (2009). Progress in Lipid Research 48(6): 375-387. Blazeck, J., A. Hill, et al. (2014). Nat Commun 5. Cao, J., J. M. Barbosa, et al. (2013). Yeast 30(4): 129-144. Cardenas, M. E., N. S. Cutler, et al. (1999). "Genes & Development 13(24): 3271-3279. Covitz, P. A., I. Herskowitz, et al. (1991). Genes & *Development* 5(11): 1982-1989. EVANS, C. T. and C. RATLEDGE (1984). Journal of General Microbiology 130(7): 1693-1704. Gebre, S., R. Connor, et al. (2012). Cell Cycle 11(11): 2176-2188. Han, Jung M., Seung J. Jeong, et al. (2012). *Cell* 149(2): 410-424. Kamei, Y., T. Tamura, et al. (2011). Biochemical and Biophysical Research Communications 407(1): 185-190. Kaufmann, E. (1993). Chromosoma 102(3): 174-179. Li, H. and R. Durbin (2009). Bioinformatics 25(14): 1754-1760. Liu, Q., Y. Guo, et al. (2012). BMC Genomics 13(Suppl 8): S8. Pablo, C., M. P. Viral, et al. (2012). Frontiers in Genetics 3. Quinlan, A. R. and I. M. Hall (2010). Bioinformatics 26(6): 841-842. Ramos, F., M. El Guezzar, et al. (1985). European Journal of Biochemistry 149(2): 401-404. Richardson, A., R. G. Gardner, et al. (2013). PLoS ONE 8(10): e76424. Staschke, K. A., S. Dey, et al. (2010). Journal of Biological Chemistry 285(22): 16893-16911. Winston, F. (2001). EMS and UV Mutagenesis in Yeast. Current Protocols in Molecular Biology, John Wiley & Sons, Inc. Xue, Z., P. L. Sharpe, et al. (2013). Nature Biotechnology 31(8): 734-740. Yuan, Z., B. Yin, et al. (2013). Journal of Structural Biology 182(2): 125-135.

TABLE 1

List of select strains used in this study

Host Strain Name	Genotype	Reference or Source
	Escherichia coli strains	
DH10B	F⁻ mcrA Δ(mrr-hsdRMS-mcrBC) ϕ80d/acZΔM15 ΔlacX74 endA1 recA1 deoR Δ(ara, leu)7697 araD139 galU galK nupG rpsL λ	Open Biosystems

TABLE 1-continued

List of select strains used in this study

Host Strain Name	Genotype	Reference or Source
	Yarrowia lipolytica base strains	
WT (PO1f)	MatA, leu2-270, ura3-302, xpr2-322, axp1-2	Madzak et al. 2000
ΔMFE1 (PO1f-Δmfe1)	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1	Blazeck et al. 2013
ΔPEX10 (PO1f-Δpex10)	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10	Blazeck et al. 2013
ΔPEX10ΔMFE1 (PO1f-Δpex10-Δmfe1)	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1	This work
ΔACO1 (PO1f-Δaco1)	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δaco1	This work
	Selected *Yarrowia lipolytica* overexpression strains	
WT-S1-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, URA3 (S1)	This work
WT-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (S2)	This work
WT-S1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, URA3, LEU2 (S1, S2)	This work
WT-pMCS	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS)	This work
WT-pMCS-TUP1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), UAS1B16-TEF-TUP1	This work
WT-pMCS-HAC1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), UAS1B16-TEF-HAC1	This work
WT-S1-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, URA3 (S1), $UAS1B_{16}$-TEF-AMPD	This work
WT-S2-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (S2), $UAS1B_{16}$-TEF-AMPD	This work
WT-S1-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, URA3 (S1), $UAS1B_{16}$-TEF-MEA1	This work
WT-S2-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (S2), $UAS1B_{16}$-TEF-MEA1	This work
WT-S1-S2-AMPD-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, URA3, LEU2 (S1, S2), UAS1B16-TEF-AMPD, UAS1B16-TEF-MEA1	This work
WT-pMCS-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
ΔMFE1-S1-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3 (S1)	This work
ΔMFE1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (S2)	This work
ΔMFE1-S1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3, LEU2 (S1, S2)	This work
ΔMFE1-S1-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3 (S1), UAS1B16-TEF-AMPD	This work
ΔMFE1-S2-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (S2), UAS1B16-TEF-AMPD	This work
ΔMFE1-S1-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3 (S1), UAS1B16-TEFMEA1	This work
ΔMFE1-S2-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (S2), UAS1B16-TEF-MEA1	This work
ΔMFE1-S1-S2-AMPD-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3, LEU2 (S1, S2), UAS1B16-TEF-AMPD, UAS1B16-TEF-MEA1	This work
ΔMFE1-S1-S2-ACL1-ACL2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, URA3, LEU2 (S1, S2), UAS1B16-TEF-ACL1, UAS1B16-TEF-ACL2	This work
ΔMFE1-pMCS-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
ΔMFE1-pMCS-DGA2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA2	This work
ΔPEX10-S1-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, URA3 (S1)	This work
ΔPEX10-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (S2)	This work
ΔPEX10-S1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, URA3, LEU2 (S1, S2)	This work
ΔPEX10-S1-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, URA3 (S1), UAS1B16-TEF-AMPD	This work
ΔPEX10-S2-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (S2), UAS1B16-TEF-AMPD	This work
ΔPEX10-S1-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, URA3 (S1), UAS1B16-TEFMEA1	This work

TABLE 1-continued

List of select strains used in this study

Host Strain Name	Genotype	Reference or Source
ΔPEX10-S2-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (S2), UAS1B16-TEF-MEA1	This work
ΔPEX10-S1-S2-AMPD-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, URA3, LEU2 (S1, S2), UAS1B16-TEF-AMPD, UAS1B16-TEF-MEA1	This work
ΔPEX10-pMCS-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10-pMCS-DGA2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA2	This work
ΔPEX10ΔMFE1-S1-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1)	This work
ΔPEX10ΔMFE1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (S2)	This work
ΔPEX10ΔMFE1-S1-S2-Ø	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3, LEU2 (S1, S2)	This work
ΔPEX10ΔMFE1-S1-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), UAS1B16-TEF-AMPD	This work
ΔPEX10ΔMFE1-S2-AMPD	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (S2), UAS1B16-TEF-AMPD	This work
ΔPEX10ΔMFE1-S1-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), UAS1B16-TEFMEA1	This work
ΔPEX10ΔMFE1-S2-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (S2), UAS1B16-TEF-MEA1	This work
ΔPEX10ΔMFE1-S1-S2-AMPD-MEA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3, LEU2 (S1, S2), UAS1B16-TEF-AMPD, UAS1B16-TEF-MEA1	This work
ΔPEX10ΔMFE1-S1-S2-ACL1-ACL2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3, LEU2 (S1, S2), UAS1B16-TEF-ACL1, UAS1B16-TEF-ACL2	This work
ΔPEX10ΔMFE1-pMCS-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-pMCS-DGA2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA2	This work
ΔPEX10ΔMFE1-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, LEU2 (S2), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-Ø-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (S2), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-AMPD-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (S2), UAS1B16-TEF-AMPD, $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-MEA1-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (S2), UAS1B16-TEF-MEA1, $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), $UAS1B_{16}$-TEF-DGA1	This work
WT-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Leu2 (S2), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, LEU2 (S2), $UAS1B_{16}$-TEF-DGA1	This work
WT-pMCS-DGA2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
ΔPEX10ΔMFE1-S1-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3, $UAS1B_{16}$-TEF-DGA1	This work
ΔMFE1-S2-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2(S2), $UAS1B_{16}$-TEF-DGA1	This work
ΔMFE1-S2-DGA2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δmfe1, LEU2 (S2), $UAS1B_{16}$-TEF-DGA2	This work
ΔPEX10ΔMFE1-S1-Ø-pMCS-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (pMCS), $UAS1B_{16}$-TEF-DGA1	This work
Po1f pMCSMga2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2 LEU2 (pMCS), UAS1B16-TEF-Mga2	This work
Po1f pMCSMga2dTM	MatA, leu2-270, ura3-302, xpr2-322, axp1-2 LEU2 (pMCS), UAS1B16-TEF-Mga2dTM (truncated of transmembrane span)	This work

TABLE 1-continued

List of select strains used in this study

Host Strain Name	Genotype	Reference or Source
Po1f pMCSMga2L36	MatA, leu2-270, ura3-302, xpr2-322, axp1-2 LEU2 (pMCS), UAS1B16-TEF-Mga2L36 (has SNP found in L36 strain)	This work
Po1f pMCSMRM2	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), $UAS1B_{16}$-TEF-MRM2	This work
Po1f pMCSO6M	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS), $UAS1B_{16}$-TEF-O6M	This work
ΔACO1-DGA1	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δaco1, URA3 (S1), LEU2 (S2), $UAS1B_{16}$-TEF-DGA1	This work
	L36 and EMS derived strains	
L36	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, LEU2 (pMCS) - isolated and fully sequenced to determine source of high lipid accumulation - most likely from mutation in MGA2 ORF.	This work
L36 E1S6-4	L36 strain mutagenized further with EMS	This work
L36 E1S6-5	L36 strain mutagenized further with EMS	This work
L36 E1S6-6	L36 strain mutagenized further with EMS	This work
ΔPEX10ΔMFE1-S2-DGA1 E1	ΔPEX10ΔMFE1-S2-DGA1 strain mutagenized with EMS	This work
ΔPEX10ΔMFE1-S2-DGA1 E6	ΔPEX10ΔMFE1-S2-DGA1 strain mutagenized with EMS	This work
ΔPEX10ΔMFE1-S2-DGA1 E12	ΔPEX10ΔMFE1-S2-DGA1 strain mutagenized with EMS	This work
E13	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (S2), $UAS1B_{16}$-TEF-DGA1 strain mutagenized with EMS and selected	This work
E26	MatA, leu2-270, ura3-302, xpr2-322, axp1-2, Δpex10, Δmfe1, URA3 (S1), LEU2 (S2), $UAS1B_{16}$-TEF-DGA1 strain mutagenized with EMS and selected	This work

TABLE 2

List of primers used in this study

JB387 YL AMPD 5' AscI	TTGGCGCGCCatgccgcagcaagcaatgg (SEQ ID NO.: 1)
JB388 YL AMPD 3' PacI	CCTTAATTAAttaaccatgcagccgctcaaac (SEQ ID NO.: 2)
JB402 YL ACL1 5' AscI	TTGGCGCGCCatgtctgccaacgagaacat (SEQ ID NO.: 3)
JB403 YL ACL1 + 4 5' AscI	TTGGCGCGCCtctgccaacgagaacatctc (SEQ ID NO.: 4)
JB404 YL ACL1 3' PacI	CCTTAATTAActatgatcgagtcttggccttg (SEQ ID NO.: 5)
JB405 YL ACL2 5' AscI	TTGGCGCGCCATGTCAGCGAAATCCATTCACG (SEQ ID NO.: 6)
JB406 YL ACL2 + 4 5' AscI	TTGGCGCGCCTCAGCGAAATCCATTCACGAG (SEQ ID NO.: 7)
JB407 YL ACL2 3' PacI	CCTTAATTAATTAAACTCCGAGAGGAGTGGAA (SEQ ID NO.: 8)
JB862 Loxleu 5' SacII	CCAccgcggataacttcgtataatgtatgctatacgaagttatgagtctttattggtgatgggaaga (SEQ ID NO.: 9)
JB863 Loxleu 3' Bstb1	CGGTTCGAAataacttcgtatagcatacattatacgaagttatcagtcgccagcttaaagatatcta (SEQ ID NO.: 10)
JB865 hygR 3' bglII	GgaacggtAGATCtCGAGCGTCCCAAAACCTTCTC (SEQ ID NO.: 11)

TABLE 2-continued

List of primers used in this study

JB883 hygR 5' NaeI	GtggacGGgccggcgtttggcgcccgttttttcg (SEQ ID NO.: 12)
JB911 DGA1 5' AscI	CattcaaaGGCGCGCCatgactatcgactcacaatactaca (SEQ ID NO.: 13)
JB912 DGA1 3' PacI	GcGGATCCTTAATTAAttactcaatcattcggaactctgg (SEQ ID NO.: 14)
JB913 DGA2 5' AscI	CattcaaaGGCGCGCCATGGAAGTCCGACGACGAAA (SEQ ID NO.: 15)
JB914 DGA2 3' PacI	GcGGATCCTTAATTAACTACTGGTTCTGCTTGTAGTTGT (SEQ ID NO.: 16)
AH011 Tup1 5' Asc	GACTGGCGCGCATGAGCTTCCCCCAACAAGTA (SEQ ID NO.: 17)
AH012 Tup1 3' PacI	GTCCTTAATTAATTATCTGTTGACAGGAAAGTATCGC (SEQ ID NO.: 18)
AH007 HacI 5' AscI	GACTGGCGCGCATGTCTATCAAGCGAGAAGAGT (SEQ ID NO.: 19)
AH008 HacI 3' PacI	GTCCTTAATTAACTAGATCAGCAATAAAGTCGTGCT (SEQ ID NO.: 20)
AH020 MAE 5' AscI	GACTGGCGCGCCATGTTACGACTACGAACCATGC (SEQ ID NO.: 21)
AH021 MAE 3' PacI	GTCCTTAATTAACTAGTCGTAATCCCGCACATG (SEQ ID NO.: 22)
LQ310 Mga2 5' AscI	ACTGGGCGCGCC atggctaaagacaaggaaatcgactttgac (SEQ ID NO.: 23)
LQ303 Mga2TM 3' PacI	ACTGTTAATTAA tcagtaaatgtaagccagaacatcgt (SEQ ID NO.: 24)
LQ309 Mga2 3' PacI	ACTGTTAATTAA tcatgcagcctgggcctgg (SEQ ID NO.: 25)
LQ294 O6M 5' AscI	ACTGGGCGCGCC atgttttacaccaagcccgacccg (SEQ ID NO.: 26)
LQ295 O6M 3' PacI	ACTGTTAATTAA ttagagagtcccccacatgtcaccc (SEQ ID NO.: 27)
LQ259 MRM2 5' AscI	ACTGGGCGCGCC Atgcgccaaaagctgccgttcaac (SEQ ID NO.: 28)
LQ260 MRM2 3' PacI	ACTGTTAATTAA ttatggcttcccttctgccacatc (SEQ ID NO.: 29)
LQ261 DGA1 5' AscI	ACTGGGCGCGCC Atgactatcgactcacaatactac (SEQ ID NO.: 30)
LQ262 DGA1 3' PacI	ACTGTTAATTAA ttactcaatcattcggaactctgg (SEQ ID NO.: 31)

TABLE 3

Media formulations used for two strain testing

Media Name	Carbon Source Glucose (g/L)	Nitrogen Source Ammonium Sulfate (g/L)
$C_{10}N_5$	10	5
$C_{20}N_{0.04}$	20	0.04
$C_{20}N_{0.2}$	20	0.2
$C_{20}N_1$	20	1
$C_{20}N_5$ (YSC)	20	5
$C_{20}N_{10}$	20	10

TABLE 3-continued

Media formulations used for two strain testing

Media Name	Carbon Source Glucose (g/L)	Nitrogen Source Ammonium Sulfate (g/L)
$C_{40}N_{0.2}$	40	0.2
$C_{40}N_1$	40	1
$C_{40}N_5$	40	5
$C_{80}N_{0.04}$	80	0.04
$C_{80}N_{0.2}$	80	0.2
$C_{80}N_1$	80	1

TABLE 3-continued

Media formulations used for two strain testing

Media Name	Carbon Source Glucose (g/L)	Nitrogen Source Ammonium Sulfate (g/L)
$C_{80}N_5$	80	5
$C_{80}N_{10}$	80	10
$C_{160}N_{0.2}$	160	0.2
$C_{160}N_1$	160	1
$C_{160}N_5$	160	5
$C_{320}N_{0.2}$	320	0.2
$C_{320}N_1$	320	1
$C_{320}N_5$	320	5

TABLE 4

ΔPex10, Mfe S1Ø, S2-DGA1 CSM vs Minimal Media (-CSM) Comparison

ΔPex10, Mfe S1Ø, S2-DGA1 CSM vs Minimal Media (-CSM) Comparison

Strain: ΔPex10, Mfe S1-ϕ, S2-DGA1

Media	Sample	Day 4 OD	Day 4 GFP Fluorescence
CSM - C80N5	A	16.83	36696
CSM - C80N5	B	16.76	34397
CSM - C80N5	C	16.31	39166
Minimal Media - C80N5	A	11.7	29365
Minimal Media - C80N5	B	11.46	52520
Minimal Media - C80N5	C	11.87	32427

TABLE 5

Media Formulations used for 12 strain testing

Media Name	Carbon Source Glucose (g/L)	Nitrogen Source Ammonium Sulfate (g/L)
$C_{20}N_{0.2}$	20	0.2
$C_{20}N_1$	20	1
$C_{20}N_5$ (YSC)	20	5
$C_{40}N_{0.2}$	40	0.2
$C_{40}N_1$	40	1
$C_{40}N_5$	40	5
$C_{80}N_{0.2}$	80	0.2
$C_{80}N_1$	80	1
$C_{80}N_5$	80	5
$C_{80}N_{10}$	80	10
$C_{160}N_{0.2}$	160	0.2

TABLE 5-continued

Media Formulations used for 12 strain testing

Media Name	Carbon Source Glucose (g/L)	Nitrogen Source Ammonium Sulfate (g/L)
$C_{160}N_1$	160	1
$C_{160}N_5$	160	5

TABLE 6

RFU and OD for EMS data

	RFU	OD
ΔPEX10ΔMFE1 S2-DGA1 Control	23750	8.81
E1	31800	21.91
E6	35400	18.86
E12	37100	22.5
L36 Control	23133.33	11.83
E1S6 4	34350	20.61
E1S6 6	34250	20.58
E1S6 8	28750	18.31

TABLE 7

List of genes and genetic changes

Gene	Type of Modification
Leucine Biosynthesis Gene (LEU2) - Note may also be able to include rest of genes of leucine biosynthetic pathway, have yet to test these additional ones	Over-expression
Uracil Biosynthesis gene (URA3)	Over-expression
multifunctional enzyme (MFE1) in b-oxidation Deletion pathway	
Transcription Factor (PEX10)	Deletion
AMP Deaminase (AMPD)	Over-expression
ATP-Citrate Lyase (ACL1 and/or ACL2)	Over-expression
Malic Enzyme (MAE/MEA)	Over-expression
Acetyl-CoA Carboxylase (ACC)	Over-expression
acyl-CoA:diacylglycerol acyltransferases (DGA1 and/or DGA2)	Over-expression
Mitochondrial 2' O-ribose methyltransferase(MRM2)	Over-expression
O-6-methylguanine-DNA methyltransferase (MGMT)	Over-expression
Aconitase (ACO1)	Deletion
Citrate Synthase (CIT1)	Over-expression

TABLE 8

Strain L36 important SNP list

Chromosome	Position	Mutation type	sequence	Gene	Accession numbers
B	1644655	SNP	C > T	mga2	12342g
D	2401168	Insertion	A > AG	sorbitol utilization protein SOU2	18964g
E	1837892	SNP	C > A	CEN0E	15444s
	1837894	SNP	T > A	CEN0E	15444s
	4025540	SNP	C > A	DEHA0A1298g IPF 95.1	33891g
	4025542	SNP	G > C	DEHA0A1298g IPF 95.1	33891g
F	2861334	Insertion	A > AGAGGG CTAGAGAG AGGGAGA A (SEQ ID NO.: 32)	RLF2 chromatin asembly complex subunit p90	21637g

Gene Targets: The reference number given for each name corresponds to the Genolevures database: http://www.genolevures.org/. YALI0 stands for *Yarrowia lipolytica*. A,B, C,D,E,F specifies chromosome, and the following number specifies location. Note: Leu2 and Ura3 given as GenBank Accession numbers

AMPD - YALI0E11495

(SEQ ID NO.: 33)

Nucleotide =

atgccgcagcaagcaatggatatcaagggcaaggccaagtctgtgcccatgcccgaagaagacgacctgg

actcgcattttgtgggtcccatctctccccgacctcacggagcagacgagattgctggctacgtgggctg

cgaagacgacgaagacgagcttgaagaactgggaatgctgggccgatctgcgtccacccacttctcttac

gcggaagaacgccacctcatcgaggttgatgccaagtacagagctcttcatggccatctgcctcatcagc

actctcagagtcccgtgtccagatcttcgtcatttgtgcgggccgaaatgaaccacccccctcccccacc

ctccagccacacccaccaacagccagaggacgatgacgcatcttccactcgatctcgatcgtcgtctcga

gcttctggacgcaagttcaacagaaacagaaccaagtctggatcttcgctgagcaagggtctccagcagc

tcaacatgaccggatcgctcgaagaagagccctacgagagcgatgacgatgcccgactatctgcggaaga

cgacattgtctatgatgctacccagaaagacacctgcaagcccatatctcctactctcaaacgcacccgc

accaaggacgacatgaagaacatgtccatcaacgacgtcaaaatcaccaccaccacagaagatcctcttg

tggcccaggagctgtccatgatgttcgaaaaggtgcagtactgccgagacctccgagacaagtaccaaac

cgtgtcgctacagaaggacggagacaaccccaaggatgacaagacacactggaaaatttaccccgagcct

ccaccaccctcctggcacgagaccgaaaagcgattccgaggctcgtccaaaaaggagcaccaaaagaaag

acccgacaatggatgaattcaaattcgaggactgcgaaatccccggacccaacgacatggtcttcaagcg

agatcctacctgtgtctatcaggtctatgaggatgaaagctctctcaacgaaaataagccgtttgttgcc

atcccctcaatccgagattactacatggatctggaggatctcattgtggcttcgtctgacggacctgcca

agtcttttgctttccgacgactgcaatatctagaagccaagtggaacctctactacctgctcaacgagta

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gttcaccactctgcctgcatgaaccagaagcatctgctgcgattcatcaaatacaagatgaagaactgcc

ctgatgaagttgtcatccaccgagacggtcgggagctgacactctcccaggtgtttgagtcacttaactt

gactgcctacgacctgtctatcgataccttgatatgcatgctcacaaggactcgttccatcgatttgac

-continued

aagttcaacctcaagtacaaccctgtcggtgagtctcgactgcgagaaatcttcctaaagaccgacaact

acatccagggtcgatacctagctgagatcacaaaggaggtgttccaggatctcgagaactcgaagtacca

gatggcggagtaccgtatttccatctacggtcggtccaaggacgagtgggacaagctggctgcctgggtg

ctggacaacaaactgttttcgcccaatgttcggtggttgatccaggtgcctcgactgtacgacatttaca

agaaggctggtctggttaacacctttgccgacattgtgcagaacgtctttgagcctcttttcgaggtcac

caaggatcccagtacccatcccaagctgcacgtgttcctgcagcgagttgtgggctttgactctgtcgat

gacgagtcgaagctggaccgacgtttccaccgaaagttcccaactgcagcatactgggacagcgcacaga

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acttatctggttgctcagggtatcaaccacggtattctgttgcgaaaggtgcccttcattcagtacctttt

actacctggaccagatccccattgccatgtctcctgtgtccaacaatgcgctgttcctcacgttcgacaa

gaaccccttctactcatacttcaagcggggtctcaacgtgtccttgtcatcggatgatcctctgcagttt

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atatgtgtgagcttgctcgaaactcggtactgcaatctggctttgagcgaatcatcaaggagcattggat

cggcgaaaactacgagatccatggccccgagggcaacaccatccagaagacaaacgtgcccaatgtgcgt

ctggccttccgagacgagactttgacccacgagcttgctctggtggacaagtacaccaatcttgaggagt

ttgagcggctgcatggtta

(SEQ ID NO.: 34)

Amino Acid =

MPQQAMDIKGKAKSVPMPEEDDLDSHFVGPISPRPHGADEIAGYVGCEDDEDELEELGMLGRSASTHFSY

AEERHLIEVDAKYRALHGHLPHQHSQSPVSRSSSFVRAEMNHPPPPPSSHTHQQPEDDDASSTRSRSSSR

ASGRKFNRNRTKSGSSLSKGLQQLNMTGSLEEEPYESDDDARLSAEDDIVYDATQKDTCKPISPTLKRTR

TKDDMKNMSINDVKITTTTEDPLVAQELSMMFEKVQYCRDLRDKYQTVSLQKDGDNPKDDKTHWKIYPEP

PPPSWHETEKRFRGSSKKEHQKKDPTMDEFKFEDCEIPGPNDMVFKRDPTCVYQVYEDESSLNENKPFVA

IPSIRDYYMDLEDLIVASSDGPAKSFAFRRLQYLEAKWNLYYLLNEYTETTESKTNPHRDFYNVRKVDTH

VHHSACMNQKHLLRFIKYKMKNCPDEVVIHRDGRELTLSQVFESLNLTAYDLSIDTLDMHAHKDSFHRFD

KFNLKYNPVGESRLREIFLKTDNYIQGRYLAEITKEVFQDLENSKYQMAEYRISIYGRSKDEWDKLAAWV

LDNKLFSPNVRWLIQVPRLYDIYKKAGLVNTFADIVQNVFEPLFEVTKDPSTHPKLHVFLQRVVGFDSVD

DESKLDRRFHRKFPTAAYWDSAQNPPYSYWQYYLYANMASINTWRQRLGYNTFELRPHAGEAGDPEHLLC

TYLVAQGINHGILLRKVPFIQYLYYLDQIPIAMSPVSNNALFLTFDKNPFYSYFKRGLNVSLSSDDPLQF

AYTKEALIEEYSVAALIYKLSNVDMCELARNSVLQSGFERIIKEHWIGENYEIHGPEGNTIQKTNVPNVR

LAFRDETLTHELALVDKYTNLEEFERLHG*

Leu2 - AF260230

(SEQ ID NO.: 35)

Nucleotide =

atggaacccgaaactaagaagaccaagactgactccaagaagattgttcttctcggcggcgacttctgtg

gccccgaggtgattgccgaggccgtcaaggtgctcaagtctgttgctgaggcctccggcaccgagtttgt

gtttgaggaccgactcattggaggagctgccattgagaaggagggcgagcccatcaccgacgctactctc

gacatctgccgaaaggctgactctattatgctcggtgctgtcggaggcgctgccaacaccgtatggacca

ctcccgacggacgaaccgacgtgcgacccgagcagggtctcctcaagctgcgaaaggacctgaacctgta

cgccaacctgcgaccctgccagctgctgtcgcccaagctcgccgatctctcccccatccgaaacgttgag

ggcaccgacttcatcattgtccgagagctcgtcggaggtatctactttggagagcgaaaggaggatgacg

gatctggcgtcgcttccgacaccgagacctactccgttcctgaggttgagcgaattgcccgaatggccgc

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caacatgtttggcgatatcatctccgacgaggcctccgtcatccccggttctctgggtctgctgccctcc

gcctctctggcttctctgcccgacaccaacgaggcgttcggtctgtacgagccctgtcacggatctgccc

ccgatctcggcaagcagaaggtcaaccccattgccaccattctgtctgccgccatgatgctcaagttctc

tcttaacatgaagcccgccggtgacgctgttgaggctgccgtcaaggagtccgtcgaggctggtatcact

accgccgatatcggaggctcttcctccacctccgaggtcggagacttgttgccaacaaggtcaaggagct

gctcaagaaggagtaagtcgtttctacgacgcattgatggaaggagcaaactgacgcgcctgcgggttgg

tctaccggcagggtccgctagtgtataa

(SEQ ID NO.: 36)

Amino Acid =
MEPETKKTKTDSKKIVLLGGDFCGPEVIAEAVKVLKSVAEASGTEFVFEDRLIGGAAIEKEGEPITDATL

DICRKADSIMLGAVGGAANTVWTTPDGRTDVRPEQGLLKLRKDLNLYANLRPCQLLSPKLADLSPIRNVE

GTDFIIVRELVGGIYFGERKEDDGSGVASDTETYSVPEVERIARMAAFLALQHNPPLPVWSLDKANVLAS

SRLWRKTVTRVLKDEFPQLELNHQLIDSAAMILIKQPSKMNGIIITTNMFGDIISDEASVIPGSLGLLPS

ASLASLPDTNEAFGLYEPCHGSAPDLGKQKVNPIATILSAAMMLKFSLNMKPAGDAVEAAVKESVEAGIT

TADIGGSSSTSEVGDLLPTRSRSCSRRSKSFLRRIDGRSKLTRLRVGLPAGSASV*

Ura3 - YLU40564

(SEQ ID NO.: 37)

Nucleotide =
atgccctcctacgaagctcgagctaacgtccacaagtccgcctttgccgctcgagtgctcaagctcgtgg

cagccaagaaaaccaacctgtgtgcttctctggatgttaccaccaccaaggagctcattgagcttgccga

taaggtcggaccttatgtgtgcatgatcaagacccatatcgacatcattgacgacttcacctacgccggc

actgtgctccccctcaaggaacttgctcttaagcacggtttcttcctgttcgaggacagaaagttcgcag

atattggcaacactgtcaagcaccagtacaagaacggtgtctaccgaatcgccgagtggtccgatatcac

caacgcccacggtgtacccggaaccggaatcattgctggcctgcgagctggtgccgaggaaactgtctct

gaacagaagaaggaggacgtctctgactacgagaactcccagtacaaggagttcctggtcccctctccca

acgagaagctggccagaggtctgctcatgctggccgagctgtcttgcaagggctctctggccactggcga

gtactccaagcagaccattgagcttgcccgatccgaccccgagtttgtggttggcttcattgcccagaac

cgacctaagggcgactctgaggactggcttattctgacccccggggtgggtcttgacgacaagggagacg

ctctcggacagcagtaccgaactgttgaggatgtcatgtctaccggaacggatatcataattgtcggccg

aggtctgtacggccagaaccgagatcctattgaggaggccaagcgataccagaaggctggctgggaggct

taccagaagattaactgttag

(SEQ ID NO.: 38)

Amino Acid =
MPSYEARANVHKSAFAARVLKLVAAKKTNLCASLDVTTTKELIELADKVGPYVCMIKTHIDIIDDFTYAG

TVLPLKELALKHGFFLFEDRKFADIGNTVKHQYKNGVYRIAEWSDITNAHGVPGTGIIAGLRAGAEETVS

EQKKEDVSDYENSQYKEFLVPSPNEKLARGLLMLAELSCKGSLATGEYSKQTIELARSDPEFVVGFIAQN

RPKGDSEDWLILTPGVGLDDKGDALGQQYRTVEDVMSTGTDIIIVGRGLYGQNRDPIEEAKRYQKAGWEA

YQKINC*

ACLsubunit1 - YALI0E34793

(SEQ ID NO.: 39)

Nucleotide =
atgtctgccaacgagaacatctcccgattcgacgcccctgtgggcaaggagcaccccgcctacgagctct

tccataaccacacacgatctttcgtctatggtctccagcctcgagcctgccagggtatgctggacttcga

-continued

cttcatctgtaagcgagagaacccctccgtggccggtgtcatctatcccttcggcggccagttcgtcacc

aagatgtactggggcaccaaggagactcttctccctgtctaccagcaggtcgagaaggccgctgccaagc

accccgaggtcgatgtcgtggtcaactttgcctcctctcgatccgtctactcctctaccatggagctgct

cgagtacccccagttccgaaccatcgccattattgccgagggtgtccccgagcgacgagcccgagagatc

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gcttcaaggttggaaacaccggaggtatgatggacaacattgtcgcctccaagctctaccgacccggctc

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ccttgccgagctctacgagaagatggtcgccaagggcgagctgtctcgaatctctgagcctgaggtcccc

aagatccccattgactactcttgggcccaggagcttggtcttatccgaaagcccgctgctttcatctcca

ctatttccgatgaccgaggccaggagcttctgtacgctggcatgcccatttccgaggttttcaaggagga

cattggtatcggcggtgtcatgtctctgctgtggttccgacgacgactccccgactacgcctccaagttt

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aggtgctcttgacggtgctgccaccgagttcaccactgcctacgacaagggtctgtccccccgacagttc

gttgataccatgcgaaagcagaacaagctgattcctggtattggccatcgagtcaagtctcgaaacaacc

ccgatttccgagtcgagcttgtcaaggactttgttaagaagaacttcccctccacccagctgctcgacta

cgcccttgctgtcgaggaggtcaccacctccaagaaggacaacctgattctgaacgttgacggtgctatt

gctgtttcttttgtcgatctcatgcgatcttgcggtgcctttactgtggaggagactgaggactacctca

agaacggtgttctcaacggtctgttcgttctcggtcgatccattggtctcattgcccaccatctcgatca

gaagcgactcaagaccggtctgtaccgacatccttgggacgatatcacctacctggttggccaggaggct

atccagaagaagcgagtcgagatcagcgccggcgacgtttccaaggccaagactcgatcatag

(SEQ ID NO.: 40)

Amino Acid =
MSANENISRFDAPVGKEHPAYELFHNHTRSFVYGLQPRACQGMLDFDFICKRENPSVAGVIYPFGGQFVT

KMYWGTKETLLPVYQQVEKAAAKHPEVDVVVNFASSRSVYSSTMELLEYPQFRTIAIIAEGVPERRAREI

LHKAQKKGVTIIGPATVGGIKPGCFKVGNTGGMMDNIVASKLYRPGSVAYVSKSGGMSNELNNIISHTTD

GVYEGIAIGGDRYPGTTFIDHILRYEADPKCKIIVLLGEVGGVEEYRVIEAVKNGQIKKPIVAWAIGTCA

SMFKTEVQFGHAGSMANSDLETAKAKNAAMKSAGFYVPDTFEDMPEVLAELYEKMVAKGELSRISEPEVP

KIPIDYSWAQELGLIRKPAAFISTISDDRGQELLYAGMPISEVFKEDIGIGGVMSLLWFRRRLPDYASKF

LEMVLMLTADHGPAVSGAMNTIITTRAGKDLISSLVAGLLTIGTRFGGALDGAATEFTTAYDKGLSPRQF

VDTMRKQNKLIPGIGHRVKSRNNPDFRVELVKDFVKKNFPSTQLLDYALAVEEVTTSKKDNLILNVDGAI

AVSFVDLMRSCGAFTVEETEDYLKNGVLNGLFVLGRSIGLIAHHLDQKRLKTGLYRHPWDDITYLVGQEA

IQKKRVEISAGDVSKAKTRS*

ACLsubunit2 - YALI0D24431

(SEQ ID NO.: 41)

Nucleotide =
atgtcagcgaaatccattcacgaggccgacggcaaggccctgctcgcacactttctgtccaaggcgcccg

tgtgggccgagcagcagcccatcaacacgtttgaaatgggcacacccaagctggcgtctctgacgttcga

-continued

ggacggcgtggcccccgagcagatcttcgccgccgctgaaaagacctacccctggctgctggagtccggc

gccaagtttgtggccaagcccgaccagctcatcaagcgacgaggcaaggccggcctgctggtactcaaca

agtcgtgggaggagtgcaagccctggatcgccgagcgggccgccaagcccatcaacgtggagggcattga

cggagtgctgcgaacgttcctggtcgagccctttgtgccccacgaccagaagcacgagtactacatcaac

atccactccgtgcgagagggcgactggatcctcttctaccacgagggaggagtcgacgtcggcgacgtgg

acgccaaggccgccaagatcctcatccccgttgacattgagaacgagtacccctccaacgccacgctcac

caaggagctgctggcacacgtgcccgaggaccagcaccagaccctgctcgacttcatcaaccggctctac

gccgtctacgtcgatctgcagtttacgtatctggagatcaacccccctggtcgtgatccccaccgcccagg

gcgtcgaggtccactacctggatcttgccggcaagctcgaccagaccgcagagtttgagtgcggccccaa

gtgggctgctgcgcggtcccccgccgctctgggccaggtegtcaecattgacgccggctccaccaaggtg

tccatcgacgccggccccgccatggtcttccccgctcctttcggtcgagagctgtccaaggaggaggcgt

acattgcggagctcgattccaagaccggagcttctctgaagctgactgttctcaatgccaagggccgaat

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gacgagctcgccaactacggcgagtactctggcgctcccaacgagacccagacctacgagtacgccaaaa

ccgtactggatctcatgacccggggcgacgctcaccccgagggcaaggtactgttcattggcggaggaat

cgccaacttcacccaggttggatccaccttcaagggcatcatccgggccttccgggactaccagtcttct

ctgcacaaccacaaggtgaagatttacgtgcgacgaggcggtcccaactggcaggagggtctgcggttga

tcaagtcggctggcgacgagctgaatctgcccatggagatttacggccccgacatgcacgtgtcgggtat

tgttcctttggctctgcttggaaagcggcccaagaatgtcaagccttttggcaccggaccttctactgag

gcttccactcctctcggagtttaa

(SEQ ID NO.: 42)

Amino Acid =
MSAKSIHEADGKALLAHFLSKAPVWAEQQPINTFEMGTPKLASLTFEDGVAPEQIFAAAEKTYPWLLESG

AKFVAKPDQLIKRBGKAGLLVLNKSWEECKPWIAERAAKPINVEGIDGVLRTFLVEPFVPHDQKHEYYIN

IHSVREGDWILFYHEGGVDVGDVDAKAAKILIPVDIENEYPSNATLTKELLAHVPEDQHQTLLDFINRLY

AVYVDLQFTYLEINPLVVIPTAQGVEVHYLDLAGKLDQTAEFECGPKWAAARSPAALGQVVTIDAGSTKV

SIDAGPAMVFPAPFGRELSKEEAYIAELDSKTGASLKLTVLNAKGRIWTLVAGGGASVVYADAIASAGFA

DELANYGEYSGAPNETQTYEYAKTVLDLMTRGDAHPEGKVLFIGGGIANFTQVGSTFKGIIRAFRDYQSS

LHNHKVKIYVRRGGPNWQEGLRLIKSAGDELNLPMEIYGPDMHVSGIVPLALLGKRPKNVKPFGTGPSTE

ASTPLGV*

MEA1 - YALI0E18634
(note: 4 nucleotide difference compared to the reference sequence.
In embodiments, MEA1 is the reference sequence associated with
YALI0E18634. In embodiments, MEA1 is the reference sequence with
the four nucleotide differences from the reference sequence
shown below.)

(SEQ ID NO.: 43)

Nucleotide =
atgttacgactacgaaccatgcgacccacacagaccagcgtcagggcggcgcttgggcccaccgctgcgg

cccgaaacatgtcctcctccagcccctccagcttcgaatactcgtcctacgtcaagggcacgcgggaaat

cggccaccgaaaggcgcccacaacccgtctgtcggttgagggccccatctacgtgggcttcgacggcatt

cgtcttctcaacctgccgcatctcaacaagggctcgggattccccctcaacgagcgacgggaattcggac

tcagtggtcttctgccctctgccgaagccaccctggaggaacaggtcgaccgagcataccaacaattcaa

aaagtgtggcactcccttagccaaaaacgggttctgcacctcgctcaagttccaaaacgaggtgctctac

tacgccctgctgctcaagcacgttaaggaggtcttccccatcatctatacaccgactcagggagaagcca

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ttgaacagtactcgcggctgttccggcggcccgaaggctgcttcctcgacatcaccagtccctacgacgt

ggaggagcgtctgggagcgtttggagaccatgacgacattgactacattgtcgtgactgactccgagggt

attctcggaattggagaccaaggagtgggcggtattggtatttccatcgccaagctggctctcatgactc

tatgtgctggagtcaacccctcacgagtcattcctgtggttctggatacgggaaccaacaaccaggagct

gctgcacgacccccctgtatctcggccgacgaatgccccgagtgcgaggaaagcagtacgacgacttcatc

gacaactttgtgcagtctgcccgaaggctgtatcccaaggcggtgatccatttcgaggactttgggctcg

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tggagccgtcactctggcctccatcacggccgctctcaaggtgctgggcaaaaatatcacagatactcga

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acttaccgacgagcagatgagcgacgtgcagaagccgtttgccaaggacaaggccaattacgagggagtg

gacaccaagactctggagcacgtggttgctgccgtcaagccccatattctcattggatgttccactcagc

ccggcgcctttaacgagaaggttgtcaaggagatgcttaaacacacccctcgacccatcattctccctct

ttccaaccccacacgtcttcatgaggctgtccctgcagatctgtacaagtggaccgacggcaaggctctg

gttgccaccggctcgccctttgacccagtcaacggcaaggagacgtctgagaacaataactgctttgttt

tccccggaatcgggctgggagccattctgtctcgatcaaagctcatcaccaacaccatgattgctgctgc

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ctcatccagatcatttcggcccgggtggccactgccgtggttcttcaggccaaggctgagggcctagcca

ctgtcgaggaagagctcaagcccggcaccaaggaacatgtgcagattcccgacaactttgacgagtgtct

cgcctgggtcgagactcagatgtggcggcccgtctaccggcctctcatccatgtgcgggattacgactag

(SEQ ID NO.: 44)

Amino Acid =
MLRLRTMRPTQTSVRAALGPTAAARNMSSSSPSSFEYSSYVKGTREIGHRKAPTTRLSVEGPIYVGFDGI

RLLNLPHLNKGSGFPLNERREFGLSGLLPSAEATLEEQVDRAYQQFKKCGTPLAKNGFCTSLKFQNEVLY

YALLLKHVKEVFPIIYTPTQGEAIEQYSRLFRRPEGCFLDITSPYDVEERLGAFGDHDDIDYIVVTDSEG

ILGIGDQGVGGIGISIAKLALMTLCAGVNPSRVIPVVLDTGTNNQELLHDPLYLGRRMPRVRGKQYDDFI

DNFVQSARRLYPKAVIHFEDFGLANAHKILDKYRPEIPCFNDDIQGTGAVTLASITAALKVLGKNITDTR

ILVYGAGSAGMGIAEQVYDNLVAQGLDDKTARQNIFLMDRPGLLTTALTDEQMSDVQKPFAKDKANYEGV

DTKTLEHVVAAVKPHILIGCSTQPGAFNEKVVKEMLKHTPRPIILPLSNPTRLHEAVPADLYKWTDGKAL

VATGSPFDPVNGKETSENNNCFVFPGIGLGAILSRSKLITNTMIAAAIECLAEQAPILKNHDEGVLPDVA

LIQIISARVATAVVLQAKAEGLATVEEELKPGTKEHVQIPDNFDECLAWVETQMWRPVYRPLIHVRDYD*

DGA1 - YALI0E32769

(SEQ ID NO.: 45)

Nucleotide =
atgactatcgactcacaatactacaagtcgcgagacaaaaacgacacggcacccaaaatcgcgggaatcc

gatatgccccgctatcgacaccattactcaaccgatgtgagaccttctctctggtctggcacattttcag

cattcccactttcctcacaattttcatgctatgctgcgcaattccactgctctggccatttgtgattgcg

tatgtagtgtacgctgttaaagacgactccccgtccaacggaggagtggtcaagcgatactcgcctattt

caagaaacttcttcatctggaagctctttggccgctacttccccataactctgcacaagacggtggatct

ggagcccacgcacacatactaccctctggacgtccaggagtatcacctgattgctgagagatactggccg

cagaacaagtacctccgagcaatcatctccaccatcgagtactttctgcccgccttcatgaaacggtctc

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gggttctcaacctgacaagtggattaaccacgacagcagatatagccgtggagaatcatctggctccaac

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ggccacgcctcgggctccgaacttaacggcaacggcaacaatggcaccactaaccgacgacctttgtcgt

ccgcctctgctggctccactgcatctgattccacgcttcttaacgggtccctcaactcctacgccaacca

gatcattggcgaaaacgacccacagctgtcgcccacaaaactcaagcccactggcagaaaatacatcttc

ggctaccacccccacggcattatcggcatgggagcctttggtggaattgccaccgagggagctggatggt

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agagtacctcatgagtctgggagtcgcttctgtctccaagaagtcctgcaaggccctcctcaagcgaaac

cagtctatctgcattgtcgttggtggagcacaggaaagtcttctggccagacccggtgtcatggacctgg

tgctactcaagcgaaagggttttgttcgacttggtatggaggtcggaaatgtcgcccttgttcccatcat

ggcctttggtgagaacgacctctatgaccaggttagcaacgacaagtcgtccaagctgtaccgattccag

cagtttgtcaagaacttccttggattcacccttcctttgatgcatgcccgaggcgtcttcaactacgatg

tcggtcttgtcccctacaggcgacccgtcaacattgtggttggttcccccattgacttgccttatctccc

acaccccaccgacgaagaagtgtccgaataccacgaccgatacatcgccgagctgcagcgaatctacaac

gagcacaaggatgaatatttcatcgattggaccgaggagggcaaaggagccccagagttccgaatgattg

agtaa

(SEQ ID NO.: 46)

Amino Acid =
MTIDSQYYKSRDKNDTAPKIAGIRYAPLSTPLLNRCETFSLVWHIFSIPTFLTIFMLCCAIPLLWPFVIA

YVVYAVKDDSPSNGGVVKRYSPISRNFFIWKLFGRYFPITLHKTVDLEPTHTYYPLDVQEYHLIAERYWP

QNKYLRAIISTIEYFLPAFMKRSLSINEQEQPAERDPLLSPVSPSSPGSQPDKWINHDSRYSRGESSGSN

GHASGSELNGNGNNGTTNRRPLSSASAGSTASDSTLLNGSLNSYANQIIGENDPQLSPTKLKPTGRKYIF

GYHPHGIIGMGAFGGIATEGAGWSKLFPGIPVSLMTLTNNFRVPLYREYLMSLGVASVSKKSCKALLKRN

QSICIVVGGAQESLLARPGVMDLVLLKRKGFVRLGMEVGNVALVPIMAFGENDLYDQVSNDKSSKLYRFQ

QFVKNFLGFTLPLMHARGVFNYDVGLVPYRRPVNIVVGSPIDLPYLPHPTDEEVSEYHDRYIAELQRIYN

EHKDEYFIDWTEEGKGAPEFRMIE*

DGA2 - YALI0D07986

(SEQ ID NO.: 47)

Nucleotide =
atggaagtccgacgacgaaaaatcgacgtgctcaaggcccagaaaaacggctacgaatcgggcccaccat

ctcgacaatcgtcgcagccctcctcaagagcatcgtccagaacccgcaacaaacactcctcgtccaccct

gtcgctcagcggactgaccatgaaagtccagaagaaacctgcgggacccccggcgaactccaaaacgcca

ttcctacacatcaagcccgtgcacacgtgctgctccacatcaatgctttcgcgcgattatgacggctcca

accccagcttcaagggcttcaaaaacatcggcatgatcattctcattgtgggaaatctacggctcgcatt

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ctctcaggcttgctcatagtcgtggcctacgcacatatcctcatggcctacgctattgagagcgctgcca

agctgctgttcctctctagcaaacaccactacatggccgtggggcttctgcataccatgaacactttgtc

gtccatctcgttgctgtcctacgtcgtctactactacctgcccaaccccgtggcaggcacaatagtcgag

tttgtggccgttattctgtctctcaaactcgcctcatacgccctcactaactcggatctccgaaaagccg

caattcatgcccagaagctcgacaagacgcaagacgataacgaaaaggaatccacctcgtcttcctcttc

ttcagatgacgcagagactttggcagacattgacgtcattcctgcatactacgcacagctgccctacccc

cagaatgtgacgctgtcgaacctgctgtacttctggtttgctcccacactggtctaccagcccgtgtacc

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cagtactttagacaccacgtctacgtgcctcttctcgctcggggcatgtcgcggttcaatgcgtcggtgg

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cgccttcttcggcatgatgtcgcaggtgcctctgatcatggctactgagaaccttcagcatattaactcc

tctctgggcccccttccttggcaactgtgcattctggttcacctttttcctgggacaacccacttgtgcat

tcctttattatctggcttacaactacaagcagaaccagtag

(SEQ ID NO.: 48)

Amino Acid =
MEVRRRKIDVLKAQKNGYESGPPSRQSSQPSSRASSRTRNKHSSSTLSLSGLTMKVQKKPAGPPANSKTP

FLHIKPVHTCCSTSMLSRDYDGSNPSFKGFKNIGMIILIVGNLRLAFENYLKYGISNPFFDPKITPSEWQ

LSGLLIVVAYAHILMAYAIESAAKLLFLSSKHHYMAVGLLHTMNTLSSISLLSYVVYYYLPNPVAGTIVE

FVAVILSLKLASYALTNSDLRKAAIHAQKLDKTQDDNEKESTSSSSSDDAETLADIDVIPAYYAQLPYP

QNVTLSNLLYFWFAPTLVYQPVYPKTERIRPKHVIRNLFELVSLCMLIQFLIFQYAYPIMQSCLALFFQP

KLDYANISERLMKLASVSMMVWLIGFYAFFQNGLNLIAELTCFGNRTFYQQWWNSRSIGQYWTLWNKPVN

QYFRHHVYVPLLARGMSRFNASVVVFFFSAVIHELLVGIPTHNIIGAAFFGMMSQVPLIMATENLQHINS

SLGPFLGNCAFWFTFFLGQPTCAFLYYLAYNYKQNQ*

MGA2- YALI0B12342

(SEQ ID NO.: 49)

Nucleotide =
atggctaaagacaaggaaatcgactttgactacacgggagaactggtgatggacgatttcgagttcccca

tcgacgacatgctccacaacgacggagatgactttgtcaagaaggaaacgtgggacgagggttttggttt

cggaacaaatggcgccgtgggtgcgcagatggacgtccagaccagcccatttagcgaccctgtttttggc

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acatgaacagcgtcgtcaagcaggaggactactacacaccgtccatgggcactcccatgaaccccaaca

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(SEQ ID NO.: 50)

Amino Acid =

MAKDKEIDFDYTGELVMDDFEFPIDDMLHNDGDDFVKKETWDEGFGFGTNGAVGAQMDVQTSPFSDPVFG

GVGAGPDMMGLMDTNMNHINGSHNMNSVVKQEDYYTPSMGTPMNPQQQQSMTPQQQHHMNHNQPSQLQSL

HQQSQKAQPQQQQQQPHQSTGVDSIITKAYTRAAGDLPYGRKYSRQLNKYPEDVEYSSFDPSLWSNLLTN

SETPYQYQIHVHSMPGKSRVETQIKCALSIYPPPPQQSVRLPTDTISRPKFQLKQGHIPDSCLSLEVYIV

GEQNPSKPVNLCSRCIKREQKRACRKKLFDESEELSWVETRQRRLAVFNCSEVLEFKDVERRVYIPESGT

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PATAGSSQPPTQVPTPAASSSTSYRPRNSLPLSPTSMEDSSSEFTSDHSHYSNYGSKRRRDGSSISDWSG

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DVVLRCLALTDIPGGRIANWQLTNAEGQTMVHLASILGYSRVLVALVARGARVDVSDNGGFTPLHFAALF

GRRKIAKKLLRCNADPYKRNRIGETVFDVACPHILDLLVGPQGMPMAVQTSYTPDYHRQRRSSSSSTLAS

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AGRGRSHSSISRMWRYLKNSSADEATRSRSRDANGAGAPPAYEEIFPGHGVVHDKKVVQMAAASAAENSS

GPVGASSSAVASTSAAAAVVPSPLAPIVEDEEQLVEAWRRQRRSMANDRMLFAFWLPVLLMAIGYMVIKA

FGLFPDQVSAVESVAETVGVHCRGAVAKLWFKQYPVHRGQPLKDTCSFEPNSLVESALRQMNGWSDREVP

IHQAQAQAA*

Mga2-L36-mutant version

(SEQ ID NO.: 51)

Nucleotide =

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(SEQ ID NO.: 52)

Amino Acid =
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HQQSQKAQPQQQQQQPHQSTGVDSIITKAYTRAAGDLPYGRKYSRQLNKYPEDVEYSSFDPSLWSNLLTN

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GEQNPSKPVNLCSRCIKREQKRACRKKLFDESEELSWVETRQRRLAVFNCSEVLEFKDVERRVYIPESGT

TVTAKQLVLPLRLACYCRHHGEKKGFRILFCLRDEGGQIVGVGQSGTTVMITDDHKVVGDAVAMPTTATA

PATAGSSQPPTQVPTPAASSSTSYRPRNSLPLSPTSMEDSSSEFTSDHSHYSNYGSKRRRDGSSISDWSG

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ELALQVVGLKMNRRLEDARNIAMRIVGNNGGVAGAQGAMAGGNMSNGDVGMESAAADSSVQPVSPPTDHE

DVVLRCLALTDIPGGRIANWQLTNAEGQTMVHLASILGYSRVLVALVARGARVDVSDNGGFTPLHFAALF

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IASIQDSREYGFYDHGMISNLSHIPSTCSIRSSTSQFDAEDEWDERDEEDGDFDDDSDEDSDDDSDALFM

SVRKHAKAKSVESPLSEEEERLVRHIEAEDQAVEARVAAGIVSSNVPDVVSSNDSDHVRSDTSTENKSFS

RYFDRTLSMASWDDVLAYIYRPKRATVPNKRSSGAPPSVRSTRSPLSDHPITSSGDESDRTISAHAPSGG

AGRGRSHSSISRMWRYLKNSSADEATRSRSRDANGAGAPPAYEEIFPGHGVVHDKKVVQMAAASAAENSS

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IHQAQAQAA*

Mga2-truncated version removing of transmembrane span.

(SEQ ID NO.: 53)

Nucleotide =

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(SEQ ID NO.: 54)

Amino Acid =
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GVGAGPDMMGLMDTNMNHINGSHNMNSVVKQEDYYTPSMGTPMNPQQQQSMTPQQQHHMNHNQPSQLQSL

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SETPYQYQIHVHSMPGKSRVETQIKCALSIYPPPPQQSVRLPTDTISRPKFQLKQGHIPDSCLSLEVYIV

GEQNPSKPVNLCSRCIKREQKRACRKKLFDESEELSWVETRQRRLAVFNCSEVLEFKDVERRVYIPESGT

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ELALQVVGLKMNGRLEDARNIAMRIVGNNGGVAGAQGAMAGGNMSNGDVGMESAAADSSVQPVSPPTDHE

DVVLRCLALTDIPGGRIANWQLTNAEGQTMVHLASILGYSRVLVALVARGARVDVSDNGGFTPLHFAALF

GRRKIAKKLLRCNADPYKRNRIGETVFDVACPHILDLLVGPQGMPMAVQTSYTPDYHRQRRSSSSSTLAS

IASIQDSREYGFYDHGMISNLSHIPSTCSIRSSTSQFDAEDEWDERDEEDGDFDDDSDEDSDDDSDALFM

SVRKHAKAKSVESPLSEEEERLVRHIEAEDQAVEARVAAGIVSSNVPDVVSSNDSDHVRSDTSTENKSFS

RYFDRTLSMASWDDVLAYIY*

Sou2L36 YALI0D18964g

(SEQ ID NO.: 55)

Nucleotide =
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ga

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CEN0EL36 YALI0D15444s

(SEQ ID NO.: 56)

Nucleotide =
Cacaaatattcttgatttactttggttttgccctattcggaaattttattgatatctaatagaagtatta

aagtaaaaatgtactaatacttaattgtaatgtcatcagaaataacatttgaggaaaatatttcaaacct

aattgatatatatattagagatgtcccgcttctctgtcattaatatattcaagcaatcga

DEHA0A1298g IPF 95.1 YALI0E33891g

(SEQ ID NO.: 57)

Nucleotide =
Atgaagtccacctccgctactctcctcgcccttgccgcccttgtcgttgccgacaacgccgtcgtctctc

agatcaacgatggccagatccaggctcctcccgctggtggtgagggtgccaagcccgcccctgctccttc

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cggtgctgccaccctcggtgcccagatcgttgccggtgttgtcgccgctgccggtgtcgctctcttctaa

RLF2 chromatin assembly complex subunit p90 YALI0F21637g

(SEQ ID NO.: 58)

Nucleotide =
atggccgacaacaagcctctgtgcacgattaccacgcccgaaccgtcacccaagcgtcgaaagatctctg

ccgaggagaaagaaaagatgcgacttgaaaaggaacagatcaagaagcagaaagaggaagagcgagagca

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gccaccattcagcactatgctgagcgacagggtcctaagagcgacaagcggtgggttctgaaggatatct

ag

TUP1 - YALI0A14542

(SEQ ID NO.: 59)

Nucleotide =
atgagcttcccccaacaagtaatagcgccgggccaacggctcaacgagcttctggaggccatcaaacagg

agttcgactccgtgaccaacgaggcgtccgtctaccggctgcacaaggacgagtttgacgtcaaggtgaa

ccagcagacgtcagatctgggccagattcgacagtcggtctacgagctagaaatggcgcaccgaaagatg

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ggaagtggagattgcaaggctcgaatctggcgatactttcctgtcaacagataa

(SEQ ID NO.: 60)

Amino Acid =
MSFPQQVIAPGQRLNELLEAIKQEFDSVTNEASVYRLHKDEFDVKVNQQTSDLGQIRQSVYELEMAHRKM

KERYEEEIMRLKSELEARGGPAANPAHSQQQQQQQQQQQQQQQNQQAQDQQARAAQQQAAQQQALAQQQ

AAQQQALAQQQAQAQQQAQAQAHHMGGVPPSQGQPPSLLRPSSNVFSGIMSGQPGTSSLAPPQGQPGQPQ

PGQPQPGQPQPYSGYVGANGYTSSPHNGPPVISAMASPNSKKRQVSTPVPGKASPQVAPQEMQQQQQQQG

PPQQQQPPQQQQQSPEEMGNYLGDMDIERVPPELKKQKADWFVVYNQRAPRLLDVDIVQSLDHNSVVCCV

RFSADGKYTATGCNRSAQIFDVQTGQLICRLQDDSVDREGDLYIRSVCFSPDGKYLATGAEDKQIRVWDI

KSQSIRHVFTGHEQDIYSLDFSRNGRHIASGSGDRTVRMWDIESGQCTLTLSIEDGVTTVAISPDGKFVA

AGSLDKSVRIWDTSTGFLVERLEAPDGHKDSVYSVAFTPNGMDLVSGSLDKTIKLWELQAPRGIQANQRG

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GVCVKTLCGHKDFVLSVASTLDGQWILSGSKDRGVQFWDPRTGQVQLMLQGHRNSVISVAPSPMGGLFAT

GSGDCKARIWRYFPVNR*

HAC1 - YALI0B12716

(SEQ ID NO.: 61)

Nucleotide =
atgtctatcaagcgagaagagtcctttactcccacccccgaggacctgggatctcccctgacagctgatt

ctcctggctctcccgagtctggagacaagcgaaagaaggatctcactctgccccttcctgctggtgctct

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acttcaccctgtttgaagacaacaagcagcctgcccagcacgactttattgctgatctag

(SEQ ID NO.: 62)

Amino Acid =
MSIKREESFTPTPEDLGSPLTADSPGSPESGDKRKKDLTLPLPAGALPPRKRAKTENEKEQRRIERIMRN

RQAAHASREKKRRHLEDLEKKCSELSSENNDLHHQVTESKKTNMHLMEQHYSLVAKLQQLSSLVNMAKSS

GALAGVDVPDMSDVSMAPKLEMPTAAPSQPMGLASAPTLFNHDNETVVPDSPIVKTEEVDSTNFLLHTES

SSPPELAESTGSGSPSSTLSCDETDYLVDRARHPAVMTVATTDQQRRHKISFSSRTSPLTTSLDCMDCRM

TSPCLKTTSSLPSTTLLLI*

MRM2- YALI0E31933

(SEQ ID NO.: 63)

Nucleotide =
Atgcgccaaaagctgccgttcaacccgctccagtcgcttctcccgcgaatctttgtgcggggcaaaaaac

acgatgcgcgcagccgctgggaaatgcgccagatgaaagacaagcatgtggccatggccaaggctgacgg

attccggtctcgagccgcgtacaagctacaggaactcgactccatgttccggctgttcaagcccggcatg

acggtggtggatttgggctttgcgcccggcgcatggagtcaagtggctgctcagcgagtgcggcctggag

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gtgcagccagcttcgatgtggcagaagggaagccataa

(SEQ ID NO.: 64)

Amino Acid =
MRQKLPFNPLQSLLPRIFVRGKKHDARSRWEMRQMKDKHVAMAKADGFRSRAAYKLQELDSMFRLFKPGM

TVVDLGFAPGAWSQVAAQRVRPGGRVIGVDILPCIPPPGVSSIQGNFLSKETQNELKRVLAVSAMGVPKD

KDSGGAIGTAPPSYLDTERELGSINSNSNEPQFGDDYPVDIVLSDMCETLPQEHGFFQRTINDPYYRMAN

VSGIAVRDHAASIVSEGRKRIGCGAASFDVAEGKP*

O6M- YALI0C10010p

-continued

(SEQ ID NO.: 65)

Nucleotide =
atgttttacaccaagcccgacccggtggttgattattcccgcctcaaggacatggacatgtatcctgagt

acgacaatggccagaacatgggcttttccaacatgaacatgaccgatctttacgacggcggtcttaacat

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agtatcatcacaacggggagatgttgggtgacatgtgggggactctctaa

(SEQ ID NO.: 66)

Amino Acid =
MFYTKPDPVVDYSRLKDMDMYPEYDNGQNMGFSNMNMTDLYDGGLNMSSMAQPVALNQMGSMGPMGSLSN

MPMGFVSQNQPQTQAQAQAQSQNQNQNQNQNQPQNHNTHVMSDNHNHTHTNNTHNTNVTHNTPSMGGH

TTSVGGHDTNDSAHVGGHASNVTSPTPATPASTSSVPATSPQIPFTVAPPAPSGKYVTDDERWQALVDRD

PEADGAFIYCVTSTKVYCRPTCSARLALRSNIVYFDTMKEAVAAGYRPCRRCNPDVSEMNSQRRAVGSVC

NLIHSLEPDKVPRVKKLAESVGLTLWHFHRLFKRYTGLTPRQYITEPHKRKRLGLPQLQVSKVVTKKSYE

RQQRRQGSNGSTPQQSPQVGASSPAGEVEAIKLETPVETVQPLYYDSNGVTHNAANVGAHSSNVTHNTSH

VGSNATSATSSIATPLSNTTSPDTSTPAQDSAYIIAHGSNASNAAPVVAPGPATGSGDNWIKTEPSMDFM

PRYEPRYDQSISIDAPMFIPDGNEYHHNGEMLGDMWGTL*

CIT1 - YALI0E02684

(SEQ ID NO.: 67)

Nucleotide =
atgatttctgctattcgtcccgccgttcgatcttccgttcgtgttgcccctatggccaacaccgccttcc

gggcctactctacccaggatgtgagtatttcttttctttcatcaattggttgctgtgcgacggatttcgt

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acgctgagctcgttggcctcaagctctaa

(SEQ ID NO.: 68)

Amino acid =
MISAIRPAVRSSVRVAPMANTAFRAYSTQDGLKERFAELIPENVEKIKKLRKEKGNTVIGEVILDQAYGG

MRGIKGLVWEGSVLDPEEGIRFRGLTIPDLQKQLPHAPGGKEPLPEGLFWLLLTGEIPTDAQVKGLSADW

ASRAEIPKHVEELIDRCPPTLHPMAQLGIAVNALESESQFTKAYEKGVNKKEYWQYTYEDSMNLIAKLPV

IASRIYRNLFKDGKIVGSIDNSLDYSANFASLLGFGDNKEFIELLRLYLTIHADHEGGNVSAHTTKLVGS

ALSSPFLSLSAGLNGLAGPLHGRANQEVLEWILEMKSKIGSDVTKEDIEKYLWDTLKAGRVVPGYGHAVL

RKTDPRYTAQREFALEHMPDYDLFHLVSTIYEVAPKVLTEHGKTKNPWPNVDSHSGVLLQYYGLTEQSYY

TVLFGVSRAIGVLPQLIMDRAYGAPIERPKSFSTEKYAELVGLKL*

ACC - YALI0C11407

(SEQ ID NO.: 69)

Nucleotide =
atgcgactgcaattgaggacactaacacgtcggtttttcaggtgagtaaacgacggtggccgtggccacg

acagccgaggcgtcacgatgggccagacgagcacattctcgccgccacaacctcgccagcacaagaaact

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gaaggacgcttctgcccagtcgtttgcttctcaactgagaaaggaccgacagggtactctccagggcatg

aagcaggctctcgcttctctttctgaggctgagcgggctgagctgctcaaggggttgtga

(SEQ ID NO.: 70)

Amino Acid =

MRLQLRTLTRRFFSMASGSSTPDVAPLVDPNIHKGLASHFFGLNSVHTAKPSKVKEFVASHGGHTVINKV

LIANNGIAAVKEIRSVRKWAYETFGDERAISFTVMATPEDLAANADYIRMADQYVEVPGGTNNNNYANVE

LIVDVAERFGVDAVWAGWGHASENPLLPESLAASPRKIVFIGPPGAAMRSLGDKISSTIVAQHAKVPCIP

WSGTGVDEVVVDKSTNLVSVSEEVYTKGCTTGPKQGLEKAKQIGFPVMIKASEGGGGKGIRKVEREEDFE

AAYHQVEGEIPGSPIFIMQLAGNARHLEVQLLADQYGNNISLFGRDCSVQRRHQKIIEEAPVTVAGQQTF

TAMEKAAVRLGKLVGYVSAGTVEYLYSHEDDKFYFLELNPRLQVEHPTTEMVTGVNLPAAQLQIAMGIPL

DRIKDIRLFYGVNPHTTTPIDFDFSGEDADKTQRRPVPRGHTTACRITSEDPGEGFKPSGGTMHELNFRS

SSNVWGYFSVGNQGGIHSFSDSQFGHIFAFGENRSASRKHMVVALKELSIRGDFRTTVEYLIKLLETPDF

EDNTITTGWLDELISNKLTAERPDSFLAVVCGAATKAHRASEDSIATYMASLEKGQVPARDILKTLFPVD

FIYEGQRYKFTATRSSEDSYTLFINGSRCDIGVRPLSDGGILCLVGGRSHNVYWKEEVGATRLSVDSKTC

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ILGILALDDPSKVKHAKPFEGQLPELGPPTLSGNKPHQRYEHCQNVLHNILLGFDNQVVMKSTLQEMVGL

LRNPELPYLQWAHQVSSLHTRMSAKLDATLAGLIDKAKQRGGEFPAKQLLRALEKEASSGEVDALFQQTL

APLFDLAREYQDGLAIHELQVAAGLLQAYYDSEARFCGPNVRDEDVILKLREENRDSLRKVVMAQLSHSR

VGAKNNLVLALLDEYKVADQAGTDSPASNVHVAKYLRPVLRKIVELESRASAKVSLKAREILIQCALPSL

KERTDQLEHILRSSVVESRYGEVGLEHRTPRADILKEVVDSKYIVFDVLAQFFAHDDPWIVLAALELYIR

RACKAYSILDINYHQDSDLPPVISWRFRLPTMSSALYNSVVSSGSKTPTSPSVSRADSVSDFSYTVERDS

APARTGAIVAVPHLDDLEDALTRVLENLPKRGAGLAISVGASNKSAAASARDAAAAAASSVDTGLSNICN

VMIGRVDESDDDDTLIARISQVIEDFKEDFEACSLRRITFSFGNSRGTYPKYFTFRGPAYEEDPTIRHIE

PALAFQLELARLSNFDIKPVHTDNRNIHVYEATGKNAASDKRFFTRGIVRPGRLRENIPTSEYLISEADR

LMSDILDALEVIGTTNSDLNHIFINFSAVFALKPEEVEAAFGGFLERFGRRLWRLRVTGAEIRMMVSDPE

TGSAFPLRAMINNVSGYVVQSELYAEAKNDKGQWIFKSLGKPGSMHMRSINTPYPTKEWLQPKRYKAHLM

GTTYCYDFPELFRQSIESDWKKYDGKAPDDLMTCNELILDEDSGELQEVNREPGANNVGMVAWKFEAKTP

EYPRGRSFIVVANDITFQIGSFGPAEDQFFFKVTELARKLGIPRIYLSANSGARIGIADELVGKYKVAWN

DETDPSKGFKYLYFTPESLATLKPDTVVTTEIEEEGPNGVEKRHVIDYIVGEKDGLGVECLRGSGLIAGA

TSRAYKDIFTLTLVTCRSVGIGAYLVRLGQRAIQIEGQPIILTGAPAINKLLGREVYSSNLQLGGTQIMY

NNGVSHLTARDDLNGVHKIMQWLSYIPASRGLPVPVLPHKTDVWDRDVTFQPVRGEQYDVRWLISGRTLE

DGAFESGLFDKDSFQETLSGWAKGVVVGRARLGGIPFGVIGVETATVDNTTPADPANPDSIEMSTSEAGQ

VWYPNSAFKTSQAINDFNHGEALPLMILANWRGFSGGQRDMYNEVLKYGSFIVDALVDYKQPIMVYIPPT

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GELRGGSWVVVDPTINSDMMEMYADVESRGGVLEPEGMVGIKYRRDKLLDTMARLDPEYSSLKKQLEESP

DSEELKVKLSVREKSLMPIYQQISVQFADLHDRAGRMEAKGVIREALVWKDARRFFFWRIRRRLVEEYLI

TKINSILPSCTRLECLARIKSWKPATLDQGSDRGVAEWFDENSDAVSARLSELKKDASAQSFASQLRKDR

QGTLQGMKQALASLSEAERAELLKGL*

Knockouts:
PEX10 - YALI0C01023g

(SEQ ID NO.: 71)

Nucleotide =
atgtggggaagttcacatgcattcgctggtgaatctgatctgacactacaactacacaccaggtccaaca

tgagcgacaatacgacaatcaaaaagccgatccgacccaaaccgatccggacggaacgcctgccttacgc

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atttccgaatgggtgagagagaagcccgagtgtcccttgtgtcggcagggtgtgagagagcagaacttgt

tgcctatcagataa

(SEQ ID NO.: 72)

Amino acid =
MWGSSHAFAGESDLTLQLHTRSNMSDNTTIKKPIRPKPIRTERLPYAGAAEIIRANQKDHYFESVLEQHL

VTFLQKWKGVRFIHQYKEELETASKFAYLGLCTLVGSKTLGEEYTNLMYTIRDRTALPGVVRRFGYVLSN

TLFPYLFVRYMGKLRAKLMREYPHLVEYDEDEPVPSPETWKERVIKTFVNKFDKFTALEGFTAIHLAIFY

VYGSYYQLSKRIWGMRYVFGHRLDKNEPRIGYEMLGLLIFARFATSFVQTGREYLGALLEKSVEKEAGEK

EDEKEAVVPKKKSSIPFIEDTEGETEDKIDLEDPRQLKFIPEASRACTLCLSYISAPACTPCGHFFCWDC

ISEWVREKPECPLCRQGVREQNLLPIR*

MFE1 - YALI0E15378

(SEQ ID NO.: 73)

Nucleotide =
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accgccatcagcaatgccgccattgagctcttccccaaggatgctaagctctaa

(SEQ ID NO.: 74)

Amino Acid =
MTDKDWDLVYKVHVFGAYKVTRAAWPYFRKQKYGRVISTSSAAGLYGNFGQTNYSAAKLALVGFGETLAK

EGAKYNITSNVIAPLAASRMTETVMPEDILKLLKPEYVVPLVGYLTHDSVTESYGIYEVGAGYMAKIRWE

RGNGAVFKGDDTFTPSAILKRWDEVTSFESPTYPNGPADFFKYAEESVKRPENPQGPTVSFKDQVVIVTG

AGAGIGRAYSHLLAKLGAKVVVNDFGNPQKVVDEIKALGGIAVADKNNVIHGEKVVQTAIDAFGAVHAVV

NNAGILRDKSFANMDDEMWQLIFDVHLNGTYSVTKAAWPHFLKQKYGRVINTTSTSGIYGNFGQANYSAA

KAGILGFSRALAREGEKYNILVNTIAPNAGTAMTASVFTEEMLELFKPDFIAPITVLLASDQAPVTGDLF

ETGSAWIGQTRWQRAGGKAFNTKKGVTPEMVRDSWAKIVDFDDGNSTHPTTPSESTTQILENIFNVPDEE

VEETALVAGPGGPGILNKEGEPFDYTYTYRDLILYNLGLGAKANELKYVFEGDDDFQTVPTFGVIPYMGG

LITTNYGDFVPNFNPMMLLHGEQYLEIRQWPIPTNATLENKAKVIDVVDKGKAALLVTATTTTNKETGEE

VFYNESSLFIRGSGGFGGKSTGTDRGAATAANKPPARAPDFVKEIKIQEDQAAIYRLSGDYNPLHIDPAF

AAVGNFDRPILHGLCSFGVSGKALYDQFGPFKNAKVRFAGHVFPGETLKVEGWKEGNKVIFQTKVVERGT

TAISNAAIELFPKDAKL*

ACO1- YALI0D09361

(SEQ ID NO.: 75)

Nucleotide =
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ttgttgtttgcgacattggctttgtgccggtcccaaaattacctcgaccaaccacacggcggcaattgaa

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tgccctcaacaagatggctgcctccaagaaataa

(SEQ ID NO.: 76)

Amino Acid =
MLASRVSIKAPRLARSLATTTNASLNLDSKVRMNNWEANNFLNFKKHTENVQIVKERLNRPLTYAEKILY

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GHLDKPHEQEIVRGQSYLKLRPDRAACQDATAQMAILQFMSAGIPTVQTPTTVHCDHLIQAQVGGEQDLA

RAIDINKEVYNFLGTASAKYDIGFWKAGSGIIHQIILENYAFPGALLIGSDSHTPNAGGLGMLAIGVGGA

DVVDVMAGLPWELKAPKIIGVKLTGKLSGWTSPKDIILKVAGILTVKGGTGAIVEYFGDGVDNLSCTGMG

TICNMGAEIGATTSTFPFNERMADYLNATGRKEIADFARLYNHFLSADEGCEYDQLIEIDLNTLEPYVNG

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It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

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<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 21

gactggcgcg ccatgttacg actacgaacc atgc 34

<210> SEQ ID NO 22
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 22

gtccttaatt aactagtcgt aatcccgcac atg 33

<210> SEQ ID NO 23
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 23

actgggcgcg ccatggctaa agacaaggaa atcgactttg ac 42

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<210> SEQ ID NO 24
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 24

actgttaatt aatcagtaaa tgtaagccag aacatcgt 38

<210> SEQ ID NO 25
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 25

actgttaatt aatcatgcag cctgggcctg g 31

<210> SEQ ID NO 26
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 26

actgggcgcg ccatgtttta caccaagccc gacccg 36

<210> SEQ ID NO 27
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 27

actgttaatt aattagagag tcccccacat gtcaccc 37

<210> SEQ ID NO 28
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 28

actgggcgcg ccatgcgcca aaagctgccg ttcaac 36

<210> SEQ ID NO 29
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 29

actgttaatt aattatggct tcccttctgc cacatc 36

<210> SEQ ID NO 30
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 30

actgggcgcg ccatgactat cgactcacaa tactac 36

<210> SEQ ID NO 31
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 31

actgttaatt aattactcaa tcattcggaa ctctgg 36

<210> SEQ ID NO 32
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 32

agagggctag agagagggag aa 22

<210> SEQ ID NO 33
<211> LENGTH: 2609
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 33

atgccgcagc aagcaatgga tatcaagggc aaggccaagt ctgtgcccat gcccgaagaa 60

gacgacctgg actcgcattt tgtgggtccc atctctcccc gacctcacgg agcagacgag 120

attgctggct acgtgggctg cgaagacgac gaagacgagc ttgaagaact gggaatgctg 180

ggccgatctg cgtccaccca cttctcttac gcggaagaac gccacctcat cgaggttgat 240

gccaagtaca gagctcttca tggccatctg cctcatcagc actctcagag tcccgtgtcc 300

agatcttcgt catttgtgcg ggccgaaatg aaccaccccc ctcccccacc ctccagccac 360

acccaccaac agccagagga cgatgacgca tcttccactc gatctcgatc gtcgtctcga 420

gcttctggac gcaagttcaa cagaaacaga accaagtctg gatcttcgct gagcaagggt 480

ctccagcagc tcaacatgac cggatcgctc gaagaagagc cctacgagag cgatgacgat 540

gcccgactat ctgcggaaga cgacattgtc tatgatgcta cccagaaaga cacctgcaag 600

cccatatctc ctactctcaa acgcacccgc accaaggacg acatgaagaa catgtccatc 660

aacgacgtca aaatcaccac caccacagaa gatcctcttg tggcccagga gctgtccatg 720

atgttcgaaa aggtgcagta ctgccgagac ctccgagaca agtaccaaac cgtgtcgcta 780

cagaaggacg gagacaaccc caaggatgac aagacacact ggaaaattta ccccgagcct 840

ccaccaccct cctggcacga gaccgaaaag cgattccgag gctcgtccaa aaaggagcac 900

caaaagaaag acccgacaat ggatgaattc aaattcgagg actgcgaaat ccccggaccc 960

aacgacatgg tcttcaagcg agatcctacc tgtgtctatc aggtctatga ggatgaaagc 1020

tctctcaacg aaaataagcc gtttgttgcc atcccctcaa tccgagatta ctacatggat 1080

ctggaggatc tcattgtggc ttcgtctgac ggacctgcca agtcttttgc tttccgacga 1140

ctgcaatatc tagaagccaa gtggaacctc tactacctgc tcaacgagta cacggagaca 1200

accgagtcca agaccaaccc ccatcgagac ttttacaacg tacgaaaggt cgacacccac 1260

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gttcaccact ctgcctgcat gaaccagaag catctgctgc gattcatcaa atacaagatg 1320

aagaactgcc ctgatgaagt tgtcatccac cgagacggtc gggagctgac actctcccag 1380

gtgtttgagt cacttaactt gactgcctac gacctgtcta tcgataccct tgatatgcat 1440

gctcacaagg actcgttcca tcgatttgac aagttcaacc tcaagtacaa ccctgtcggt 1500

gagtctcgac tgcgagaaat cttcctaaag accgacaact acatccaggg tcgataccta 1560

gctgagatca caaaggaggt gttccaggat ctcgagaact cgaagtacca gatggcggag 1620

taccgtattt ccatctacgg tcggtccaag gacgagtggg acaagctggc tgcctgggtg 1680

ctggacaaca aactgttttc gcccaatgtt cggtggttga tccaggtgcc tcgactgtac 1740

gacatttaca agaaggctgg tctggttaac acctttgccg acattgtgca gaacgtcttt 1800

gagcctcttt tcgaggtcac caaggatccc agtacccatc ccaagctgca cgtgttcctg 1860

cagcgagttg tgggctttga ctctgtcgat gacgagtcga agctggaccg acgtttccac 1920

cgaaagttcc caactgcagc atactgggac agcgcacaga accctcccta ctcgtactgg 1980

cagtactatc tatacgccaa catggcctcc atcaacacct ggagacagcg tttgggctat 2040

aatacttttg agttgcgacc ccatgctgga gaggctggtg acccagagca tcttctgtgc 2100

acttatctgg ttgctcaggg tatcaaccac ggtattctgt tgcgaaaggt gcccttcatt 2160

cagtaccttt actacctgga ccagatcccc attgccatgt ctcctgtgtc caacaatgcg 2220

ctgttcctca cgttcgacaa gaaccccttc tactcatact tcaagcgggg tctcaacgtg 2280

tccttgtcat cggatgatcc tctgcagttt gcttacacta aggaggctct gattgaggag 2340

tactctgtgg ctgcgctcat ttacaagctt tccaacgtgg atatgtgtga gcttgctcga 2400

aactcggtac tgcaatctgg ctttgagcga atcatcaagg agcattggat cggcgaaaac 2460

tacgagatcc atggccccga gggcaacacc atccagaaga caaacgtgcc caatgtgcgt 2520

ctggccttcc gagacgagac tttgacccac gagcttgctc tggtggacaa gtacaccaat 2580

cttgaggagt ttgagcggct gcatggtta 2609

<210> SEQ ID NO 34
<211> LENGTH: 869
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 34

Met Pro Gln Gln Ala Met Asp Ile Lys Gly Lys Ala Lys Ser Val Pro
1 5 10 15

Met Pro Glu Glu Asp Asp Leu Asp Ser His Phe Val Gly Pro Ile Ser
20 25 30

Pro Arg Pro His Gly Ala Asp Glu Ile Ala Gly Tyr Val Gly Cys Glu
35 40 45

Asp Asp Glu Asp Glu Leu Glu Glu Leu Gly Met Leu Gly Arg Ser Ala
50 55 60

Ser Thr His Phe Ser Tyr Ala Glu Glu Arg His Leu Ile Glu Val Asp
65 70 75 80

Ala Lys Tyr Arg Ala Leu His Gly His Leu Pro His Gln His Ser Gln
85 90 95

Ser Pro Val Ser Arg Ser Ser Ser Phe Val Arg Ala Glu Met Asn His
100 105 110

Pro Pro Pro Pro Pro Ser Ser His Thr His Gln Gln Pro Glu Asp Asp
115 120 125

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Asp Ala Ser Ser Thr Arg Ser Arg Ser Ser Ser Arg Ala Ser Gly Arg
    130                 135                 140

Lys Phe Asn Arg Asn Arg Thr Lys Ser Gly Ser Ser Leu Ser Lys Gly
145                 150                 155                 160

Leu Gln Gln Leu Asn Met Thr Gly Ser Leu Glu Glu Glu Pro Tyr Glu
                165                 170                 175

Ser Asp Asp Asp Ala Arg Leu Ser Ala Glu Asp Asp Ile Val Tyr Asp
            180                 185                 190

Ala Thr Gln Lys Asp Thr Cys Lys Pro Ile Ser Pro Thr Leu Lys Arg
        195                 200                 205

Thr Arg Thr Lys Asp Asp Met Lys Asn Met Ser Ile Asn Asp Val Lys
    210                 215                 220

Ile Thr Thr Thr Thr Glu Asp Pro Leu Val Ala Gln Glu Leu Ser Met
225                 230                 235                 240

Met Phe Glu Lys Val Gln Tyr Cys Arg Asp Leu Arg Asp Lys Tyr Gln
                245                 250                 255

Thr Val Ser Leu Gln Lys Asp Gly Asp Asn Pro Lys Asp Asp Lys Thr
            260                 265                 270

His Trp Lys Ile Tyr Pro Glu Pro Pro Pro Pro Ser Trp His Glu Thr
        275                 280                 285

Glu Lys Arg Phe Arg Gly Ser Ser Lys Lys Glu His Gln Lys Lys Asp
    290                 295                 300

Pro Thr Met Asp Glu Phe Lys Phe Glu Asp Cys Glu Ile Pro Gly Pro
305                 310                 315                 320

Asn Asp Met Val Phe Lys Arg Asp Pro Thr Cys Val Tyr Gln Val Tyr
                325                 330                 335

Glu Asp Glu Ser Ser Leu Asn Glu Asn Lys Pro Phe Val Ala Ile Pro
            340                 345                 350

Ser Ile Arg Asp Tyr Tyr Met Asp Leu Glu Asp Leu Ile Val Ala Ser
        355                 360                 365

Ser Asp Gly Pro Ala Lys Ser Phe Ala Phe Arg Arg Leu Gln Tyr Leu
    370                 375                 380

Glu Ala Lys Trp Asn Leu Tyr Tyr Leu Leu Asn Glu Tyr Thr Glu Thr
385                 390                 395                 400

Thr Glu Ser Lys Thr Asn Pro His Arg Asp Phe Tyr Asn Val Arg Lys
                405                 410                 415

Val Asp Thr His Val His His Ser Ala Cys Met Asn Gln Lys His Leu
            420                 425                 430

Leu Arg Phe Ile Lys Tyr Lys Met Lys Asn Cys Pro Asp Glu Val Val
        435                 440                 445

Ile His Arg Asp Gly Arg Glu Leu Thr Leu Ser Gln Val Phe Glu Ser
    450                 455                 460

Leu Asn Leu Thr Ala Tyr Asp Leu Ser Ile Asp Thr Leu Asp Met His
465                 470                 475                 480

Ala His Lys Asp Ser Phe His Arg Phe Asp Lys Phe Asn Leu Lys Tyr
                485                 490                 495

Asn Pro Val Gly Glu Ser Arg Leu Arg Glu Ile Phe Leu Lys Thr Asp
            500                 505                 510

Asn Tyr Ile Gln Gly Arg Tyr Leu Ala Glu Ile Thr Lys Glu Val Phe
        515                 520                 525

Gln Asp Leu Glu Asn Ser Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser
    530                 535                 540

Ile Tyr Gly Arg Ser Lys Asp Glu Trp Asp Lys Leu Ala Ala Trp Val
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545                 550                 555                 560

Leu Asp Asn Lys Leu Phe Ser Pro Asn Val Arg Trp Leu Ile Gln Val
                565                 570                 575

Pro Arg Leu Tyr Asp Ile Tyr Lys Lys Ala Gly Leu Val Asn Thr Phe
            580                 585                 590

Ala Asp Ile Val Gln Asn Val Phe Glu Pro Leu Phe Glu Val Thr Lys
        595                 600                 605

Asp Pro Ser Thr His Pro Lys Leu His Val Phe Leu Gln Arg Val Val
    610                 615                 620

Gly Phe Asp Ser Val Asp Asp Glu Ser Lys Leu Asp Arg Arg Phe His
625                 630                 635                 640

Arg Lys Phe Pro Thr Ala Ala Tyr Trp Asp Ser Ala Gln Asn Pro Pro
                645                 650                 655

Tyr Ser Tyr Trp Gln Tyr Tyr Leu Tyr Ala Asn Met Ala Ser Ile Asn
            660                 665                 670

Thr Trp Arg Gln Arg Leu Gly Tyr Asn Thr Phe Glu Leu Arg Pro His
        675                 680                 685

Ala Gly Glu Ala Gly Asp Pro Glu His Leu Leu Cys Thr Tyr Leu Val
    690                 695                 700

Ala Gln Gly Ile Asn His Gly Ile Leu Leu Arg Lys Val Pro Phe Ile
705                 710                 715                 720

Gln Tyr Leu Tyr Tyr Leu Asp Gln Ile Pro Ile Ala Met Ser Pro Val
                725                 730                 735

Ser Asn Asn Ala Leu Phe Leu Thr Phe Asp Lys Asn Pro Phe Tyr Ser
            740                 745                 750

Tyr Phe Lys Arg Gly Leu Asn Val Ser Leu Ser Ser Asp Asp Pro Leu
        755                 760                 765

Gln Phe Ala Tyr Thr Lys Glu Ala Leu Ile Glu Glu Tyr Ser Val Ala
    770                 775                 780

Ala Leu Ile Tyr Lys Leu Ser Asn Val Asp Met Cys Glu Leu Ala Arg
785                 790                 795                 800

Asn Ser Val Leu Gln Ser Gly Phe Glu Arg Ile Ile Lys Glu His Trp
                805                 810                 815

Ile Gly Glu Asn Tyr Glu Ile His Gly Pro Glu Gly Asn Thr Ile Gln
            820                 825                 830

Lys Thr Asn Val Pro Asn Val Arg Leu Ala Phe Arg Asp Glu Thr Leu
        835                 840                 845

Thr His Glu Leu Ala Leu Val Asp Lys Tyr Thr Asn Leu Glu Glu Phe
    850                 855                 860

Glu Arg Leu His Gly
865


<210> SEQ ID NO 35
<211> LENGTH: 1218
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 35

atggaacccg aaactaagaa gaccaagact gactccaaga agattgttct tctcggcggc     60

gacttctgtg gccccgaggt gattgccgag gccgtcaagg tgctcaagtc tgttgctgag    120

gcctccggca ccgagtttgt gtttgaggac cgactcattg gaggagctgc cattgagaag    180

gagggcgagc ccatcaccga cgctactctc gacatctgcc gaaaggctga ctctattatg    240

ctcggtgctg tcggaggcgc tgccaacacc gtatggacca ctcccgacgg acgaaccgac    300
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gtgcgacccg agcagggtct cctcaagctg cgaaaggacc tgaacctgta cgccaacctg    360

cgaccctgcc agctgctgtc gcccaagctc gccgatctct cccccatccg aaacgttgag    420

ggcaccgact tcatcattgt ccgagagctc gtcggaggta tctactttgg agagcgaaag    480

gaggatgacg gatctggcgt cgcttccgac accgagacct actccgttcc tgaggttgag    540

cgaattgccc gaatggccgc cttcctggcc cttcagcaca acccccctct tcccgtgtgg    600

tctcttgaca aggccaacgt gctggcctcc tctcgacttt ggcgaaagac tgtcactcga    660

gtcctcaagg acgaattccc ccagctcgag ctcaaccacc agctgatcga ctcggccgcc    720

atgatcctca tcaagcagcc ctccaagatg aatggtatca tcatcaccac caacatgttt    780

ggcgatatca tctccgacga ggcctccgtc atccccggtt ctctgggtct gctgccctcc    840

gcctctctgg cttctctgcc cgacaccaac gaggcgttcg gtctgtacga gccctgtcac    900

ggatctgccc ccgatctcgg caagcagaag gtcaacccca ttgccaccat tctgtctgcc    960

gccatgatgc tcaagttctc tcttaacatg aagcccgccg gtgacgctgt tgaggctgcc   1020

gtcaaggagt ccgtcgaggc tggtatcact accgccgata tcggaggctc ttcctccacc   1080

tccgaggtcg gagacttgtt gccaacaagg tcaaggagct gctcaagaag gagtaagtcg   1140

tttctacgac gcattgatgg aaggagcaaa ctgacgcgcc tgcgggttgg tctaccggca   1200

gggtccgcta gtgtataa                                                 1218
```

<210> SEQ ID NO 36
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 36

```
Met Glu Pro Glu Thr Lys Lys Thr Lys Thr Asp Ser Lys Lys Ile Val
1               5                   10                  15

Leu Leu Gly Gly Asp Phe Cys Gly Pro Glu Val Ile Ala Glu Ala Val
            20                  25                  30

Lys Val Leu Lys Ser Val Ala Glu Ala Ser Gly Thr Glu Phe Val Phe
        35                  40                  45

Glu Asp Arg Leu Ile Gly Gly Ala Ala Ile Glu Lys Glu Gly Glu Pro
    50                  55                  60

Ile Thr Asp Ala Thr Leu Asp Ile Cys Arg Lys Ala Asp Ser Ile Met
65                  70                  75                  80

Leu Gly Ala Val Gly Gly Ala Ala Asn Thr Val Trp Thr Thr Pro Asp
                85                  90                  95

Gly Arg Thr Asp Val Arg Pro Glu Gln Gly Leu Leu Lys Leu Arg Lys
            100                 105                 110

Asp Leu Asn Leu Tyr Ala Asn Leu Arg Pro Cys Gln Leu Leu Ser Pro
        115                 120                 125

Lys Leu Ala Asp Leu Ser Pro Ile Arg Asn Val Glu Gly Thr Asp Phe
    130                 135                 140

Ile Ile Val Arg Glu Leu Val Gly Gly Ile Tyr Phe Gly Glu Arg Lys
145                 150                 155                 160

Glu Asp Asp Gly Ser Gly Val Ala Ser Asp Thr Glu Thr Tyr Ser Val
                165                 170                 175

Pro Glu Val Glu Arg Ile Ala Arg Met Ala Ala Phe Leu Ala Leu Gln
            180                 185                 190

His Asn Pro Pro Leu Pro Val Trp Ser Leu Asp Lys Ala Asn Val Leu
        195                 200                 205
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Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Thr Arg Val Leu Lys Asp
    210                 215                 220

Glu Phe Pro Gln Leu Glu Leu Asn His Gln Leu Ile Asp Ser Ala Ala
225                 230                 235                 240

Met Ile Leu Ile Lys Gln Pro Ser Lys Met Asn Gly Ile Ile Ile Thr
                245                 250                 255

Thr Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala Ser Val Ile Pro
            260                 265                 270

Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala Ser Leu Pro Asp
        275                 280                 285

Thr Asn Glu Ala Phe Gly Leu Tyr Glu Pro Cys His Gly Ser Ala Pro
    290                 295                 300

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

Ala Met Met Leu Lys Phe Ser Leu Asn Met Lys Pro Ala Gly Asp Ala
                325                 330                 335

Val Glu Ala Ala Val Lys Glu Ser Val Glu Ala Gly Ile Thr Thr Ala
            340                 345                 350

Asp Ile Gly Gly Ser Ser Ser Thr Ser Glu Val Gly Asp Leu Leu Pro
        355                 360                 365

Thr Arg Ser Arg Ser Cys Ser Arg Arg Ser Lys Ser Phe Leu Arg Arg
    370                 375                 380

Ile Asp Gly Arg Ser Lys Leu Thr Arg Leu Arg Val Gly Leu Pro Ala
385                 390                 395                 400


<210> SEQ ID NO 37
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 37

atgccctcct acgaagctcg agctaacgtc cacaagtccg cctttgccgc tcgagtgctc     60

aagctcgtgg cagccaagaa aaccaacctg tgtgcttctc tggatgttac caccaccaag    120

gagctcattg agcttgccga taaggtcgga ccttatgtgt gcatgatcaa gacccatatc    180

gacatcattg acgacttcac ctacgccggc actgtgctcc ccctcaagga acttgctctt    240

aagcacggtt tcttcctgtt cgaggacaga aagttcgcag atattggcaa cactgtcaag    300

caccagtaca agaacggtgt ctaccgaatc gccgagtggt ccgatatcac caacgcccac    360

ggtgtacccg gaaccggaat cattgctggc ctgcgagctg gtgccgagga aactgtctct    420

gaacagaaga aggaggacgt ctctgactac gagaactccc agtacaagga gttcctggtc    480

ccctctccca acgagaagct ggccagaggt ctgctcatgc tggccgagct gtcttgcaag    540

ggctctctgg ccactggcga gtactccaag cagaccattg agcttgcccg atccgacccc    600

gagtttgtgg ttggcttcat tgcccagaac cgacctaagg gcgactctga ggactggctt    660

attctgaccc ccggggtggg tcttgacgac aagggagacg ctctcggaca gcagtaccga    720

actgttgagg atgtcatgtc taccggaacg gatatcataa ttgtcggccg aggtctgtac    780

ggccagaacc gagatcctat tgaggaggcc aagcgatacc agaaggctgg ctgggaggct    840

taccagaaga ttaactgtta g                                              861


<210> SEQ ID NO 38
<211> LENGTH: 286
<212> TYPE: PRT
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<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 38

Met Pro Ser Tyr Glu Ala Arg Ala Asn Val His Lys Ser Ala Phe Ala
1 5 10 15

Ala Arg Val Leu Lys Leu Val Ala Ala Lys Lys Thr Asn Leu Cys Ala
20 25 30

Ser Leu Asp Val Thr Thr Thr Lys Glu Leu Ile Glu Leu Ala Asp Lys
35 40 45

Val Gly Pro Tyr Val Cys Met Ile Lys Thr His Ile Asp Ile Ile Asp
50 55 60

Asp Phe Thr Tyr Ala Gly Thr Val Leu Pro Leu Lys Glu Leu Ala Leu
65 70 75 80

Lys His Gly Phe Phe Leu Phe Glu Asp Arg Lys Phe Ala Asp Ile Gly
85 90 95

Asn Thr Val Lys His Gln Tyr Lys Asn Gly Val Tyr Arg Ile Ala Glu
100 105 110

Trp Ser Asp Ile Thr Asn Ala His Gly Val Pro Gly Thr Gly Ile Ile
115 120 125

Ala Gly Leu Arg Ala Gly Ala Glu Glu Thr Val Ser Glu Gln Lys Lys
130 135 140

Glu Asp Val Ser Asp Tyr Glu Asn Ser Gln Tyr Lys Glu Phe Leu Val
145 150 155 160

Pro Ser Pro Asn Glu Lys Leu Ala Arg Gly Leu Leu Met Leu Ala Glu
165 170 175

Leu Ser Cys Lys Gly Ser Leu Ala Thr Gly Glu Tyr Ser Lys Gln Thr
180 185 190

Ile Glu Leu Ala Arg Ser Asp Pro Glu Phe Val Val Gly Phe Ile Ala
195 200 205

Gln Asn Arg Pro Lys Gly Asp Ser Glu Asp Trp Leu Ile Leu Thr Pro
210 215 220

Gly Val Gly Leu Asp Asp Lys Gly Asp Ala Leu Gly Gln Gln Tyr Arg
225 230 235 240

Thr Val Glu Asp Val Met Ser Thr Gly Thr Asp Ile Ile Ile Val Gly
245 250 255

Arg Gly Leu Tyr Gly Gln Asn Arg Asp Pro Ile Glu Glu Ala Lys Arg
260 265 270

Tyr Gln Lys Ala Gly Trp Glu Ala Tyr Gln Lys Ile Asn Cys
275 280 285

<210> SEQ ID NO 39
<211> LENGTH: 1953
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 39

atgtctgcca acgagaacat ctcccgattc gacgcccctg tgggcaagga gcaccccgcc 60

tacgagctct tccataacca cacacgatct ttcgtctatg gtctccagcc tcgagcctgc 120

cagggtatgc tggacttcga cttcatctgt aagcgagaga acccctccgt ggccggtgtc 180

atctatccct tcggcggcca gttcgtcacc aagatgtact ggggcaccaa ggagactctt 240

ctccctgtct accagcaggt cgagaaggcc gctgccaagc accccgaggt cgatgtcgtg 300

gtcaactttg cctcctctcg atccgtctac tcctctacca tggagctgct cgagtacccc 360

cagttccgaa ccatcgccat tattgccgag ggtgtccccg agcgacgagc ccgagagatc 420

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ctccacaagg cccagaagaa gggtgtgacc atcattggtc ccgctaccgt cggaggtatc    480

aagcccggtt gcttcaaggt tggaaacacc ggaggtatga tggacaacat tgtcgcctcc    540

aagctctacc gacccggctc cgttgcctac gtctccaagt ccggaggaat gtccaacgag    600

ctgaacaaca ttatctctca caccaccgac ggtgtctacg agggtattgc tattggtggt    660

gaccgatacc ctggtactac cttcattgac catatcctgc gatacgaggc cgaccccaag    720

tgtaagatca tcgtcctcct tggtgaggtt ggtggtgttg aggagtaccg agtcatcgag    780

gctgttaaga acggccagat caagaagccc atcgtcgctt gggccattgg tacttgtgcc    840

tccatgttca agactgaggt tcagttcggc cacgccggct ccatggccaa ctccgacctg    900

gagactgcca aggctaagaa cgccgccatg aagtctgctg gcttctacgt ccccgatacc    960

ttcgaggaca tgcccgaggt ccttgccgag ctctacgaga agatggtcgc caagggcgag   1020

ctgtctcgaa tctctgagcc tgaggtcccc aagatcccca ttgactactc ttgggcccag   1080

gagcttggtc ttatccgaaa gcccgctgct ttcatctcca ctatttccga tgaccgaggc   1140

caggagcttc tgtacgctgg catgcccatt tccgaggttt tcaaggagga cattggtatc   1200

ggcggtgtca tgtctctgct gtggttccga cgacgactcc ccgactacgc ctccaagttt   1260

cttgagatgg ttctcatgct tactgctgac cacggtcccg ccgtatccgg tgccatgaac   1320

accattatca ccacccgagc tggtaaggat ctcatttctt ccctggttgc tggtctcctg   1380

accattggta cccgattcgg aggtgctctt gacggtgctg ccaccgagtt caccactgcc   1440

tacgacaagg gtctgtcccc ccgacagttc gttgatacca tgcgaaagca gaacaagctg   1500

attcctggta ttggccatcg agtcaagtct cgaaacaacc ccgatttccg agtcgagctt   1560

gtcaaggact ttgttaagaa gaacttcccc tccacccagc tgctcgacta cgcccttgct   1620

gtcgaggagg tcaccacctc caagaaggac aacctgattc tgaacgttga cggtgctatt   1680

gctgtttctt ttgtcgatct catgcgatct tgcggtgcct ttactgtgga ggagactgag   1740

gactacctca agaacggtgt tctcaacggt ctgttcgttc tcggtcgatc cattggtctc   1800

attgcccacc atctcgatca gaagcgactc aagaccggtc tgtaccgaca tccttgggac   1860

gatatcacct acctggttgg ccaggaggct atccagaaga agcgagtcga gatcagcgcc   1920

ggcgacgttt ccaaggccaa gactcgatca tag                                1953
```

<210> SEQ ID NO 40
<211> LENGTH: 650
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 40

```
Met Ser Ala Asn Glu Asn Ile Ser Arg Phe Asp Ala Pro Val Gly Lys
1               5                  10                  15

Glu His Pro Ala Tyr Glu Leu Phe His Asn His Thr Arg Ser Phe Val
            20                  25                  30

Tyr Gly Leu Gln Pro Arg Ala Cys Gln Gly Met Leu Asp Phe Asp Phe
        35                  40                  45

Ile Cys Lys Arg Glu Asn Pro Ser Val Ala Gly Val Ile Tyr Pro Phe
    50                  55                  60

Gly Gly Gln Phe Val Thr Lys Met Tyr Trp Gly Thr Lys Glu Thr Leu
65                  70                  75                  80

Leu Pro Val Tyr Gln Gln Val Glu Lys Ala Ala Ala Lys His Pro Glu
                85                  90                  95
```

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```
Val Asp Val Val Val Asn Phe Ala Ser Ser Arg Ser Val Tyr Ser Ser
            100                 105                 110

Thr Met Glu Leu Leu Glu Tyr Pro Gln Phe Arg Thr Ile Ala Ile Ile
        115                 120                 125

Ala Glu Gly Val Pro Glu Arg Arg Ala Arg Glu Ile Leu His Lys Ala
    130                 135                 140

Gln Lys Lys Gly Val Thr Ile Ile Gly Pro Ala Thr Val Gly Gly Ile
145                 150                 155                 160

Lys Pro Gly Cys Phe Lys Val Gly Asn Thr Gly Gly Met Met Asp Asn
                165                 170                 175

Ile Val Ala Ser Lys Leu Tyr Arg Pro Gly Ser Val Ala Tyr Val Ser
            180                 185                 190

Lys Ser Gly Gly Met Ser Asn Glu Leu Asn Asn Ile Ile Ser His Thr
        195                 200                 205

Thr Asp Gly Val Tyr Glu Gly Ile Ala Ile Gly Gly Asp Arg Tyr Pro
    210                 215                 220

Gly Thr Thr Phe Ile Asp His Ile Leu Arg Tyr Glu Ala Asp Pro Lys
225                 230                 235                 240

Cys Lys Ile Ile Val Leu Leu Gly Glu Val Gly Gly Val Glu Glu Tyr
                245                 250                 255

Arg Val Ile Glu Ala Val Lys Asn Gly Gln Ile Lys Lys Pro Ile Val
            260                 265                 270

Ala Trp Ala Ile Gly Thr Cys Ala Ser Met Phe Lys Thr Glu Val Gln
        275                 280                 285

Phe Gly His Ala Gly Ser Met Ala Asn Ser Asp Leu Glu Thr Ala Lys
    290                 295                 300

Ala Lys Asn Ala Ala Met Lys Ser Ala Gly Phe Tyr Val Pro Asp Thr
305                 310                 315                 320

Phe Glu Asp Met Pro Glu Val Leu Ala Glu Leu Tyr Glu Lys Met Val
                325                 330                 335

Ala Lys Gly Glu Leu Ser Arg Ile Ser Glu Pro Glu Val Pro Lys Ile
            340                 345                 350

Pro Ile Asp Tyr Ser Trp Ala Gln Glu Leu Gly Leu Ile Arg Lys Pro
        355                 360                 365

Ala Ala Phe Ile Ser Thr Ile Ser Asp Asp Arg Gly Gln Glu Leu Leu
    370                 375                 380

Tyr Ala Gly Met Pro Ile Ser Glu Val Phe Lys Glu Asp Ile Gly Ile
385                 390                 395                 400

Gly Gly Val Met Ser Leu Leu Trp Phe Arg Arg Arg Leu Pro Asp Tyr
                405                 410                 415

Ala Ser Lys Phe Leu Glu Met Val Leu Met Leu Thr Ala Asp His Gly
            420                 425                 430

Pro Ala Val Ser Gly Ala Met Asn Thr Ile Ile Thr Thr Arg Ala Gly
        435                 440                 445

Lys Asp Leu Ile Ser Ser Leu Val Ala Gly Leu Leu Thr Ile Gly Thr
    450                 455                 460

Arg Phe Gly Gly Ala Leu Asp Gly Ala Ala Thr Glu Phe Thr Thr Ala
465                 470                 475                 480

Tyr Asp Lys Gly Leu Ser Pro Arg Gln Phe Val Asp Thr Met Arg Lys
                485                 490                 495

Gln Asn Lys Leu Ile Pro Gly Ile Gly His Arg Val Lys Ser Arg Asn
            500                 505                 510

Asn Pro Asp Phe Arg Val Glu Leu Val Lys Asp Phe Val Lys Lys Asn
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        515                 520                 525

Phe Pro Ser Thr Gln Leu Leu Asp Tyr Ala Leu Ala Val Glu Glu Val
    530                 535                 540

Thr Thr Ser Lys Lys Asp Asn Leu Ile Leu Asn Val Asp Gly Ala Ile
545                 550                 555                 560

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

Glu Glu Thr Glu Asp Tyr Leu Lys Asn Gly Val Leu Asn Gly Leu Phe
            580                 585                 590

Val Leu Gly Arg Ser Ile Gly Leu Ile Ala His His Leu Asp Gln Lys
        595                 600                 605

Arg Leu Lys Thr Gly Leu Tyr Arg His Pro Trp Asp Asp Ile Thr Tyr
    610                 615                 620

Leu Val Gly Gln Glu Ala Ile Gln Lys Lys Arg Val Glu Ile Ser Ala
625                 630                 635                 640

Gly Asp Val Ser Lys Ala Lys Thr Arg Ser
                645                 650


<210> SEQ ID NO 41
<211> LENGTH: 1494
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 41

atgtcagcga aatccattca cgaggccgac ggcaaggccc tgctcgcaca ctttctgtcc     60

aaggcgcccg tgtgggccga gcagcagccc atcaacacgt ttgaaatggg cacacccaag    120

ctggcgtctc tgacgttcga ggacggcgtg gcccccgagc agatcttcgc cgccgctgaa    180

aagacctacc cctggctgct ggagtccggc gccaagtttg tggccaagcc cgaccagctc    240

atcaagcgac gaggcaaggc cggcctgctg gtactcaaca agtcgtggga ggagtgcaag    300

ccctggatcg ccgagcgggc cgccaagccc atcaacgtgg agggcattga cggagtgctg    360

cgaacgttcc tggtcgagcc ctttgtgccc cacgaccaga agcacgagta ctacatcaac    420

atccactccg tgcgagaggg cgactggatc ctcttctacc acgagggagg agtcgacgtc    480

ggcgacgtgg acgccaaggc cgccaagatc ctcatccccg ttgacattga gaacgagtac    540

ccctccaacg ccacgctcac caaggagctg ctggcacacg tgcccgagga ccagcaccag    600

accctgctcg acttcatcaa ccggctctac gccgtctacg tcgatctgca gtttacgtat    660

ctggagatca acccctggt cgtgatcccc accgcccagg gcgtcgaggt ccactacctg    720

gatcttgccg gcaagctcga ccagaccgca gagtttgagt gcggccccaa gtgggctgct    780

gcgcggtccc ccgccgctct gggccaggtc gtcaccattg acgccggctc caccaaggtg    840

tccatcgacg ccggccccgc catggtcttc cccgctcctt tcggtcgaga gctgtccaag    900

gaggaggcgt acattgcgga gctcgattcc aagaccggag cttctctgaa gctgactgtt    960

ctcaatgcca agggccgaat ctggaccctt gtggctggtg gaggagcctc cgtcgtctac   1020

gccgacgcca ttgcgtctgc cggctttgct gacgagctcg ccaactacgg cgagtactct   1080

ggcgctccca acgagaccca gacctacgag tacgccaaaa ccgtactgga tctcatgacc   1140

cggggcgacg ctcaccccga gggcaaggta ctgttcattg gcggaggaat cgccaacttc   1200

acccaggttg gatccacctt caagggcatc atccgggcct tccgggacta ccagtcttct   1260

ctgcacaacc acaaggtgaa gatttacgtg cgacgaggcg gtcccaactg gcaggagggt   1320

ctgcggttga tcaagtcggc tggcgacgag ctgaatctgc ccatggagat ttacggcccc   1380
```

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gacatgcacg tgtcgggtat tgttcctttg gctctgcttg gaaagcggcc caagaatgtc 1440

aagccttttg gcaccggacc ttctactgag gcttccactc ctctcggagt ttaa 1494

<210> SEQ ID NO 42
<211> LENGTH: 497
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 42

Met Ser Ala Lys Ser Ile His Glu Ala Asp Gly Lys Ala Leu Leu Ala
1 5 10 15

His Phe Leu Ser Lys Ala Pro Val Trp Ala Glu Gln Gln Pro Ile Asn
20 25 30

Thr Phe Glu Met Gly Thr Pro Lys Leu Ala Ser Leu Thr Phe Glu Asp
35 40 45

Gly Val Ala Pro Glu Gln Ile Phe Ala Ala Ala Glu Lys Thr Tyr Pro
50 55 60

Trp Leu Leu Glu Ser Gly Ala Lys Phe Val Ala Lys Pro Asp Gln Leu
65 70 75 80

Ile Lys Arg Arg Gly Lys Ala Gly Leu Leu Val Leu Asn Lys Ser Trp
85 90 95

Glu Glu Cys Lys Pro Trp Ile Ala Glu Arg Ala Ala Lys Pro Ile Asn
100 105 110

Val Glu Gly Ile Asp Gly Val Leu Arg Thr Phe Leu Val Glu Pro Phe
115 120 125

Val Pro His Asp Gln Lys His Glu Tyr Tyr Ile Asn Ile His Ser Val
130 135 140

Arg Glu Gly Asp Trp Ile Leu Phe Tyr His Glu Gly Gly Val Asp Val
145 150 155 160

Gly Asp Val Asp Ala Lys Ala Ala Lys Ile Leu Ile Pro Val Asp Ile
165 170 175

Glu Asn Glu Tyr Pro Ser Asn Ala Thr Leu Thr Lys Glu Leu Leu Ala
180 185 190

His Val Pro Glu Asp Gln His Gln Thr Leu Leu Asp Phe Ile Asn Arg
195 200 205

Leu Tyr Ala Val Tyr Val Asp Leu Gln Phe Thr Tyr Leu Glu Ile Asn
210 215 220

Pro Leu Val Val Ile Pro Thr Ala Gln Gly Val Glu Val His Tyr Leu
225 230 235 240

Asp Leu Ala Gly Lys Leu Asp Gln Thr Ala Glu Phe Glu Cys Gly Pro
245 250 255

Lys Trp Ala Ala Ala Arg Ser Pro Ala Ala Leu Gly Gln Val Val Thr
260 265 270

Ile Asp Ala Gly Ser Thr Lys Val Ser Ile Asp Ala Gly Pro Ala Met
275 280 285

Val Phe Pro Ala Pro Phe Gly Arg Glu Leu Ser Lys Glu Glu Ala Tyr
290 295 300

Ile Ala Glu Leu Asp Ser Lys Thr Gly Ala Ser Leu Lys Leu Thr Val
305 310 315 320

Leu Asn Ala Lys Gly Arg Ile Trp Thr Leu Val Ala Gly Gly Gly Ala
325 330 335

Ser Val Val Tyr Ala Asp Ala Ile Ala Ser Ala Gly Phe Ala Asp Glu
340 345 350

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```
Leu Ala Asn Tyr Gly Glu Tyr Ser Gly Ala Pro Asn Glu Thr Gln Thr
        355                 360                 365

Tyr Glu Tyr Ala Lys Thr Val Leu Asp Leu Met Thr Arg Gly Asp Ala
    370                 375                 380

His Pro Glu Gly Lys Val Leu Phe Ile Gly Gly Gly Ile Ala Asn Phe
385                 390                 395                 400

Thr Gln Val Gly Ser Thr Phe Lys Gly Ile Ile Arg Ala Phe Arg Asp
                405                 410                 415

Tyr Gln Ser Ser Leu His Asn His Lys Val Lys Ile Tyr Val Arg Arg
            420                 425                 430

Gly Gly Pro Asn Trp Gln Glu Gly Leu Arg Leu Ile Lys Ser Ala Gly
        435                 440                 445

Asp Glu Leu Asn Leu Pro Met Glu Ile Tyr Gly Pro Asp Met His Val
    450                 455                 460

Ser Gly Ile Val Pro Leu Ala Leu Leu Gly Lys Arg Pro Lys Asn Val
465                 470                 475                 480

Lys Pro Phe Gly Thr Gly Pro Ser Thr Glu Ala Ser Thr Pro Leu Gly
                485                 490                 495

Val
```

<210> SEQ ID NO 43
<211> LENGTH: 1890
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 43

```
atgttacgac tacgaaccat gcgacccaca cagaccagcg tcagggcggc gcttgggccc     60

accgctgcgg cccgaaacat gtcctcctcc agcccctcca gcttcgaata ctcgtcctac    120

gtcaagggca cgcgggaaat cggccaccga aaggcgccca caacccgtct gtcggttgag    180

ggccccatct acgtgggctt cgacggcatt cgtcttctca acctgccgca tctcaacaag    240

ggctcgggat tccccctcaa cgagcgacgg gaattcggac tcagtggtct tctgccctct    300

gccgaagcca ccctggagga acaggtcgac cgagcatacc aacaattcaa aaagtgtggc    360

actcccttag ccaaaaacgg gttctgcacc tcgctcaagt tccaaaacga ggtgctctac    420

tacgccctgc tgctcaagca cgttaaggag gtcttcccca tcatctatac accgactcag    480

ggagaagcca ttgaacagta ctcgcggctg ttccggcggc ccgaaggctg cttcctcgac    540

atcaccagtc cctacgacgt ggaggagcgt ctgggagcgt ttggagacca tgacgacatt    600

gactacattg tcgtgactga ctccgagggt attctcggaa ttggagacca aggagtgggc    660

ggtattggta tttccatcgc caagctggct ctcatgactc tatgtgctgg agtcaacccc    720

tcacgagtca ttcctgtggt tctggatacg ggaaccaaca accaggagct gctgcacgac    780

cccctgtatc tcggccgacg aatgccccga gtgcgaggaa agcagtacga cgacttcatc    840

gacaactttg tgcagtctgc ccgaaggctg tatcccaagg cggtgatcca tttcgaggac    900

tttgggctcg ctaacgcaca caagatcctc gacaagtatc gaccggagat cccctgcttc    960

aacgacgaca tccagggcac tggagccgtc actctggcct ccatcacggc cgctctcaag   1020

gtgctgggca aaaatatcac agatactcga attctcgtgt acggagctgg ttcggccggc   1080

atgggtattg ctgaacaggt ctatgataac ctggttgccc agggtctcga cgacaagact   1140

gcgcgacaaa acatctttct catggaccga ccgggtctac tgaccaccgc acttaccgac   1200
```

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gagcagatga gcgacgtgca gaagccgttt gccaaggaca aggccaatta cgagggagtg 1260

gacaccaaga ctctggagca cgtggttgct gccgtcaagc cccatattct cattggatgt 1320

tccactcagc ccggcgcctt taacgagaag gttgtcaagg agatgcttaa acacacccct 1380

cgacccatca ttctccctct ttccaacccc acacgtcttc atgaggctgt ccctgcagat 1440

ctgtacaagt ggaccgacgg caaggctctg gttgccaccg gctcgccctt tgacccagtc 1500

aacggcaagg agacgtctga gaacaataac tgctttgttt tccccggaat cgggctggga 1560

gccattctgt ctcgatcaaa gctcatcacc aacaccatga ttgctgctgc catcgagtgc 1620

ctcgccgaac aggcccccat tctcaagaac cacgacgagg gagtacttcc cgacgtagct 1680

ctcatccaga tcatttcggc ccgggtggcc actgccgtgg ttcttcaggc caaggctgag 1740

ggcctagcca ctgtcgagga agagctcaag cccggcacca aggaacatgt gcagattccc 1800

gacaactttg acgagtgtct cgcctgggtc gagactcaga tgtggcggcc cgtctaccgg 1860

cctctcatcc atgtgcggga ttacgactag 1890

<210> SEQ ID NO 44
<211> LENGTH: 629
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 44

Met Leu Arg Leu Arg Thr Met Arg Pro Thr Gln Thr Ser Val Arg Ala
1 5 10 15

Ala Leu Gly Pro Thr Ala Ala Ala Arg Asn Met Ser Ser Ser Ser Pro
20 25 30

Ser Ser Phe Glu Tyr Ser Ser Tyr Val Lys Gly Thr Arg Glu Ile Gly
35 40 45

His Arg Lys Ala Pro Thr Thr Arg Leu Ser Val Glu Gly Pro Ile Tyr
50 55 60

Val Gly Phe Asp Gly Ile Arg Leu Leu Asn Leu Pro His Leu Asn Lys
65 70 75 80

Gly Ser Gly Phe Pro Leu Asn Glu Arg Arg Glu Phe Gly Leu Ser Gly
85 90 95

Leu Leu Pro Ser Ala Glu Ala Thr Leu Glu Glu Gln Val Asp Arg Ala
100 105 110

Tyr Gln Gln Phe Lys Lys Cys Gly Thr Pro Leu Ala Lys Asn Gly Phe
115 120 125

Cys Thr Ser Leu Lys Phe Gln Asn Glu Val Leu Tyr Tyr Ala Leu Leu
130 135 140

Leu Lys His Val Lys Glu Val Phe Pro Ile Ile Tyr Thr Pro Thr Gln
145 150 155 160

Gly Glu Ala Ile Glu Gln Tyr Ser Arg Leu Phe Arg Arg Pro Glu Gly
165 170 175

Cys Phe Leu Asp Ile Thr Ser Pro Tyr Asp Val Glu Glu Arg Leu Gly
180 185 190

Ala Phe Gly Asp His Asp Asp Ile Asp Tyr Ile Val Val Thr Asp Ser
195 200 205

Glu Gly Ile Leu Gly Ile Gly Asp Gln Gly Val Gly Gly Ile Gly Ile
210 215 220

Ser Ile Ala Lys Leu Ala Leu Met Thr Leu Cys Ala Gly Val Asn Pro
225 230 235 240

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```
Ser Arg Val Ile Pro Val Val Leu Asp Thr Gly Thr Asn Asn Gln Glu
                245                 250                 255

Leu Leu His Asp Pro Leu Tyr Leu Gly Arg Arg Met Pro Arg Val Arg
            260                 265                 270

Gly Lys Gln Tyr Asp Asp Phe Ile Asp Asn Phe Val Gln Ser Ala Arg
        275                 280                 285

Arg Leu Tyr Pro Lys Ala Val Ile His Phe Glu Asp Phe Gly Leu Ala
    290                 295                 300

Asn Ala His Lys Ile Leu Asp Lys Tyr Arg Pro Glu Ile Pro Cys Phe
305                 310                 315                 320

Asn Asp Asp Ile Gln Gly Thr Gly Ala Val Thr Leu Ala Ser Ile Thr
                325                 330                 335

Ala Ala Leu Lys Val Leu Gly Lys Asn Ile Thr Asp Thr Arg Ile Leu
            340                 345                 350

Val Tyr Gly Ala Gly Ser Ala Gly Met Gly Ile Ala Glu Gln Val Tyr
        355                 360                 365

Asp Asn Leu Val Ala Gln Gly Leu Asp Asp Lys Thr Ala Arg Gln Asn
    370                 375                 380

Ile Phe Leu Met Asp Arg Pro Gly Leu Leu Thr Thr Ala Leu Thr Asp
385                 390                 395                 400

Glu Gln Met Ser Asp Val Gln Lys Pro Phe Ala Lys Asp Lys Ala Asn
                405                 410                 415

Tyr Glu Gly Val Asp Thr Lys Thr Leu Glu His Val Val Ala Ala Val
            420                 425                 430

Lys Pro His Ile Leu Ile Gly Cys Ser Thr Gln Pro Gly Ala Phe Asn
        435                 440                 445

Glu Lys Val Val Lys Glu Met Leu Lys His Thr Pro Arg Pro Ile Ile
    450                 455                 460

Leu Pro Leu Ser Asn Pro Thr Arg Leu His Glu Ala Val Pro Ala Asp
465                 470                 475                 480

Leu Tyr Lys Trp Thr Asp Gly Lys Ala Leu Val Ala Thr Gly Ser Pro
                485                 490                 495

Phe Asp Pro Val Asn Gly Lys Glu Thr Ser Glu Asn Asn Asn Cys Phe
            500                 505                 510

Val Phe Pro Gly Ile Gly Leu Gly Ala Ile Leu Ser Arg Ser Lys Leu
        515                 520                 525

Ile Thr Asn Thr Met Ile Ala Ala Ala Ile Glu Cys Leu Ala Glu Gln
    530                 535                 540

Ala Pro Ile Leu Lys Asn His Asp Glu Gly Val Leu Pro Asp Val Ala
545                 550                 555                 560

Leu Ile Gln Ile Ile Ser Ala Arg Val Ala Thr Ala Val Val Leu Gln
                565                 570                 575

Ala Lys Ala Glu Gly Leu Ala Thr Val Glu Glu Glu Leu Lys Pro Gly
            580                 585                 590

Thr Lys Glu His Val Gln Ile Pro Asp Asn Phe Asp Glu Cys Leu Ala
        595                 600                 605

Trp Val Glu Thr Gln Met Trp Arg Pro Val Tyr Arg Pro Leu Ile His
    610                 615                 620

Val Arg Asp Tyr Asp
625
```

<210> SEQ ID NO 45
<211> LENGTH: 1545
<212> TYPE: DNA

-continued

<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 45

atgactatcg actcacaata ctacaagtcg cgagacaaaa acgacacggc acccaaaatc 60

gcgggaatcc gatatgcccc gctatcgaca ccattactca accgatgtga gaccttctct 120

ctggtctggc acattttcag cattcccact ttcctcacaa ttttcatgct atgctgcgca 180

attccactgc tctggccatt tgtgattgcg tatgtagtgt acgctgttaa agacgactcc 240

ccgtccaacg gaggagtggt caagcgatac tcgcctattt caagaaactt cttcatctgg 300

aagctctttg gccgctactt ccccataact ctgcacaaga cggtggatct ggagcccacg 360

cacacatact accctctgga cgtccaggag tatcacctga ttgctgagag atactggccg 420

cagaacaagt acctccgagc aatcatctcc accatcgagt actttctgcc cgccttcatg 480

aaacggtctc tttctatcaa cgagcaggag cagcctgccg agcgagatcc tctcctgtct 540

cccgtttctc ccagctctcc gggttctcaa cctgacaagt ggattaacca cgacagcaga 600

tatagccgtg gagaatcatc tggctccaac ggccacgcct cgggctccga acttaacggc 660

aacggcaaca atggcaccac taaccgacga cctttgtcgt ccgcctctgc tggctccact 720

gcatctgatt ccacgcttct taacgggtcc ctcaactcct acgccaacca gatcattggc 780

gaaaacgacc cacagctgtc gcccacaaaa ctcaagccca ctggcagaaa atacatcttc 840

ggctaccacc cccacggcat tatcggcatg ggagcctttg gtggaattgc caccgaggga 900

gctggatggt ccaagctctt tccgggcatc cctgtttctc ttatgactct caccaacaac 960

ttccgagtgc ctctctacag agagtacctc atgagtctgg gagtcgcttc tgtctccaag 1020

aagtcctgca aggccctcct caagcgaaac cagtctatct gcattgtcgt tggtggagca 1080

caggaaagtc ttctggccag acccggtgtc atggacctgg tgctactcaa gcgaaagggt 1140

tttgttcgac ttggtatgga ggtcggaaat gtcgcccttg ttcccatcat ggcctttggt 1200

gagaacgacc tctatgacca ggttagcaac gacaagtcgt ccaagctgta ccgattccag 1260

cagtttgtca agaacttcct tggattcacc cttcctttga tgcatgcccg aggcgtcttc 1320

aactacgatg tcggtcttgt cccctacagg cgacccgtca acattgtggt tggttccccc 1380

attgacttgc cttatctccc acaccccacc gacgaagaag tgtccgaata ccacgaccga 1440

tacatcgccg agctgcagcg aatctacaac gagcacaagg atgaatattt catcgattgg 1500

accgaggagg gcaaaggagc cccagagttc cgaatgattg agtaa 1545

<210> SEQ ID NO 46
<211> LENGTH: 514
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 46

Met Thr Ile Asp Ser Gln Tyr Tyr Lys Ser Arg Asp Lys Asn Asp Thr
1 5 10 15

Ala Pro Lys Ile Ala Gly Ile Arg Tyr Ala Pro Leu Ser Thr Pro Leu
20 25 30

Leu Asn Arg Cys Glu Thr Phe Ser Leu Val Trp His Ile Phe Ser Ile
35 40 45

Pro Thr Phe Leu Thr Ile Phe Met Leu Cys Cys Ala Ile Pro Leu Leu
50 55 60

Trp Pro Phe Val Ile Ala Tyr Val Val Tyr Ala Val Lys Asp Asp Ser
65 70 75 80

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```
Pro Ser Asn Gly Gly Val Val Lys Arg Tyr Ser Pro Ile Ser Arg Asn
                85                  90                  95

Phe Phe Ile Trp Lys Leu Phe Gly Arg Tyr Phe Pro Ile Thr Leu His
            100                 105                 110

Lys Thr Val Asp Leu Glu Pro Thr His Thr Tyr Tyr Pro Leu Asp Val
        115                 120                 125

Gln Glu Tyr His Leu Ile Ala Glu Arg Tyr Trp Pro Gln Asn Lys Tyr
    130                 135                 140

Leu Arg Ala Ile Ile Ser Thr Ile Glu Tyr Phe Leu Pro Ala Phe Met
145                 150                 155                 160

Lys Arg Ser Leu Ser Ile Asn Glu Gln Glu Gln Pro Ala Glu Arg Asp
                165                 170                 175

Pro Leu Leu Ser Pro Val Ser Pro Ser Ser Pro Gly Ser Gln Pro Asp
            180                 185                 190

Lys Trp Ile Asn His Asp Ser Arg Tyr Ser Arg Gly Glu Ser Ser Gly
        195                 200                 205

Ser Asn Gly His Ala Ser Gly Ser Glu Leu Asn Gly Asn Gly Asn Asn
    210                 215                 220

Gly Thr Thr Asn Arg Arg Pro Leu Ser Ser Ala Ser Ala Gly Ser Thr
225                 230                 235                 240

Ala Ser Asp Ser Thr Leu Leu Asn Gly Ser Leu Asn Ser Tyr Ala Asn
                245                 250                 255

Gln Ile Ile Gly Glu Asn Asp Pro Gln Leu Ser Pro Thr Lys Leu Lys
            260                 265                 270

Pro Thr Gly Arg Lys Tyr Ile Phe Gly Tyr His Pro His Gly Ile Ile
        275                 280                 285

Gly Met Gly Ala Phe Gly Gly Ile Ala Thr Glu Gly Ala Gly Trp Ser
    290                 295                 300

Lys Leu Phe Pro Gly Ile Pro Val Ser Leu Met Thr Leu Thr Asn Asn
305                 310                 315                 320

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

Ser Val Ser Lys Lys Ser Cys Lys Ala Leu Leu Lys Arg Asn Gln Ser
            340                 345                 350

Ile Cys Ile Val Val Gly Gly Ala Gln Glu Ser Leu Leu Ala Arg Pro
        355                 360                 365

Gly Val Met Asp Leu Val Leu Leu Lys Arg Lys Gly Phe Val Arg Leu
    370                 375                 380

Gly Met Glu Val Gly Asn Val Ala Leu Val Pro Ile Met Ala Phe Gly
385                 390                 395                 400

Glu Asn Asp Leu Tyr Asp Gln Val Ser Asn Asp Lys Ser Ser Lys Leu
                405                 410                 415

Tyr Arg Phe Gln Gln Phe Val Lys Asn Phe Leu Gly Phe Thr Leu Pro
            420                 425                 430

Leu Met His Ala Arg Gly Val Phe Asn Tyr Asp Val Gly Leu Val Pro
        435                 440                 445

Tyr Arg Arg Pro Val Asn Ile Val Val Gly Ser Pro Ile Asp Leu Pro
    450                 455                 460

Tyr Leu Pro His Pro Thr Asp Glu Glu Val Ser Glu Tyr His Asp Arg
465                 470                 475                 480

Tyr Ile Ala Glu Leu Gln Arg Ile Tyr Asn Glu His Lys Asp Glu Tyr
                485                 490                 495

Phe Ile Asp Trp Thr Glu Glu Gly Lys Gly Ala Pro Glu Phe Arg Met
```

-continued

500 505 510

Ile Glu

<210> SEQ ID NO 47
<211> LENGTH: 1581
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 47

atggaagtcc gacgacgaaa aatcgacgtg ctcaaggccc agaaaaacgg ctacgaatcg 60

ggcccaccat ctcgacaatc gtcgcagccc tcctcaagag catcgtccag aacccgcaac 120

aaacactcct cgtccaccct gtcgctcagc ggactgacca tgaaagtcca gaagaaacct 180

gcgggacccc cggcgaactc caaaacgcca ttcctacaca tcaagcccgt gcacacgtgc 240

tgctccacat caatgctttc gcgcgattat gacggctcca accccagctt caagggcttc 300

aaaaacatcg gcatgatcat tctcattgtg ggaaatctac ggctcgcatt cgaaaactac 360

ctcaaatacg gcatttccaa cccgttcttc gaccccaaaa ttactccttc cgagtggcag 420

ctctcaggct tgctcatagt cgtggcctac gcacatatcc tcatggccta cgctattgag 480

agcgctgcca agctgctgtt cctctctagc aaacaccact acatggccgt ggggcttctg 540

cataccatga acactttgtc gtccatctcg ttgctgtcct acgtcgtcta ctactacctg 600

cccaaccccg tggcaggcac aatagtcgag tttgtggccg ttattctgtc tctcaaactc 660

gcctcatacg ccctcactaa ctcggatctc cgaaaagccg caattcatgc ccagaagctc 720

gacaagacgc aagacgataa cgaaaaggaa tccacctcgt cttcctcttc ttcagatgac 780

gcagagactt tggcagacat tgacgtcatt cctgcatact acgcacagct gccctacccc 840

cagaatgtga cgctgtcgaa cctgctgtac ttctggtttg ctcccacact ggtctaccag 900

cccgtgtacc ccaagacgga gcgtattcga cccaagcacg tgatccgaaa cctgtttgag 960

ctcgtctctc tgtgcatgct tattcagttt ctcatcttcc agtacgccta ccccatcatg 1020

cagtcgtgtc tggctctgtt cttccagccc aagctcgatt atgccaacat ctccgagcgc 1080

ctcatgaagt tggcctccgt gtctatgatg gtctggctca ttggattcta cgctttcttc 1140

cagaacggtc tcaatcttat tgccgagctc acctgttttg gaaacagaac cttctaccag 1200

cagtggtgga attcccgctc cattggccag tactggactc tatggaacaa gccagtcaac 1260

cagtacttta gacaccacgt ctacgtgcct cttctcgctc ggggcatgtc gcggttcaat 1320

gcgtcggtgg tggttttctt tttctccgcc gtcatccatg aactgcttgt cggcatcccc 1380

actcacaaca tcatcggagc cgccttcttc ggcatgatgt cgcaggtgcc tctgatcatg 1440

gctactgaga accttcagca tattaactcc tctctgggcc ccttccttgg caactgtgca 1500

ttctggttca ccttttttcct gggacaaccc acttgtgcat tcctttatta tctggcttac 1560

aactacaagc agaaccagta g 1581

<210> SEQ ID NO 48
<211> LENGTH: 526
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 48

Met Glu Val Arg Arg Arg Lys Ile Asp Val Leu Lys Ala Gln Lys Asn
1 5 10 15

Gly Tyr Glu Ser Gly Pro Pro Ser Arg Gln Ser Ser Gln Pro Ser Ser
20 25 30

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```
Arg Ala Ser Ser Arg Thr Arg Asn Lys His Ser Ser Ser Thr Leu Ser
        35                  40                  45

Leu Ser Gly Leu Thr Met Lys Val Gln Lys Lys Pro Ala Gly Pro Pro
    50                  55                  60

Ala Asn Ser Lys Thr Pro Phe Leu His Ile Lys Pro Val His Thr Cys
65                  70                  75                  80

Cys Ser Thr Ser Met Leu Ser Arg Asp Tyr Asp Gly Ser Asn Pro Ser
                85                  90                  95

Phe Lys Gly Phe Lys Asn Ile Gly Met Ile Ile Leu Ile Val Gly Asn
            100                 105                 110

Leu Arg Leu Ala Phe Glu Asn Tyr Leu Lys Tyr Gly Ile Ser Asn Pro
        115                 120                 125

Phe Phe Asp Pro Lys Ile Thr Pro Ser Glu Trp Gln Leu Ser Gly Leu
    130                 135                 140

Leu Ile Val Val Ala Tyr Ala His Ile Leu Met Ala Tyr Ala Ile Glu
145                 150                 155                 160

Ser Ala Ala Lys Leu Leu Phe Leu Ser Ser Lys His His Tyr Met Ala
                165                 170                 175

Val Gly Leu Leu His Thr Met Asn Thr Leu Ser Ser Ile Ser Leu Leu
            180                 185                 190

Ser Tyr Val Val Tyr Tyr Tyr Leu Pro Asn Pro Val Ala Gly Thr Ile
        195                 200                 205

Val Glu Phe Val Ala Val Ile Leu Ser Leu Lys Leu Ala Ser Tyr Ala
    210                 215                 220

Leu Thr Asn Ser Asp Leu Arg Lys Ala Ala Ile His Ala Gln Lys Leu
225                 230                 235                 240

Asp Lys Thr Gln Asp Asp Asn Glu Lys Glu Ser Thr Ser Ser Ser Ser
                245                 250                 255

Ser Ser Asp Asp Ala Glu Thr Leu Ala Asp Ile Asp Val Ile Pro Ala
            260                 265                 270

Tyr Tyr Ala Gln Leu Pro Tyr Pro Gln Asn Val Thr Leu Ser Asn Leu
        275                 280                 285

Leu Tyr Phe Trp Phe Ala Pro Thr Leu Val Tyr Gln Pro Val Tyr Pro
    290                 295                 300

Lys Thr Glu Arg Ile Arg Pro Lys His Val Ile Arg Asn Leu Phe Glu
305                 310                 315                 320

Leu Val Ser Leu Cys Met Leu Ile Gln Phe Leu Ile Phe Gln Tyr Ala
                325                 330                 335

Tyr Pro Ile Met Gln Ser Cys Leu Ala Leu Phe Phe Gln Pro Lys Leu
            340                 345                 350

Asp Tyr Ala Asn Ile Ser Glu Arg Leu Met Lys Leu Ala Ser Val Ser
        355                 360                 365

Met Met Val Trp Leu Ile Gly Phe Tyr Ala Phe Phe Gln Asn Gly Leu
    370                 375                 380

Asn Leu Ile Ala Glu Leu Thr Cys Phe Gly Asn Arg Thr Phe Tyr Gln
385                 390                 395                 400

Gln Trp Trp Asn Ser Arg Ser Ile Gly Gln Tyr Trp Thr Leu Trp Asn
                405                 410                 415

Lys Pro Val Asn Gln Tyr Phe Arg His His Val Tyr Val Pro Leu Leu
            420                 425                 430

Ala Arg Gly Met Ser Arg Phe Asn Ala Ser Val Val Val Phe Phe Phe
        435                 440                 445
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Ser Ala Val Ile His Glu Leu Leu Val Gly Ile Pro Thr His Asn Ile
    450                 455                 460

Ile Gly Ala Ala Phe Phe Gly Met Met Ser Gln Val Pro Leu Ile Met
465                 470                 475                 480

Ala Thr Glu Asn Leu Gln His Ile Asn Ser Ser Leu Gly Pro Phe Leu
                485                 490                 495

Gly Asn Cys Ala Phe Trp Phe Thr Phe Phe Leu Gly Gln Pro Thr Cys
            500                 505                 510

Ala Phe Leu Tyr Tyr Leu Ala Tyr Asn Tyr Lys Gln Asn Gln
        515                 520                 525


<210> SEQ ID NO 49
<211> LENGTH: 3810
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 49

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gagttcccca tcgacgacat gctccacaac gacggagatg actttgtcaa gaaggaaacg    120

tgggacgagg gttttggttt cggaacaaat ggcgccgtgg gtgcgcagat ggacgtccag    180

accagcccat ttagcgaccc tgtttttggc ggcgtgggag caggccctga catgatgggt    240

ctcatggata caaacatgaa ccacatcaac ggtagtcaca acatgaacag cgtcgtcaag    300

caggaggact actacacacc gtccatgggc actcccatga acccccaaca gcaacagtcc    360

atgacccctc aacagcagca tcacatgaac cacaaccagc cctctcagct ccaatctttg    420

catcaacagt cccagaaggc tcaaccacag cagcaacaac aacagccaca tcagtcgaca    480

ggagtcgata gcataatcac aaaggcatac accagggcag caggagacct accgtacgga    540

cgaaagtact cacgacaact caacaagtac cccgaggacg tggagtattc atctttcgac    600

ccatcgctat ggagcaattt gctgaccaac tcggaaactc cgtaccaata ccagatacat    660

gtccattcca tgcccggaaa atcacgtgtg gagacccaaa tcaaatgtgc attatcaatc    720

taccctccgc ctccacagca gtccgttcga cttccgacag acaccatttc gcgtcccaag    780

ttccagctca agcagggcca cattccagac tcgtgtctct ccttggaagt atacattgtg    840

ggcgagcaga accccagcaa gcccgtcaat ttgtgttcta gatgcatcaa acgagaacag    900

aagcgagcct gtcgaaagaa actctttgac gagtcggagg agctgtcgtg ggtcgagact    960

cgtcaacgac gtctggctgt cttcaactgc tccgaggtgc ttgagttcaa ggatgtggaa   1020

cggcgagtat acatccccga gtccggcact acagttaccg ccaagcagct ggttctgccc   1080

ctgcgtctgg cttgctactg tagacaccac ggggagaaaa agggatttcg aatcctcttt   1140

tgtcttagag acgagggagg ccagattgtg ggtgtgggcc agagtggaac gaccgtcatg   1200

atcactgacg accacaaggt tgtgggagac gcggttgcca tgccgactac agccactgct   1260

cctgccaccg ctggctcttc acaacccccc acccaggttc ctacccccgc tgcatcttcg   1320

tcgacgagct atcgtcctcg aaactcgctt cctctatcgc ctacttccat ggaagactct   1380

tcgtcggagt tcacctcgga ccattctcat tactccaact atggttctaa acgacgacga   1440

gacggctctt ccatcagcga ttggagcggc atgatgaacg tgcgaggcat ggatagacag   1500

gcttccatta ccagcattcc cgaaatggtt ggtggcatgt cgaacatgac tgtggccagt   1560

gcttcgggta gcgccactaa tctggctgct cacaacatga acaaccccgc agacgaaaac   1620

ctgcccgtca tcaagcgaat catcccctcg cagggttcca ttcgaggcgg cattgaagta   1680
```

-continued

accctgcttg gatctggctt caagtccaat ctggtggctg ttttcggtga caacaaggcc 1740

gtgggcaccc actgctggtc tgattcgacc atcgtgaccc atctgccgcc ttcgaccatc 1800

gtgggtcccg ttgtggtgtc tttcgaaggt tttgtgctcg acaagcctca gatttttacc 1860

tattttgacg acacagacgg ccagttgatt gagttggcgc tccaggttgt gggtctcaag 1920

atgaacggac ggctggaaga cgcccgaaac attgccatgc gaatcgtggg caacaatgga 1980

ggcgttgcgg gcgcacaagg cgccatggca ggcgggaaca tgtctaacgg agacgttgga 2040

atggaaagtg ctgctgcaga cagttcggtt caacccgtat cgcctcccac agaccacgaa 2100

gatgtggttc tgcgatgtct ggctctcaca gacattcctg gaggccgaat tgccaactgg 2160

caactcacca acgccgaggg acagaccatg gttcatctgg ccagtattct gggttactcg 2220

cgtgttctgg tggctcttgt ggctcgagga gctcgtgtgg atgtttccga caatggtgga 2280

ttcactcctc ttcatttcgc tgctctcttt ggccgtcgaa agattgccaa gaaactactt 2340

cggtgcaacg ctgaccccta caaacgtaac cgaattggcg aaaccgtgtt tgatgttgct 2400

tgtcctcaca ttctcgatct tctggtcggt cctcagggca tgcctatggc cgttcagacg 2460

tcgtatactc ccgattacca tcgtcagcgt cgatcttcat cttcttccac tctggcttcc 2520

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ctgtcgcata ttccgtccac gtgctccatt cgatcatcga cttctcagtt tgacgctgaa 2640

gacgagtggg acgagcgaga tgaggaggat ggagactttg acgacgattc agatgaggac 2700

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gtggaatctc ctctctctga ggaggaagag cgacttgtgc gacacattga ggccgaagac 2820

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cggtactttg accgtactct cagcatggca tcttgggacg atgttctggc ttacatttac 3000

agacccaagc gagctactgt gcccaacaag cggtcttctg gagctcctcc ttcagtcaga 3060

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accatttctg cacatgcccc ttccggcggt gccggtcgag gccggtctca ttcgtccatc 3180

tcgcgaatgt ggcgatacct gaagaactcg tctgccgatg aggccacccg gtctcgatct 3240

cgagatgcaa acggagccgg tgctcccccc gcctacgaag aaatcttccc tggccatggg 3300

gttgtccacg acaagaaggt tgtgcagatg gccgctgctt ctgctgccga gaactcgtct 3360

gggcctgttg gagcctcatc ttcagcagtt gcgtccactt ctgcggctgc cgctgtggtg 3420

ccctccccac tagcccccat tgtggaggac gaggagcagc tggtagaggc ctggagacga 3480

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gttgagtctg tggctgagac tgtgggtgtc cactgccgtg gagcagttgc caagctatgg 3660

ttcaagcagt accctgttca ccgaggccag ccactcaagg acacctgttc atttgagccc 3720

aacagtctgg tagagtcagc tcttcgtcag atgaatgggt ggtccgaccg ggaggttccc 3780

attcatcaag cccaggccca ggctgcatga 3810

<210> SEQ ID NO 50
<211> LENGTH: 1269
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 50

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```
Met Ala Lys Asp Lys Glu Ile Asp Phe Asp Tyr Thr Gly Glu Leu Val
1               5                  10                  15

Met Asp Asp Phe Glu Phe Pro Ile Asp Asp Met Leu His Asn Asp Gly
            20                  25                  30

Asp Asp Phe Val Lys Lys Glu Thr Trp Asp Glu Gly Phe Gly Phe Gly
        35                  40                  45

Thr Asn Gly Ala Val Gly Ala Gln Met Asp Val Gln Thr Ser Pro Phe
    50                  55                  60

Ser Asp Pro Val Phe Gly Gly Val Gly Ala Gly Pro Asp Met Met Gly
65                  70                  75                  80

Leu Met Asp Thr Asn Met Asn His Ile Asn Gly Ser His Asn Met Asn
                85                  90                  95

Ser Val Val Lys Gln Glu Asp Tyr Tyr Thr Pro Ser Met Gly Thr Pro
            100                 105                 110

Met Asn Pro Gln Gln Gln Gln Ser Met Thr Pro Gln Gln Gln His His
        115                 120                 125

Met Asn His Asn Gln Pro Ser Gln Leu Gln Ser Leu His Gln Gln Ser
    130                 135                 140

Gln Lys Ala Gln Pro Gln Gln Gln Gln Gln Pro His Gln Ser Thr
145                 150                 155                 160

Gly Val Asp Ser Ile Ile Thr Lys Ala Tyr Thr Arg Ala Ala Gly Asp
                165                 170                 175

Leu Pro Tyr Gly Arg Lys Tyr Ser Arg Gln Leu Asn Lys Tyr Pro Glu
            180                 185                 190

Asp Val Glu Tyr Ser Ser Phe Asp Pro Ser Leu Trp Ser Asn Leu Leu
        195                 200                 205

Thr Asn Ser Glu Thr Pro Tyr Gln Tyr Gln Ile His Val His Ser Met
    210                 215                 220

Pro Gly Lys Ser Arg Val Glu Thr Gln Ile Lys Cys Ala Leu Ser Ile
225                 230                 235                 240

Tyr Pro Pro Pro Pro Gln Gln Ser Val Arg Leu Pro Thr Asp Thr Ile
                245                 250                 255

Ser Arg Pro Lys Phe Gln Leu Lys Gln Gly His Ile Pro Asp Ser Cys
            260                 265                 270

Leu Ser Leu Glu Val Tyr Ile Val Gly Glu Gln Asn Pro Ser Lys Pro
        275                 280                 285

Val Asn Leu Cys Ser Arg Cys Ile Lys Arg Glu Gln Lys Arg Ala Cys
    290                 295                 300

Arg Lys Lys Leu Phe Asp Glu Ser Glu Glu Leu Ser Trp Val Glu Thr
305                 310                 315                 320

Arg Gln Arg Arg Leu Ala Val Phe Asn Cys Ser Glu Val Leu Glu Phe
                325                 330                 335

Lys Asp Val Glu Arg Arg Val Tyr Ile Pro Glu Ser Gly Thr Thr Val
            340                 345                 350

Thr Ala Lys Gln Leu Val Leu Pro Leu Arg Leu Ala Cys Tyr Cys Arg
        355                 360                 365

His His Gly Glu Lys Lys Gly Phe Arg Ile Leu Phe Cys Leu Arg Asp
    370                 375                 380

Glu Gly Gly Gln Ile Val Gly Val Gly Gln Ser Gly Thr Thr Val Met
385                 390                 395                 400

Ile Thr Asp Asp His Lys Val Val Gly Asp Ala Val Ala Met Pro Thr
                405                 410                 415
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```
Thr Ala Thr Ala Pro Ala Thr Ala Gly Ser Ser Gln Pro Pro Thr Gln
            420                 425                 430

Val Pro Thr Pro Ala Ala Ser Ser Ser Thr Ser Tyr Arg Pro Arg Asn
        435                 440                 445

Ser Leu Pro Leu Ser Pro Thr Ser Met Glu Asp Ser Ser Ser Glu Phe
    450                 455                 460

Thr Ser Asp His Ser His Tyr Ser Asn Tyr Gly Ser Lys Arg Arg Arg
465                 470                 475                 480

Asp Gly Ser Ser Ile Ser Asp Trp Ser Gly Met Met Asn Val Arg Gly
                485                 490                 495

Met Asp Arg Gln Ala Ser Ile Thr Ser Ile Pro Glu Met Val Gly Gly
            500                 505                 510

Met Ser Asn Met Thr Val Ala Ser Ala Ser Gly Ser Ala Thr Asn Leu
        515                 520                 525

Ala Ala His Asn Met Asn Asn Pro Ala Asp Glu Asn Leu Pro Val Ile
    530                 535                 540

Lys Arg Ile Ile Pro Ser Gln Gly Ser Ile Arg Gly Gly Ile Glu Val
545                 550                 555                 560

Thr Leu Leu Gly Ser Gly Phe Lys Ser Asn Leu Val Ala Val Phe Gly
                565                 570                 575

Asp Asn Lys Ala Val Gly Thr His Cys Trp Ser Asp Ser Thr Ile Val
            580                 585                 590

Thr His Leu Pro Pro Ser Thr Ile Val Gly Pro Val Val Val Ser Phe
        595                 600                 605

Glu Gly Phe Val Leu Asp Lys Pro Gln Ile Phe Thr Tyr Phe Asp Asp
    610                 615                 620

Thr Asp Gly Gln Leu Ile Glu Leu Ala Leu Gln Val Val Gly Leu Lys
625                 630                 635                 640

Met Asn Gly Arg Leu Glu Asp Ala Arg Asn Ile Ala Met Arg Ile Val
                645                 650                 655

Gly Asn Asn Gly Gly Val Ala Gly Ala Gln Gly Ala Met Ala Gly Gly
            660                 665                 670

Asn Met Ser Asn Gly Asp Val Gly Met Glu Ser Ala Ala Ala Asp Ser
        675                 680                 685

Ser Val Gln Pro Val Ser Pro Pro Thr Asp His Glu Asp Val Val Leu
    690                 695                 700

Arg Cys Leu Ala Leu Thr Asp Ile Pro Gly Gly Arg Ile Ala Asn Trp
705                 710                 715                 720

Gln Leu Thr Asn Ala Glu Gly Gln Thr Met Val His Leu Ala Ser Ile
                725                 730                 735

Leu Gly Tyr Ser Arg Val Leu Val Ala Leu Val Ala Arg Gly Ala Arg
            740                 745                 750

Val Asp Val Ser Asp Asn Gly Gly Phe Thr Pro Leu His Phe Ala Ala
        755                 760                 765

Leu Phe Gly Arg Arg Lys Ile Ala Lys Lys Leu Leu Arg Cys Asn Ala
    770                 775                 780

Asp Pro Tyr Lys Arg Asn Arg Ile Gly Glu Thr Val Phe Asp Val Ala
785                 790                 795                 800

Cys Pro His Ile Leu Asp Leu Leu Val Gly Pro Gln Gly Met Pro Met
                805                 810                 815

Ala Val Gln Thr Ser Tyr Thr Pro Asp Tyr His Arg Gln Arg Arg Ser
            820                 825                 830

Ser Ser Ser Ser Thr Leu Ala Ser Ile Ala Ser Ile Gln Asp Ser Arg
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        835                 840                 845

Glu Tyr Gly Phe Tyr Asp His Gly Met Ile Ser Asn Leu Ser His Ile
    850                 855                 860

Pro Ser Thr Cys Ser Ile Arg Ser Ser Thr Ser Gln Phe Asp Ala Glu
865                 870                 875                 880

Asp Glu Trp Asp Glu Arg Asp Glu Glu Asp Gly Asp Phe Asp Asp Asp
                885                 890                 895

Ser Asp Glu Asp Ser Asp Asp Asp Ser Asp Ala Leu Phe Met Ser Val
            900                 905                 910

Arg Lys His Ala Lys Ala Lys Ser Val Glu Ser Pro Leu Ser Glu Glu
        915                 920                 925

Glu Glu Arg Leu Val Arg His Ile Glu Ala Glu Asp Gln Ala Val Glu
    930                 935                 940

Ala Arg Val Ala Ala Gly Ile Val Ser Ser Asn Val Pro Asp Val Val
945                 950                 955                 960

Ser Ser Asn Asp Ser Asp His Val Arg Ser Asp Thr Ser Thr Glu Asn
                965                 970                 975

Lys Ser Phe Ser Arg Tyr Phe Asp Arg Thr Leu Ser Met Ala Ser Trp
            980                 985                 990

Asp Asp Val Leu Ala Tyr Ile Tyr  Arg Pro Lys Arg Ala  Thr Val Pro
        995                 1000                1005

Asn Lys  Arg Ser Ser Gly Ala  Pro Pro Ser Val Arg  Ser Thr Arg
    1010                1015                1020

Ser Pro  Leu Ser Asp His Pro  Ile Thr Ser Ser Gly  Asp Glu Ser
    1025                1030                1035

Asp Arg  Thr Ile Ser Ala His  Ala Pro Ser Gly Gly  Ala Gly Arg
    1040                1045                1050

Gly Arg  Ser His Ser Ser Ile  Ser Arg Met Trp Arg  Tyr Leu Lys
    1055                1060                1065

Asn Ser  Ser Ala Asp Glu Ala  Thr Arg Ser Arg Ser  Arg Asp Ala
    1070                1075                1080

Asn Gly  Ala Gly Ala Pro Pro  Ala Tyr Glu Glu Ile  Phe Pro Gly
    1085                1090                1095

His Gly  Val Val His Asp Lys  Lys Val Val Gln Met  Ala Ala Ala
    1100                1105                1110

Ser Ala  Ala Glu Asn Ser Ser  Gly Pro Val Gly Ala  Ser Ser Ser
    1115                1120                1125

Ala Val  Ala Ser Thr Ser Ala  Ala Ala Ala Val Val  Pro Ser Pro
    1130                1135                1140

Leu Ala  Pro Ile Val Glu Asp  Glu Glu Gln Leu Val  Glu Ala Trp
    1145                1150                1155

Arg Arg  Gln Arg Arg Ser Met  Ala Asn Asp Arg Met  Leu Phe Ala
    1160                1165                1170

Phe Trp  Leu Pro Val Leu Leu  Met Ala Ile Gly Tyr  Met Val Ile
    1175                1180                1185

Lys Ala  Phe Gly Leu Phe Pro  Asp Gln Val Ser Ala  Val Glu Ser
    1190                1195                1200

Val Ala  Glu Thr Val Gly Val  His Cys Arg Gly Ala  Val Ala Lys
    1205                1210                1215

Leu Trp  Phe Lys Gln Tyr Pro  Val His Arg Gly Gln  Pro Leu Lys
    1220                1225                1230

Asp Thr  Cys Ser Phe Glu Pro  Asn Ser Leu Val Glu  Ser Ala Leu
    1235                1240                1245
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-continued

Arg Gln Met Asn Gly Trp Ser Asp Arg Glu Val Pro Ile His Gln
1250 1255 1260

Ala Gln Ala Gln Ala Ala
1265

<210> SEQ ID NO 51
<211> LENGTH: 3810
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 51

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gagttcccca tcgacgacat gctccacaac gacggagatg actttgtcaa gaaggaaacg 120

tgggacgagg gttttggttt cggaacaaat ggcgccgtgg gtgcgcagat ggacgtccag 180

accagcccat ttagcgaccc tgtttttggc ggcgtgggag caggccctga catgatgggt 240

ctcatggata caaacatgaa ccacatcaac ggtagtcaca acatgaacag cgtcgtcaag 300

caggaggact actacacacc gtccatgggc actcccatga acccccaaca gcaacagtcc 360

atgacccctc aacagcagca tcacatgaac cacaaccagc cctctcagct ccaatctttg 420

catcaacagt cccagaaggc tcaaccacag cagcaacaac aacagccaca tcagtcgaca 480

ggagtcgata gcataatcac aaaggcatac accagggcag caggagacct accgtacgga 540

cgaaagtact cacgacaact caacaagtac cccgaggacg tggagtattc atctttcgac 600

ccatcgctat ggagcaattt gctgaccaac tcggaaactc cgtaccaata ccagatacat 660

gtccattcca tgcccggaaa atcacgtgtg gagacccaaa tcaaatgtgc attatcaatc 720

taccctccgc ctccacagca gtccgttcga cttccgacag acaccatttc gcgtcccaag 780

ttccagctca agcagggcca cattccagac tcgtgtctct ccttggaagt atacattgtg 840

ggcgagcaga accccagcaa gcccgtcaat ttgtgttcta gatgcatcaa acgagaacag 900

aagcgagcct gtcgaaagaa actctttgac gagtcggagg agctgtcgtg ggtcgagact 960

cgtcaacgac gtctggctgt cttcaactgc tccgaggtgc ttgagttcaa ggatgtggaa 1020

cggcgagtat acatccccga gtccggcact acagttaccg ccaagcagct ggttctgccc 1080

ctgcgtctgg cttgctactg tagacaccac ggggagaaaa agggatttcg aatcctcttt 1140

tgtcttagag acgagggagg ccagattgtg ggtgtgggcc agagtggaac gaccgtcatg 1200

atcactgacg accacaaggt tgtgggagac gcggttgcca tgccgactac agccactgct 1260

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gcttccatta ccagcattcc cgaaatggtt ggtggcatgt cgaacatgac tgtggccagt 1560

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accctgcttg gatctggctt caagtccaat ctggtggctg ttttcggtga caacaaggcc 1740

gtgggcaccc actgctggtc tgattcgacc atcgtgaccc atctgccgcc ttcgaccatc 1800

gtgggtcccg ttgtggtgtc tttcgaaggt tttgtgctcg acaagcctca gatttttacc 1860

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tattttgacg acacagacgg ccagttgatt gagttggcgc tccaggttgt gggtctcaag 1920

atgaacagac ggctggaaga cgcccgaaac attgccatgc gaatcgtggg caacaatgga 1980

ggcgttgcgg gcgcacaagg cgccatggca ggcgggaaca tgtctaacgg agacgttgga 2040

atggaaagtg ctgctgcaga cagttcggtt caacccgtat cgcctcccac agaccacgaa 2100

gatgtggttc tgcgatgtct ggctctcaca gacattcctg gaggccgaat tgccaactgg 2160

caactcacca acgccgaggg acagaccatg gttcatctgg ccagtattct gggttactcg 2220

cgtgttctgg tggctcttgt ggctcgagga gctcgtgtgg atgtttccga caatggtgga 2280

ttcactcctc ttcatttcgc tgctctcttt ggccgtcgaa agattgccaa gaaactactt 2340

cggtgcaacg ctgaccccta caaacgtaac cgaattggcg aaaccgtgtt tgatgttgct 2400

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tcgtatactc ccgattacca tcgtcagcgt cgatcttcat cttcttccac tctggcttcc 2520

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caggctgtgg aggcccgtgt ggctgccgga atcgtcagta gcaatgtacc cgacgtggtg 2880

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agacccaagc gagctactgt gcccaacaag cggtcttctg gagctcctcc ttcagtcaga 3060

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tcgcgaatgt ggcgatacct gaagaactcg tctgccgatg aggccacccg gtctcgatct 3240

cgagatgcaa acggagccgg tgctcccccc gcctacgaag aaatcttccc tggccatggg 3300

gttgtccacg acaagaaggt tgtgcagatg gccgctgctt ctgctgccga gaactcgtct 3360

gggcctgttg gagcctcatc ttcagcagtt gcgtccactt ctgcggctgc cgctgtggtg 3420

ccctccccac tagcccccat tgtggaggac gaggagcagc tggtagaggc ctggagacga 3480

cagcgacgat ccatggctaa cgatcgcatg ttatttgcct tctggctgcc tgtgctgctc 3540

atggctattg gttatatggt catcaaggcg tttggtctgt tccccgacca ggtctctgcc 3600

gttgagtctg tggctgagac tgtgggtgtc cactgccgtg gagcagttgc caagctatgg 3660

ttcaagcagt accctgttca ccgaggccag ccactcaagg acacctgttc atttgagccc 3720

aacagtctgg tagagtcagc tcttcgtcag atgaatgggt ggtccgaccg ggaggttccc 3780

attcatcaag cccaggccca ggctgcatga 3810

<210> SEQ ID NO 52
<211> LENGTH: 1269
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 52

Met Ala Lys Asp Lys Glu Ile Asp Phe Asp Tyr Thr Gly Glu Leu Val
1 5 10 15

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Met Asp Asp Phe Glu Phe Pro Ile Asp Asp Met Leu His Asn Asp Gly
            20                  25                  30

Asp Asp Phe Val Lys Lys Glu Thr Trp Asp Glu Gly Phe Gly Phe Gly
        35                  40                  45

Thr Asn Gly Ala Val Gly Ala Gln Met Asp Val Gln Thr Ser Pro Phe
    50                  55                  60

Ser Asp Pro Val Phe Gly Gly Val Gly Ala Gly Pro Asp Met Met Gly
65                  70                  75                  80

Leu Met Asp Thr Asn Met Asn His Ile Asn Gly Ser His Asn Met Asn
                85                  90                  95

Ser Val Val Lys Gln Glu Asp Tyr Tyr Thr Pro Ser Met Gly Thr Pro
            100                 105                 110

Met Asn Pro Gln Gln Gln Gln Ser Met Thr Pro Gln Gln Gln His His
        115                 120                 125

Met Asn His Asn Gln Pro Ser Gln Leu Gln Ser Leu His Gln Gln Ser
    130                 135                 140

Gln Lys Ala Gln Pro Gln Gln Gln Gln Gln Gln Pro His Gln Ser Thr
145                 150                 155                 160

Gly Val Asp Ser Ile Ile Thr Lys Ala Tyr Thr Arg Ala Ala Gly Asp
                165                 170                 175

Leu Pro Tyr Gly Arg Lys Tyr Ser Arg Gln Leu Asn Lys Tyr Pro Glu
            180                 185                 190

Asp Val Glu Tyr Ser Ser Phe Asp Pro Ser Leu Trp Ser Asn Leu Leu
        195                 200                 205

Thr Asn Ser Glu Thr Pro Tyr Gln Tyr Gln Ile His Val His Ser Met
    210                 215                 220

Pro Gly Lys Ser Arg Val Glu Thr Gln Ile Lys Cys Ala Leu Ser Ile
225                 230                 235                 240

Tyr Pro Pro Pro Pro Gln Gln Ser Val Arg Leu Pro Thr Asp Thr Ile
                245                 250                 255

Ser Arg Pro Lys Phe Gln Leu Lys Gln Gly His Ile Pro Asp Ser Cys
            260                 265                 270

Leu Ser Leu Glu Val Tyr Ile Val Gly Glu Gln Asn Pro Ser Lys Pro
        275                 280                 285

Val Asn Leu Cys Ser Arg Cys Ile Lys Arg Glu Gln Lys Arg Ala Cys
    290                 295                 300

Arg Lys Lys Leu Phe Asp Glu Ser Glu Glu Leu Ser Trp Val Glu Thr
305                 310                 315                 320

Arg Gln Arg Arg Leu Ala Val Phe Asn Cys Ser Glu Val Leu Glu Phe
                325                 330                 335

Lys Asp Val Glu Arg Arg Val Tyr Ile Pro Glu Ser Gly Thr Thr Val
            340                 345                 350

Thr Ala Lys Gln Leu Val Leu Pro Leu Arg Leu Ala Cys Tyr Cys Arg
        355                 360                 365

His His Gly Glu Lys Lys Gly Phe Arg Ile Leu Phe Cys Leu Arg Asp
    370                 375                 380

Glu Gly Gly Gln Ile Val Gly Val Gly Gln Ser Gly Thr Thr Val Met
385                 390                 395                 400

Ile Thr Asp Asp His Lys Val Val Gly Asp Ala Val Ala Met Pro Thr
                405                 410                 415

Thr Ala Thr Ala Pro Ala Thr Ala Gly Ser Ser Gln Pro Pro Thr Gln
            420                 425                 430

Val Pro Thr Pro Ala Ala Ser Ser Ser Thr Ser Tyr Arg Pro Arg Asn
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        435                 440                 445

Ser Leu Pro Leu Ser Pro Thr Ser Met Glu Asp Ser Ser Ser Glu Phe
    450                 455                 460

Thr Ser Asp His Ser His Tyr Ser Asn Tyr Gly Ser Lys Arg Arg Arg
465                 470                 475                 480

Asp Gly Ser Ser Ile Ser Asp Trp Ser Gly Met Met Asn Val Arg Gly
                485                 490                 495

Met Asp Arg Gln Ala Ser Ile Thr Ser Ile Pro Glu Met Val Gly Gly
            500                 505                 510

Met Ser Asn Met Thr Val Ala Ser Ala Ser Gly Ser Ala Thr Asn Leu
        515                 520                 525

Ala Ala His Asn Met Asn Asn Pro Ala Asp Glu Asn Leu Pro Val Ile
    530                 535                 540

Lys Arg Ile Ile Pro Ser Gln Gly Ser Ile Arg Gly Gly Ile Glu Val
545                 550                 555                 560

Thr Leu Leu Gly Ser Gly Phe Lys Ser Asn Leu Val Ala Val Phe Gly
                565                 570                 575

Asp Asn Lys Ala Val Gly Thr His Cys Trp Ser Asp Ser Thr Ile Val
            580                 585                 590

Thr His Leu Pro Pro Ser Thr Ile Val Gly Pro Val Val Val Ser Phe
        595                 600                 605

Glu Gly Phe Val Leu Asp Lys Pro Gln Ile Phe Thr Tyr Phe Asp Asp
    610                 615                 620

Thr Asp Gly Gln Leu Ile Glu Leu Ala Leu Gln Val Val Gly Leu Lys
625                 630                 635                 640

Met Asn Arg Arg Leu Glu Asp Ala Arg Asn Ile Ala Met Arg Ile Val
                645                 650                 655

Gly Asn Asn Gly Gly Val Ala Gly Ala Gln Gly Ala Met Ala Gly Gly
            660                 665                 670

Asn Met Ser Asn Gly Asp Val Gly Met Glu Ser Ala Ala Ala Asp Ser
        675                 680                 685

Ser Val Gln Pro Val Ser Pro Pro Thr Asp His Glu Asp Val Val Leu
    690                 695                 700

Arg Cys Leu Ala Leu Thr Asp Ile Pro Gly Gly Arg Ile Ala Asn Trp
705                 710                 715                 720

Gln Leu Thr Asn Ala Glu Gly Gln Thr Met Val His Leu Ala Ser Ile
                725                 730                 735

Leu Gly Tyr Ser Arg Val Leu Val Ala Leu Val Ala Arg Gly Ala Arg
            740                 745                 750

Val Asp Val Ser Asp Asn Gly Gly Phe Thr Pro Leu His Phe Ala Ala
        755                 760                 765

Leu Phe Gly Arg Arg Lys Ile Ala Lys Lys Leu Leu Arg Cys Asn Ala
    770                 775                 780

Asp Pro Tyr Lys Arg Asn Arg Ile Gly Glu Thr Val Phe Asp Val Ala
785                 790                 795                 800

Cys Pro His Ile Leu Asp Leu Leu Val Gly Pro Gln Gly Met Pro Met
                805                 810                 815

Ala Val Gln Thr Ser Tyr Thr Pro Asp Tyr His Arg Gln Arg Arg Ser
            820                 825                 830

Ser Ser Ser Ser Thr Leu Ala Ser Ile Ala Ser Ile Gln Asp Ser Arg
        835                 840                 845

Glu Tyr Gly Phe Tyr Asp His Gly Met Ile Ser Asn Leu Ser His Ile
    850                 855                 860
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Pro Ser Thr Cys Ser Ile Arg Ser Ser Thr Ser Gln Phe Asp Ala Glu
865                 870                 875                 880

Asp Glu Trp Asp Glu Arg Asp Glu Glu Asp Gly Asp Phe Asp Asp Asp
                885                 890                 895

Ser Asp Glu Asp Ser Asp Asp Asp Ser Asp Ala Leu Phe Met Ser Val
            900                 905                 910

Arg Lys His Ala Lys Ala Lys Ser Val Glu Ser Pro Leu Ser Glu Glu
        915                 920                 925

Glu Glu Arg Leu Val Arg His Ile Glu Ala Glu Asp Gln Ala Val Glu
    930                 935                 940

Ala Arg Val Ala Ala Gly Ile Val Ser Ser Asn Val Pro Asp Val Val
945                 950                 955                 960

Ser Ser Asn Asp Ser Asp His Val Arg Ser Asp Thr Ser Thr Glu Asn
                965                 970                 975

Lys Ser Phe Ser Arg Tyr Phe Asp Arg Thr Leu Ser Met Ala Ser Trp
            980                 985                 990

Asp Asp Val Leu Ala Tyr Ile Tyr  Arg Pro Lys Arg Ala  Thr Val Pro
        995                 1000                1005

Asn Lys  Arg Ser Ser Gly Ala  Pro Pro Ser Val Arg  Ser Thr Arg
    1010                1015                1020

Ser Pro  Leu Ser Asp His Pro  Ile Thr Ser Ser Gly  Asp Glu Ser
    1025                1030                1035

Asp Arg  Thr Ile Ser Ala His  Ala Pro Ser Gly Gly  Ala Gly Arg
    1040                1045                1050

Gly Arg  Ser His Ser Ser Ile  Ser Arg Met Trp Arg  Tyr Leu Lys
    1055                1060                1065

Asn Ser  Ser Ala Asp Glu Ala  Thr Arg Ser Arg Ser  Arg Asp Ala
    1070                1075                1080

Asn Gly  Ala Gly Ala Pro Pro  Ala Tyr Glu Glu Ile  Phe Pro Gly
    1085                1090                1095

His Gly  Val Val His Asp Lys  Lys Val Val Gln Met  Ala Ala Ala
    1100                1105                1110

Ser Ala  Ala Glu Asn Ser Ser  Gly Pro Val Gly Ala  Ser Ser Ser
    1115                1120                1125

Ala Val  Ala Ser Thr Ser Ala  Ala Ala Ala Val Val  Pro Ser Pro
    1130                1135                1140

Leu Ala  Pro Ile Val Glu Asp  Glu Glu Gln Leu Val  Glu Ala Trp
    1145                1150                1155

Arg Arg  Gln Arg Arg Ser Met  Ala Asn Asp Arg Met  Leu Phe Ala
    1160                1165                1170

Phe Trp  Leu Pro Val Leu Leu  Met Ala Ile Gly Tyr  Met Val Ile
    1175                1180                1185

Lys Ala  Phe Gly Leu Phe Pro  Asp Gln Val Ser Ala  Val Glu Ser
    1190                1195                1200

Val Ala  Glu Thr Val Gly Val  His Cys Arg Gly Ala  Val Ala Lys
    1205                1210                1215

Leu Trp  Phe Lys Gln Tyr Pro  Val His Arg Gly Gln  Pro Leu Lys
    1220                1225                1230

Asp Thr  Cys Ser Phe Glu Pro  Asn Ser Leu Val Glu  Ser Ala Leu
    1235                1240                1245

Arg Gln  Met Asn Gly Trp Ser  Asp Arg Glu Val Pro  Ile His Gln
    1250                1255                1260
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Ala Gln Ala Gln Ala Ala
1265

<210> SEQ ID NO 53
<211> LENGTH: 3003
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 53

atggctaaag acaaggaaat cgactttgac tacacgggag aactggtgat ggacgatttc 60

gagttcccca tcgacgacat gctccacaac gacggagatg actttgtcaa gaaggaaacg 120

tgggacgagg gttttggttt cggaacaaat ggcgccgtgg gtgcgcagat ggacgtccag 180

accagcccat ttagcgaccc tgtttttggc ggcgtgggag caggccctga catgatgggt 240

ctcatggata caaacatgaa ccacatcaac ggtagtcaca acatgaacag cgtcgtcaag 300

caggaggact actacacacc gtccatgggc actcccatga acccccaaca gcaacagtcc 360

atgacccctc aacagcagca tcacatgaac cacaaccagc cctctcagct ccaatctttg 420

catcaacagt cccagaaggc tcaaccacag cagcaacaac aacagccaca tcagtcgaca 480

ggagtcgata gcataatcac aaaggcatac accagggcag caggagacct accgtacgga 540

cgaaagtact cacgacaact caacaagtac cccgaggacg tggagtattc atctttcgac 600

ccatcgctat ggagcaattt gctgaccaac tcggaaactc cgtaccaata ccagatacat 660

gtccattcca tgcccggaaa atcacgtgtg gagacccaaa tcaaatgtgc attatcaatc 720

taccctccgc ctccacagca gtccgttcga cttccgacag acaccatttc gcgtcccaag 780

ttccagctca agcagggcca cattccagac tcgtgtctct ccttggaagt atacattgtg 840

ggcgagcaga accccagcaa gcccgtcaat ttgtgttcta gatgcatcaa acgagaacag 900

aagcgagcct gtcgaaagaa actctttgac gagtcggagg agctgtcgtg ggtcgagact 960

cgtcaacgac gtctggctgt cttcaactgc tccgaggtgc ttgagttcaa ggatgtggaa 1020

cggcgagtat acatccccga gtccggcact acagttaccg ccaagcagct ggttctgccc 1080

ctgcgtctgg cttgctactg tagacaccac ggggagaaaa agggatttcg aatcctcttt 1140

tgtcttagag acgagggagg ccagattgtg ggtgtgggcc agagtggaac gaccgtcatg 1200

atcactgacg accacaaggt tgtgggagac gcggttgcca tgccgactac agccactgct 1260

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tattttgacg acacagacgg ccagttgatt gagttggcgc tccaggttgt gggtctcaag 1920

atgaacggac ggctggaaga cgcccgaaac attgccatgc gaatcgtggg caacaatgga 1980

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ggcgttgcgg gcgcacaagg cgccatggca ggcgggaaca tgtctaacgg agacgttgga 2040

atggaaagtg ctgctgcaga cagttcggtt caacccgtat cgcctcccac agaccacgaa 2100

gatgtggttc tgcgatgtct ggctctcaca gacattcctg gaggccgaat tgccaactgg 2160

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cggtactttg accgtactct cagcatggca tcttgggacg atgttctggc ttacatttac 3000

tga 3003

<210> SEQ ID NO 54
<211> LENGTH: 1000
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 54

Met Ala Lys Asp Lys Glu Ile Asp Phe Asp Tyr Thr Gly Glu Leu Val
1 5 10 15

Met Asp Asp Phe Glu Phe Pro Ile Asp Asp Met Leu His Asn Asp Gly
20 25 30

Asp Asp Phe Val Lys Lys Glu Thr Trp Asp Glu Gly Phe Gly Phe Gly
35 40 45

Thr Asn Gly Ala Val Gly Ala Gln Met Asp Val Gln Thr Ser Pro Phe
50 55 60

Ser Asp Pro Val Phe Gly Gly Val Gly Ala Gly Pro Asp Met Met Gly
65 70 75 80

Leu Met Asp Thr Asn Met Asn His Ile Asn Gly Ser His Asn Met Asn
85 90 95

Ser Val Val Lys Gln Glu Asp Tyr Tyr Thr Pro Ser Met Gly Thr Pro
100 105 110

Met Asn Pro Gln Gln Gln Gln Ser Met Thr Pro Gln Gln Gln His His
115 120 125

Met Asn His Asn Gln Pro Ser Gln Leu Gln Ser Leu His Gln Gln Ser
130 135 140

Gln Lys Ala Gln Pro Gln Gln Gln Gln Gln Pro His Gln Ser Thr
145 150 155 160

Gly Val Asp Ser Ile Ile Thr Lys Ala Tyr Thr Arg Ala Ala Gly Asp
165 170 175

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Leu Pro Tyr Gly Arg Lys Tyr Ser Arg Gln Leu Asn Lys Tyr Pro Glu
            180                 185                 190

Asp Val Glu Tyr Ser Ser Phe Asp Pro Ser Leu Trp Ser Asn Leu Leu
        195                 200                 205

Thr Asn Ser Glu Thr Pro Tyr Gln Tyr Gln Ile His Val His Ser Met
    210                 215                 220

Pro Gly Lys Ser Arg Val Glu Thr Gln Ile Lys Cys Ala Leu Ser Ile
225                 230                 235                 240

Tyr Pro Pro Pro Pro Gln Gln Ser Val Arg Leu Pro Thr Asp Thr Ile
                245                 250                 255

Ser Arg Pro Lys Phe Gln Leu Lys Gln Gly His Ile Pro Asp Ser Cys
            260                 265                 270

Leu Ser Leu Glu Val Tyr Ile Val Gly Glu Gln Asn Pro Ser Lys Pro
        275                 280                 285

Val Asn Leu Cys Ser Arg Cys Ile Lys Arg Glu Gln Lys Arg Ala Cys
    290                 295                 300

Arg Lys Lys Leu Phe Asp Glu Ser Glu Glu Leu Ser Trp Val Glu Thr
305                 310                 315                 320

Arg Gln Arg Arg Leu Ala Val Phe Asn Cys Ser Glu Val Leu Glu Phe
                325                 330                 335

Lys Asp Val Glu Arg Arg Val Tyr Ile Pro Glu Ser Gly Thr Thr Val
            340                 345                 350

Thr Ala Lys Gln Leu Val Leu Pro Leu Arg Leu Ala Cys Tyr Cys Arg
        355                 360                 365

His His Gly Glu Lys Lys Gly Phe Arg Ile Leu Phe Cys Leu Arg Asp
    370                 375                 380

Glu Gly Gly Gln Ile Val Gly Val Gly Gln Ser Gly Thr Thr Val Met
385                 390                 395                 400

Ile Thr Asp Asp His Lys Val Val Gly Asp Ala Val Ala Met Pro Thr
                405                 410                 415

Thr Ala Thr Ala Pro Ala Thr Ala Gly Ser Ser Gln Pro Pro Thr Gln
            420                 425                 430

Val Pro Thr Pro Ala Ala Ser Ser Ser Thr Ser Tyr Arg Pro Arg Asn
        435                 440                 445

Ser Leu Pro Leu Ser Pro Thr Ser Met Glu Asp Ser Ser Ser Glu Phe
    450                 455                 460

Thr Ser Asp His Ser His Tyr Ser Asn Tyr Gly Ser Lys Arg Arg Arg
465                 470                 475                 480

Asp Gly Ser Ser Ile Ser Asp Trp Ser Gly Met Met Asn Val Arg Gly
                485                 490                 495

Met Asp Arg Gln Ala Ser Ile Thr Ser Ile Pro Glu Met Val Gly Gly
            500                 505                 510

Met Ser Asn Met Thr Val Ala Ser Ala Ser Gly Ser Ala Thr Asn Leu
        515                 520                 525

Ala Ala His Asn Met Asn Asn Pro Ala Asp Glu Asn Leu Pro Val Ile
    530                 535                 540

Lys Arg Ile Ile Pro Ser Gln Gly Ser Ile Arg Gly Gly Ile Glu Val
545                 550                 555                 560

Thr Leu Leu Gly Ser Gly Phe Lys Ser Asn Leu Val Ala Val Phe Gly
                565                 570                 575

Asp Asn Lys Ala Val Gly Thr His Cys Trp Ser Asp Ser Thr Ile Val
            580                 585                 590

Thr His Leu Pro Pro Ser Thr Ile Val Gly Pro Val Val Val Ser Phe
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595 600 605

Glu Gly Phe Val Leu Asp Lys Pro Gln Ile Phe Thr Tyr Phe Asp Asp
610 615 620

Thr Asp Gly Gln Leu Ile Glu Leu Ala Leu Gln Val Val Gly Leu Lys
625 630 635 640

Met Asn Gly Arg Leu Glu Asp Ala Arg Asn Ile Ala Met Arg Ile Val
645 650 655

Gly Asn Asn Gly Gly Val Ala Gly Ala Gln Gly Ala Met Ala Gly Gly
660 665 670

Asn Met Ser Asn Gly Asp Val Gly Met Glu Ser Ala Ala Ala Asp Ser
675 680 685

Ser Val Gln Pro Val Ser Pro Pro Thr Asp His Glu Asp Val Val Leu
690 695 700

Arg Cys Leu Ala Leu Thr Asp Ile Pro Gly Gly Arg Ile Ala Asn Trp
705 710 715 720

Gln Leu Thr Asn Ala Glu Gly Gln Thr Met Val His Leu Ala Ser Ile
725 730 735

Leu Gly Tyr Ser Arg Val Leu Val Ala Leu Val Ala Arg Gly Ala Arg
740 745 750

Val Asp Val Ser Asp Asn Gly Gly Phe Thr Pro Leu His Phe Ala Ala
755 760 765

Leu Phe Gly Arg Arg Lys Ile Ala Lys Lys Leu Leu Arg Cys Asn Ala
770 775 780

Asp Pro Tyr Lys Arg Asn Arg Ile Gly Glu Thr Val Phe Asp Val Ala
785 790 795 800

Cys Pro His Ile Leu Asp Leu Leu Val Gly Pro Gln Gly Met Pro Met
805 810 815

Ala Val Gln Thr Ser Tyr Thr Pro Asp Tyr His Arg Gln Arg Arg Ser
820 825 830

Ser Ser Ser Ser Thr Leu Ala Ser Ile Ala Ser Ile Gln Asp Ser Arg
835 840 845

Glu Tyr Gly Phe Tyr Asp His Gly Met Ile Ser Asn Leu Ser His Ile
850 855 860

Pro Ser Thr Cys Ser Ile Arg Ser Ser Thr Ser Gln Phe Asp Ala Glu
865 870 875 880

Asp Glu Trp Asp Glu Arg Asp Glu Glu Asp Gly Asp Phe Asp Asp Asp
885 890 895

Ser Asp Glu Asp Ser Asp Asp Asp Ser Asp Ala Leu Phe Met Ser Val
900 905 910

Arg Lys His Ala Lys Ala Lys Ser Val Glu Ser Pro Leu Ser Glu Glu
915 920 925

Glu Glu Arg Leu Val Arg His Ile Glu Ala Glu Asp Gln Ala Val Glu
930 935 940

Ala Arg Val Ala Ala Gly Ile Val Ser Ser Asn Val Pro Asp Val Val
945 950 955 960

Ser Ser Asn Asp Ser Asp His Val Arg Ser Asp Thr Ser Thr Glu Asn
965 970 975

Lys Ser Phe Ser Arg Tyr Phe Asp Arg Thr Leu Ser Met Ala Ser Trp
980 985 990

Asp Asp Val Leu Ala Tyr Ile Tyr
995 1000

<210> SEQ ID NO 55

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<211> LENGTH: 772
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 55

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ttccccacca acatcatgga ccgattctcc ctcaagggta aggttgcctc cgtcaccggc 120

tcctcgtcag gtatcggcta ctgcgtggcc gaggcctacg cccaggccgg tgccgacgtg 180

gccatctggt acaactccca ccccgccgac gcaaaggctg agcacctcgc taagacctac 240

ggcgtcaagg ccaaggccta caagtgccct gtcaccgacg ccgccgccgt ggagtccacc 300

atccagcaga tcgagaagga ctttggcacc attgacatct tcgtcgccaa cgctggtgtc 360

ccctggaccg ccggccccat gatcgacgtg cccgacaaca aggagtggga caaggtcatc 420

aacctggatc tcaacggtgc ctactactgc gccaagtacg ccggccagat cttcaagaag 480

aagggcaagg gatccttcat cttcaccgcc tccatgtccg gccacattgt caacatcccc 540

cagatgcagg cctgctacaa cgccgccaag gccgctctgc tgcacctgtc tcgatcgctg 600

gccgtcgagt gggccggctt tgcccgatgc aacacagtct cccctggcta catggccacc 660

gagatctccg actttgtccc caaggagacc aaggagaagt ggtggcagct cattcccatg 720

ggccgagagg gagacccctc cgagctctag cctacctcta ccttgcctct ga 772

<210> SEQ ID NO 56
<211> LENGTH: 200
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 56

cacaaatatt cttgatttac tttggttttg ccctattcgg aaattttatt gatatctaat 60

agaagtatta aagtaaaaat gtactaatac ttaattgtaa tgtcatcaga aataacattt 120

gaggaaaata tttcaaacct aattgatata tatattagag atgtcccgct tctctgtcat 180

taatatattc aagcaatcga 200

<210> SEQ ID NO 57
<211> LENGTH: 840
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 57

atgaagttca cctccgctac tctcctcgcc cttgccgccc ttgtcgttgc cgacaacgcc 60

gttgtctctc agatcaacga tggccagatc caggctcctc ccgctggtgg tgagggtgcc 120

aagcccgccc ctgctccttc tggagctgcc cccggtgccc ccggtgctgg tgctcccggc 180

gctggtgctc ccggcgctgg tgcccctggc gctggcgagg gtgctaagcc ctctggagct 240

gcccccggtg cccccggcgc tggtgctccc ggtgctggtg agggtgctaa gccttctggc 300

ggtgcccccg gtgctggcgc tcctggtgct ggcgagggtg ctaagccctc tggtggtgcc 360

cctggtgccc ccggcgctgg tgctcccggt gctggtgagg gtgctaagcc ctctggtggt 420

gcccccggtg cccccggcgc tggtgagggt gccaagccct ccggctctgc tcccggtgct 480

cctggcgctg gtgagggtgc caagccctcc ggctctgctc ccggtgctcc tggcgctggt 540

gagggtgcca agccctctgg ctctgctccc ggtgctcctg gtgctggtga gggtgccaag 600

ccctctggct ctgctcccgg tgctcctgga gctggtgcag gtgctaagcc ctccgctgga 660

ggtgagcacc ccgctgctga ggccactggt gtcgtcactc agatccacga cggccagatc 720

caggctcccg agcagaccca gccccccgct gccggccctg cccaggctaa cggtgctgcc 780

accctcggtg cccagatcgt tgccggtgtt gtcgccgctg ccggtgtcgc tctcttctaa 840

<210> SEQ ID NO 58
<211> LENGTH: 1542
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 58

atggccgaca acaagcctct gtgcacgatt accacgcccg aaccgtcacc caagcgtcga 60

aagatctctg ccgaggagaa agaaaagatg cgacttgaaa aggaacagat caagaagcag 120

aaagaggaag agcgagagca gcttcgaaga cagaaggaag aagagaaaga gctactgaga 180

aagcagaaag aggaggagaa ggaacaactg aggaaacaga aggaggagga gaagagggct 240

aaagaggagg agagagggct agagagaggg agaaaacgac gacgagaaga ggaacgaaag 300

aaggctgccg aagagaagga gcttgagcga gccaagattg cagaggagaa ggctaagttg 360

gctgaagaga aggaggccaa gagacttgaa aaagaagctg aactcaagaa gaaggagcaa 420

gaacagactc gaatcatgtc tttctttaac aagaagacca aaaagaagac caagaaggaa 480

gctgttaaca gtgacaagtg tttggacttt gataaagact tcctaccctt ccacatcaaa 540

gataccgtgt gtatggcaga caagacggag tgtgaagtga tggatcagga tcctgttgac 600

tggctcaaca gtctcaacct ttctgatgac agcaacaccg ccgaagcaga agaaccacct 660

gttcccgtca aaaccatcat tactcacatc cagaccgctg ccactctggg tctcaatcct 720

gataattaca acggtactcc tttagacacg ctggtcaatg ctcttcctag acgatacttg 780

cagttctatg gtgacgagcg acccgcatac ctgggcacgt actccaagag ctgctcgcgt 840

gatctgttgc agaaccctct cttccaggtg cctggtttgg actacgagta cgacagtgag 900

gcagactggg aagatgaagg agaagatatt gaagatgatg aaattagtgg agacgaggag 960

atggaggacg acgaaatggc cgactttgtg tgttctgatg atgccaagag tcccagcacc 1020

atgacttcaa aggtcacgac agcccaggaa cctgttgttg tctggggctg ctcagatatg 1080

gttggtatga cttttggagg actgattgtc caggggggcaa ttgacccatt caaagactat 1140

tggactgttg caaaagttga gcagaagacc gatactaaga gtgacgtgac aatgactagt 1200

gcgacatcag cttctggtac agctattaaa tctactacaa ccaaaaccga actcagcccg 1260

tttgaagtcc tctccaaaac tctgtcacct tccccagcgg ttgcttcagc cacgaaacag 1320

tttctggctg ctgccaagcc tcagaagctc attgctggag acgacctgac tgctcttttg 1380

aagcgagtag atggatccga cgataacaag acgctgttga ccgagctgct ttgtaagcag 1440

tatccccagt acacacgcaa gatggtcacg gccaccattc agcactatgc tgagcgacag 1500

ggtcctaaga gcgacaagcg gtgggttctg aaggatatct ag 1542

<210> SEQ ID NO 59
<211> LENGTH: 1944
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

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<400> SEQUENCE: 59

atgagcttcc cccaacaagt aatagcgccg ggccaacggc tcaacgagct tctggaggcc 60

atcaaacagg agttcgactc cgtgaccaac gaggcgtccg tctaccggct gcacaaggac 120

gagtttgacg tcaaggtgaa ccagcagacg tcagatctgg gccagattcg acagtcggtc 180

tacgagctag aaatggcgca ccgaaagatg aaggagcgct acgaggagga aatcatgcgg 240

ctcaagagcg agctggaggc ccgaggtgga cccgctgcga accccgcaca ctcccagcag 300

cagcaacagc agcaacagca acagcagcaa cagcagcagc agaaccagca ggcacaggac 360

caacaagcac gggccgcgca acaacaggca gcccagcagc aggccctcgc ccagcagcag 420

gccgcccagc agcaggctct ggcccaacag caggcccagg ctcaacagca ggcccaggcc 480

caggcccacc acatgggtgg tgtgcccccc tcgcaaggac agcccccgtc gctgctgcgt 540

ccatcatcca acgtgttcag cggcatcatg tccggtcagc ccggcacctc ttctctggct 600

cccccgcagg gacagcccgg tcagccccag cctggtcagc cccaacctgg tcaaccccag 660

ccctactccg gctacgtggg tgctaacggc tacacgtctt cgccacataa cggacccccc 720

gtcatcagcg caatggcctc gcccaacagc aagaagcgac aggtgtcgac ccccgttccc 780

ggcaaggcgt ctccccaggt ggcccccccaa gagatgcaac agcagcagca acagcagggc 840

cctccacagc agcagcaacc tccccagcag cagcaacaga gccccgaaga gatgggcaac 900

tacctgggcg acatggacat tgagcgggta cctccggagc tcaaaaaaca aaaggccgac 960

tggtttgtcg tttacaacca gcgagcacca cggctgctgg acgtggatat tgtgcagtcg 1020

ctggaccaca actctgtagt gtgctgtgtg cggttctccg ctgacggcaa gtacattgcc 1080

actggctgta accgatctgc ccagattttc gacgtgcaga ctggccagct catctgccgg 1140

ctgcaggacg actcggtcga ccgagaaggc gacctgtaca tccggtccgt gtgtttctcg 1200

ccggacggta agtacctggc caccggcgcc gaggacaagc agatccgagt gtgggacatt 1260

aaatctcaga gcatacggca cgtgttcact ggccacgagc aggacattta ctcgctggac 1320

ttttcgcgaa acggccgaca cattgcctct ggctctggcg accgcacagt ccgaatgtgg 1380

gatattgaga gcggccagtg tactctaacc ctgtcgatcg aggacggcgt caccacggtg 1440

gccatctcgc ccgacggcaa gtttgtggct gcaggcagct tggacaagtc tgtgcgaatc 1500

tgggacacct ctaccggttt cctggttgag cgtctggagg cccctgatgg acacaaggac 1560

tccgtctata gtgtagcttt caccccaac ggtatggatc ttgtttccgg ctcgctggac 1620

aagacgatca agctgtggga gctgcaggct cctcgaggca ttcaggccaa ccagcgagga 1680

ggcgtctgcg tcaagacgct gtgtggacac aaggactttg ttctgagtgt ggccagcacg 1740

ctggatgggc agtggattct ttccggctcc aaggaccggg gtgtgcaatt ctgggaccct 1800

cgaacgggcc aggtgcaact catgctgcag ggtcatcgaa attcggtcat cagtgtggct 1860

cctagtccca tgggcgggtt gtttgctact ggaagtggag attgcaaggc tcgaatctgg 1920

cgatactttc ctgtcaacag ataa 1944

<210> SEQ ID NO 60
<211> LENGTH: 647
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 60

Met Ser Phe Pro Gln Gln Val Ile Ala Pro Gly Gln Arg Leu Asn Glu
1 5 10 15

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Leu Leu Glu Ala Ile Lys Gln Glu Phe Asp Ser Val Thr Asn Glu Ala
            20                  25                  30

Ser Val Tyr Arg Leu His Lys Asp Glu Phe Asp Val Lys Val Asn Gln
        35                  40                  45

Gln Thr Ser Asp Leu Gly Gln Ile Arg Gln Ser Val Tyr Glu Leu Glu
    50                  55                  60

Met Ala His Arg Lys Met Lys Glu Arg Tyr Glu Glu Glu Ile Met Arg
65                  70                  75                  80

Leu Lys Ser Glu Leu Glu Ala Arg Gly Gly Pro Ala Ala Asn Pro Ala
                85                  90                  95

His Ser Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
            100                 105                 110

Gln Gln Asn Gln Gln Ala Gln Asp Gln Gln Ala Arg Ala Ala Gln Gln
        115                 120                 125

Gln Ala Ala Gln Gln Gln Ala Leu Ala Gln Gln Gln Ala Ala Gln Gln
    130                 135                 140

Gln Ala Leu Ala Gln Gln Gln Ala Gln Ala Gln Gln Gln Ala Gln Ala
145                 150                 155                 160

Gln Ala His His Met Gly Gly Val Pro Pro Ser Gln Gly Gln Pro Pro
                165                 170                 175

Ser Leu Leu Arg Pro Ser Ser Asn Val Phe Ser Gly Ile Met Ser Gly
            180                 185                 190

Gln Pro Gly Thr Ser Ser Leu Ala Pro Pro Gln Gly Gln Pro Gly Gln
        195                 200                 205

Pro Gln Pro Gly Gln Pro Gln Pro Gly Gln Pro Gln Pro Tyr Ser Gly
    210                 215                 220

Tyr Val Gly Ala Asn Gly Tyr Thr Ser Ser Pro His Asn Gly Pro Pro
225                 230                 235                 240

Val Ile Ser Ala Met Ala Ser Pro Asn Ser Lys Lys Arg Gln Val Ser
                245                 250                 255

Thr Pro Val Pro Gly Lys Ala Ser Pro Gln Val Ala Pro Gln Glu Met
            260                 265                 270

Gln Gln Gln Gln Gln Gln Gln Gly Pro Pro Gln Gln Gln Gln Pro Pro
        275                 280                 285

Gln Gln Gln Gln Gln Ser Pro Glu Glu Met Gly Asn Tyr Leu Gly Asp
    290                 295                 300

Met Asp Ile Glu Arg Val Pro Pro Glu Leu Lys Lys Gln Lys Ala Asp
305                 310                 315                 320

Trp Phe Val Val Tyr Asn Gln Arg Ala Pro Arg Leu Leu Asp Val Asp
                325                 330                 335

Ile Val Gln Ser Leu Asp His Asn Ser Val Val Cys Cys Val Arg Phe
            340                 345                 350

Ser Ala Asp Gly Lys Tyr Ile Ala Thr Gly Cys Asn Arg Ser Ala Gln
        355                 360                 365

Ile Phe Asp Val Gln Thr Gly Gln Leu Ile Cys Arg Leu Gln Asp Asp
    370                 375                 380

Ser Val Asp Arg Glu Gly Asp Leu Tyr Ile Arg Ser Val Cys Phe Ser
385                 390                 395                 400

Pro Asp Gly Lys Tyr Leu Ala Thr Gly Ala Glu Asp Lys Gln Ile Arg
                405                 410                 415

Val Trp Asp Ile Lys Ser Gln Ser Ile Arg His Val Phe Thr Gly His
            420                 425                 430

Glu Gln Asp Ile Tyr Ser Leu Asp Phe Ser Arg Asn Gly Arg His Ile
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        435                 440                 445

Ala Ser Gly Ser Gly Asp Arg Thr Val Arg Met Trp Asp Ile Glu Ser
    450                 455                 460

Gly Gln Cys Thr Leu Thr Leu Ser Ile Glu Asp Gly Val Thr Thr Val
465                 470                 475                 480

Ala Ile Ser Pro Asp Gly Lys Phe Val Ala Ala Gly Ser Leu Asp Lys
                485                 490                 495

Ser Val Arg Ile Trp Asp Thr Ser Thr Gly Phe Leu Val Glu Arg Leu
            500                 505                 510

Glu Ala Pro Asp Gly His Lys Asp Ser Val Tyr Ser Val Ala Phe Thr
        515                 520                 525

Pro Asn Gly Met Asp Leu Val Ser Gly Ser Leu Asp Lys Thr Ile Lys
    530                 535                 540

Leu Trp Glu Leu Gln Ala Pro Arg Gly Ile Gln Ala Asn Gln Arg Gly
545                 550                 555                 560

Gly Val Cys Val Lys Thr Leu Cys Gly His Lys Asp Phe Val Leu Ser
                565                 570                 575

Val Ala Ser Thr Leu Asp Gly Gln Trp Ile Leu Ser Gly Ser Lys Asp
            580                 585                 590

Arg Gly Val Gln Phe Trp Asp Pro Arg Thr Gly Gln Val Gln Leu Met
        595                 600                 605

Leu Gln Gly His Arg Asn Ser Val Ile Ser Val Ala Pro Ser Pro Met
    610                 615                 620

Gly Gly Leu Phe Ala Thr Gly Ser Gly Asp Cys Lys Ala Arg Ile Trp
625                 630                 635                 640

Arg Tyr Phe Pro Val Asn Arg
                645
```

<210> SEQ ID NO 61
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 61

```
atgtctatca agcgagaaga gtcctttact cccacccccg aggacctggg atctcccctg     60

acagctgatt ctcctggctc tcccgagtct ggagacaagc gaaagaagga tctcactctg    120

ccccttcctg ctggtgctct tccccctcga aagagagcta agacagagaa cgaaaaggag    180

cagagacgca tcgagcggat catgcgaaac cggcaggcgg cacatgcgtc tcgagagaag    240

aagcgacgac atttggagga cctggagaag aagtgctcgg agttgtcgtc cgaaaacaac    300

gatctacacc accaggtgac tgagtccaag aagaccaaca tgcacctcat ggaacaacac    360

tactcgctgg tggccaagct gcagcagctc tcgtcgctcg tcaacatggc caagtcttcc    420

ggagctttgg ccggcgttga tgtccccgac atgagcgatg tgtctatggc ccccaagttg    480

gagatgccca ccgcggctcc ttcccagccc atgggtctcg ccagcgcgcc caccctcttc    540

aaccacgata atgagaccgt cgtccccgac tctcctattg tgaagaccga ggaagtcgac    600

tctacaaact ttctcctcca cacggagtcc tcctcccccc ccgaactagc tgagagcact    660

ggctcaggct cgccatcgtc gactctgtcc tgcgacgaaa ctgattatct tgtggaccgg    720

gcgcgtcatc cagcagtgat gactgtcgca actactgacc agcagcgtcg gcacaagatt    780

tcattttcat caaggacgag cccgttgacg acgagcttgg actgcatgga ctgtcggatg    840

acttcaccct gtttgaagac aacaagcagc ctgcccagca cgactttatt gctgatctag    900
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<210> SEQ ID NO 62
<211> LENGTH: 299
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 62

Met Ser Ile Lys Arg Glu Glu Ser Phe Thr Pro Thr Pro Glu Asp Leu
1 5 10 15

Gly Ser Pro Leu Thr Ala Asp Ser Pro Gly Ser Pro Glu Ser Gly Asp
20 25 30

Lys Arg Lys Lys Asp Leu Thr Leu Pro Leu Pro Ala Gly Ala Leu Pro
35 40 45

Pro Arg Lys Arg Ala Lys Thr Glu Asn Glu Lys Glu Gln Arg Arg Ile
50 55 60

Glu Arg Ile Met Arg Asn Arg Gln Ala Ala His Ala Ser Arg Glu Lys
65 70 75 80

Lys Arg Arg His Leu Glu Asp Leu Glu Lys Lys Cys Ser Glu Leu Ser
85 90 95

Ser Glu Asn Asn Asp Leu His His Gln Val Thr Glu Ser Lys Lys Thr
100 105 110

Asn Met His Leu Met Glu Gln His Tyr Ser Leu Val Ala Lys Leu Gln
115 120 125

Gln Leu Ser Ser Leu Val Asn Met Ala Lys Ser Ser Gly Ala Leu Ala
130 135 140

Gly Val Asp Val Pro Asp Met Ser Asp Val Ser Met Ala Pro Lys Leu
145 150 155 160

Glu Met Pro Thr Ala Ala Pro Ser Gln Pro Met Gly Leu Ala Ser Ala
165 170 175

Pro Thr Leu Phe Asn His Asp Asn Glu Thr Val Val Pro Asp Ser Pro
180 185 190

Ile Val Lys Thr Glu Glu Val Asp Ser Thr Asn Phe Leu Leu His Thr
195 200 205

Glu Ser Ser Ser Pro Pro Glu Leu Ala Glu Ser Thr Gly Ser Gly Ser
210 215 220

Pro Ser Ser Thr Leu Ser Cys Asp Glu Thr Asp Tyr Leu Val Asp Arg
225 230 235 240

Ala Arg His Pro Ala Val Met Thr Val Ala Thr Thr Asp Gln Gln Arg
245 250 255

Arg His Lys Ile Ser Phe Ser Ser Arg Thr Ser Pro Leu Thr Thr Ser
260 265 270

Leu Asp Cys Met Asp Cys Arg Met Thr Ser Pro Cys Leu Lys Thr Thr
275 280 285

Ser Ser Leu Pro Ser Thr Thr Leu Leu Leu Ile
290 295

<210> SEQ ID NO 63
<211> LENGTH: 738
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 63

atgcgccaaa agctgccgtt caacccgctc cagtcgcttc tcccgcgaat ctttgtgcgg 60

ggcaaaaaac acgatgcgcg cagccgctgg gaaatgcgcc agatgaaaga caagcatgtg 120

gccatggcca aggctgacgg attccggtct cgagccgcgt acaagctaca ggaactcgac 180

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tccatgttcc ggctgttcaa gcccggcatg acggtggtgg atttgggctt tgcgcccggc 240

gcatggagtc aagtggctgc tcagcgagtg cggcctggag gcagagttat tggagtggat 300

atccttcctt gcattcctcc tccaggagtg tccagcatcc agggaaattt cctgtccaaa 360

gaaacacaaa acgagctcaa acgtgtgctg gccgtctcgg cgatgggagt tcccaaggac 420

aaggactctg gtggcgccat aggcactgct cctccgtctt atctggacac tgaacgcgag 480

cttggcagta ttaacagcaa cagcaacgaa ccccaatttg gcgacgacta cccggtagat 540

atagtgctta gtgacatgtg cgaaacgtta ccccaggaac acggattttt tcaaagaact 600

attaatgacc catactatag gatggccaat gtttccggca tagctgtgag ggaccatgct 660

gccagtattg tgagtgaagg aaggaagcgc attgggtgtg gtgcagccag cttcgatgtg 720

gcagaaggga agccataa 738

<210> SEQ ID NO 64
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 64

Met Arg Gln Lys Leu Pro Phe Asn Pro Leu Gln Ser Leu Leu Pro Arg
1 5 10 15

Ile Phe Val Arg Gly Lys Lys His Asp Ala Arg Ser Arg Trp Glu Met
20 25 30

Arg Gln Met Lys Asp Lys His Val Ala Met Ala Lys Ala Asp Gly Phe
35 40 45

Arg Ser Arg Ala Ala Tyr Lys Leu Gln Glu Leu Asp Ser Met Phe Arg
50 55 60

Leu Phe Lys Pro Gly Met Thr Val Val Asp Leu Gly Phe Ala Pro Gly
65 70 75 80

Ala Trp Ser Gln Val Ala Ala Gln Arg Val Arg Pro Gly Gly Arg Val
85 90 95

Ile Gly Val Asp Ile Leu Pro Cys Ile Pro Pro Pro Gly Val Ser Ser
100 105 110

Ile Gln Gly Asn Phe Leu Ser Lys Glu Thr Gln Asn Glu Leu Lys Arg
115 120 125

Val Leu Ala Val Ser Ala Met Gly Val Pro Lys Asp Lys Asp Ser Gly
130 135 140

Gly Ala Ile Gly Thr Ala Pro Pro Ser Tyr Leu Asp Thr Glu Arg Glu
145 150 155 160

Leu Gly Ser Ile Asn Ser Asn Ser Asn Glu Pro Gln Phe Gly Asp Asp
165 170 175

Tyr Pro Val Asp Ile Val Leu Ser Asp Met Cys Glu Thr Leu Pro Gln
180 185 190

Glu His Gly Phe Phe Gln Arg Thr Ile Asn Asp Pro Tyr Tyr Arg Met
195 200 205

Ala Asn Val Ser Gly Ile Ala Val Arg Asp His Ala Ala Ser Ile Val
210 215 220

Ser Glu Gly Arg Lys Arg Ile Gly Cys Gly Ala Ala Ser Phe Asp Val
225 230 235 240

Ala Glu Gly Lys Pro
245

<210> SEQ ID NO 65
<211> LENGTH: 1590

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<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 65

atgttttaca ccaagcccga cccggtggtt gattattccc gcctcaagga catggacatg 60

tatcctgagt acgacaatgg ccagaacatg ggcttttcca acatgaacat gaccgatctt 120

tacgacggcg gtcttaacat gtcgtcgatg gcgcaacccg tggcgttgaa ccagatgggc 180

agcatgggcc ccatgggctc tttaagtaac atgcccatgg gttttgtgtc ccagaaccag 240

cctcaaactc aggctcaggc ccaggcccag agccagaacc agaatcagaa ccagaaccag 300

aaccagaacc agcctcagaa tcacaacacc catgttatga gcgataacca caaccatacc 360

cacaccaaca atactcacaa caccaacgtc acccacaaca ccccctccat gggtggtcac 420

acaacctctg tcgggggcca cgacaccaat gactcggccc atgttggggg tcacgccagc 480

aatgtcacat ccccgacccc ggcaacccct gcctccacat cttccgtacc cgcaacctcg 540

cctcagattc ccttcacggt cgcgccaccc gcaccgtcag gcaaatatgt gaccgatgac 600

gagcgatggc aggcactggt cgaccgagac cccgaggctg acggcgcctt catctactgc 660

gtcaccagca ccaaggtgta ctgccggccc acgtgctcgg cccggctcgc gctgcggtcc 720

aacattgtgt attttgacac catgaaggag gctgtggccg ccggctaccg cccctgccga 780

cggtgcaacc ccgacgtgag cgagatgaac tcgcagcgac gcgccgtggg ctccgtgtgt 840

aacctcatcc actcgctgga gcccgacaag gtgccacgtg tcaagaagct agccgagtcc 900

gtcggcctca cgctctggca ctttcaccgt ctcttcaagc ggtacacggg cctcacgcct 960

cgacagtaca tcactgagtt ccacaagcga aagcgccttg ggctgccgca gttgcaagtc 1020

agcaaggtgg taaccaagaa gagctatgag cgacagcagc gtcgccaggg cagcaacggt 1080

tccacgcccc agcagtctcc ccaagtcggc gcctcttcgc cagccggcga ggtggaggcc 1140

atcaagctcg agacccccgt cgaaaccgtc cagccgctat actacgacag caacggcgtg 1200

actcacaacg ctgccaacgt cggggctcac agctccaatg tcactcacaa cactagccat 1260

gtcggaagca acgcaacctc cgccacgagc tccattgcca ctcctctttc caacacaacg 1320

tcacccgaca cctcgacgcc ggcccaggac tcggcataca tcattgccca cggttccaac 1380

gccagcaacg ccgctcctgt ggttgctccg gggcctgcca ccggctctgg cgacaactgg 1440

atcaagacgg agccctcgat ggattttatg cctcggtacg agccgcggta cgaccagtct 1500

atctccattg acgcccccat gtttattcct gatggtaacg agtatcatca caacggggag 1560

atgttgggtg acatgtgggg gactctctaa 1590

<210> SEQ ID NO 66
<211> LENGTH: 529
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 66

Met Phe Tyr Thr Lys Pro Asp Pro Val Val Asp Tyr Ser Arg Leu Lys
1 5 10 15

Asp Met Asp Met Tyr Pro Glu Tyr Asp Asn Gly Gln Asn Met Gly Phe
20 25 30

Ser Asn Met Asn Met Thr Asp Leu Tyr Asp Gly Gly Leu Asn Met Ser
35 40 45

Ser Met Ala Gln Pro Val Ala Leu Asn Gln Met Gly Ser Met Gly Pro
50 55 60

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Met Gly Ser Leu Ser Asn Met Pro Met Gly Phe Val Ser Gln Asn Gln
65                  70                  75                  80

Pro Gln Thr Gln Ala Gln Ala Gln Ala Gln Ser Gln Asn Gln Asn Gln
                85                  90                  95

Asn Gln Asn Gln Asn Gln Asn Gln Pro Gln Asn His Asn Thr His Val
            100                 105                 110

Met Ser Asp Asn His Asn His Thr His Thr Asn Asn Thr His Asn Thr
        115                 120                 125

Asn Val Thr His Asn Thr Pro Ser Met Gly Gly His Thr Thr Ser Val
    130                 135                 140

Gly Gly His Asp Thr Asn Asp Ser Ala His Val Gly Gly His Ala Ser
145                 150                 155                 160

Asn Val Thr Ser Pro Thr Pro Ala Thr Pro Ala Ser Thr Ser Ser Val
                165                 170                 175

Pro Ala Thr Ser Pro Gln Ile Pro Phe Thr Val Ala Pro Pro Ala Pro
            180                 185                 190

Ser Gly Lys Tyr Val Thr Asp Asp Glu Arg Trp Gln Ala Leu Val Asp
        195                 200                 205

Arg Asp Pro Glu Ala Asp Gly Ala Phe Ile Tyr Cys Val Thr Ser Thr
    210                 215                 220

Lys Val Tyr Cys Arg Pro Thr Cys Ser Ala Arg Leu Ala Leu Arg Ser
225                 230                 235                 240

Asn Ile Val Tyr Phe Asp Thr Met Lys Glu Ala Val Ala Ala Gly Tyr
                245                 250                 255

Arg Pro Cys Arg Arg Cys Asn Pro Asp Val Ser Glu Met Asn Ser Gln
            260                 265                 270

Arg Arg Ala Val Gly Ser Val Cys Asn Leu Ile His Ser Leu Glu Pro
        275                 280                 285

Asp Lys Val Pro Arg Val Lys Lys Leu Ala Glu Ser Val Gly Leu Thr
    290                 295                 300

Leu Trp His Phe His Arg Leu Phe Lys Arg Tyr Thr Gly Leu Thr Pro
305                 310                 315                 320

Arg Gln Tyr Ile Thr Glu Phe His Lys Arg Lys Arg Leu Gly Leu Pro
                325                 330                 335

Gln Leu Gln Val Ser Lys Val Val Thr Lys Lys Ser Tyr Glu Arg Gln
            340                 345                 350

Gln Arg Arg Gln Gly Ser Asn Gly Ser Thr Pro Gln Gln Ser Pro Gln
        355                 360                 365

Val Gly Ala Ser Ser Pro Ala Gly Glu Val Glu Ala Ile Lys Leu Glu
    370                 375                 380

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

Thr His Asn Ala Ala Asn Val Gly Ala His Ser Ser Asn Val Thr His
                405                 410                 415

Asn Thr Ser His Val Gly Ser Asn Ala Thr Ser Ala Thr Ser Ser Ile
            420                 425                 430

Ala Thr Pro Leu Ser Asn Thr Thr Ser Pro Asp Thr Ser Thr Pro Ala
        435                 440                 445

Gln Asp Ser Ala Tyr Ile Ile Ala His Gly Ser Asn Ala Ser Asn Ala
    450                 455                 460

Ala Pro Val Val Ala Pro Gly Pro Ala Thr Gly Ser Gly Asp Asn Trp
465                 470                 475                 480

Ile Lys Thr Glu Pro Ser Met Asp Phe Met Pro Arg Tyr Glu Pro Arg
```

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485 490 495

Tyr Asp Gln Ser Ile Ser Ile Asp Ala Pro Met Phe Ile Pro Asp Gly
500 505 510

Asn Glu Tyr His His Asn Gly Glu Met Leu Gly Asp Met Trp Gly Thr
515 520 525

Leu

<210> SEQ ID NO 67
<211> LENGTH: 1709
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 67

atgatttctg ctattcgtcc cgccgttcga tcttccgttc gtgttgcccc tatggccaac 60

accgccttcc gggcctactc tacccaggat gtgagtattt cttttctttc atcaattggt 120

tgctgtgcga cggatttcgt tgcgtcagcc tgattgcaac agccttaggc cccattttcg 180

acctgttctt gcctcggcaa aagtttttcc gaatgcatgt gacacgtcga atgtggtgct 240

ttcaagcagc agcagcagca taaaatatgg aatgtgttgt gtgcagaagt cgacattaca 300

taaccccgcg gcaaccatac gagatggcag tcataacaat tgcaattgag caatacaaac 360

cacactgcaa cccactaaaa agaaacacga ctaacaaata gggtcttaag gagcgattcg 420

ccgagctcat ccccgagaac gtcgagaaga tcaagaagct ccgaaaggag aagggtaaca 480

ccgtcatcgg cgaggtcatc ctcgaccagg cttacggtgg tatgcgaggt attaagggtc 540

tcgtctggga gggatccgtc ctcgaccccg aggagggtat ccgattccga ggtctgacta 600

tccccgacct ccagaagcag ctcccccacg cccctggcgg aaaggagcct ctccccgagg 660

gtcttttctg gctcctgctc accggcgaga tccccactga tgctcaggtc aagggtctgt 720

ccgctgactg ggcctctcga gccgagatcc ccaagcatgt tgaggagctc atcgaccgat 780

gccccccccac cctccacccc atggctcagc tcggtattgc cgtcaacgct ctggagtccg 840

agtctcagtt caccaaggct tacgagaagg gtgttaacaa gaaggagtac tggcagtaca 900

cctacgagga ttccatgaac ctcattgcca agctccccgt cattgcttct cgaatctacc 960

gaaaccttttt caaggacgga aagattgttg gctccattga caactctctt gactactctg 1020

ctaacttcgc ctctctgctc ggctttggcg acaacaagga gttcattgag cttctgcgac 1080

tctacctcac catccacgct gaccacgagg gaggtaacgt ctctgcccac accaccaagc 1140

ttgttggttc tgctctctcc tctcccttcc tctctctgtc cgctggtctc aacggtcttg 1200

ccggtcctct ccacggccga gctaaccagg aggtccttga gtggattctc gagatgaagt 1260

ccaagattgg ctctgatgtc accaaggagg acattgagaa gtacctctgg gataccctta 1320

aggccggtcg agtcgtcccc ggttacggac acgccgttct ccgaaagacc gatcctcgat 1380

acaccgccca gcgagagttc gccctcgagc acatgcccga ctacgacctc ttccacctcg 1440

tttccaccat ctacgaggtt gcccccaagg ttctcaccga gcacggcaag accaagaacc 1500

cctggcccaa tgtggactcc cactccggtg tcctcctcca gtactacggt ctcactgagc 1560

agtcttacta cactgttctc ttcggtgttt cccgagctat cggtgtcctg ccccagctca 1620

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acgctgagct cgttggcctc aagctctaa 1709

<210> SEQ ID NO 68
<211> LENGTH: 465

-continued

<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 68

Met Ile Ser Ala Ile Arg Pro Ala Val Arg Ser Ser Val Arg Val Ala
1 5 10 15

Pro Met Ala Asn Thr Ala Phe Arg Ala Tyr Ser Thr Gln Asp Gly Leu
20 25 30

Lys Glu Arg Phe Ala Glu Leu Ile Pro Glu Asn Val Glu Lys Ile Lys
35 40 45

Lys Leu Arg Lys Glu Lys Gly Asn Thr Val Ile Gly Glu Val Ile Leu
50 55 60

Asp Gln Ala Tyr Gly Gly Met Arg Gly Ile Lys Gly Leu Val Trp Glu
65 70 75 80

Gly Ser Val Leu Asp Pro Glu Glu Gly Ile Arg Phe Arg Gly Leu Thr
85 90 95

Ile Pro Asp Leu Gln Lys Gln Leu Pro His Ala Pro Gly Gly Lys Glu
100 105 110

Pro Leu Pro Glu Gly Leu Phe Trp Leu Leu Leu Thr Gly Glu Ile Pro
115 120 125

Thr Asp Ala Gln Val Lys Gly Leu Ser Ala Asp Trp Ala Ser Arg Ala
130 135 140

Glu Ile Pro Lys His Val Glu Glu Leu Ile Asp Arg Cys Pro Pro Thr
145 150 155 160

Leu His Pro Met Ala Gln Leu Gly Ile Ala Val Asn Ala Leu Glu Ser
165 170 175

Glu Ser Gln Phe Thr Lys Ala Tyr Glu Lys Gly Val Asn Lys Lys Glu
180 185 190

Tyr Trp Gln Tyr Thr Tyr Glu Asp Ser Met Asn Leu Ile Ala Lys Leu
195 200 205

Pro Val Ile Ala Ser Arg Ile Tyr Arg Asn Leu Phe Lys Asp Gly Lys
210 215 220

Ile Val Gly Ser Ile Asp Asn Ser Leu Asp Tyr Ser Ala Asn Phe Ala
225 230 235 240

Ser Leu Leu Gly Phe Gly Asp Asn Lys Glu Phe Ile Glu Leu Leu Arg
245 250 255

Leu Tyr Leu Thr Ile His Ala Asp His Glu Gly Gly Asn Val Ser Ala
260 265 270

His Thr Thr Lys Leu Val Gly Ser Ala Leu Ser Ser Pro Phe Leu Ser
275 280 285

Leu Ser Ala Gly Leu Asn Gly Leu Ala Gly Pro Leu His Gly Arg Ala
290 295 300

Asn Gln Glu Val Leu Glu Trp Ile Leu Glu Met Lys Ser Lys Ile Gly
305 310 315 320

Ser Asp Val Thr Lys Glu Asp Ile Glu Lys Tyr Leu Trp Asp Thr Leu
325 330 335

Lys Ala Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
340 345 350

Thr Asp Pro Arg Tyr Thr Ala Gln Arg Glu Phe Ala Leu Glu His Met
355 360 365

Pro Asp Tyr Asp Leu Phe His Leu Val Ser Thr Ile Tyr Glu Val Ala
370 375 380

Pro Lys Val Leu Thr Glu His Gly Lys Thr Lys Asn Pro Trp Pro Asn
385 390 395 400

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Val Asp Ser His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Leu Thr Glu
                405                 410                 415

Gln Ser Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg Ala Ile Gly Val
            420                 425                 430

Leu Pro Gln Leu Ile Met Asp Arg Ala Tyr Gly Ala Pro Ile Glu Arg
        435                 440                 445

Pro Lys Ser Phe Ser Thr Glu Lys Tyr Ala Glu Leu Val Gly Leu Lys
    450                 455                 460

Leu
465
```

<210> SEQ ID NO 69
<211> LENGTH: 7270
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 69

```
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cgtggccacg acagccgagg cgtcacgatg ggccagacga gcacattctc gccgccacaa    120

cctcgccagc acaagaaact aacccagtat ggcttcagga tcttcaacgc cagatgtggc    180

tcccttggtg gaccccaaca ttcacaaagg tctcgcctct catttctttg gactcaattc    240

tgtccacaca gccaagccct caaaagtcaa ggagtttgtg gcttctcacg gaggtcatac    300

agttatcaac aaggtgagta tttgacgttt agactgtata acaggcggcc gcagtgcaac    360

aacgaccaaa aagggtcgaa aaagggtcga aaacggacac aaaagctgga aaacaagagt    420

gtaatacatt cttacacgtc caattgttag acaaacacgg ctgttcggtc ccaaaaccac    480

cagtatcacc tattttccac ttgtgtctcg gatctgatca taatctgatc tcaagatgaa    540

atttacgcca ccgacatgat attgtgattt tcggattctc cagaccgagc agattccagc    600

aataccacca cttgcccacc ttcagcggcc tctcggcgcg attcgccact ttccccaacg    660

agtgttacta acccaggtcc tcatcgctaa caacggtatt gccgcagtaa aggagatccg    720

ttcagtacga aaatgggcct acgagacctt tggcgacgag cgagcaatct cgttcaccgt    780

catggccacc cccgaagatc tcgctgccaa cgccgactac attagaatgg ccgatcagta    840

cgtcgaggtg cccggaggaa ccaacaacaa caactacgcc aacgtcgagc tgattgtcga    900

cgtggctgag cgattcggcg tcgatgccgt gtgggccgga tggggccatg ccagtgaaaa    960

tcccctgctc cccgagtcgc tagcggcctc tccccgcaag attgtcttca tcggccctcc   1020

cggagctgcc atgagatctc tgggagacaa aatttcttct accattgtgg cccagcacgc   1080

aaaggtcccg tgtatcccgt ggtctggaac cggagtggac gaggttgtgg ttgacaagag   1140

caccaacctc gtgtccgtgt ccgaggaggt gtacaccaag ggctgcacca ccggtcccaa   1200

gcagggtctg gagaaggcta agcagattgg attccccgtg atgatcaagg cttccgaggg   1260

aggaggagga aagggtattc gaaaggttga gcgagaggag gacttcgagg ctgcttacca   1320

ccaggtcgag ggagagatcc ccggctcgcc catcttcatt atgcagcttg caggcaatgc   1380

ccggcatttg gaggtgcagc ttctggctga tcagtacggc aacaatattt cactgtttgg   1440

tcgagattgt tcggttcagc gacggcatca aaagattatt gaggaggctc ctgtgactgt   1500

ggctggccag cagaccttca ctgccatgga gaaggctgcc gtgcgactcg gtaagcttgt   1560

cggatatgtc tctgcaggta ccgttgaata tctgtattcc catgaggacg acaagttcta   1620

cttcttggag ctgaatcctc gtcttcaggt cgaacatcct accaccgaga tggtcaccgg   1680
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tgtcaacctg cccgctgccc agcttcagat cgccatgggt atccccctcg atcgaatcaa 1740

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ctcgggcgag gatgctgata agacacagcg acgtcccgtc ccccgaggtc acaccactgc 1860

ttgccgaatc acatccgagg accctggaga gggtttcaag ccctccggag gtactatgca 1920

cgagctcaac ttccgatcct cgtccaacgt gtggggttac ttctccgttg gtaaccaggg 1980

aggtatccat tcgttctcgg attcgcagtt tggtcacatc ttcgccttcg gtgagaaccg 2040

aagtgcgtct cgaaagcaca tggttgttgc tttgaaggaa ctatctattc gaggtgactt 2100

ccgaaccacc gtcgagtacc tcatcaagct gctggagaca ccggacttcg aggacaacac 2160

catcaccacc ggctggctgg atgagcttat ctccaacaag ctgactgccg agcgacccga 2220

ctcgttcctc gctgttgttt gtggtgctgc taccaaggcc catcgagctt ccgaggactc 2280

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gaaggaggag gttggagcca cgcgactgtc tgttgactcc aagacctgcc ttctcgaggt 2580

ggagaacgac cccactcagc ttcgatctcc ctctcccggt aagctggtta agttcctggt 2640

cgagaacggc gaccacgtgc gagccaacca gccctatgcc gagattgagg tcatgaagat 2700

gtacatgact ctcactgctc aggaggacgg tattgtccag ctgatgaagc agcccggttc 2760

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tgagcttcct tatctccagt gggctcatca ggtgtcttct ctgcacaccc gaatgagcgc 3060

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tcctgccaag cagcttctgc gagcccttga gaaggaggcg agctctggcg aggtcgatgc 3180

gctcttccag caaactcttg ctcctctgtt tgaccttgct cgagagtacc aggacggtct 3240

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ggcctactcc atcctggaca tcaactacca ccaggactcg gacctgcctc ccgtcatctc 3900

gtggcgattt agactgccta ccatgtcgtc tgctttgtac aactcagtag tgtcttctgg 3960

ctccaaaacc cccacttccc cctcggtgtc tcgagctgat tccgtctccg acttttcgta 4020

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ggatgatctg gaggatgctc tgactcgtgt tctggagaac ctgcccaaac ggggcgctgg 4140

tcttgccatc tctgttggtg ctagcaacaa gagtgccgct gcttctgctc gtgacgctgc 4200

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ctcccgaggt acttatccca agtatttcac gttccgaggc cccgcatacg aggaggaccc 4440

cactatccga cacattgagc ctgctctggc cttccagctg gagctcgccc gtctgtccaa 4500

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caagaacgct gcttccgaca agcggttctt cacccgaggt atcgtacgac ctggtcgtct 4620

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cgagctgcag gaggtgaacc gagagcccgg cgccaacaac gtcggtatgg ttgcgtggaa 5280

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tatcaccttc cagattggtt cgtttggccc tgctgaggac cagttcttct tcaaggtgac 5400

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aatcggcatt gctgacgagc tcgttggcaa gtacaaggtt gcgtggaacg acgagactga 5520

cccctccaag ggcttcaagt acctttactt caccccctgag tctcttgcca ccctcaagcc 5580

cgacactgtt gtcaccactg agattgagga ggagggtccc aacggcgtgg agaagcgtca 5640

tgtgatcgac tacattgtcg gagagaagga cggtctcgga gtcgagtgtc tgcggggctc 5700

tggtctcatt gcaggcgcca cttctcgagc ctacaaggat atcttcactc tcactcttgt 5760

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gtctcatctg actgcccgag atgatctcaa cggtgtccac aagatcatgc agtggctgtc 6000

atacatccct gcttctcgag gtcttccagt gcctgttctc cctcacaaga ccgatgtgtg 6060

ggatcgagac gtgacgttcc agcctgtccg aggcgagcag tacgatgtta gatggcttat 6120

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tcccgccaac ccggactcta ttgagatgag cacctctgaa gccggccagg tttggtaccc 6360

caactcggcc ttcaagacct ctcaggccat caacgacttc aaccatggtg aggcgcttcc 6420

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tctcatgatt cttgctaact ggcgaggctt ttctggtggt cagcgagaca tgtacaatga   6480

ggttctcaag tacggatctt tcattgttga tgctctggtt gactacaagc agcccatcat   6540

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tctggatccc gagtactcct ctctcaagaa gcagcttgag gagtctcccg attctgagga   6780

gctcaaggtc aagctcagcg tgcgagagaa gtctctcatg cccatctacc agcagatctc   6840

cgtgcagttt gccgacttgc atgaccgagc tggccgaatg gaggccaagg gtgtcattcg   6900

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gaaggacgct tctgcccagt cgtttgcttc tcaactgaga aaggaccgac agggtactct   7200

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ggggttgtga                                                          7270
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<210> SEQ ID NO 70
<211> LENGTH: 2266
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 70

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Met Arg Leu Gln Leu Arg Thr Leu Thr Arg Arg Phe Phe Ser Met Ala
1               5                   10                  15

Ser Gly Ser Ser Thr Pro Asp Val Ala Pro Leu Val Asp Pro Asn Ile
            20                  25                  30

His Lys Gly Leu Ala Ser His Phe Phe Gly Leu Asn Ser Val His Thr
        35                  40                  45

Ala Lys Pro Ser Lys Val Lys Glu Phe Val Ala Ser His Gly Gly His
    50                  55                  60

Thr Val Ile Asn Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val
65                  70                  75                  80

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp
                85                  90                  95

Glu Arg Ala Ile Ser Phe Thr Val Met Ala Thr Pro Glu Asp Leu Ala
            100                 105                 110

Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro
        115                 120                 125

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp
    130                 135                 140

Val Ala Glu Arg Phe Gly Val Asp Ala Val Trp Ala Gly Trp Gly His
145                 150                 155                 160

Ala Ser Glu Asn Pro Leu Leu Pro Glu Ser Leu Ala Ala Ser Pro Arg
                165                 170                 175

Lys Ile Val Phe Ile Gly Pro Pro Gly Ala Ala Met Arg Ser Leu Gly
            180                 185                 190

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

Ile Pro Trp Ser Gly Thr Gly Val Asp Glu Val Val Val Asp Lys Ser
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    210                 215                 220

Thr Asn Leu Val Ser Val Ser Glu Glu Val Tyr Thr Lys Gly Cys Thr
225                 230                 235                 240

Thr Gly Pro Lys Gln Gly Leu Glu Lys Ala Lys Gln Ile Gly Phe Pro
                245                 250                 255

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys
            260                 265                 270

Val Glu Arg Glu Glu Asp Phe Glu Ala Ala Tyr His Gln Val Glu Gly
        275                 280                 285

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Gln Leu Ala Gly Asn Ala
    290                 295                 300

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile
305                 310                 315                 320

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile
                325                 330                 335

Ile Glu Glu Ala Pro Val Thr Val Ala Gly Gln Gln Thr Phe Thr Ala
            340                 345                 350

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser
        355                 360                 365

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Glu Asp Asp Lys Phe Tyr
    370                 375                 380

Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu
385                 390                 395                 400

Met Val Thr Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met
                405                 410                 415

Gly Ile Pro Leu Asp Arg Ile Lys Asp Ile Arg Leu Phe Tyr Gly Val
            420                 425                 430

Asn Pro His Thr Thr Thr Pro Ile Asp Phe Asp Phe Ser Gly Glu Asp
        435                 440                 445

Ala Asp Lys Thr Gln Arg Arg Pro Val Pro Arg Gly His Thr Thr Ala
    450                 455                 460

Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Gly
465                 470                 475                 480

Gly Thr Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
                485                 490                 495

Tyr Phe Ser Val Gly Asn Gln Gly Gly Ile His Ser Phe Ser Asp Ser
            500                 505                 510

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Ser Ala Ser Arg
        515                 520                 525

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe
    530                 535                 540

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Pro Asp Phe
545                 550                 555                 560

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Asn
                565                 570                 575

Lys Leu Thr Ala Glu Arg Pro Asp Ser Phe Leu Ala Val Val Cys Gly
            580                 585                 590

Ala Ala Thr Lys Ala His Arg Ala Ser Glu Asp Ser Ile Ala Thr Tyr
        595                 600                 605

Met Ala Ser Leu Glu Lys Gly Gln Val Pro Ala Arg Asp Ile Leu Lys
    610                 615                 620

Thr Leu Phe Pro Val Asp Phe Ile Tyr Glu Gly Gln Arg Tyr Lys Phe
625                 630                 635                 640
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Thr Ala Thr Arg Ser Ser Glu Asp Ser Tyr Thr Leu Phe Ile Asn Gly
                645                 650                 655

Ser Arg Cys Asp Ile Gly Val Arg Pro Leu Ser Asp Gly Gly Ile Leu
            660                 665                 670

Cys Leu Val Gly Gly Arg Ser His Asn Val Tyr Trp Lys Glu Glu Val
        675                 680                 685

Gly Ala Thr Arg Leu Ser Val Asp Ser Lys Thr Cys Leu Leu Glu Val
    690                 695                 700

Glu Asn Asp Pro Thr Gln Leu Arg Ser Pro Ser Pro Gly Lys Leu Val
705                 710                 715                 720

Lys Phe Leu Val Glu Asn Gly Asp His Val Arg Ala Asn Gln Pro Tyr
                725                 730                 735

Ala Glu Ile Glu Val Met Lys Met Tyr Met Thr Leu Thr Ala Gln Glu
            740                 745                 750

Asp Gly Ile Val Gln Leu Met Lys Gln Pro Gly Ser Thr Ile Glu Ala
        755                 760                 765

Gly Asp Ile Leu Gly Ile Leu Ala Leu Asp Asp Pro Ser Lys Val Lys
    770                 775                 780

His Ala Lys Pro Phe Glu Gly Gln Leu Pro Glu Leu Gly Pro Pro Thr
785                 790                 795                 800

Leu Ser Gly Asn Lys Pro His Gln Arg Tyr Glu His Cys Gln Asn Val
                805                 810                 815

Leu His Asn Ile Leu Leu Gly Phe Asp Asn Gln Val Val Met Lys Ser
            820                 825                 830

Thr Leu Gln Glu Met Val Gly Leu Leu Arg Asn Pro Glu Leu Pro Tyr
        835                 840                 845

Leu Gln Trp Ala His Gln Val Ser Ser Leu His Thr Arg Met Ser Ala
    850                 855                 860

Lys Leu Asp Ala Thr Leu Ala Gly Leu Ile Asp Lys Ala Lys Gln Arg
865                 870                 875                 880

Gly Gly Glu Phe Pro Ala Lys Gln Leu Leu Arg Ala Leu Glu Lys Glu
                885                 890                 895

Ala Ser Ser Gly Glu Val Asp Ala Leu Phe Gln Gln Thr Leu Ala Pro
            900                 905                 910

Leu Phe Asp Leu Ala Arg Glu Tyr Gln Asp Gly Leu Ala Ile His Glu
        915                 920                 925

Leu Gln Val Ala Ala Gly Leu Leu Gln Ala Tyr Tyr Asp Ser Glu Ala
    930                 935                 940

Arg Phe Cys Gly Pro Asn Val Arg Asp Glu Asp Val Ile Leu Lys Leu
945                 950                 955                 960

Arg Glu Glu Asn Arg Asp Ser Leu Arg Lys Val Val Met Ala Gln Leu
                965                 970                 975

Ser His Ser Arg Val Gly Ala Lys Asn Asn Leu Val Leu Ala Leu Leu
            980                 985                 990

Asp Glu Tyr Lys Val Ala Asp Gln  Ala Gly Thr Asp Ser  Pro Ala Ser
        995                 1000                1005

Asn Val  His Val Ala Lys Tyr  Leu Arg Pro Val Leu  Arg Lys Ile
    1010                1015                1020

Val Glu  Leu Glu Ser Arg Ala  Ser Ala Lys Val Ser  Leu Lys Ala
    1025                1030                1035

Arg Glu  Ile Leu Ile Gln Cys  Ala Leu Pro Ser Leu  Lys Glu Arg
    1040                1045                1050
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Thr Asp  Gln Leu Glu His Ile  Leu Arg Ser Ser Val  Val Glu Ser
    1055                1060                1065

Arg Tyr  Gly Glu Val Gly Leu  Glu His Arg Thr Pro  Arg Ala Asp
    1070                1075                1080

Ile Leu  Lys Glu Val Val Asp  Ser Lys Tyr Ile Val  Phe Asp Val
    1085                1090                1095

Leu Ala  Gln Phe Phe Ala His  Asp Asp Pro Trp Ile  Val Leu Ala
    1100                1105                1110

Ala Leu  Glu Leu Tyr Ile Arg  Arg Ala Cys Lys Ala  Tyr Ser Ile
    1115                1120                1125

Leu Asp  Ile Asn Tyr His Gln  Asp Ser Asp Leu Pro  Pro Val Ile
    1130                1135                1140

Ser Trp  Arg Phe Arg Leu Pro  Thr Met Ser Ser Ala  Leu Tyr Asn
    1145                1150                1155

Ser Val  Val Ser Ser Gly Ser  Lys Thr Pro Thr Ser  Pro Ser Val
    1160                1165                1170

Ser Arg  Ala Asp Ser Val Ser  Asp Phe Ser Tyr Thr  Val Glu Arg
    1175                1180                1185

Asp Ser  Ala Pro Ala Arg Thr  Gly Ala Ile Val Ala  Val Pro His
    1190                1195                1200

Leu Asp  Asp Leu Glu Asp Ala  Leu Thr Arg Val Leu  Glu Asn Leu
    1205                1210                1215

Pro Lys  Arg Gly Ala Gly Leu  Ala Ile Ser Val Gly  Ala Ser Asn
    1220                1225                1230

Lys Ser  Ala Ala Ala Ser Ala  Arg Asp Ala Ala Ala  Ala Ala Ala
    1235                1240                1245

Ser Ser  Val Asp Thr Gly Leu  Ser Asn Ile Cys Asn  Val Met Ile
    1250                1255                1260

Gly Arg  Val Asp Glu Ser Asp  Asp Asp Asp Thr Leu  Ile Ala Arg
    1265                1270                1275

Ile Ser  Gln Val Ile Glu Asp  Phe Lys Glu Asp Phe  Glu Ala Cys
    1280                1285                1290

Ser Leu  Arg Arg Ile Thr Phe  Ser Phe Gly Asn Ser  Arg Gly Thr
    1295                1300                1305

Tyr Pro  Lys Tyr Phe Thr Phe  Arg Gly Pro Ala Tyr  Glu Glu Asp
    1310                1315                1320

Pro Thr  Ile Arg His Ile Glu  Pro Ala Leu Ala Phe  Gln Leu Glu
    1325                1330                1335

Leu Ala  Arg Leu Ser Asn Phe  Asp Ile Lys Pro Val  His Thr Asp
    1340                1345                1350

Asn Arg  Asn Ile His Val Tyr  Glu Ala Thr Gly Lys  Asn Ala Ala
    1355                1360                1365

Ser Asp  Lys Arg Phe Phe Thr  Arg Gly Ile Val Arg  Pro Gly Arg
    1370                1375                1380

Leu Arg  Glu Asn Ile Pro Thr  Ser Glu Tyr Leu Ile  Ser Glu Ala
    1385                1390                1395

Asp Arg  Leu Met Ser Asp Ile  Leu Asp Ala Leu Glu  Val Ile Gly
    1400                1405                1410

Thr Thr  Asn Ser Asp Leu Asn  His Ile Phe Ile Asn  Phe Ser Ala
    1415                1420                1425

Val Phe  Ala Leu Lys Pro Glu  Glu Val Glu Ala Ala  Phe Gly Gly
    1430                1435                1440

Phe Leu  Glu Arg Phe Gly Arg  Arg Leu Trp Arg Leu  Arg Val Thr
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    1445                1450                1455

Gly Ala  Glu Ile Arg Met Met  Val Ser Asp Pro Glu  Thr Gly Ser
    1460                1465                1470

Ala Phe  Pro Leu Arg Ala Met  Ile Asn Asn Val Ser  Gly Tyr Val
    1475                1480                1485

Val Gln  Ser Glu Leu Tyr Ala  Glu Ala Lys Asn Asp  Lys Gly Gln
    1490                1495                1500

Trp Ile  Phe Lys Ser Leu Gly  Lys Pro Gly Ser Met  His Met Arg
    1505                1510                1515

Ser Ile  Asn Thr Pro Tyr Pro  Thr Lys Glu Trp Leu  Gln Pro Lys
    1520                1525                1530

Arg Tyr  Lys Ala His Leu Met  Gly Thr Thr Tyr Cys  Tyr Asp Phe
    1535                1540                1545

Pro Glu  Leu Phe Arg Gln Ser  Ile Glu Ser Asp Trp  Lys Lys Tyr
    1550                1555                1560

Asp Gly  Lys Ala Pro Asp Asp  Leu Met Thr Cys Asn  Glu Leu Ile
    1565                1570                1575

Leu Asp  Glu Asp Ser Gly Glu  Leu Gln Glu Val Asn  Arg Glu Pro
    1580                1585                1590

Gly Ala  Asn Asn Val Gly Met  Val Ala Trp Lys Phe  Glu Ala Lys
    1595                1600                1605

Thr Pro  Glu Tyr Pro Arg Gly  Arg Ser Phe Ile Val  Val Ala Asn
    1610                1615                1620

Asp Ile  Thr Phe Gln Ile Gly  Ser Phe Gly Pro Ala  Glu Asp Gln
    1625                1630                1635

Phe Phe  Phe Lys Val Thr Glu  Leu Ala Arg Lys Leu  Gly Ile Pro
    1640                1645                1650

Arg Ile  Tyr Leu Ser Ala Asn  Ser Gly Ala Arg Ile  Gly Ile Ala
    1655                1660                1665

Asp Glu  Leu Val Gly Lys Tyr  Lys Val Ala Trp Asn  Asp Glu Thr
    1670                1675                1680

Asp Pro  Ser Lys Gly Phe Lys  Tyr Leu Tyr Phe Thr  Pro Glu Ser
    1685                1690                1695

Leu Ala  Thr Leu Lys Pro Asp  Thr Val Val Thr Thr  Glu Ile Glu
    1700                1705                1710

Glu Glu  Gly Pro Asn Gly Val  Glu Lys Arg His Val  Ile Asp Tyr
    1715                1720                1725

Ile Val  Gly Glu Lys Asp Gly  Leu Gly Val Glu Cys  Leu Arg Gly
    1730                1735                1740

Ser Gly  Leu Ile Ala Gly Ala  Thr Ser Arg Ala Tyr  Lys Asp Ile
    1745                1750                1755

Phe Thr  Leu Thr Leu Val Thr  Cys Arg Ser Val Gly  Ile Gly Ala
    1760                1765                1770

Tyr Leu  Val Arg Leu Gly Gln  Arg Ala Ile Gln Ile  Glu Gly Gln
    1775                1780                1785

Pro Ile  Ile Leu Thr Gly Ala  Pro Ala Ile Asn Lys  Leu Leu Gly
    1790                1795                1800

Arg Glu  Val Tyr Ser Ser Asn  Leu Gln Leu Gly Gly  Thr Gln Ile
    1805                1810                1815

Met Tyr  Asn Asn Gly Val Ser  His Leu Thr Ala Arg  Asp Asp Leu
    1820                1825                1830

Asn Gly  Val His Lys Ile Met  Gln Trp Leu Ser Tyr  Ile Pro Ala
    1835                1840                1845
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Ser Arg  Gly Leu Pro Val Pro  Val Leu Pro His Lys  Thr Asp Val
    1850                 1855                 1860

Trp Asp  Arg Asp Val Thr Phe  Gln Pro Val Arg Gly  Glu Gln Tyr
    1865                 1870                 1875

Asp Val  Arg Trp Leu Ile Ser  Gly Arg Thr Leu Glu  Asp Gly Ala
    1880                 1885                 1890

Phe Glu  Ser Gly Leu Phe Asp  Lys Asp Ser Phe Gln  Glu Thr Leu
    1895                 1900                 1905

Ser Gly  Trp Ala Lys Gly Val  Val Val Gly Arg Ala  Arg Leu Gly
    1910                 1915                 1920

Gly Ile  Pro Phe Gly Val Ile  Gly Val Glu Thr Ala  Thr Val Asp
    1925                 1930                 1935

Asn Thr  Thr Pro Ala Asp Pro  Ala Asn Pro Asp Ser  Ile Glu Met
    1940                 1945                 1950

Ser Thr  Ser Glu Ala Gly Gln  Val Trp Tyr Pro Asn  Ser Ala Phe
    1955                 1960                 1965

Lys Thr  Ser Gln Ala Ile Asn  Asp Phe Asn His Gly  Glu Ala Leu
    1970                 1975                 1980

Pro Leu  Met Ile Leu Ala Asn  Trp Arg Gly Phe Ser  Gly Gly Gln
    1985                 1990                 1995

Arg Asp  Met Tyr Asn Glu Val  Leu Lys Tyr Gly Ser  Phe Ile Val
    2000                 2005                 2010

Asp Ala  Leu Val Asp Tyr Lys  Gln Pro Ile Met Val  Tyr Ile Pro
    2015                 2020                 2025

Pro Thr  Gly Glu Leu Arg Gly  Gly Ser Trp Val Val  Val Asp Pro
    2030                 2035                 2040

Thr Ile  Asn Ser Asp Met Met  Glu Met Tyr Ala Asp  Val Glu Ser
    2045                 2050                 2055

Arg Gly  Gly Val Leu Glu Pro  Glu Gly Met Val Gly  Ile Lys Tyr
    2060                 2065                 2070

Arg Arg  Asp Lys Leu Leu Asp  Thr Met Ala Arg Leu  Asp Pro Glu
    2075                 2080                 2085

Tyr Ser  Ser Leu Lys Lys Gln  Leu Glu Glu Ser Pro  Asp Ser Glu
    2090                 2095                 2100

Glu Leu  Lys Val Lys Leu Ser  Val Arg Glu Lys Ser  Leu Met Pro
    2105                 2110                 2115

Ile Tyr  Gln Gln Ile Ser Val  Gln Phe Ala Asp Leu  His Asp Arg
    2120                 2125                 2130

Ala Gly  Arg Met Glu Ala Lys  Gly Val Ile Arg Glu  Ala Leu Val
    2135                 2140                 2145

Trp Lys  Asp Ala Arg Arg Phe  Phe Phe Trp Arg Ile  Arg Arg Arg
    2150                 2155                 2160

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

Ser Cys  Thr Arg Leu Glu Cys  Leu Ala Arg Ile Lys  Ser Trp Lys
    2180                 2185                 2190

Pro Ala  Thr Leu Asp Gln Gly  Ser Asp Arg Gly Val  Ala Glu Trp
    2195                 2200                 2205

Phe Asp  Glu Asn Ser Asp Ala  Val Ser Ala Arg Leu  Ser Glu Leu
    2210                 2215                 2220

Lys Lys  Asp Ala Ser Ala Gln  Ser Phe Ala Ser Gln  Leu Arg Lys
    2225                 2230                 2235
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Asp Arg  Gln Gly Thr Leu Gln  Gly Met Lys Gln Ala  Leu Ala Ser
    2240                2245                2250

Leu Ser  Glu Ala Glu Arg Ala  Glu Leu Leu Lys Gly  Leu
    2255                2260                2265


<210> SEQ ID NO 71
<211> LENGTH: 1134
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 71

atgtggggaa gttcacatgc attcgctggt gaatctgatc tgacactaca actacacacc     60

aggtccaaca tgagcgacaa tacgacaatc aaaaagccga tccgacccaa accgatccgg    120

acggaacgcc tgccttacgc tggggccgca gaaatcatcc gagccaacca gaaagaccac    180

tactttgagt ccgtgcttga acagcatctc gtcacgtttc tgcagaaatg gaagggagta    240

cgatttatcc accagtacaa ggaggagctg gagacggcgt ccaagtttgc atatctcggt    300

ttgtgtacgc ttgtgggctc caagactctc ggagaagagt acaccaatct catgtacact    360

atcagagacc gaacagctct accgggggtg gtgagacggt ttggctacgt gctttccaac    420

actctgtttc catacctgtt tgtgcgctac atgggcaagt tgcgcgccaa actgatgcgc    480

gagtatcccc atctggtgga gtacgacgaa gatgagcctg tgcccagccc ggaaacatgg    540

aaggagcggg tcatcaagac gtttgtgaac aagtttgaca agttcacggc gctggagggg    600

tttaccgcga tccacttggc gattttctac gtctacggct cgtactacca gctcagtaag    660

cggatctggg gcatgcgtta tgtatttgga caccgactgg acaagaatga gcctcgaatc    720

ggttacgaga tgctcggtct gctgattttc gcccggtttg ccacgtcatt tgtgcagacg    780

ggaagagagt acctcggagc gctgctggaa aagagcgtgg agaaagaggc aggggagaag    840

gaagatgaaa aggaagcggt tgtgccgaaa aagaagtcgt caattccgtt cattgaggat    900

acagaagggg agacggaaga caagatcgat ctggaggacc ctcgacagct caagttcatt    960

cctgaggcgt ccagagcgtg cactctgtgt ctgtcataca ttagtgcgcc ggcatgtacg   1020

ccatgtggac actttttctg ttgggactgt atttccgaat gggtgagaga gaagcccgag   1080

tgtcccttgt gtcggcaggg tgtgagagag cagaacttgt tgcctatcag ataa         1134


<210> SEQ ID NO 72
<211> LENGTH: 377
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 72

Met Trp Gly Ser Ser His Ala Phe Ala Gly Glu Ser Asp Leu Thr Leu
1               5                  10                  15

Gln Leu His Thr Arg Ser Asn Met Ser Asp Asn Thr Thr Ile Lys Lys
            20                  25                  30

Pro Ile Arg Pro Lys Pro Ile Arg Thr Glu Arg Leu Pro Tyr Ala Gly
        35                  40                  45

Ala Ala Glu Ile Ile Arg Ala Asn Gln Lys Asp His Tyr Phe Glu Ser
    50                  55                  60

Val Leu Glu Gln His Leu Val Thr Phe Leu Gln Lys Trp Lys Gly Val
65                  70                  75                  80

Arg Phe Ile His Gln Tyr Lys Glu Glu Leu Glu Thr Ala Ser Lys Phe
                85                  90                  95

Ala Tyr Leu Gly Leu Cys Thr Leu Val Gly Ser Lys Thr Leu Gly Glu
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            100                 105                 110

Glu Tyr Thr Asn Leu Met Tyr Thr Ile Arg Asp Arg Thr Ala Leu Pro
        115                 120                 125

Gly Val Val Arg Arg Phe Gly Tyr Val Leu Ser Asn Thr Leu Phe Pro
    130                 135                 140

Tyr Leu Phe Val Arg Tyr Met Gly Lys Leu Arg Ala Lys Leu Met Arg
145                 150                 155                 160

Glu Tyr Pro His Leu Val Glu Tyr Asp Glu Asp Glu Pro Val Pro Ser
                165                 170                 175

Pro Glu Thr Trp Lys Glu Arg Val Ile Lys Thr Phe Val Asn Lys Phe
            180                 185                 190

Asp Lys Phe Thr Ala Leu Glu Gly Phe Thr Ala Ile His Leu Ala Ile
        195                 200                 205

Phe Tyr Val Tyr Gly Ser Tyr Tyr Gln Leu Ser Lys Arg Ile Trp Gly
    210                 215                 220

Met Arg Tyr Val Phe Gly His Arg Leu Asp Lys Asn Glu Pro Arg Ile
225                 230                 235                 240

Gly Tyr Glu Met Leu Gly Leu Leu Ile Phe Ala Arg Phe Ala Thr Ser
                245                 250                 255

Phe Val Gln Thr Gly Arg Glu Tyr Leu Gly Ala Leu Leu Glu Lys Ser
            260                 265                 270

Val Glu Lys Glu Ala Gly Glu Lys Glu Asp Glu Lys Glu Ala Val Val
        275                 280                 285

Pro Lys Lys Lys Ser Ser Ile Pro Phe Ile Glu Asp Thr Glu Gly Glu
    290                 295                 300

Thr Glu Asp Lys Ile Asp Leu Glu Asp Pro Arg Gln Leu Lys Phe Ile
305                 310                 315                 320

Pro Glu Ala Ser Arg Ala Cys Thr Leu Cys Leu Ser Tyr Ile Ser Ala
                325                 330                 335

Pro Ala Cys Thr Pro Cys Gly His Phe Phe Cys Trp Asp Cys Ile Ser
            340                 345                 350

Glu Trp Val Arg Glu Lys Pro Glu Cys Pro Leu Cys Arg Gln Gly Val
        355                 360                 365

Arg Glu Gln Asn Leu Leu Pro Ile Arg
    370                 375


<210> SEQ ID NO 73
<211> LENGTH: 2364
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 73

atgaccgaca aggactggga tcttgtctac aaggtccacg ttttcggtgc ctacaaggtt     60

acccgagctg cctggcctta cttccgaaag cagaagtacg gtcgagttat ctctacctct    120

tccgctgctg gtctttacgg aaacttcggc cagaccaact actccgctgc caagctcgcc    180

ctggttggtt tcggtgagac tctcgccaag gagggtgcca agtacaacat tacttccaac    240

gtcatcgctc ctcttgctgc ttcccgaatg accgagacag tcatgcccga ggatatcctc    300

aagctcctca agcctgagta cgttgttcct ctggtcggct acctcaccca cgactctgtc    360

accgagtctt atggtattta cgaggtcggt gctggttaca tggctaaaat ccgatgggag    420

cgaggcaacg gtgctgtttt caagggcgac gacactttca ccccgtctgc tattctgaag    480

cgatgggatg aggtcacctc ttttgagagc cccacctacc ctaacggccc tgctgacttc    540
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ttcaaatacg ctgaggagtc tgttaagcga cccgagaacc cccagggacc caccgtctcc    600

ttcaaggacc aggttgtcat tgtcactgga gccggtgctg gcattggccg agcttactct    660

cacctccttg ctaagcttgg tgccaaggtc gttgttaacg atttcggtaa ccctcagaag    720

gttgtcgatg aaattaaggc cctcggtggt atcgccgtcg ctgacaagaa caacgtcatc    780

cacggtgaga aggttgttca gaccgctatc gacgccttcg gtgctgtcca cgccgttgtc    840

aacaacgctg gtattctccg agacaagtct ttcgccaaca tggatgatga gatgtggcag    900

ctgatctttg atgtccacct caacggtact tactccgtta ccaaggccgc gtggccccac    960

ttccttaagc agaagtacgg ccgtgtcatc aacaccacct caacttctgg tatctacggt   1020

aacttcggcc aggccaacta ctctgccgcc aaggctggta tcctcggttt ctcccgagct   1080

cttgctcgag agggtgagaa gtacaacatt cttgtcaaca ccattgcccc taacgctggt   1140

actgccatga ctgcttctgt cttcactgag gagatgctcg agctcttcaa gcccgatttc   1200

atcgcaccca tcaccgtcct gcttgcttcc gatcaggctc ccgtcaccgg tgatctgttt   1260

gagactggtt ctgcttggat cggacagact cgatggcagc gagctggtgg taaggccttc   1320

aacaccaaga agggtgtcac ccccgaaatg gttcgagaca gctgggctaa gatcgtcgac   1380

ttcgatgatg gtaactccac ccatcccacc actccctccg agtctactac tcagattctt   1440

gagaacatct tcaacgtgcc tgatgaggag gttgaggaga ctgctctcgt tgctggtccc   1500

ggtggtcccg gtatcctcaa caaggagggc gaacctttcg actacactta cacttaccga   1560

gacctcattc tttacaacct tggtctcggt gccaaggcta atgagctcaa gtatgtcttc   1620

gagggtgatg atgacttcca gaccgtgccc actttcggtg ttatccctta catgggtggc   1680

ctcatcacta ccaactatgg cgacttcgtt cctaacttca accctatgat gcttctccac   1740

ggtgagcagt accttgaaat ccgacagtgg cctattccta ccaatgctac attggagaac   1800

aaggctaagg tcatcgatgt cgttgacaag ggcaaggctg ccctccttgt cactgctacc   1860

accaccacga acaaggagac tggtgaggag gttttctaca acgagtcttc tctcttcatc   1920

cgaggctctg gtggtttcgg tggtaagtct accggtactg accgtggcgc tgccactgct   1980

gccaacaagc cccctgctcg agctcctgac ttcgttaagg agatcaagat ccaggaggac   2040

caggctgcca tttaccgact ttctggtgat tacaaccctc ttcacatcga ccctgctttt   2100

gctgctgttg gtaactttga ccgacctatt ctccacggtc tctgctcttt tggtgtctcc   2160

ggtaaggctc tttacgatca gtttggtcct ttcaagaacg ctaaggtccg atttgctggt   2220

cacgtcttcc ctggtgagac cctgaaggtt gagggctgga aggagggcaa caaggtcatt   2280

ttccagacca aggttgttga gcgaggtact accgccatca gcaatgccgc cattgagctc   2340

ttccccaagg atgctaagct ctaa                                          2364
```

<210> SEQ ID NO 74
<211> LENGTH: 787
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 74

```
Met Thr Asp Lys Asp Trp Asp Leu Val Tyr Lys Val His Val Phe Gly
1               5                   10                  15

Ala Tyr Lys Val Thr Arg Ala Ala Trp Pro Tyr Phe Arg Lys Gln Lys
            20                  25                  30

Tyr Gly Arg Val Ile Ser Thr Ser Ser Ala Ala Gly Leu Tyr Gly Asn
        35                  40                  45
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```
Phe Gly Gln Thr Asn Tyr Ser Ala Ala Lys Leu Ala Leu Val Gly Phe
    50                  55                  60

Gly Glu Thr Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Thr Ser Asn
65                  70                  75                  80

Val Ile Ala Pro Leu Ala Ala Ser Arg Met Thr Glu Thr Val Met Pro
                85                  90                  95

Glu Asp Ile Leu Lys Leu Leu Lys Pro Glu Tyr Val Val Pro Leu Val
            100                 105                 110

Gly Tyr Leu Thr His Asp Ser Val Thr Glu Ser Tyr Gly Ile Tyr Glu
        115                 120                 125

Val Gly Ala Gly Tyr Met Ala Lys Ile Arg Trp Glu Arg Gly Asn Gly
    130                 135                 140

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

Arg Trp Asp Glu Val Thr Ser Phe Glu Ser Pro Thr Tyr Pro Asn Gly
                165                 170                 175

Pro Ala Asp Phe Phe Lys Tyr Ala Glu Glu Ser Val Lys Arg Pro Glu
            180                 185                 190

Asn Pro Gln Gly Pro Thr Val Ser Phe Lys Asp Gln Val Val Ile Val
        195                 200                 205

Thr Gly Ala Gly Ala Gly Ile Gly Arg Ala Tyr Ser His Leu Leu Ala
    210                 215                 220

Lys Leu Gly Ala Lys Val Val Val Asn Asp Phe Gly Asn Pro Gln Lys
225                 230                 235                 240

Val Val Asp Glu Ile Lys Ala Leu Gly Gly Ile Ala Val Ala Asp Lys
                245                 250                 255

Asn Asn Val Ile His Gly Glu Lys Val Val Gln Thr Ala Ile Asp Ala
            260                 265                 270

Phe Gly Ala Val His Ala Val Val Asn Asn Ala Gly Ile Leu Arg Asp
        275                 280                 285

Lys Ser Phe Ala Asn Met Asp Asp Glu Met Trp Gln Leu Ile Phe Asp
    290                 295                 300

Val His Leu Asn Gly Thr Tyr Ser Val Thr Lys Ala Ala Trp Pro His
305                 310                 315                 320

Phe Leu Lys Gln Lys Tyr Gly Arg Val Ile Asn Thr Thr Ser Thr Ser
                325                 330                 335

Gly Ile Tyr Gly Asn Phe Gly Gln Ala Asn Tyr Ser Ala Ala Lys Ala
            340                 345                 350

Gly Ile Leu Gly Phe Ser Arg Ala Leu Ala Arg Glu Gly Glu Lys Tyr
        355                 360                 365

Asn Ile Leu Val Asn Thr Ile Ala Pro Asn Ala Gly Thr Ala Met Thr
    370                 375                 380

Ala Ser Val Phe Thr Glu Glu Met Leu Glu Leu Phe Lys Pro Asp Phe
385                 390                 395                 400

Ile Ala Pro Ile Thr Val Leu Leu Ala Ser Asp Gln Ala Pro Val Thr
                405                 410                 415

Gly Asp Leu Phe Glu Thr Gly Ser Ala Trp Ile Gly Gln Thr Arg Trp
            420                 425                 430

Gln Arg Ala Gly Gly Lys Ala Phe Asn Thr Lys Lys Gly Val Thr Pro
        435                 440                 445

Glu Met Val Arg Asp Ser Trp Ala Lys Ile Val Asp Phe Asp Asp Gly
    450                 455                 460

Asn Ser Thr His Pro Thr Thr Pro Ser Glu Ser Thr Thr Gln Ile Leu
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465                 470                 475                 480

Glu Asn Ile Phe Asn Val Pro Asp Glu Glu Val Glu Glu Thr Ala Leu
                485                 490                 495

Val Ala Gly Pro Gly Gly Pro Gly Ile Leu Asn Lys Glu Gly Glu Pro
            500                 505                 510

Phe Asp Tyr Thr Tyr Thr Tyr Arg Asp Leu Ile Leu Tyr Asn Leu Gly
        515                 520                 525

Leu Gly Ala Lys Ala Asn Glu Leu Lys Tyr Val Phe Glu Gly Asp Asp
    530                 535                 540

Asp Phe Gln Thr Val Pro Thr Phe Gly Val Ile Pro Tyr Met Gly Gly
545                 550                 555                 560

Leu Ile Thr Thr Asn Tyr Gly Asp Phe Val Pro Asn Phe Asn Pro Met
                565                 570                 575

Met Leu Leu His Gly Glu Gln Tyr Leu Glu Ile Arg Gln Trp Pro Ile
            580                 585                 590

Pro Thr Asn Ala Thr Leu Glu Asn Lys Ala Lys Val Ile Asp Val Val
        595                 600                 605

Asp Lys Gly Lys Ala Ala Leu Leu Val Thr Ala Thr Thr Thr Thr Asn
    610                 615                 620

Lys Glu Thr Gly Glu Glu Val Phe Tyr Asn Glu Ser Ser Leu Phe Ile
625                 630                 635                 640

Arg Gly Ser Gly Gly Phe Gly Gly Lys Ser Thr Gly Thr Asp Arg Gly
                645                 650                 655

Ala Ala Thr Ala Ala Asn Lys Pro Pro Ala Arg Ala Pro Asp Phe Val
            660                 665                 670

Lys Glu Ile Lys Ile Gln Glu Asp Gln Ala Ala Ile Tyr Arg Leu Ser
        675                 680                 685

Gly Asp Tyr Asn Pro Leu His Ile Asp Pro Ala Phe Ala Ala Val Gly
    690                 695                 700

Asn Phe Asp Arg Pro Ile Leu His Gly Leu Cys Ser Phe Gly Val Ser
705                 710                 715                 720

Gly Lys Ala Leu Tyr Asp Gln Phe Gly Pro Phe Lys Asn Ala Lys Val
                725                 730                 735

Arg Phe Ala Gly His Val Phe Pro Gly Glu Thr Leu Lys Val Glu Gly
            740                 745                 750

Trp Lys Glu Gly Asn Lys Val Ile Phe Gln Thr Lys Val Val Glu Arg
        755                 760                 765

Gly Thr Thr Ala Ile Ser Asn Ala Ala Ile Glu Leu Phe Pro Lys Asp
    770                 775                 780

Ala Lys Leu
785


<210> SEQ ID NO 75
<211> LENGTH: 2694
<212> TYPE: DNA
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 75

atgctggctt ctcgagtttc catcaaggct gtgagtatcg atggtgaaga aagacaccga     60

caatcgccac gttgtgccac agacacagac gcgtttctac acacacacac acaagagtcg    120

acgtgtggtt tagccgaggt atttcgacag ggaggaaaaa cgacaacgaa aggaccgaca    180

gataccaaag caacccaatc accacctcaa tcaatgatcc ccgcccgcgg gaatgcggaa    240

aaggcttctg cgacattaca acaaagccaa ctctgttgat ttgttgtttg cgacattggc    300
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tttgtgccgg tcccaaaatt acctcgacca accacacggc ggcaattgaa gacaatgcaa    360
attaaatagc acatactaac ccagccccgc cttgcacgat ctctcgcgac taccactaat    420
gcctccctca acttggactc caaggtccga atgaacaact gggaggccaa caacttcctc    480
aacttcaaga agcacaccga gaacgtccag attgtcaagg agcgactcaa ccgacccctg    540
acctacgctg agaagattct ctacggccat ctcgacaagc cccatgagca ggagattgtc    600
cgaggtcagt cctacctcaa gctgcgaccc gatcgagccg cctgccagga tgccaccgcc    660
cagatggcca ttctgcagtt catgtctgcc ggtatcccca ccgtccagac ccccaccacc    720
gtccactgtg accatcttat ccaggcccag gttggtggtg agcaggatct tgctcgagcc    780
atcgacatca acaaggaggt ctacaacttc cttggcaccg cctccgccaa gtacgacatt    840
ggtttctgga aggccggatc cggtattatc caccagatca ttctcgagaa ctacgccttc    900
cccggtgccc ttctcattgg ttccgactct catacccccа acgccggtgg tctcggtatg    960
ctcgccatcg gtgtcggtgg tgccgatgtc gtcgacgtca tggccggtct cccctgggag   1020
cttaaggccc ccaagattat cggtgtcaag ctgaccggta agctctctgg ctggacctcc   1080
cccaaggata ttatcctgaa ggtcgctggt atcctcaccg tcaagggtgg aaccggtgct   1140
atcgtcgagt acttcggtga tggtgtcgat aacctgtcct gcactggtat gggaaccatc   1200
tgtaacatgg gtgccgagat tggtgctacc acctccacct tccccttcaa cgagcgaatg   1260
gccgactacc ttaacgccac tggccgaaag gagattgccg actttgctcg actttacaac   1320
cacttcctct ctgccgatga gggttgtgag tacgatcagc tcatcgagat tgacctgaac   1380
acccttgagc cttacgtcaa cggtcccttc actcccgatc ttgccacccc catctccaag   1440
ctcaaggatg tcgccgtcga gaacggatgg ccccttgagg tcaaggtcgg tcttatcggc   1500
tcttgcacca actcctctta cgaggatatg gagcgatccg cctccattgc caaggacgcc   1560
atggcccacg gtcttaagtc caagtccatc tacaccgtca cccccggttc cgagcagatc   1620
cgagccacca ttgagcgaga tggtcagctc cagaccttcc tcgacttcgg tggtatcgtc   1680
cttgctaacg cttgtggccc ctgcattggt cagtgggacc gacgagacat caagaagggt   1740
gagaagaaca ccattgtctc ttcttacaac cgaaacttca ctggccgaaa cgattctaac   1800
cctgccaccc acgctttcgt cacctctccc gatctcgtca ccgctttcgc cattgctggt   1860
gacctccgat tcaaccctct cactgactcc ctgaaggatt ctgagggtaa ggagttcaag   1920
ctcaaggagc ccactggaaa gggtctgccc gaccgaggtt acgaccccgg catggacacc   1980
taccaggctc cccccgccga ccgatctgcc gtcgaggttg atgtttcccc cacttccgac   2040
cgactccaga tcctcaagcc cttcaagcct tgggacggca aggacggtat tgacatgccc   2100
atcctcatca agtctcttgg taagaccacc actgaccata tctctcaggc cggtccctgg   2160
cttaagtacc gaggccatct ccagaacatc tccaacaact acatgattgg agccatcaac   2220
gctgagaacg aggaggccaa caacgtccga aaccagatca ctggcgagtg gggaggagtt   2280
cccgagactg ccattgctta ccgagacaac ggtatccgat gggttgttgt cggaggtgat   2340
aacttcggtg agggttcttc tcgagagcac gctgctcttg agccccgatt cctcggtggt   2400
ttcgccatca tcaccaagtc ttttgcccga attcacgaga ctaacctgaa gaagcagggt   2460
ctcctgcccc ttaacttcgt caacggtgct gactacgaca agatccagcc ctccgataag   2520
atctccattc ttggtcttaa ggaccttgcc cccggcaaga acgtcaccat tgaggttacc   2580
cccaaggacg gtgccaagtg gaccaccgag gtttctcaca cctacaactc tgagcagctc   2640
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gagtggttca agtacggctc tgccctcaac aagatggctg cctccaagaa ataa 2694

<210> SEQ ID NO 76
<211> LENGTH: 779
<212> TYPE: PRT
<213> ORGANISM: Yarrowia lipolytica

<400> SEQUENCE: 76

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

Leu Ala Thr Thr Thr Asn Ala Ser Leu Asn Leu Asp Ser Lys Val Arg
20 25 30

Met Asn Asn Trp Glu Ala Asn Asn Phe Leu Asn Phe Lys Lys His Thr
35 40 45

Glu Asn Val Gln Ile Val Lys Glu Arg Leu Asn Arg Pro Leu Thr Tyr
50 55 60

Ala Glu Lys Ile Leu Tyr Gly His Leu Asp Lys Pro His Glu Gln Glu
65 70 75 80

Ile Val Arg Gly Gln Ser Tyr Leu Lys Leu Arg Pro Asp Arg Ala Ala
85 90 95

Cys Gln Asp Ala Thr Ala Gln Met Ala Ile Leu Gln Phe Met Ser Ala
100 105 110

Gly Ile Pro Thr Val Gln Thr Pro Thr Thr Val His Cys Asp His Leu
115 120 125

Ile Gln Ala Gln Val Gly Gly Glu Gln Asp Leu Ala Arg Ala Ile Asp
130 135 140

Ile Asn Lys Glu Val Tyr Asn Phe Leu Gly Thr Ala Ser Ala Lys Tyr
145 150 155 160

Asp Ile Gly Phe Trp Lys Ala Gly Ser Gly Ile Ile His Gln Ile Ile
165 170 175

Leu Glu Asn Tyr Ala Phe Pro Gly Ala Leu Leu Ile Gly Ser Asp Ser
180 185 190

His Thr Pro Asn Ala Gly Gly Leu Gly Met Leu Ala Ile Gly Val Gly
195 200 205

Gly Ala Asp Val Val Asp Val Met Ala Gly Leu Pro Trp Glu Leu Lys
210 215 220

Ala Pro Lys Ile Ile Gly Val Lys Leu Thr Gly Lys Leu Ser Gly Trp
225 230 235 240

Thr Ser Pro Lys Asp Ile Ile Leu Lys Val Ala Gly Ile Leu Thr Val
245 250 255

Lys Gly Gly Thr Gly Ala Ile Val Glu Tyr Phe Gly Asp Gly Val Asp
260 265 270

Asn Leu Ser Cys Thr Gly Met Gly Thr Ile Cys Asn Met Gly Ala Glu
275 280 285

Ile Gly Ala Thr Thr Ser Thr Phe Pro Phe Asn Glu Arg Met Ala Asp
290 295 300

Tyr Leu Asn Ala Thr Gly Arg Lys Glu Ile Ala Asp Phe Ala Arg Leu
305 310 315 320

Tyr Asn His Phe Leu Ser Ala Asp Glu Gly Cys Glu Tyr Asp Gln Leu
325 330 335

Ile Glu Ile Asp Leu Asn Thr Leu Glu Pro Tyr Val Asn Gly Pro Phe
340 345 350

Thr Pro Asp Leu Ala Thr Pro Ile Ser Lys Leu Lys Asp Val Ala Val
355 360 365

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Glu Asn Gly Trp Pro Leu Glu Val Lys Val Gly Leu Ile Gly Ser Cys
    370                 375                 380

Thr Asn Ser Ser Tyr Glu Asp Met Glu Arg Ser Ala Ser Ile Ala Lys
385                 390                 395                 400

Asp Ala Met Ala His Gly Leu Lys Ser Lys Ser Ile Tyr Thr Val Thr
                405                 410                 415

Pro Gly Ser Glu Gln Ile Arg Ala Thr Ile Glu Arg Asp Gly Gln Leu
            420                 425                 430

Gln Thr Phe Leu Asp Phe Gly Gly Ile Val Leu Ala Asn Ala Cys Gly
        435                 440                 445

Pro Cys Ile Gly Gln Trp Asp Arg Arg Asp Ile Lys Lys Gly Glu Lys
    450                 455                 460

Asn Thr Ile Val Ser Ser Tyr Asn Arg Asn Phe Thr Gly Arg Asn Asp
465                 470                 475                 480

Ser Asn Pro Ala Thr His Ala Phe Val Thr Ser Pro Asp Leu Val Thr
                485                 490                 495

Ala Phe Ala Ile Ala Gly Asp Leu Arg Phe Asn Pro Leu Thr Asp Ser
            500                 505                 510

Leu Lys Asp Ser Glu Gly Lys Glu Phe Lys Leu Lys Glu Pro Thr Gly
        515                 520                 525

Lys Gly Leu Pro Asp Arg Gly Tyr Asp Pro Gly Met Asp Thr Tyr Gln
    530                 535                 540

Ala Pro Pro Ala Asp Arg Ser Ala Val Glu Val Asp Val Ser Pro Thr
545                 550                 555                 560

Ser Asp Arg Leu Gln Ile Leu Lys Pro Phe Lys Pro Trp Asp Gly Lys
                565                 570                 575

Asp Gly Ile Asp Met Pro Ile Leu Ile Lys Ser Leu Gly Lys Thr Thr
            580                 585                 590

Thr Asp His Ile Ser Gln Ala Gly Pro Trp Leu Lys Tyr Arg Gly His
        595                 600                 605

Leu Gln Asn Ile Ser Asn Asn Tyr Met Ile Gly Ala Ile Asn Ala Glu
    610                 615                 620

Asn Glu Glu Ala Asn Asn Val Arg Asn Gln Ile Thr Gly Glu Trp Gly
625                 630                 635                 640

Gly Val Pro Glu Thr Ala Ile Ala Tyr Arg Asp Asn Gly Ile Arg Trp
                645                 650                 655

Val Val Val Gly Gly Asp Asn Phe Gly Glu Gly Ser Ser Arg Glu His
            660                 665                 670

Ala Ala Leu Glu Pro Arg Phe Leu Gly Gly Phe Ala Ile Ile Thr Lys
        675                 680                 685

Ser Phe Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu
    690                 695                 700

Pro Leu Asn Phe Val Asn Gly Ala Asp Tyr Asp Lys Ile Gln Pro Ser
705                 710                 715                 720

Asp Lys Ile Ser Ile Leu Gly Leu Lys Asp Leu Ala Pro Gly Lys Asn
                725                 730                 735

Val Thr Ile Glu Val Thr Pro Lys Asp Gly Ala Lys Trp Thr Thr Glu
            740                 745                 750

Val Ser His Thr Tyr Asn Ser Glu Gln Leu Glu Trp Phe Lys Tyr Gly
        755                 760                 765

Ser Ala Leu Asn Lys Met Ala Ala Ser Lys Lys
    770                 775
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<210> SEQ ID NO 77
<211> LENGTH: 1464
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 77

atggatctgg cgaaaatcac cgacggcttc gtcaagcacg agacctcgtc gtcgtcctct 60

tcttgctcca ccaccaacac agggcccacc ccagacttgt ctccagtgac gccctccaag 120

gaatgtgaga agcggccacg agaggacgac cctgaagagt cgcacgacac gagcgccggc 180

gccaacagca acaacaacgc tagcgtgtct ctcatgtcca ccccagagcc caagtcgtcg 240

tctccccccg gactgtcgca tttcgcacac ctgatgcaaa agtcggacac catgtaccga 300

cagaacctca actcggacca gtacatctac tcggacgagg agaaggagaa ccacaagact 360

tcgggcaagc cccacacccc ccaggtgcct catacgccct ccagtgtgcc gacacaacaa 420

ccccaatatg catttatttc acattccatc acctcgtacc cgtcgaacga gcctcagatt 480

gacaacgcac ggctggcgcg ccgaaaacga cgccgaacgt ctcccacgga actcgcgctg 540

ctggagcagg agtttgcccg caaccagaag cctcccaagc acattcgcgt cgacattgcc 600

cgccgagtcg acatgactga aaaggctgtg caggtgtggt tccagaacaa gcggcagagc 660

gtgcgaaaga gcatgaacaa gagcatgacc gatgacacct ctttcgccga ctcttcgttc 720

gctgaaacta cctttgacga gacagacggt aactccacat tcctgtccaa ttccaacgtc 780

agcaccagcg taagcaacaa gtcaatcact tcttccatca cagacaacaa gtcgcccctg 840

gcacagtcaa ccaccgccga ctctggtgcc aacgccaacg ccaacgccaa cgccaacgcc 900

aacaacaaca ccgcatccac ttcctccaca aacgactccg aaattgcatc cgtcgccccc 960

aaaacaaacg gcagctcatt ctctgttttc gaagataccc ccgagactcc cgcgaaaaag 1020

aaacccagtg ctccgcgact gtccatgcgt ggtgggaagg ctactgttat ctacgccggc 1080

aagcccaagg gtgtcacgct gtcctcggga agacgtcttg gggtccctgc cacaccctcc 1140

tctcccgcca acaacaatct tggcctggga ggctcgcctc tggccacatc gtctcctatg 1200

acccagcgga ccgcgtcgca actgaaccag gcatctgcat cttctccccc atcggctgtt 1260

aagtccaagt cttttggaac tgccgaggaa agcctggctg cgacgctcaa gaagcggctt 1320

ccgtccatgc actacgacct gcccgtgacc aacaagacgt cgtctgtgcg ccatggcgtg 1380

agctctcccg tggtcgacgc cggcagccgt gaggccgagt gtatttccaa tctcctctct 1440

cttcgaaacg gaggacgatg gtaa 1464

<210> SEQ ID NO 78
<211> LENGTH: 1548
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 78

atgttgcgag ccctgaatac cgtccagcga ctttccagca cccgagccat gtccacctct 60

tccatttcgt ctctgcttaa gaaccccaat cttctgcgaa accagggcta tgtcaatggt 120

cagtgggtct cctccaagac cggagacact ttcagcgttg agaacccagc cactggcgag 180

actctgggcc aggtgcccga gttctctgtc gccgaggccg atgaggctgt ccagcacgca 240

cagactgcct tcaagacctt caaacatacc actggacgag agcgatccaa gatgctgcga 300

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aagtggtacg atctgatgca ggagaatgct ggtgatctgg ccaccctggt gactctggag 360

aacggtaagt ccctcgctga cgccaagggc gagattggct acggagcatc tttcttcgag 420

tggttctccg aggaagctcc tcgaatctac ggagacatca ttccatccgc caaccccgcc 480

aaccgaatct acacaatcaa gcagcccatc ggagtctgcg gaatcatcac cccctggaac 540

ttcccctcgg ccatgatcac ccgaaaggct gctgctgctg ttgctgctgg ctgtaccatg 600

gtgatcaagc ctggttccga aacctcctac tctgcccttg ctctggctta cctggctgaa 660

caggccggca tccctaaggg tgttgtcaac gtggtcacta ctaagaagaa cactcgagct 720

tttggtaacg ccctgtgcga gaacccgacc gtcaaaaagg tttctttcac gggctccact 780

ggtgtcggaa agacccttat gggcgcatcg gcctccactc ttaagaagct gtcctttgag 840

ctcggtggca acgctccctt cattgtgttt gaggacgccg atattgaccg ggctgtcgac 900

ggagctattg cgtccaagtt ccgaggcact ggccagacct gtgtctgtgc aaaccgaatt 960

tatgtgcacg agagcatcgc cgagaagttt gctgagcgaa tggcagccgt ggtcaaggac 1020

ttcaaggttg gaaacggtct cgaccctaac accacccatg gccctcttat ccacgaggga 1080

gccaagggca agatccagga gcaggttgac gatgctgtca agaagggagg aaaggtactc 1140

attggaggct ccgacgcccc tgagatcgga aaggcctttt tccagcctac cgtcatttcc 1200

ggggccaagt ctgatatgct gattgcctcc gaggagacgt ttggtcccat tgctgccatc 1260

ttccccttta agaccgacgc tgaggtcatt gagcttgcca acaaggcaga ggtcggtctg 1320

gccggctact tctactccaa ggacgtgtac cgaatccaac aggttgccga ggctctcgag 1380

gtcggaatgg tcggtgttaa caccggtctg atgacggagt gtgctctgcc ctttggcggt 1440

atcaaggagt ctggctttgg ccgagagggc tccaagtacg gcctggatga ctacatggtg 1500

ctcaagacta ttgttgtgtc tggcgtcgag ccccacattc agccttaa 1548

<210> SEQ ID NO 79
<211> LENGTH: 627
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 79

atgtattcat tcgacttcaa ctttgacacg gcatatccgc cacagactga atattccaaa 60

caagacgact gtctgggata catgcccatc acgcctcctt acctggactg gagctcgctg 120

acattcccgc cggttgaata cgcacccatc gtcgataacg tgctcccgga agaaccctcg 180

gagccctcgg acgtgtcttc ttcttccgga gaagaaagcc cctacttttt cgacgaatac 240

tgcaccattc cctctctggt cgaccagctc aaagaaaacc ccaacatttg ggccatggca 300

aacaccgtca agaaaggagc ctacgtgtgt agccactgca ctaagcaggg caccccccgtc 360

aagttcaaaa ccatggtcga ctttgccacc cacctcgact cgcattctca tgaccgaagc 420

tgcaaatgcg ccgacacaaa atgtccctgg tccattgtgg gcttctctac tcgatcggaa 480

atgcgaagac acacaaactc ggtccatcga caaacaccct tcacatgcaa aatctgtgac 540

cgcgggtttg tacgagaaga ctctctcaaa cggcatgtca aactactcca catttctccc 600

ctcaaaacca gacgaaagag tacctga 627

<210> SEQ ID NO 80
<211> LENGTH: 1683
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 80

atgcaccacc acctcaaccc caaggcgctc ttttctggtg agtatggcgg acagaaatgg 60

acggaggaac gtggcagagc cgattgacca gccacgcagg ccgaccaagc cccattgagt 120

gagccattgg acgtccttgg cccgaataga cgctctctcc caggtttgcc ggaaaaacga 180

gctgttatat ccgaacgagc tgtttgtgcc caaaaaagcc cctactaacc cccaggccga 240

aaggagagca cctctcccca gacacaagcc gcgtccggct ccggagccgt gtctccaggc 300

cgacctctgg attcgtccac caacgtcgaa gatgtggatg agcttgacgg agacggccag 360

aacatcatca tgggaattat cgcgcagctg cgacccggcg ctgatctgtc tcgaatcaca 420

cttcccacct tcattctcga gcgaaagtcc atgctcgagc gaatcacaaa ctccctgcag 480

caccccacat atgtcattga ggcccacgcc accaaggacc ccatgcagcg gttcatccaa 540

gtggtaaagt ggtaccactc cggctggcac atcaccccca aggccgtcaa aaagcccctg 600

aaccccattc tcggcgagtt cttcacatgc tactgggact acgacgacgg ttcccacgga 660

tactacatct ccgagcagac ctcccaccac cctcccaagt catcctactt ttacatgatc 720

cctgagcaca acatccgagt cgacggtaca ctggctccca agtcccgttt cctgggtaac 780

tcagctgctt ctctcatgga gggcgccacc attctcaagt tcctggacat tgtagatgcc 840

aagggcgctc ccgaggagta cgaaatcact tcgcccaatg cctacgcccg aggtattctc 900

tttgaacggc tcaagtacga gtactgcgac cactcgatca tcaagtgtcc cgctctggac 960

ctgactctgg acctggactt caaggccaag ggcttcattt ccggtacata caatgccttc 1020

gagggccaga tcaagaagat ctccaccggc gaggcctttt acgatgttta tggaaagtgg 1080

gatgaaatca tcgagctcaa gaacctcaag accggcgaga agtcggtgct gtttgacgtg 1140

actaaggccg ccctgcaccc tcccaaggtg cgacccatcg ctgagcaggc cgccaccgag 1200

tcccgacgac tgtgggagcc cgtcaccgac gctcttgcta agcgagacca caccgttgct 1260

accgacgaaa agttcaagat tgaggacaaa cagcgaacgc tggccaagga gcgagaagag 1320

cacggcgtca agttcctgcc caaactgttc aagcccgccc ccgctcccct ggacttcatt 1380

ctgtataagg atctgcacgg cactcccgaa gagatcacca aggagattct cagcatagtc 1440

cccattctgc ccggccaaca gttcaccaag gactttgaaa tgtccggcga gaagaaatac 1500

aagctggaga agagcggcca ggccagcagc gagactcagc ccaccgccac gaccactgcg 1560

gctgcccccc aagcaggcgc tgtccccaca acccctgcta acggccagac tcccctggcc 1620

aagacttctg atcttcagga ggctcttccc accgaagagg acgagttcca cgacgcccag 1680

tag 1683

<210> SEQ ID NO 81
<211> LENGTH: 5510
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic polynucleotide

<400> SEQUENCE: 81

atgacaagtg atgcgataaa cgccatggaa aacgacagta cgacggtggt agaggtggaa 60

acgacatttg tgaacgataa cgtggtccgt ggcttcctcg atgttgcacg tgatacgctg 120

ccagacgtcc aaggactcct tccactggtc caagtgcagc tggtggcgga tatctcaaga 180

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gagatgctgg agggcgaaga agtgctggaa atcaccgatc cagagtcaca tggcgtcaaa 240

aataccgaag caggtgacga aacgaactca cgtgacccca tcgtcgcttc tgcgcctgct 300

accctggttc ctaacgagag cacattagag attcatgtca cgcccaagta caccaccaag 360

gacaagaaac gaggccgcaa aaagaccaag aaggacgaag attggttggt aacatgcttg 420

ggtgttgttc aactaggaaa cgtggaaacc agtgaccacg tgcttaccgc tttgaaacag 480

gctctttcgg tagccaaatt taacccgcga aatcgagtca gtgtcttttc agtgaatcct 540

cacgtcactg ttaccaaaaa caatggtgtt tacagcattt ccatcacttt tggagtcttt 600

gcgaagcctt ttgatggcca cgtcaaccct gagatccata tggcaggtca cctcaacatt 660

gtgaatgtca tccgacagtt cctgggcgta actaagataa aacagctaca taagaacgac 720

tatgtgactc ctgaatactt ctacgagtgc ctggaactca aggatgatac cgaggttgag 780

atcaacagag atcttcagcc ggaagggatg agatcaaaac ttttggatta ccagcttgaa 840

actgtggggt gggttctgga tagagaaaag ggagaatcgc gtgagaagac gatagaggga 900

attccttcac catggaaacg gttcagggct catggtatca actggttggt tgattttgtg 960

ggtctcaaca ttggtcctga gaaggaggtg atggagattt tgacacgaga tacgaaacca 1020

acaactgagg accccgagat tcaagcagta tcacgtgacg cagattttaa ggctggatat 1080

ggacttattg ctgatgaaat gggtcttgga aagacagttg agctactagc tgtagtcctg 1140

aataacccca gacctgaatt tccaccgcaa acacactacg atctgtactc tgacagagac 1200

gtgttaccta ccaagacgac tctcatttta tgtcctgcca gtatcagtca acagtggatt 1260

gctgaggtta ctaaacatgc tcccagtctc tctgtctttc tgtacactgg tcgagcagct 1320

ttggatgctc aaagagagaa ggaaggtact cccgataccg atattgaggt tggaattgac 1380

tcagatactg attcagaagg ccctcttgtt tcaaaacatg cacaatttct ctctcagttc 1440

gacattgtag tcacatccta tgaagttgca tctcgcgagg ttgccaacgc tctttacaac 1500

cctctgagag gtcgtgtaac tcgcaccaag acgaagctaa agtcgaaaga tacccgagat 1560

gtcgatctcg tgcaagaccg gctttccctc caatctccac tgagtcagct tcagttctgg 1620

cgtgtgattc tggacgaggt tcagatggtg ggaaacacgg tctccaacgc agctgttgta 1680

gctcgtatta ttccccgagt gcatgcatgg ggagtcagtg gtactcctat aaagaagggc 1740

atgcctgact tacttggcat gtgtgtgttt ttgagatgtg aacccggcga gttttatgga 1800

agaagtgatt gtgagtatac taaaggaaca gtcagagtgg catgtgacaa aaaaacaaaa 1860

aaccatatgg ctcaatgaag ggctacgact aacacagatg cgtataacta ctcttggcaa 1920

aacggatacc tcagcacaac tatgacagca tctggagtaa gtcatcaaaa acactgggag 1980

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What is claimed is:

1. A method of producing a lipid, lipid precursor, or oleochemical comprising:

a) culturing a genetically modified yeast cell in a growth medium; and

b) isolating said lipid, lipid precursor, or oleochemical,

wherein the dry weight of said genetically modified yeast cell comprises greater than 60% wt/wt lipids, lipid precursors, and oleochemicals; and

wherein said genetically modified yeast cell comprises (i) a recombinant acyl-CoA:diacylglycerol acyltransferase 1 (DGA1) gene and a UGA2 succinate semialdehyde dehydrogenase (UGA2) gene comprising a mutation, wherein said mutation results in a loss of function of succinate semialdehyde dehydrogenase of 20% or more compared to succinate semialdehyde dehydrogenase encoded by UGA2 without the mutation; or (ii) a recombinant acyl-CoA:diacylglycerol acyltransferase 2 (DGA2) gene and a UGA2 succinate semialdehyde dehydrogenase (UGA2) gene comprising a mutation, wherein said mutation results in a loss of function of succinate semialdehyde dehydrogenase of 20% or more compared to succinate semialdehyde dehydrogenase encoded by UGA2 without the mutation.

2. The method of claim **1**, wherein said growth medium comprises a majority carbon source selected from the group consisting of glucose, glycerol, xylose, fructose, mannose, ribose, sucrose, and lignocellulosic biomass.

3. The method of claim **1**, wherein said growth medium comprises lignocellulosic biomass as the majority carbon source.

4. The method of claim **1**, wherein said growth medium comprises cobalt, iron, magnesium, potassium, zinc, nickel, molybdenum, manganese, copper, or boron.

5. The method of claim **1**, wherein said growth medium comprises 5.77×10^{-5} M to 1.73×10^{-4} M cobalt, 0.001 M to 0.003 M magnesium, 4.52×10^{-5} M to 1.35×10^{-4} M potassium, 4.05×10^{-5} M to 1.22×10^{-4} zinc, 3.55×10^{-5} M to 1.06×10^{-4} manganese, 9.07×10^{-5} M to 2.91×10^{-4} boron, 3.76×10^{-5} M to 1.10×10^{-5} molybdenum, 2.28×10^{-5} M to 6.84×10^{-5} nickel, 3.60×10^{-5} M to 1.08×10^{-4} iron, or 4.70×10^{-5} M to 1.41×10^{-4} copper.

6. The method of claim **1**, wherein said genetically modified yeast cell comprises a recombinant Lipid synthesis regulator (MGA2) gene, a genetically modified Lipid synthesis regulator (MGA2) gene, a recombinant Leucine Biosynthesis gene (LEU2), a genetically modified multifunctional enzyme (MFEI) gene, a genetically modified PEX10 Transcription Factor (PEX10) gene or a recombinant AMP Deaminase (AMPD) gene.

7. The method of claim **1**, wherein said genetically modified yeast cell comprises a genetically modified multifunctional enzyme (MFE1) gene and a genetically modified PEX10 Transcription Factor (PEX10) gene.

8. The method of claim **1**, wherein said genetically modified yeast cell comprises a recombinant Leucine Biosynthesis gene (LEU2), a genetically modified multifunctional enzyme (MFEI) gene and a genetically modified PEX10 Transcription Factor (PEX10) gene.

9. The method of claim **1**, wherein said genetically modified yeast cell comprises a genetically modified multifunctional enzyme (MFEI) gene, a genetically modified PEX10 Transcription Factor (PEX10) gene and a recombinant AMP Deaminase (AMPD) gene.

10. The method of claim **1**, wherein said genetically modified yeast cell comprises a recombinant Leucine Biosynthesis gene (LEU2), a genetically modified multifunctional enzyme (MFEI) gene, a genetically modified PEX10 Transcription Factor (PEX10) gene and a recombinant AMP Deaminase (AMPD)) gene.

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