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(54) **COMPOSITIONS AND METHODS FOR METABOLIC CONTROL OF A BIOFERMENTATION PROCESS WITH SYNTHETIC METABOLIC VALVES**

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(73) Assignee: **DUKE UNIVERSITY**, Durham, NC (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.

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(22) Filed: **Jan. 14, 2022**

(65) **Prior Publication Data**

US 2022/0220514 A1 Jul. 14, 2022

Related U.S. Application Data

(63) Continuation of application No. 16/487,542, filed as application No. PCT/US2018/019040 on Feb. 21, 2018, now Pat. No. 11,268,111.

(60) Provisional application No. 62/461,436, filed on Feb. 21, 2017.

(51) **Int. Cl.**

C12P 7/42	(2006.01)
C12N 9/04	(2006.01)
C12N 9/02	(2006.01)
C12N 9/06	(2006.01)
C12N 9/10	(2006.01)
C12N 15/74	(2006.01)
C12P 13/06	(2006.01)

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

CPC ***C12P 7/42*** (2013.01); ***C12N 9/001*** (2013.01); ***C12N 9/0006*** (2013.01); ***C12N 9/0008*** (2013.01); ***C12N 9/0016*** (2013.01); ***C12N 9/0051*** (2013.01); ***C12N 9/1025*** (2013.01); ***C12N 15/746*** (2013.01); ***C12P 13/06*** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The present disclosure provides compositions and methods for rapid production of chemicals in genetically engineered microorganisms in a large scale. Also provided herein is a high-throughput metabolic engineering platform enabling the rapid optimization of microbial production strains. The platform, which bridges a gap between current in vivo and in vitro bio-production approaches, relies on dynamic minimization of the active metabolic network.

17 Claims, 117 Drawing Sheets

Specification includes a Sequence Listing.

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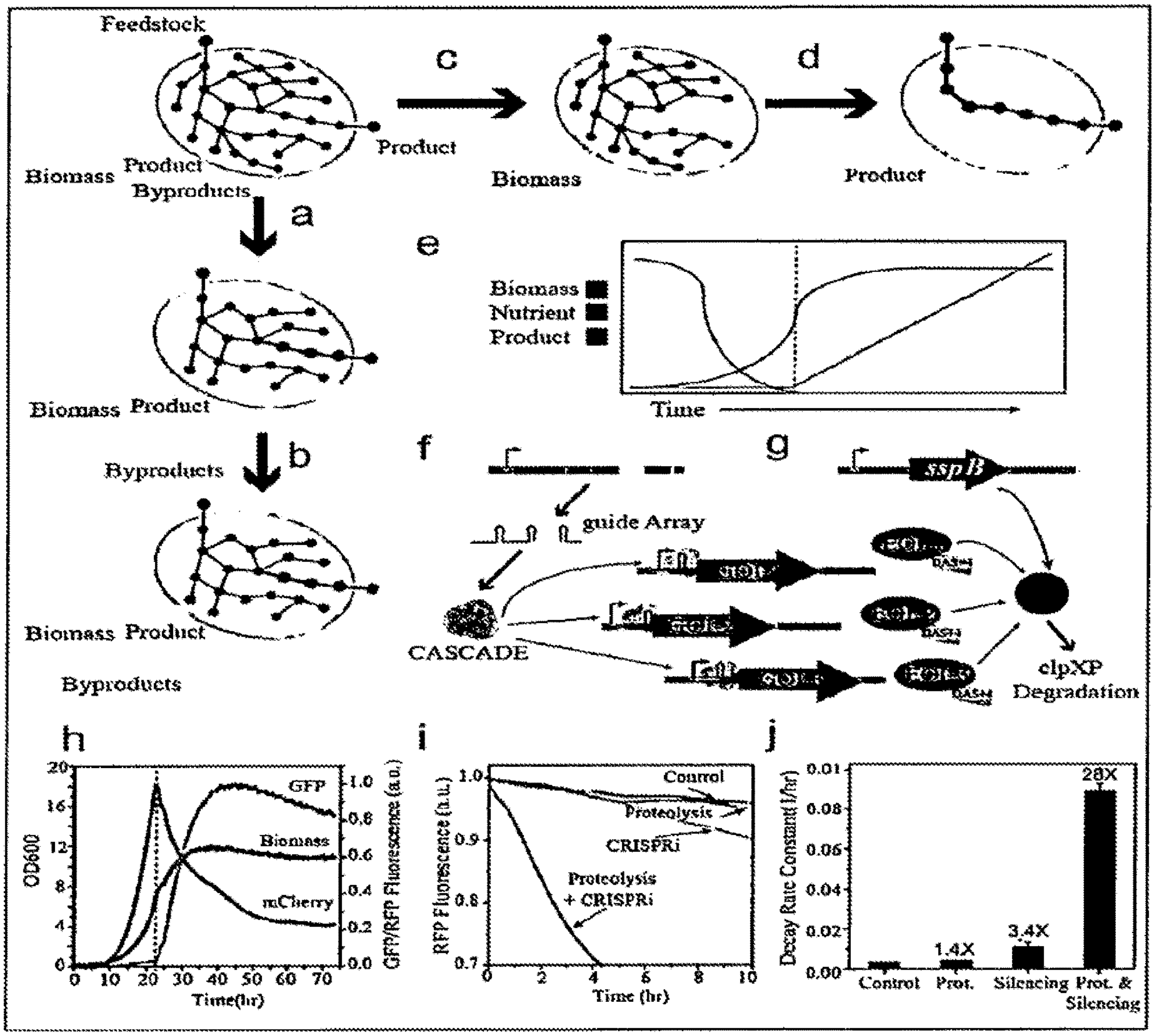
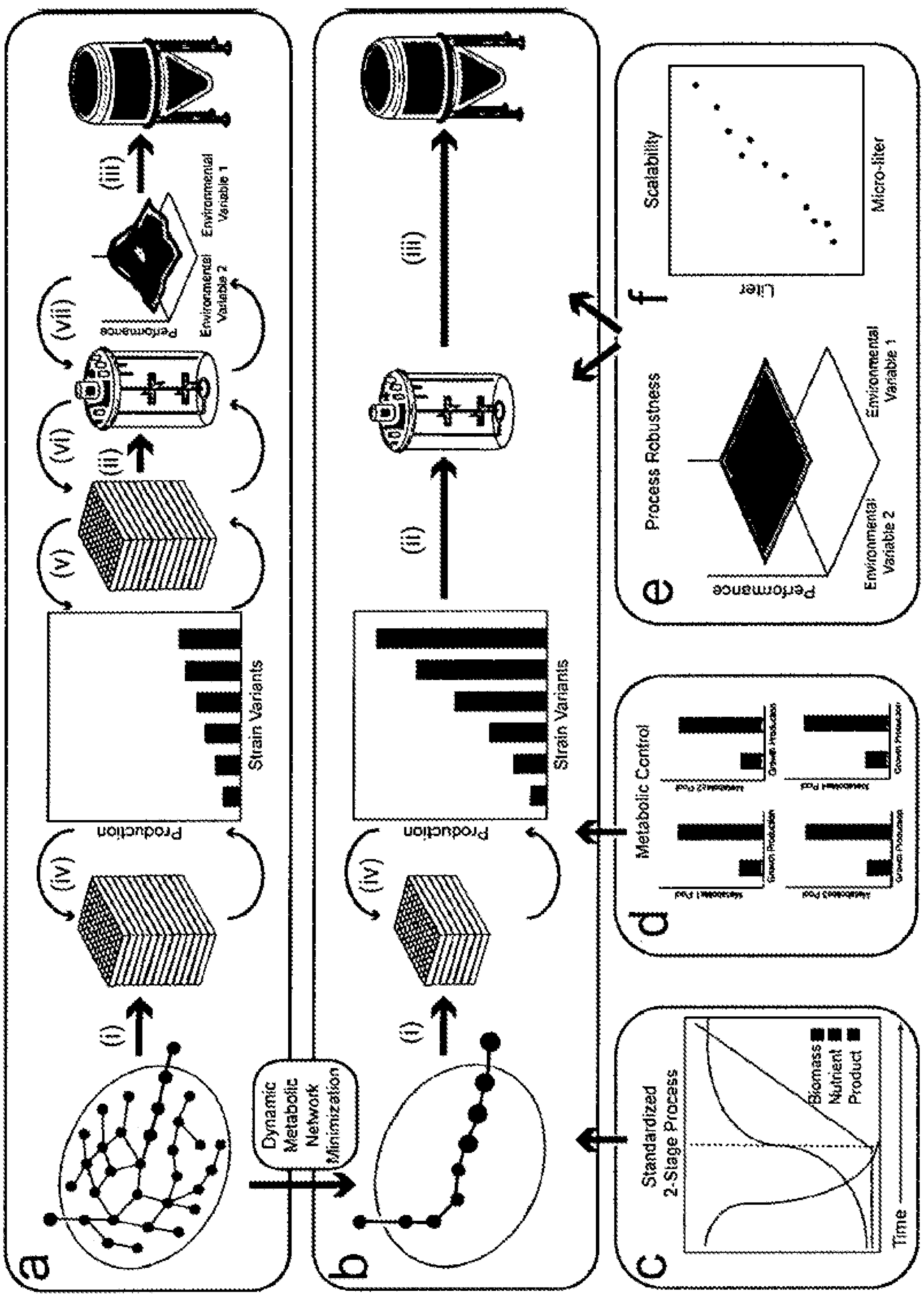

Feedstock
c
d
Product
Biomass
Product
Byproducts
Biomass
Product
a
e
Biomass
Nutrient
Product
Time
Biomass Product
b
Byproducts
Biomass Product
Byproducts
f
g
sspB
guide Array
CASCADE
clpXP
Degradation
h
i
j
GFP
Biomass
mCherry
OD600
GFP/RFP Fluorescence (a.u.)
Time(hr)
Control
Proteolysis
CRISPRi
Proteolysis
+ CRISPRi
RFP Fluorescence (a.u.)
Time (hr)
Decay Rate Constant (1/hr)
28X
1.4X
3.4X
Control
Prot.
Silencing
Prot. &
Silencing

FIGURE 1A



a
(i)
(iv)
Production
Strain Variants
(v)
(vi)
(ii)
(vii)
Performance
Environmental Variable 2
Environmental Variable 1
(iii)
Dynamic Metabolic Network Minimization
b
(i)
(iv)
Production
Strain Variants
(ii)
(iii)
c
Standardized 2-Stage Process
Biomass
Nutrient
Product
Time
d
Metabolic Control
e
Process Robustness
Performance
Environmental Variable 2
Environmental Variable 1
f
Scalability
Liter
Micro-liter

FIGURE 1B

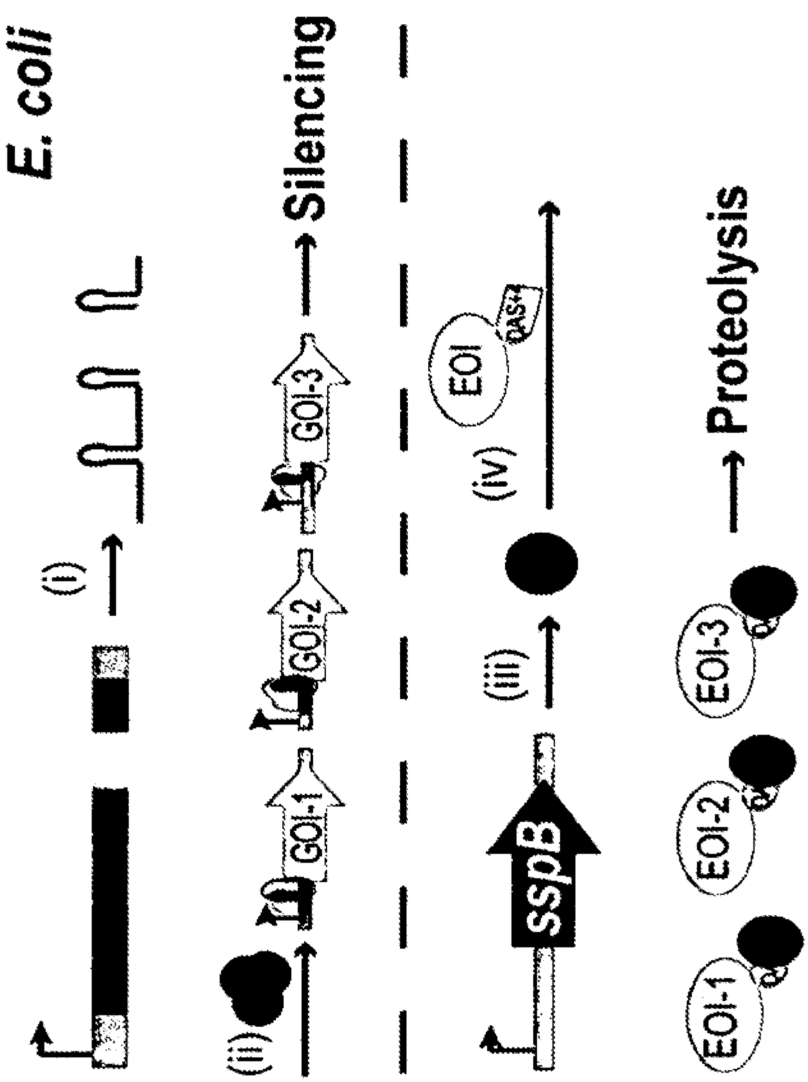

E. coli
(i)
(ii)
GOI-1
GOI-2
GOI-3
Silencing
(iii)
(iv)
sspB
EOI
DAS+4
EOI-1
EOI-2
EOI-3
Proteolysis

FIGURE 2A

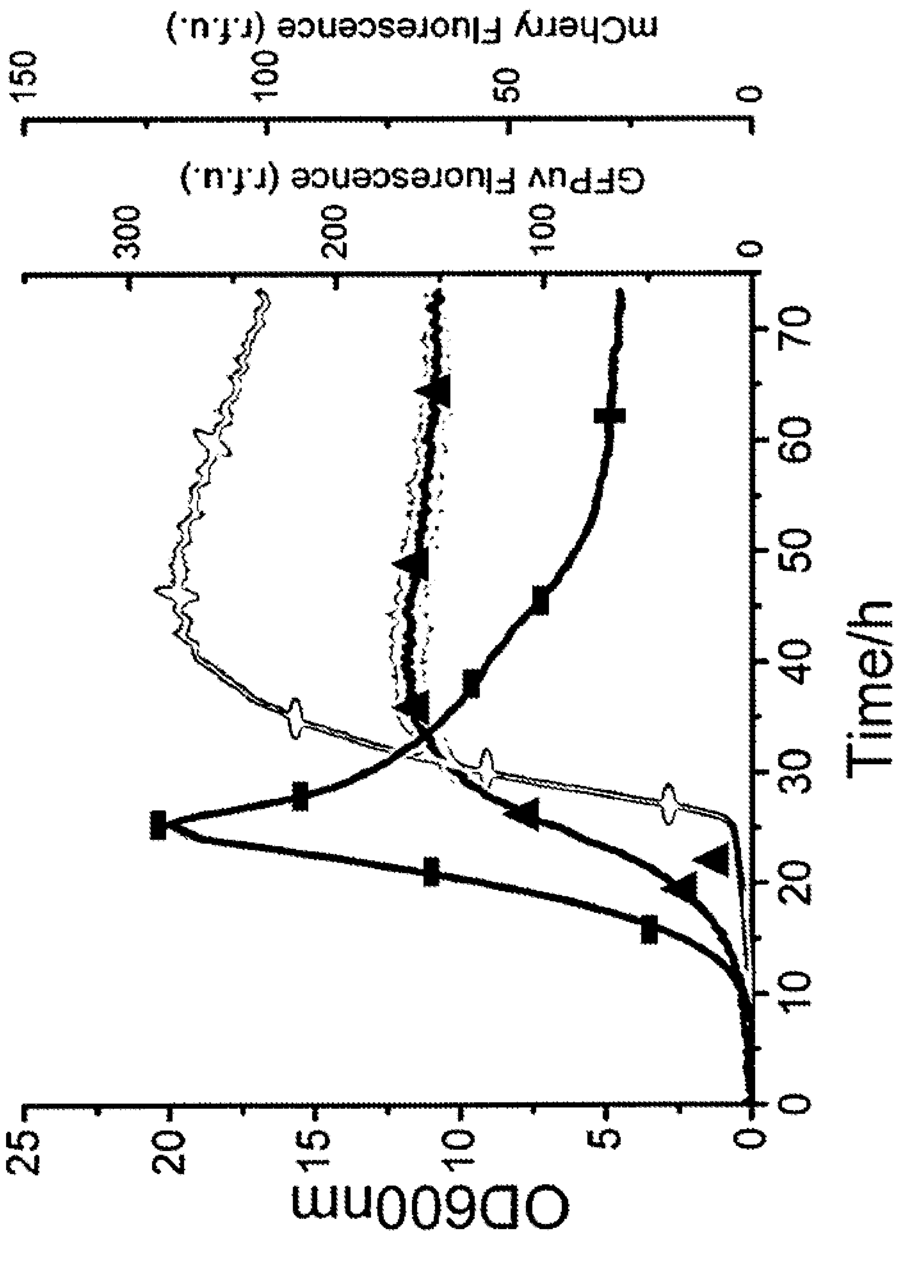
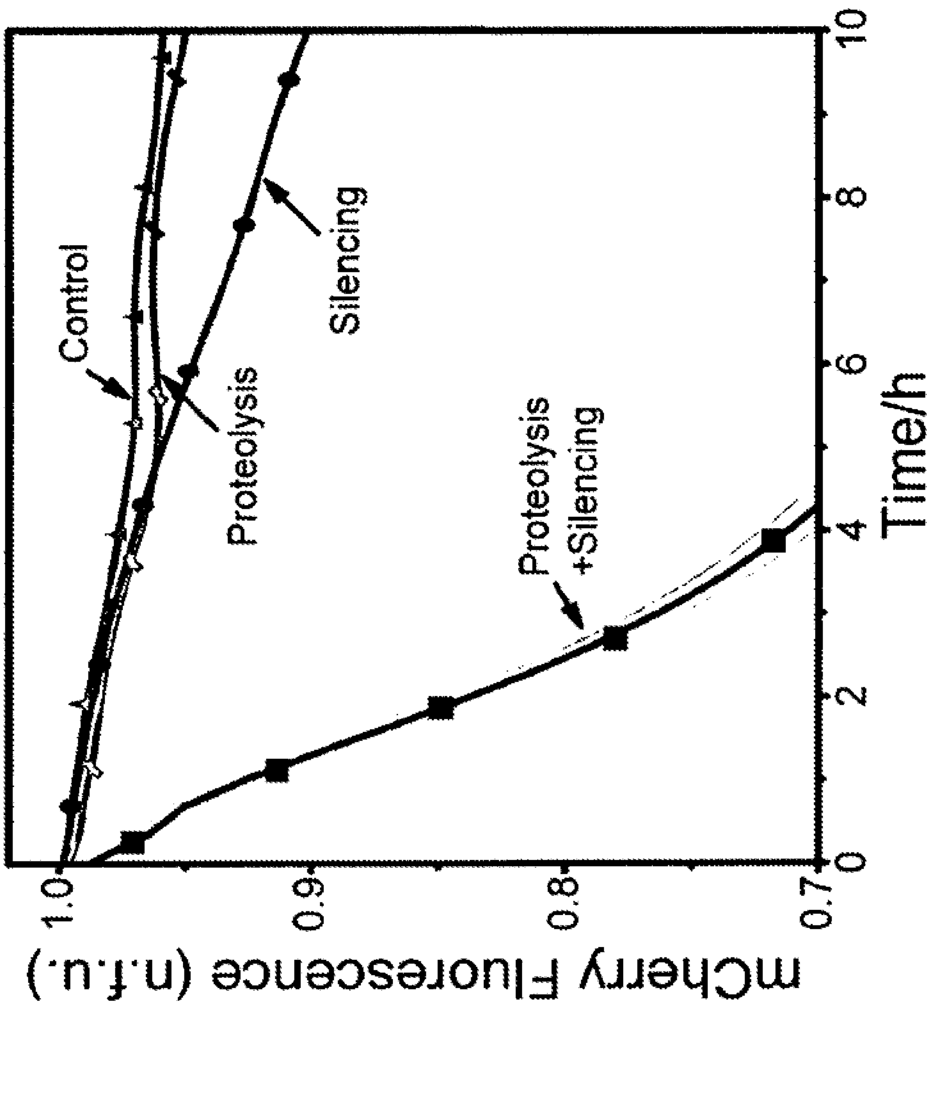

mCherry Fluorescence (r.f.u.)
150
100
50
0
GFPuv Fluorescence (r.f.u.)
300
200
100
0
OD600nm
25
20
15
10
5
0
0
10
20
30
40
50
60
70
Time/h

FIGURE 2B



mCherry Fluorescence (n.f.u.)
1.0
0.9
0.8
0.7
0
2
4
6
8
10
Time/h
Control
Proteolysis
Silencing
Proteolysis
+Silencing

FIGURE 2C

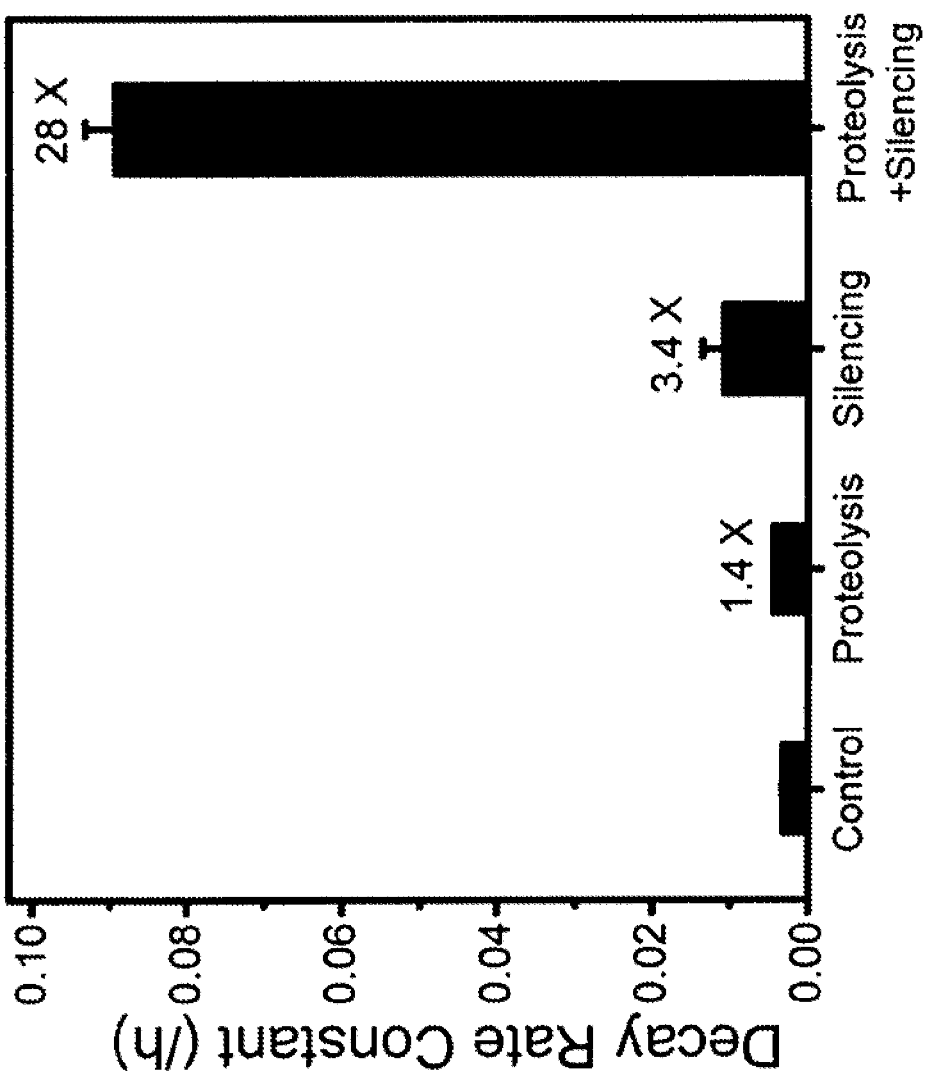
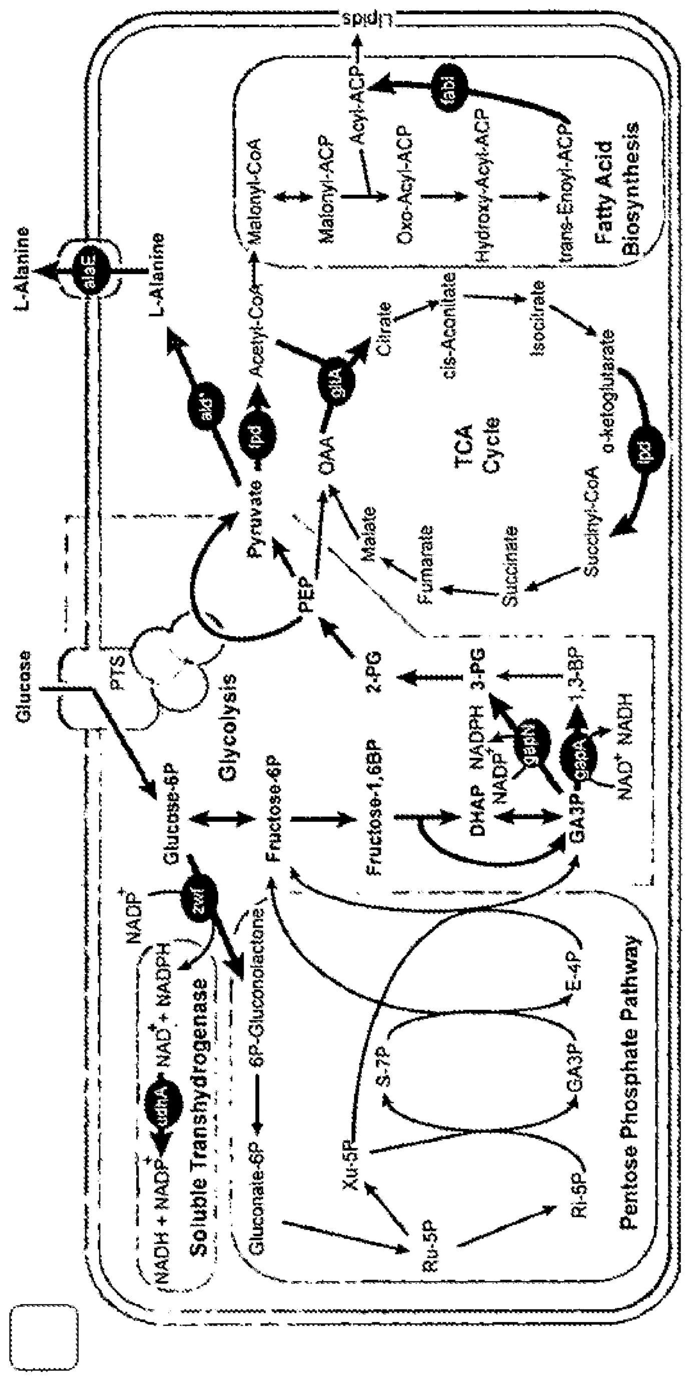

Decay Rate Constant (/h)
0.10
0.08
0.06
0.04
0.02
0.00
Control
Proteolysis
Silencing
Proteolysis
+Silencing
1.4 X
3.4 X
28 X

FIGURE 2D



Glucose
PTS
L-Alanine
alaE
L-Alanine
Lipids
Glucose-6P
Glycolysis
Fructose-6P
Fructose-1,6BP
DHAP
GA3P
NADP+
NADPH
gapN
gapA
NAD+
NADH
1,3-BP
3-PG
2-PG
PEP
Pyruvate
ald
lpd
Acetyl-CoA
gltA
OAA
Citrate
cis-Aconitate
Isocitrate
α-ketoglutarate
lpd
Succinyl-CoA
Succinate
Fumarate
Malate
TCA
Cycle
Malonyl-CoA
Malonyl-ACP
Oxo-Acyl-ACP
Hydroxy-Acyl-ACP
trans-Enoyl-ACP
Acyl-ACP
fabI
Fatty Acid
Biosynthesis
zwf
NADP+
NADH + NADP+
udhA
NAD+ + NADPH
Soluble Transhydrogenase
6P-Gluconolactone
Gluconate-6P
Ru-5P
Xu-5P
Ri-5P
S-7P
GA3P
E-4P
Pentose Phosphate Pathway

FIGURE 3A

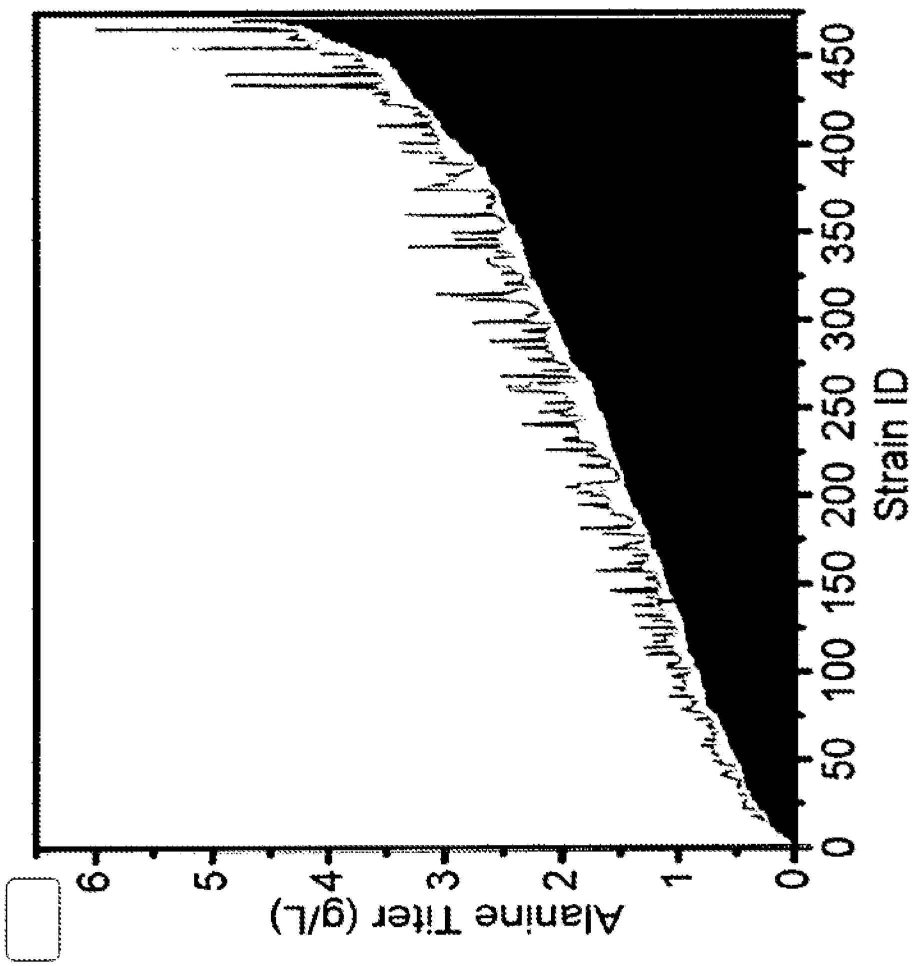

Alanine Titer (g/L)
0
1
2
3
4
5
6
Strain ID
0
50
100
150
200
250
300
350
400
450

FIGURE 3B

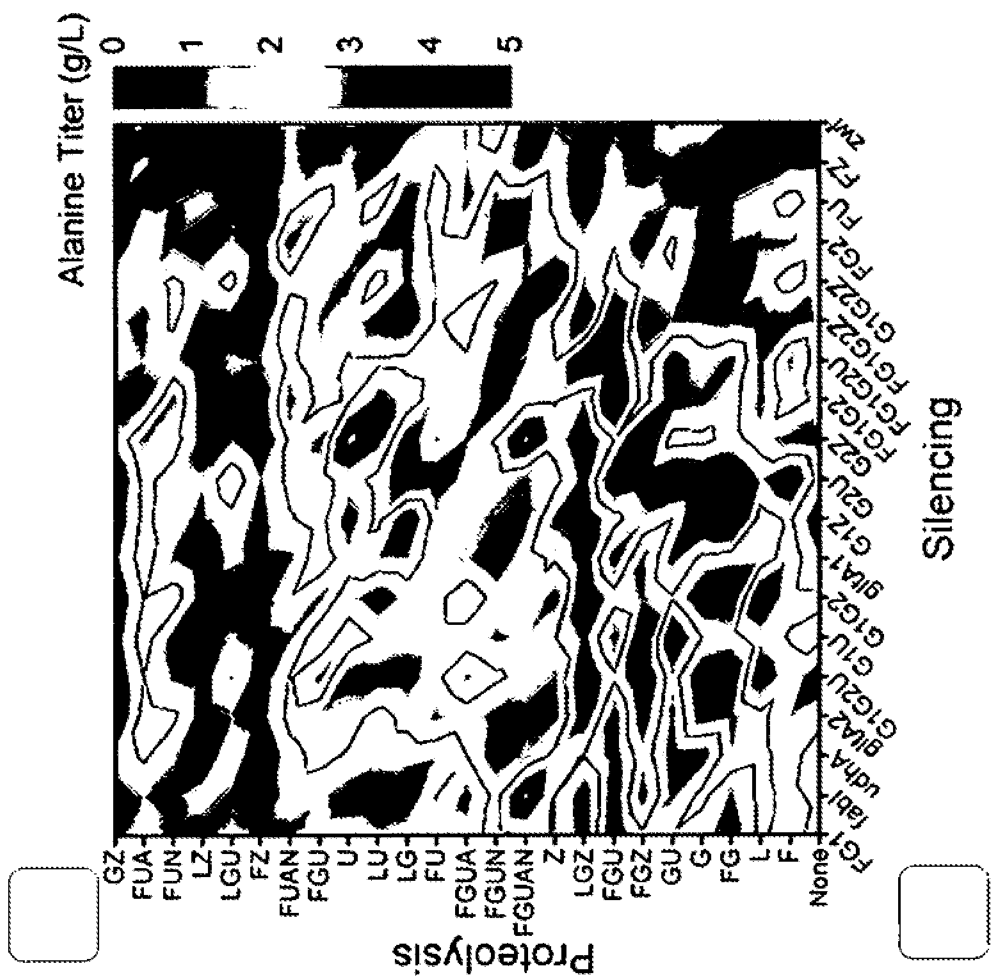

Alanine Titer (g/L)
0
1
2
3
4
5
Silencing
Proteolysis
GZ
FUA
FUN
LZ
LGU
FZ
FUAN
FGU
U
LU
LG
FU
FGUA
FGUN
FGUAN
Z
LGZ
FGU
FGZ
GU
G
FG
L
F
None
FG1
fabI
udhA
gltA2
G1G2U
G1U
G1G2
gltA1
G1Z
G2U
G2Z
FG1G2
FG1G2U
G1G2Z
FG2
FU
FZ
zwf

FIGURE 3C

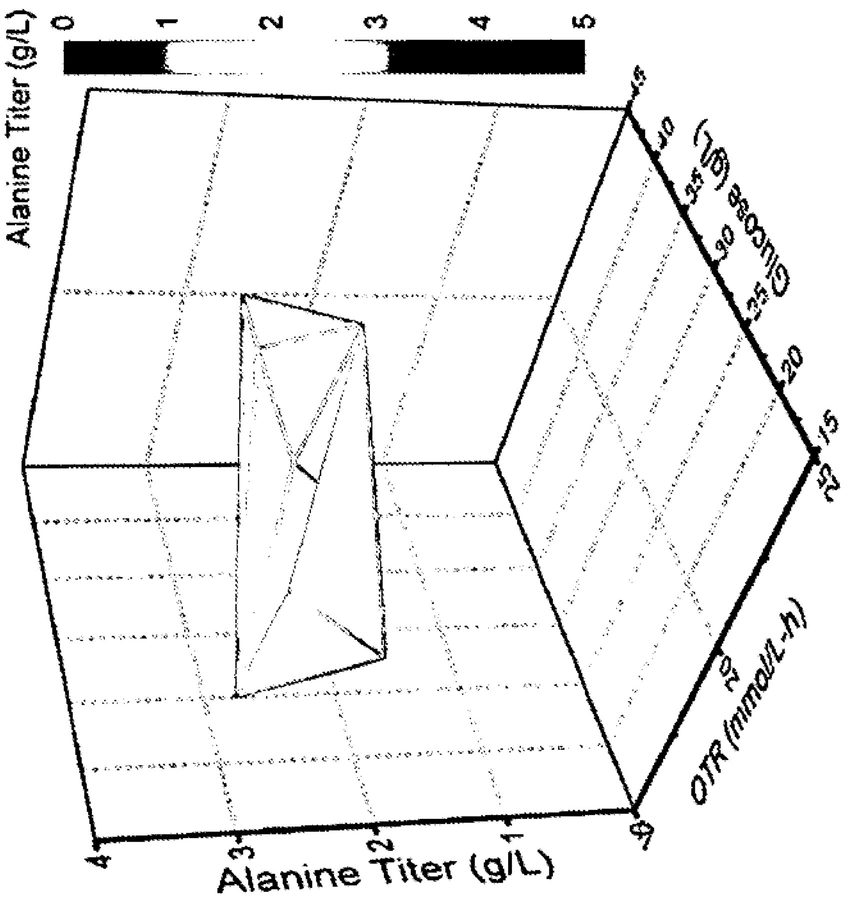

Alanine Titer (g/L)
0
1
2
3
4
5
Alanine Titer (g/L)
4
3
2
1
0
Glucose (g/L)
15
20
OTR (mmol/L-h)

FIGURE 3D

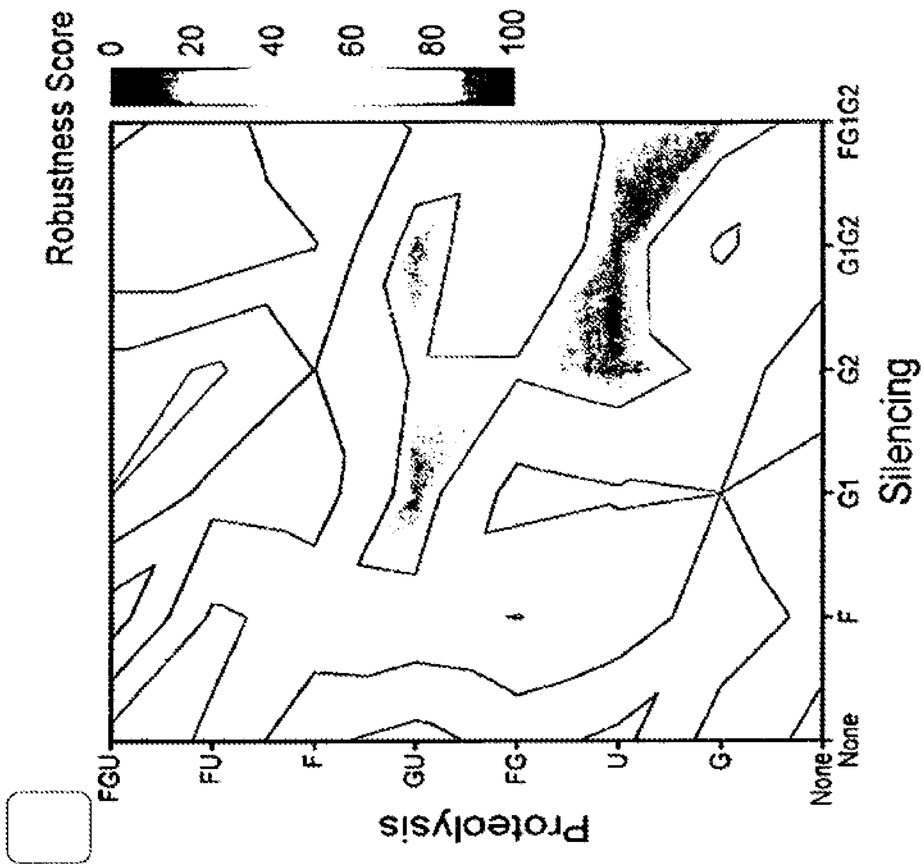

Robustness Score
0
20
40
60
80
100
Proteolysis
FGU
FU
F
GU
FG
U
G
None
Silencing
None
F
G1
G2
G1G2
FG1G2

FIGURE 3E

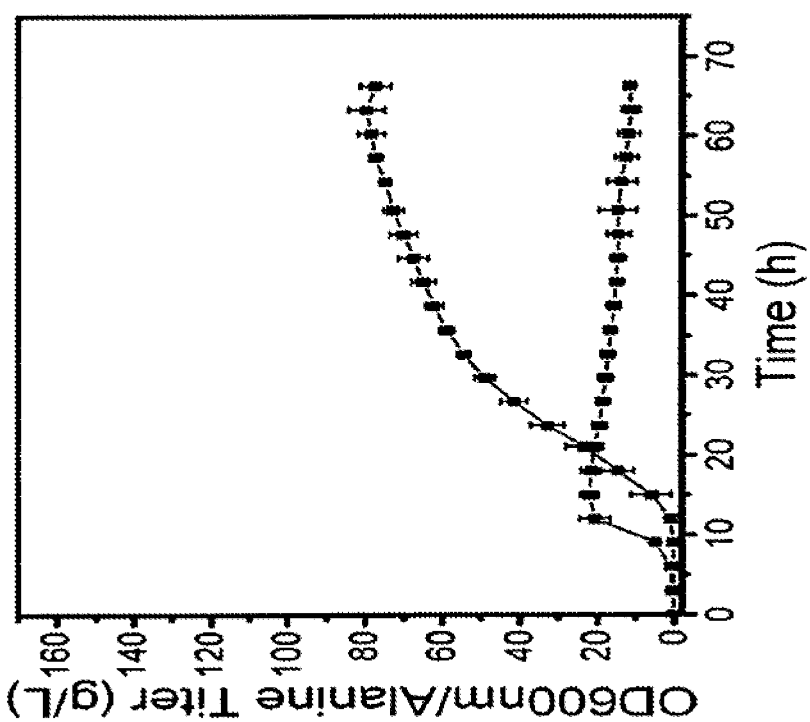


FIGURE 3F

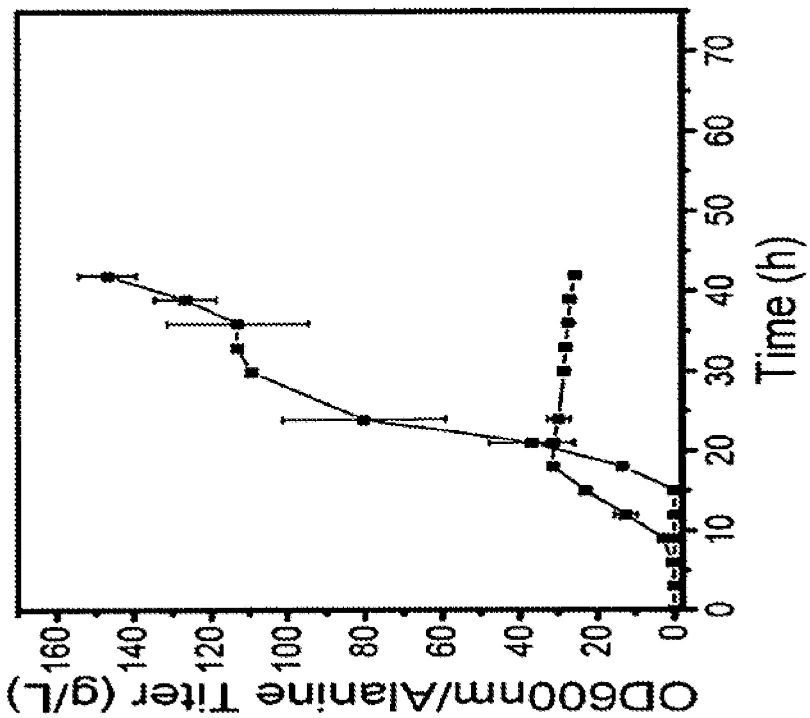
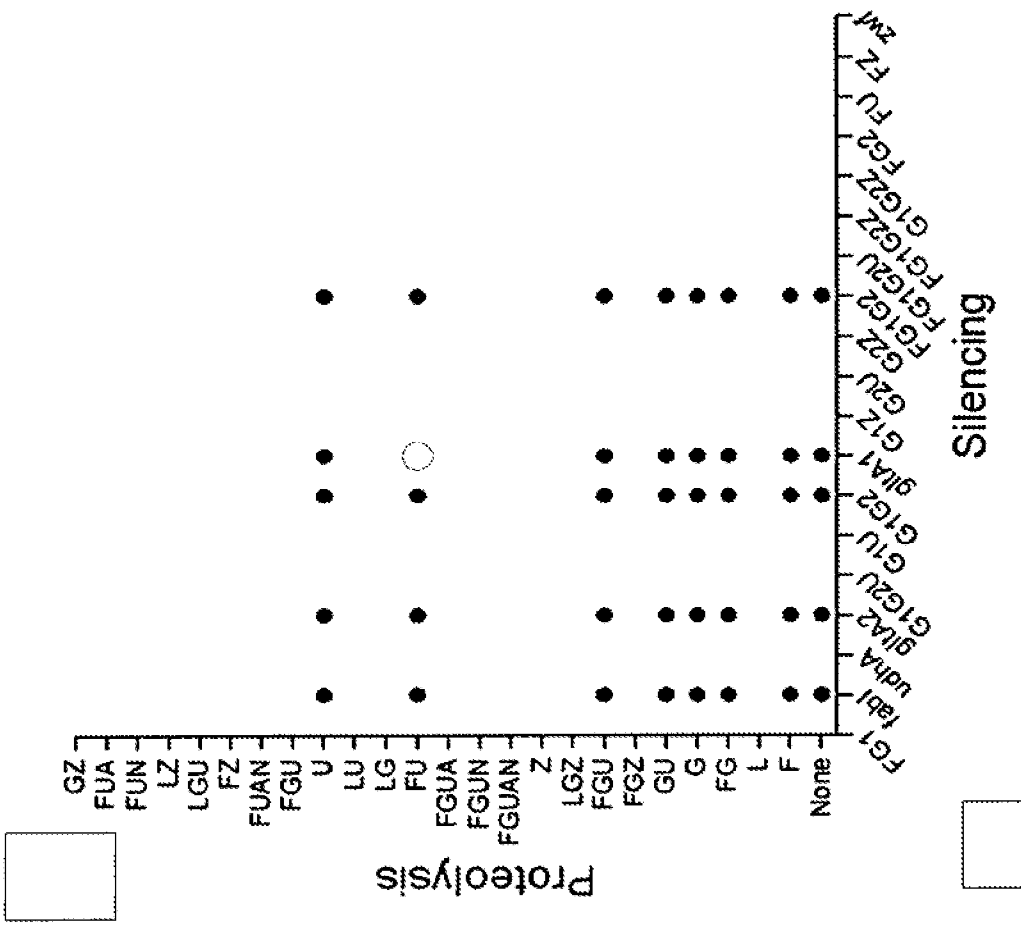


FIGURE 3G



Silencing
FG1
fabI
udhA
gltA2
G1G2U
G1U
G1G2
gltA1
G1Z
G2U
G2Z
FG1G2
FG1G2U
G1G2Z
FG2
FU
FZ
zwf
Proteolysis
GZ
FUA
FUN
LZ
LGU
FZ
FUAN
FGU
U
LU
LG
FU
FGUA
FGUN
FGUAN
Z
LGZ
FGU
FGZ
GU
G
FG
L
F
None

FIGURE 3H

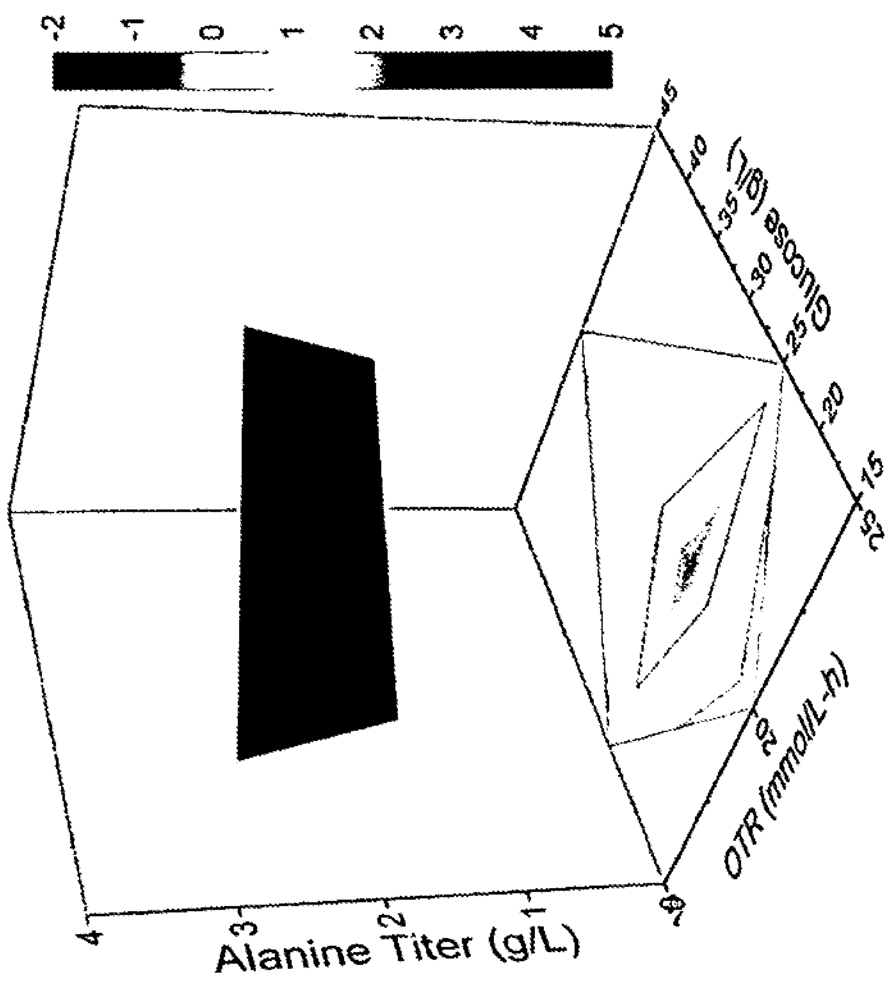

-2
-1
0
1
2
3
4
5
Alanine Titer (g/L)
4
3
2
1
0
Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
20

FIGURE 3I

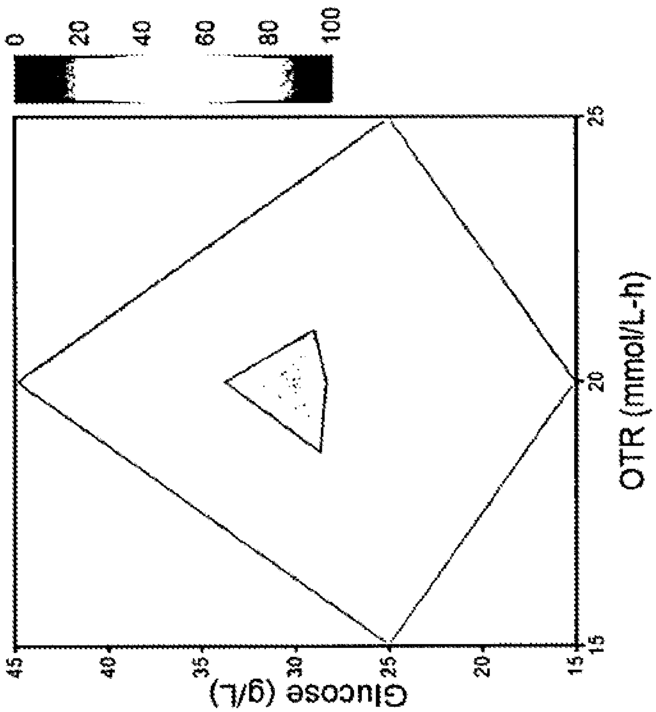


FIGURE 3K

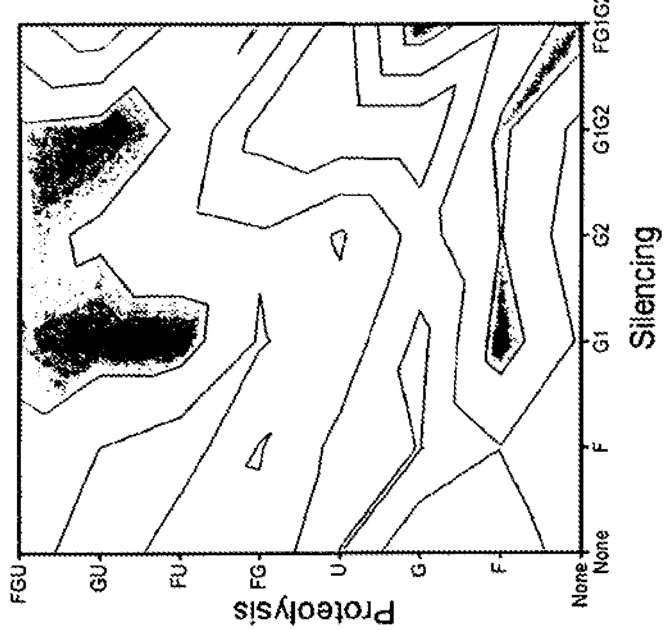


FIGURE 3J

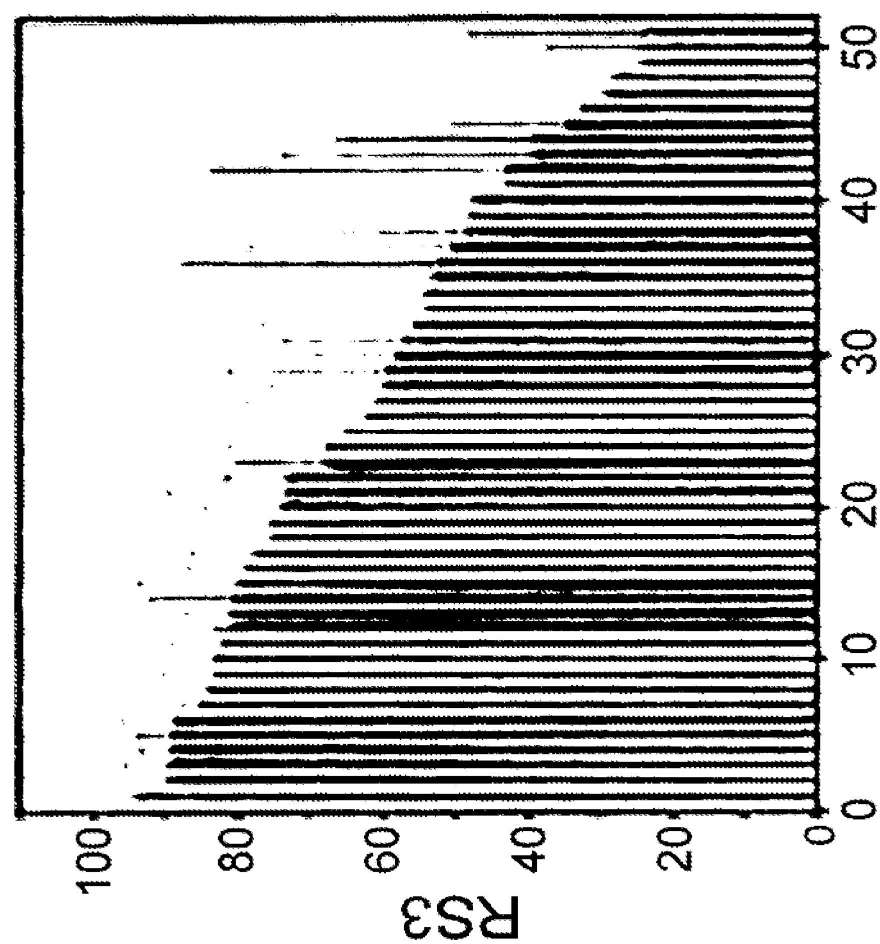


FIGURE 4A

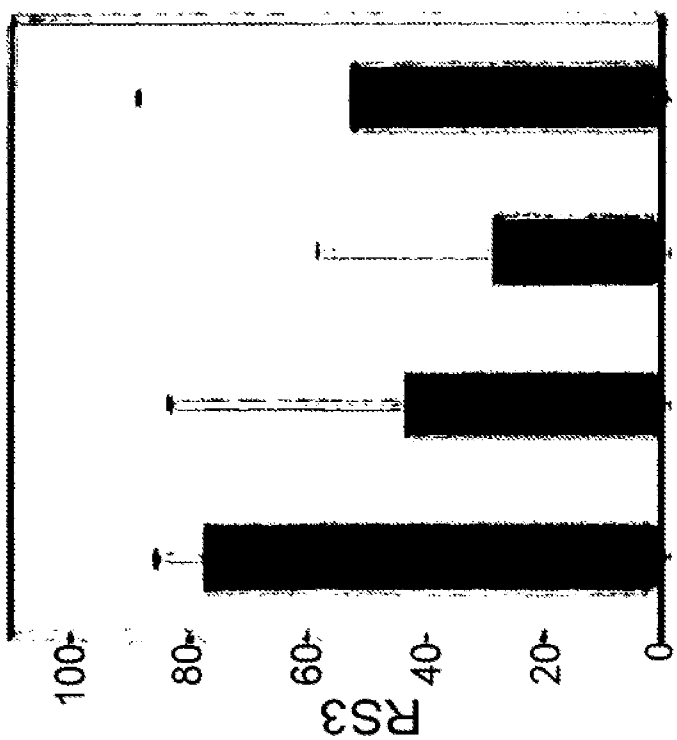


FIGURE 4B

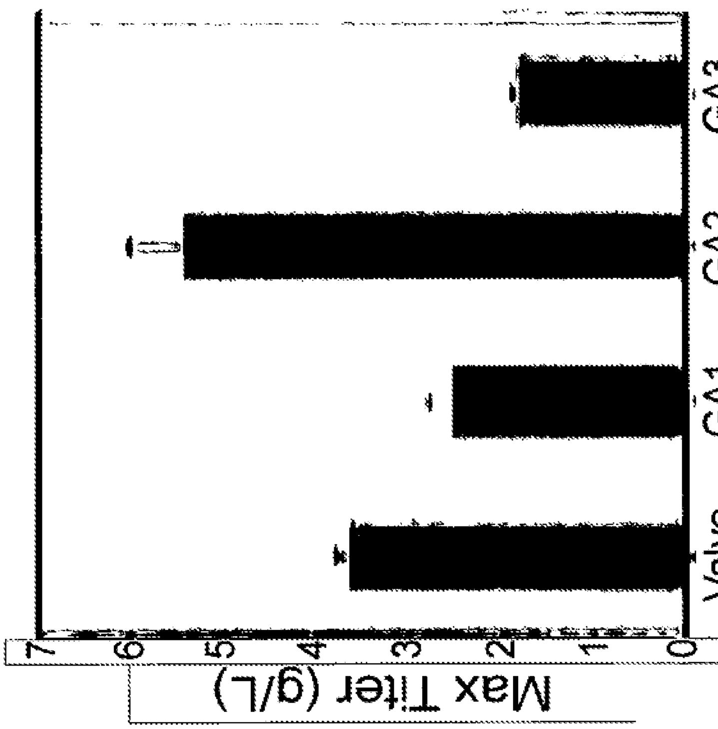


FIGURE 4C

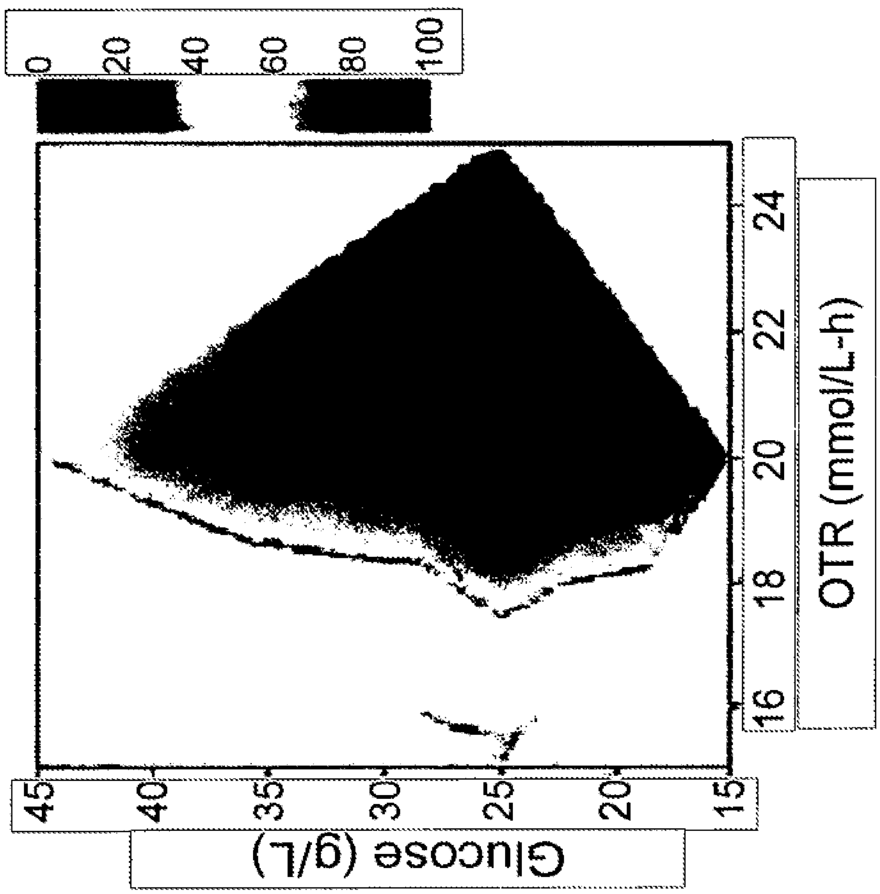

Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
16
18
20
22
24
0
20
40
60
80
100

FIGURE 4D

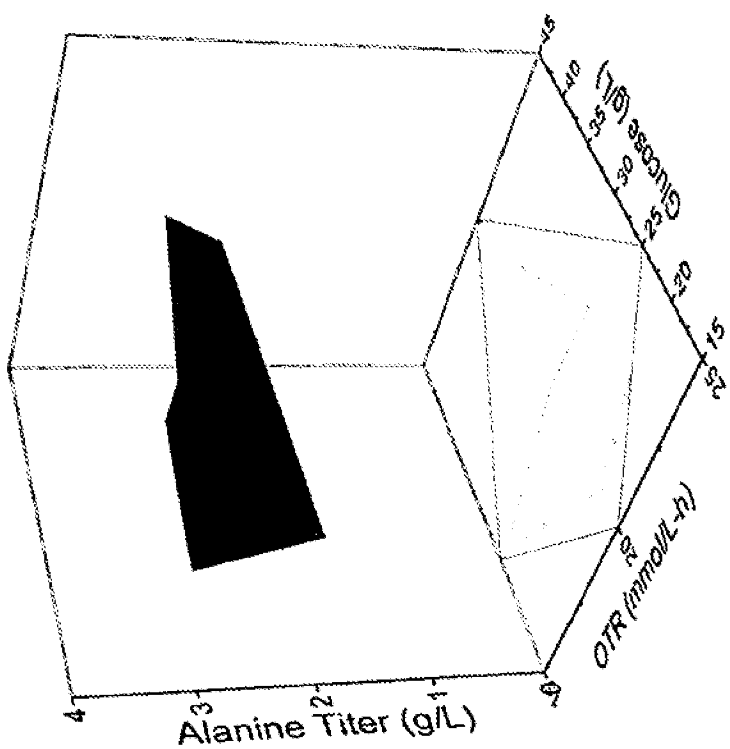


FIGURE 4E

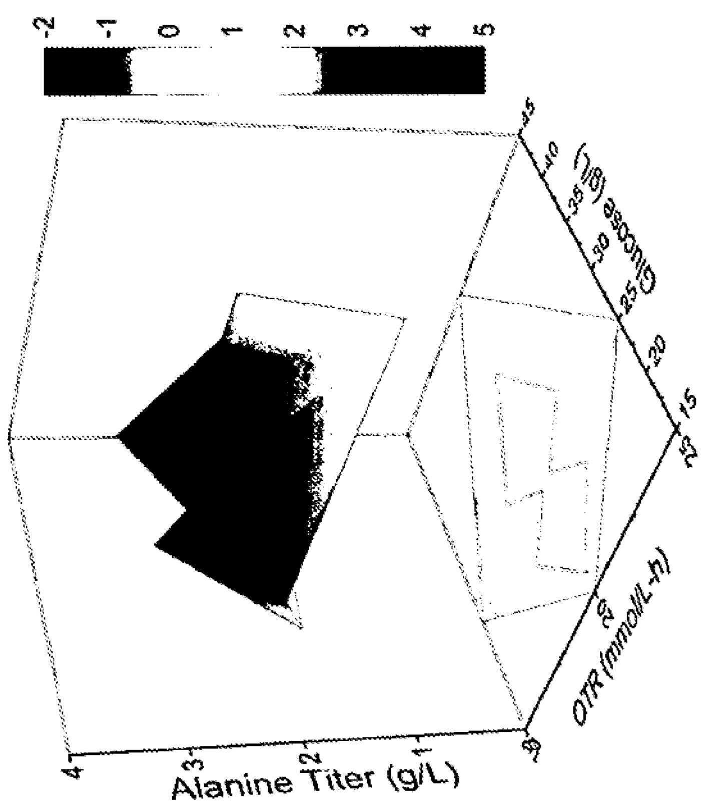


FIGURE 4F

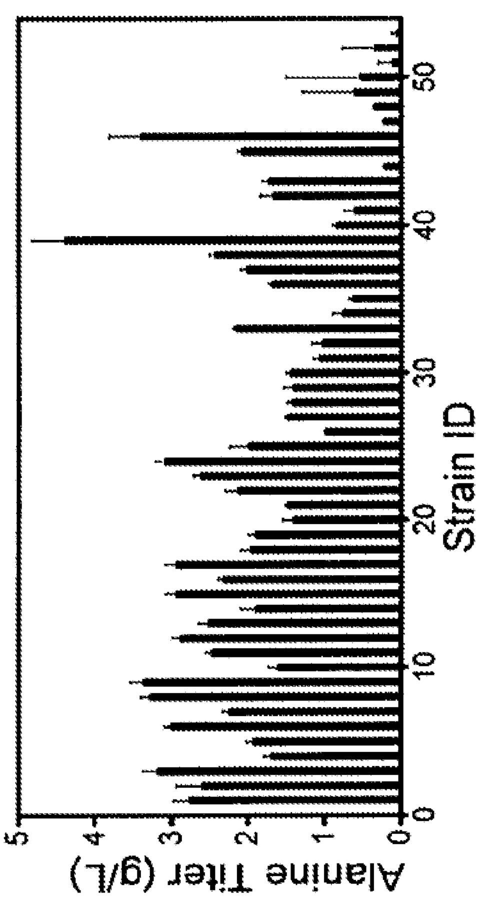


FIGURE 5A

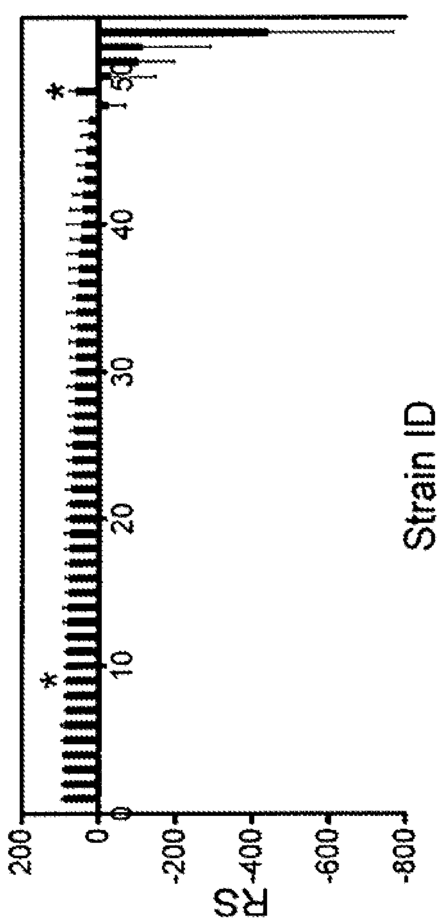


FIGURE 5B

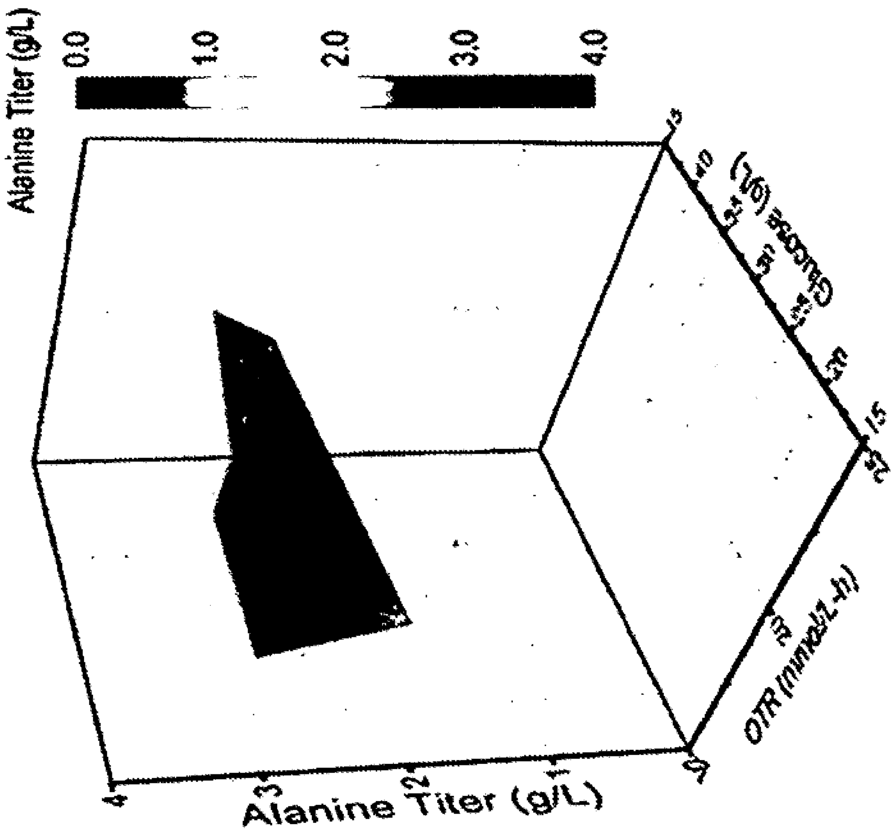

Alanine Titer (g/L)
0.0
1.0
2.0
3.0
4.0
Glucose (g/L)
OTR (mmol/L-h)
4
3
2
1
0
Alanine Titer (g/L)

FIGURE 5C

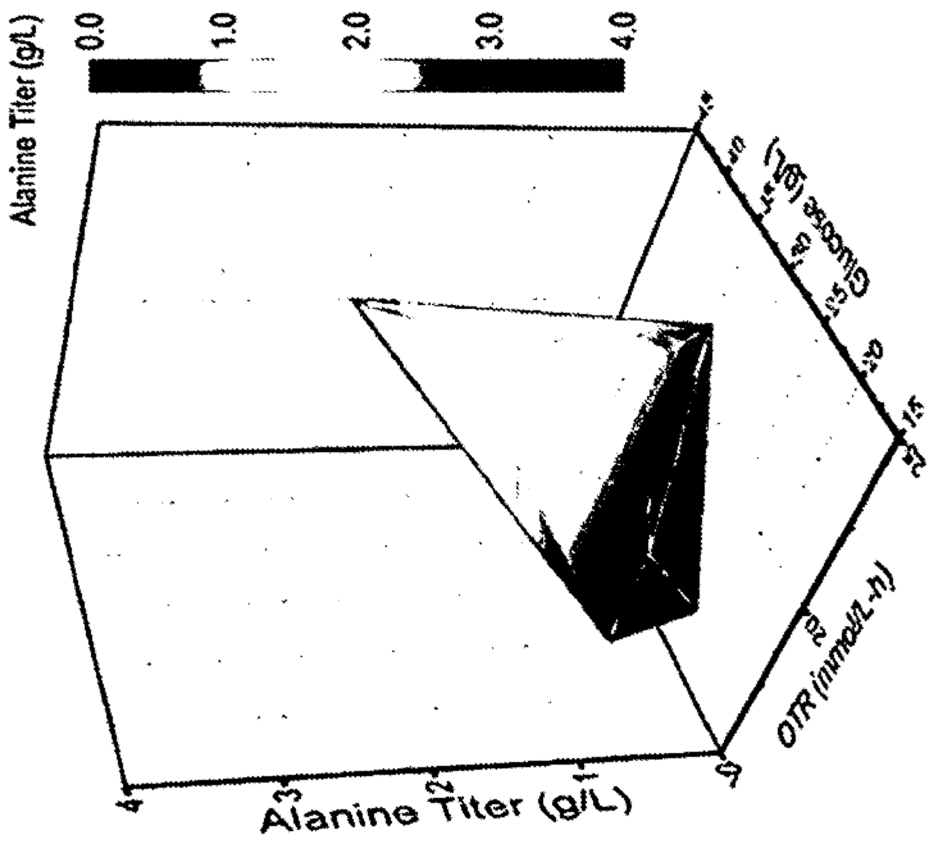

Alanine Titer (g/L)
0.0
1.0
2.0
3.0
4.0
Glucose (g/L)
OTR (mmol/L-h)
Alanine Titer (g/L)
4
3
2
1
0

FIGURE 5D

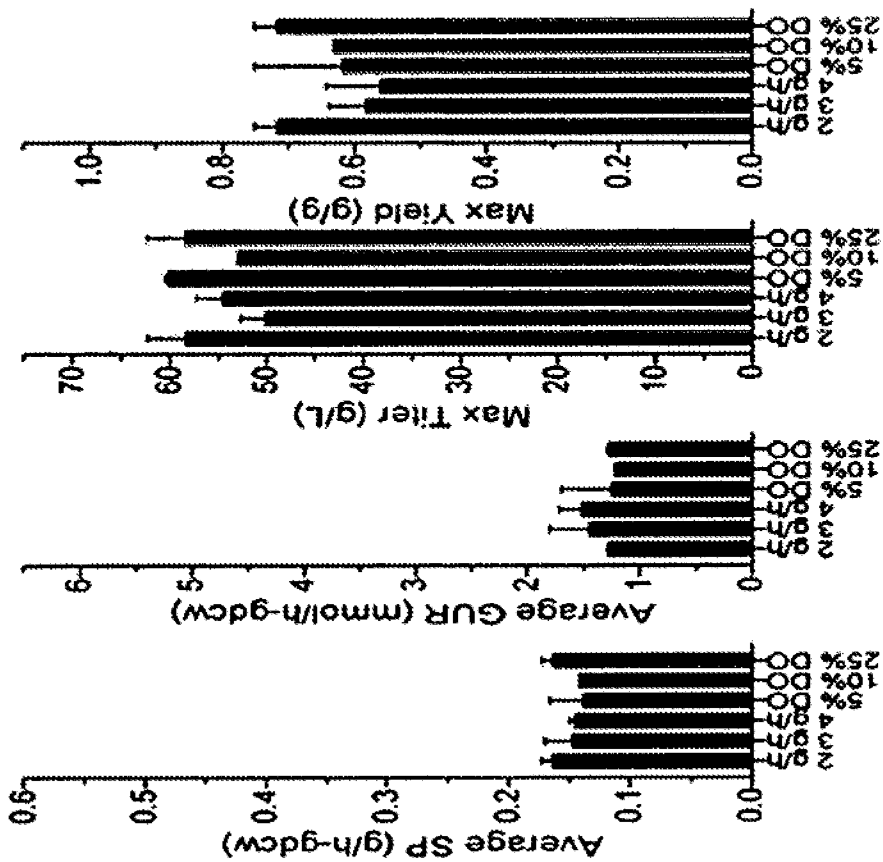

Average SP (g/h-gdcw)
Average GUR (mmol/h-gdcw)
Max Titer (g/L)
Max Yield (g/g)
2 g/L
3 g/L
4 g/L
5% DO
10% DO
25% DO

FIGURE 5E

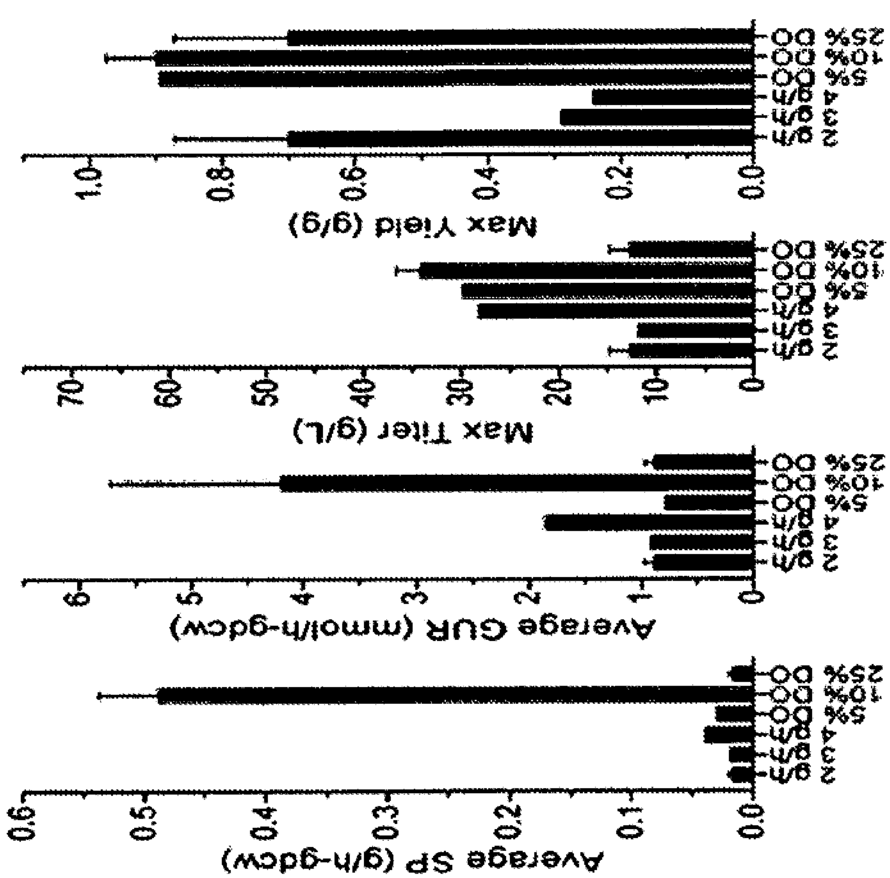

Average SP (g/h-gdcw)
Average GUR (mmol/h-gdcw)
Max Titer (g/L)
Max Yield (g/g)
2 g/L
3 g/L
4 g/L
5% DO
10% DO
25% DO

FIGURE 5F

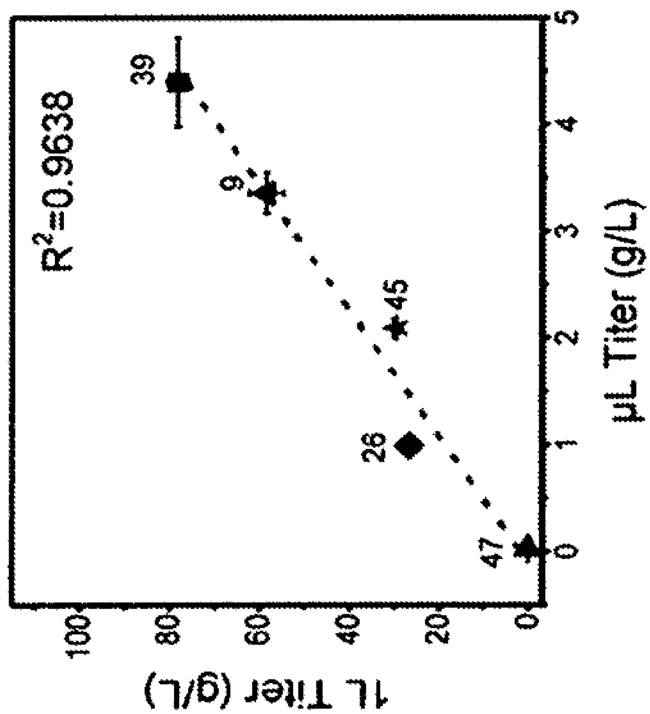

R^2=0.9638
39
9
45
26
47
1L Titer (g/L)
0
20
40
60
80
100
µL Titer (g/L)
0
1
2
3
4
5

FIGURE 5G

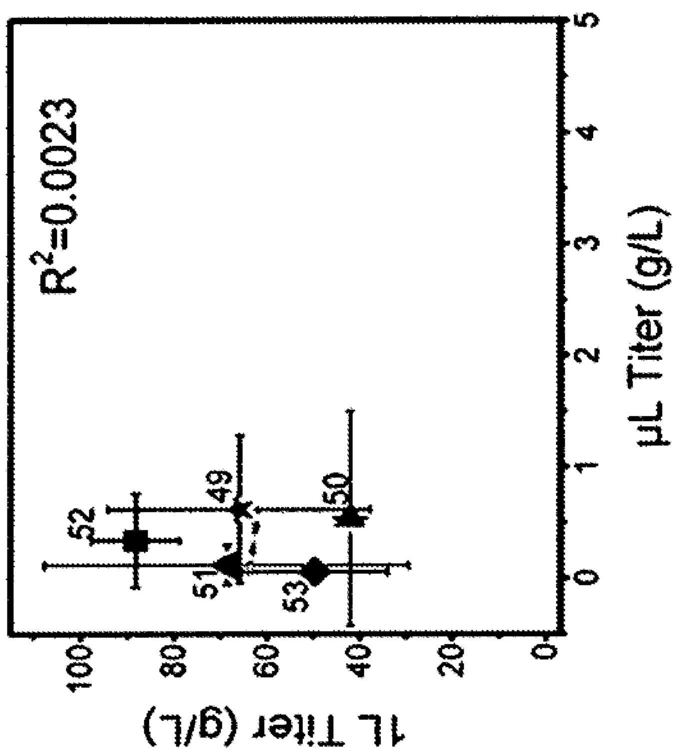

R²=0.0023
1L Titer (g/L)
μL Titer (g/L)
0
20
40
60
80
100
0
1
2
3
4
5
49
50
51
52
53

FIGURE 5H

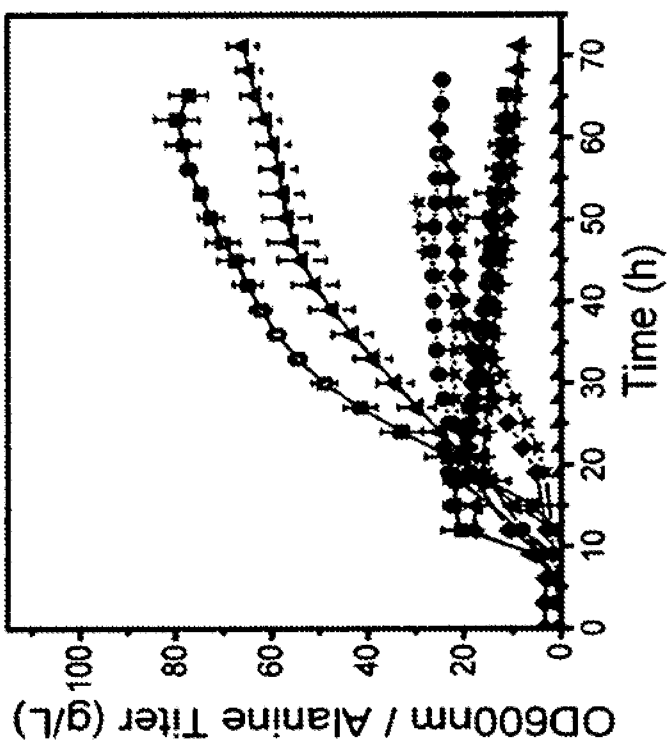

OD600nm / Alanine Titer (g/L)
100
80
60
40
20
0
0
10
20
30
40
50
60
70
Time (h)

FIGURE 5I

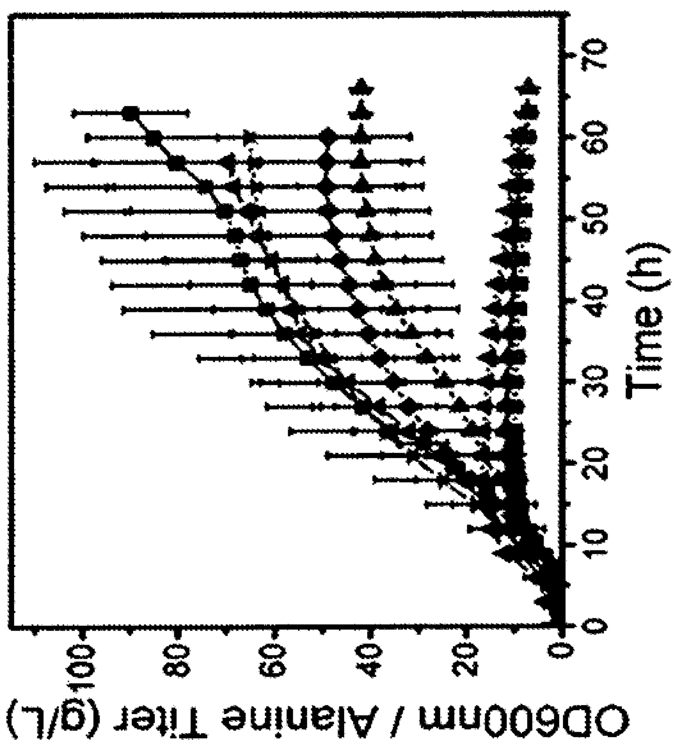

OD600nm / Alanine Titer (g/L)
0
20
40
60
80
100
0
10
20
30
40
50
60
70
Time (h)

FIGURE 5J

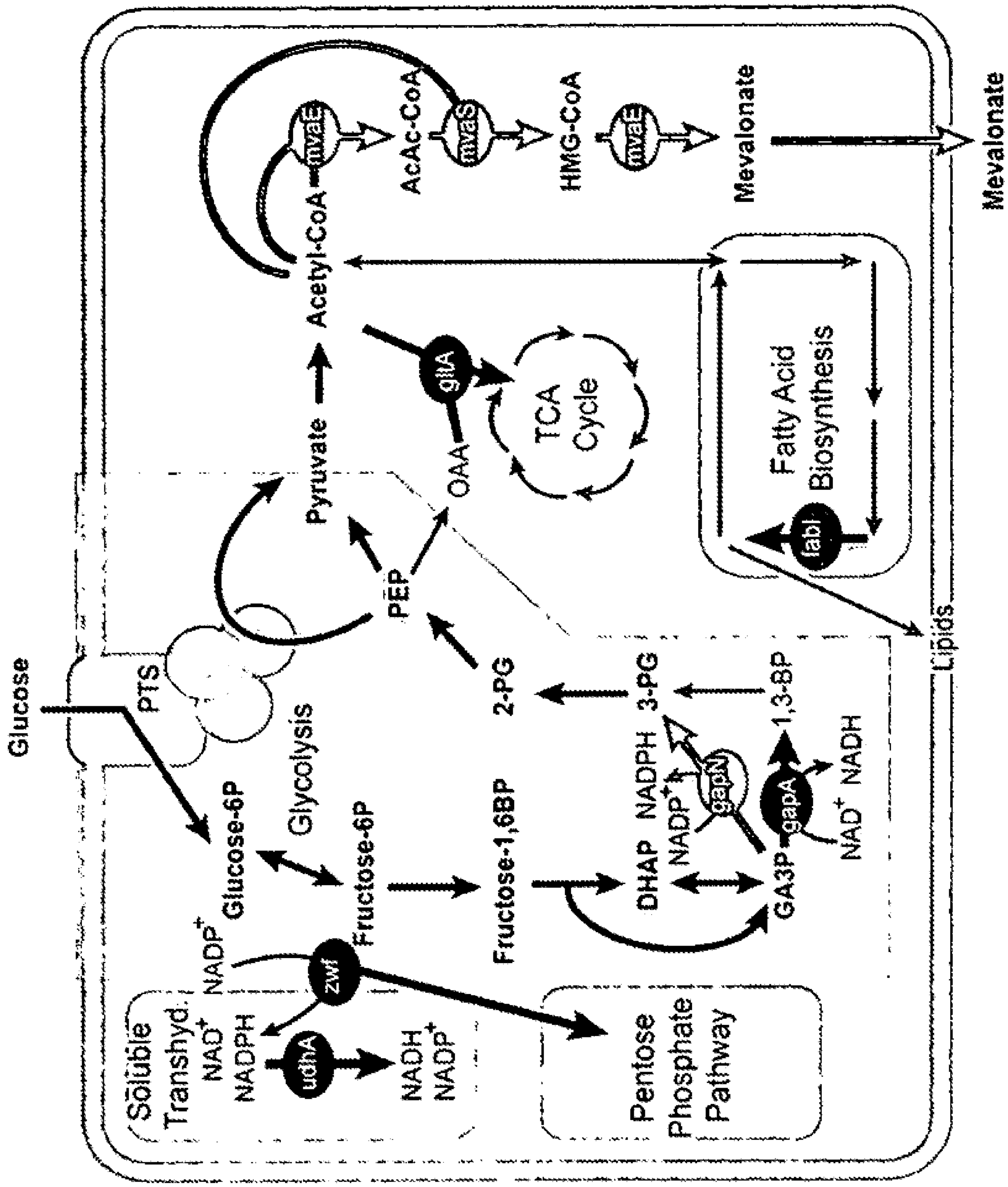

Glucose
PTS
Glucose-6P
Glycolysis
Fructose-6P
Fructose-1,6BP
DHAP
GA3P
NADP+
NADPH
gapN
gapA
NAD+
NADH
3-PG
1,3-BP
2-PG
PEP
Pyruvate
OAA
gltA
TCA Cycle
Acetyl-CoA
mvaE
AcAc-CoA
mvaS
HMG-CoA
Mevalonate
Mevalonate
Fatty Acid Biosynthesis
fabI
Lipids
Soluble Transhyd.
NAD+
NADPH
udhA
NADH
NADP+
zwf
Pentose Phosphate Pathway

FIGURE 6A

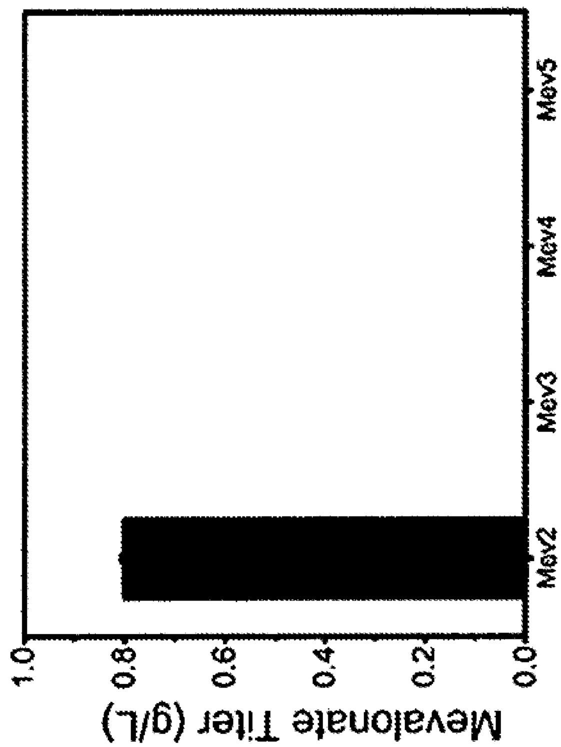


FIGURE 6B

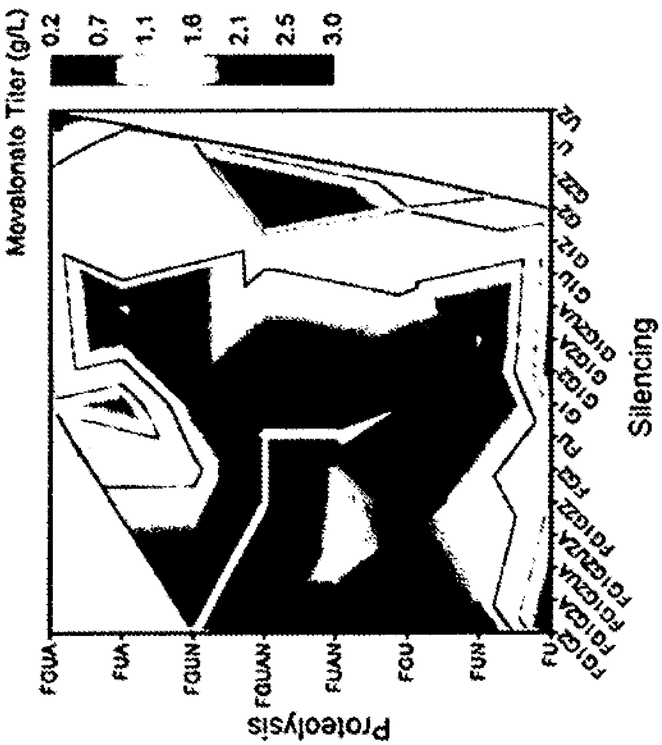

Mevalonate Titer (g/L)
0.2
0.7
1.1
1.6
2.1
2.5
3.0
Proteolysis
FGUA
FUA
FGUN
FGUAN
FUAN
FGU
FUN
FU
Silencing

FIGURE 6C

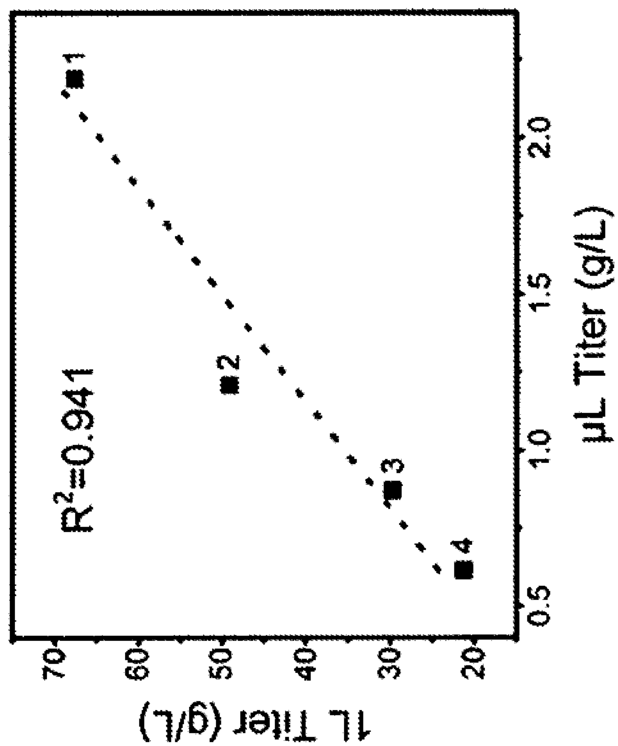


FIGURE 6D

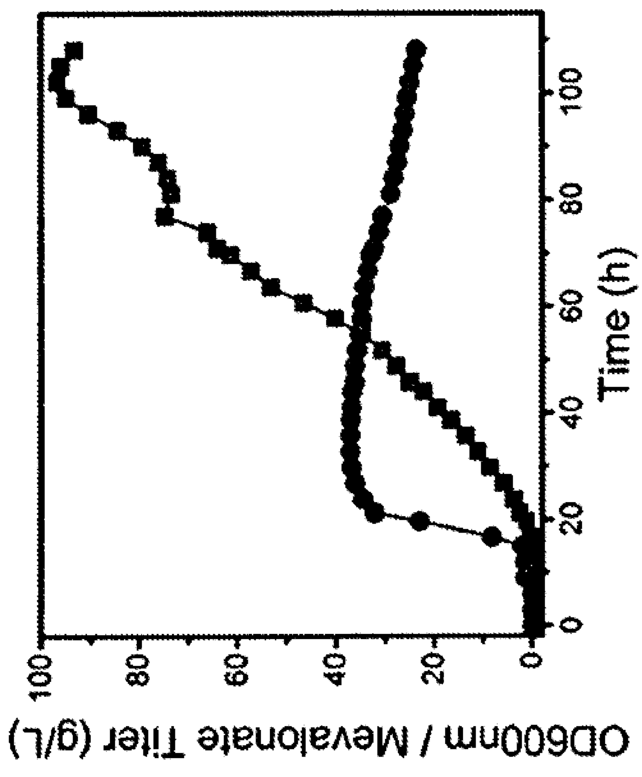

OD600nm / Mevalonate Titer (g/L)
0
20
40
60
80
100
Time (h)
0
20
40
60
80
100

FIGURE 6E

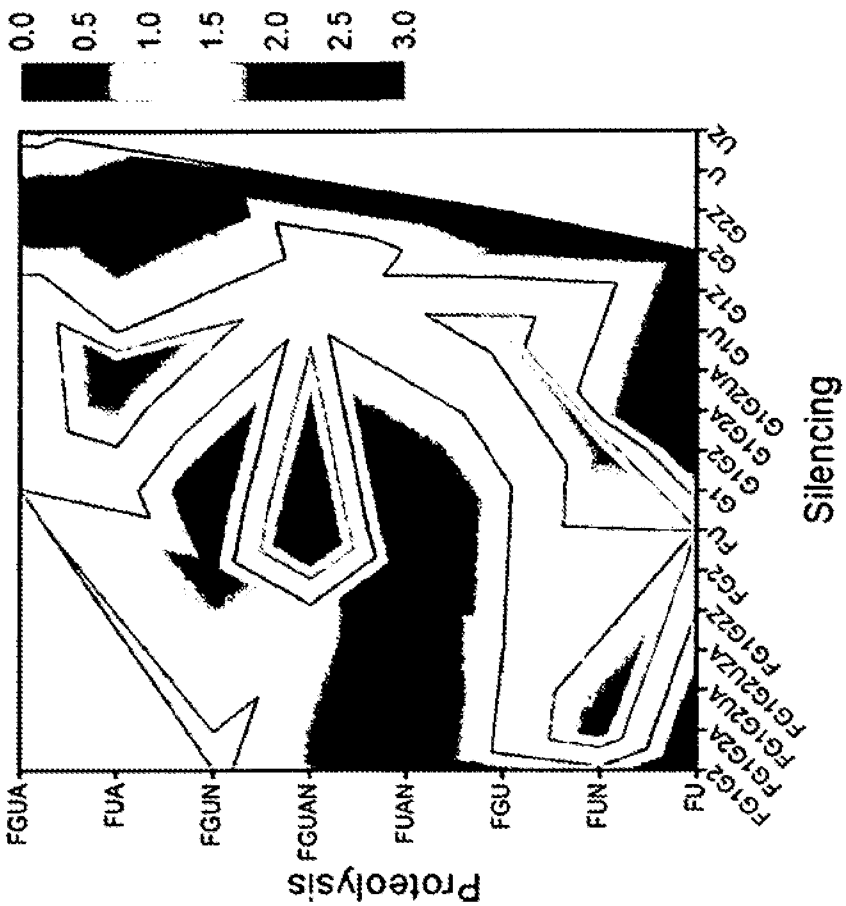

0.0
0.5
1.0
1.5
2.0
2.5
3.0
FGUA
FUA
FGUN
FGUAN
FUAN
FGU
FUN
FU
Proteolysis
Silencing

FIGURE 6F

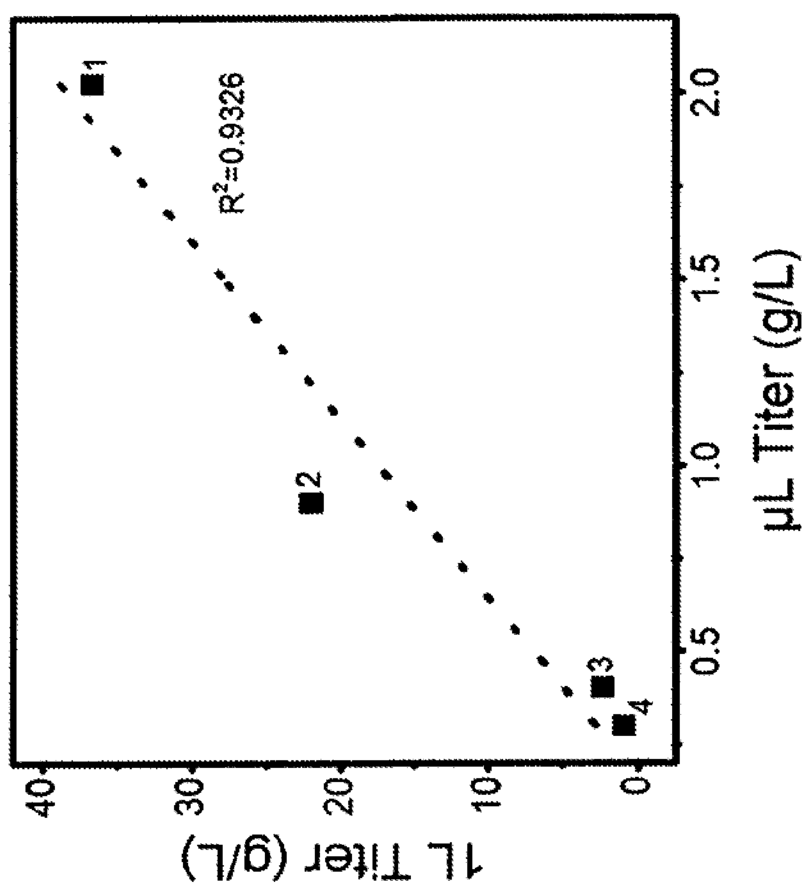


FIGURE 6G

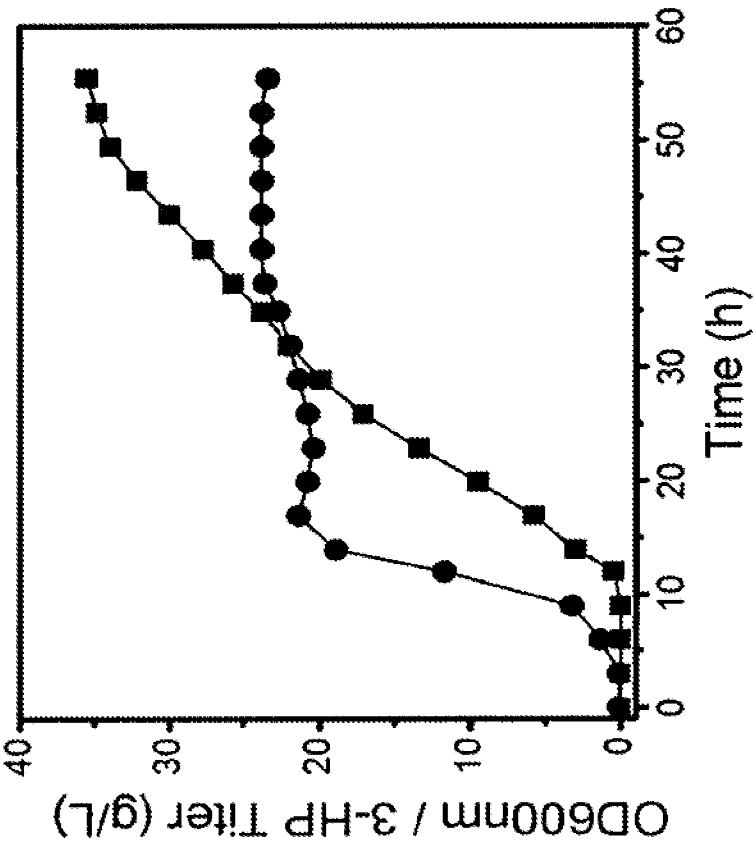


FIGURE 6H

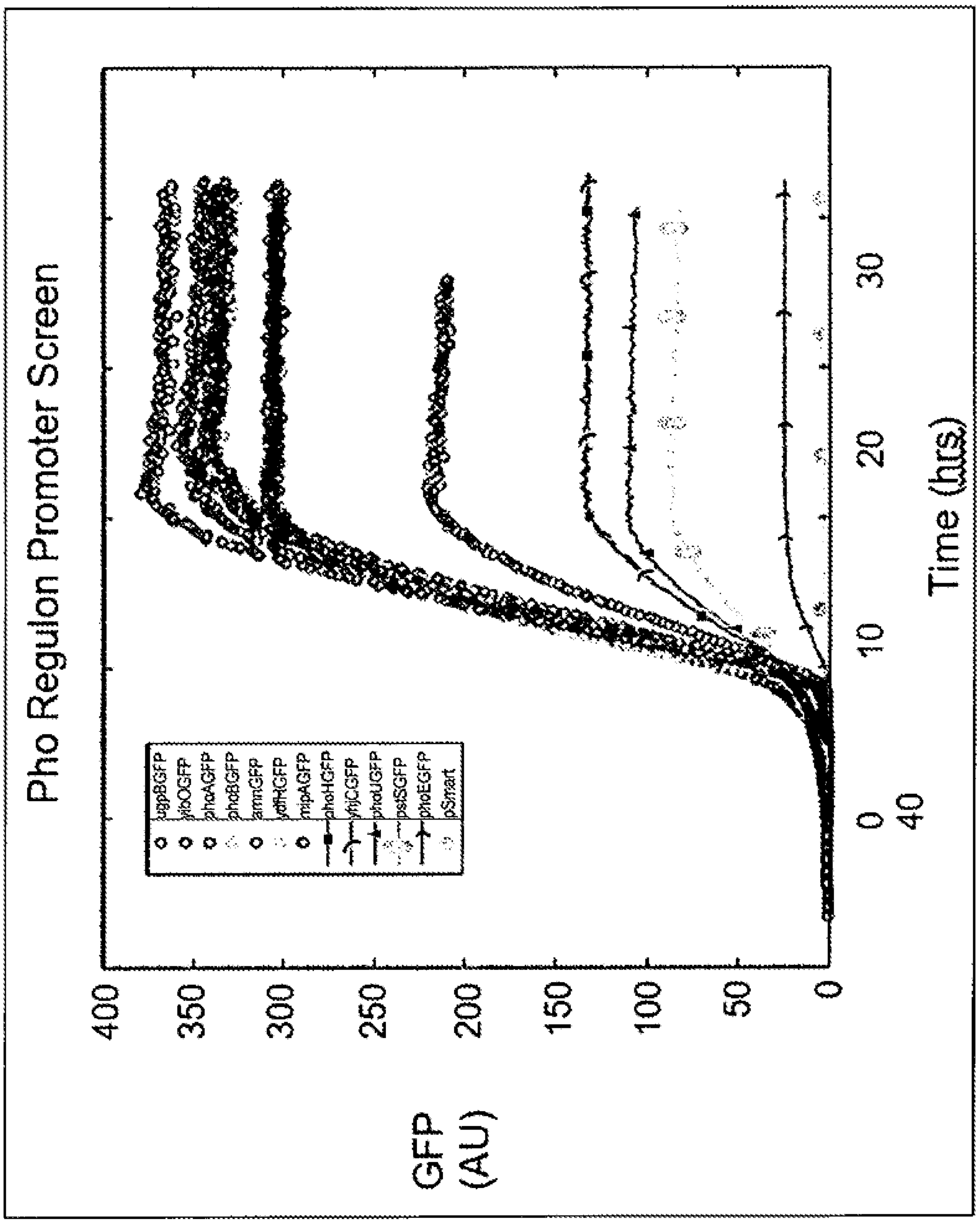

Pho Regulon Promoter Screen
GFP (AU)
400
350
300
250
200
150
100
50
0
0
10
20
30
40
Time (hrs)
ugpBGFP
yjbOGFP
phoAGFP
phoBGFP
amnGFP
ydfHGFP
mipAGFP
phoHGFP
yfijCGFP
phoUGFP
pstSGFP
phoEGFP
pSmart

FIGURE 7

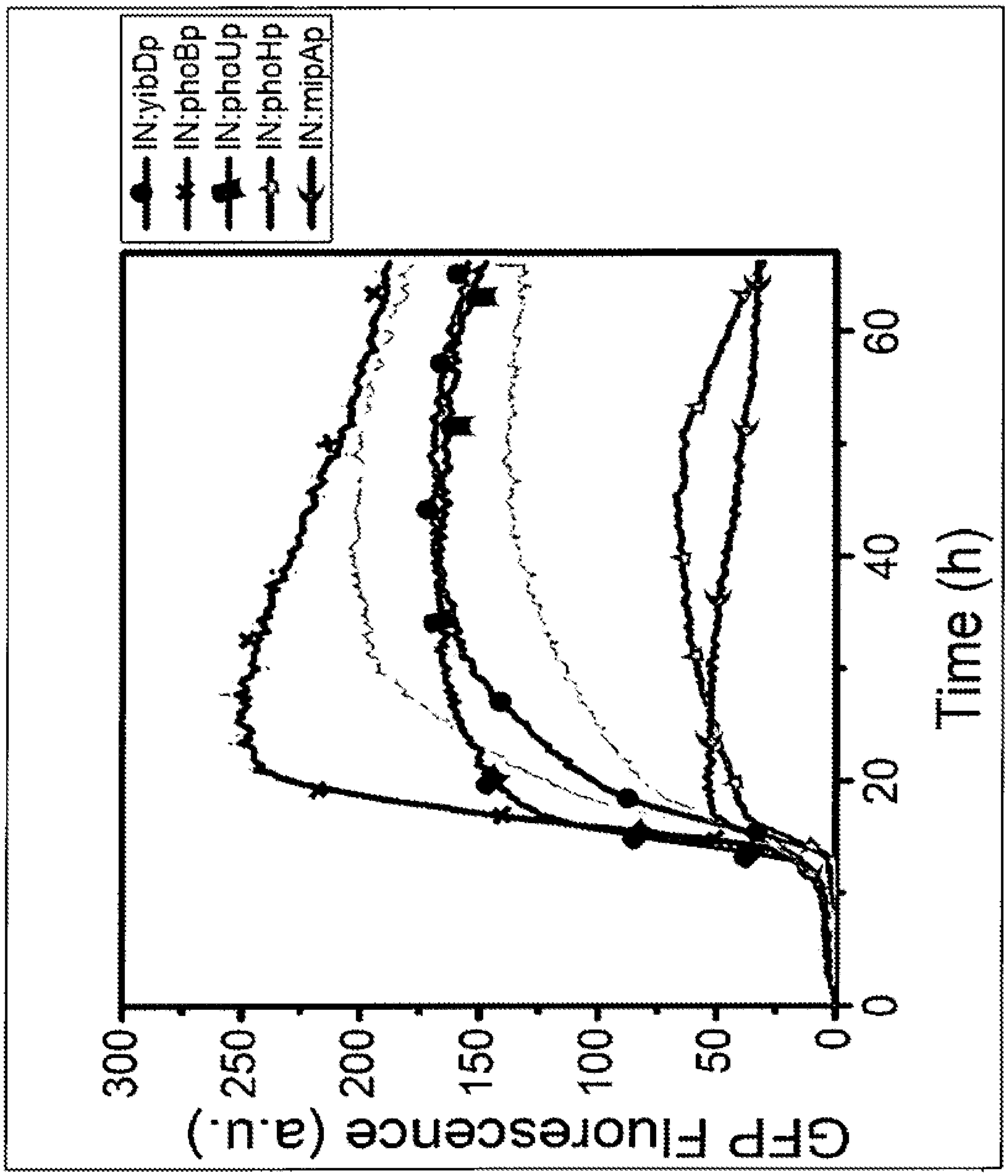

IN:yibDp
IN:phoBp
IN:phoUp
IN:phoHp
IN:mipAp
GFP Fluorescence (a.u.)
300
250
200
150
100
50
0
0
20
40
60
Time (h)

FIGURE 8

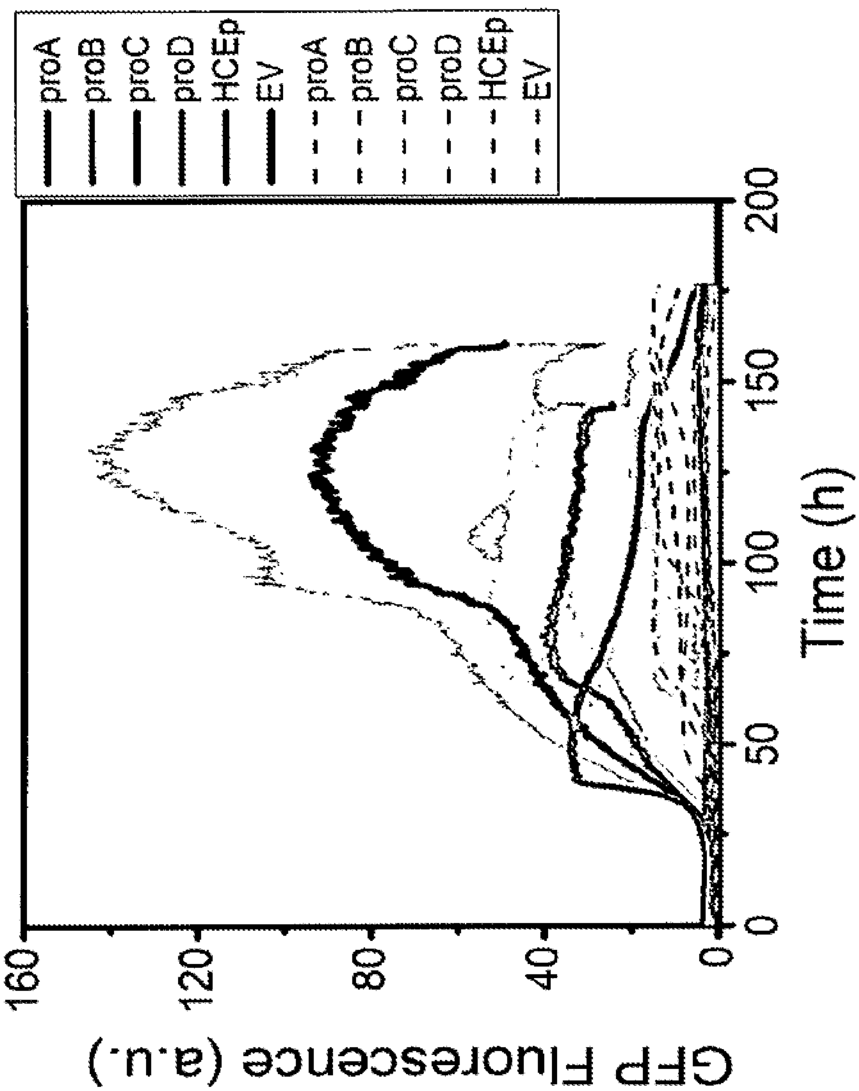

proA
proB
proC
proD
HCEp
EV
proA
proB
proC
proD
HCEp
EV
GFP Fluorescence (a.u.)
0
40
80
120
160
Time (h)
0
50
100
150
200

FIGURE 9

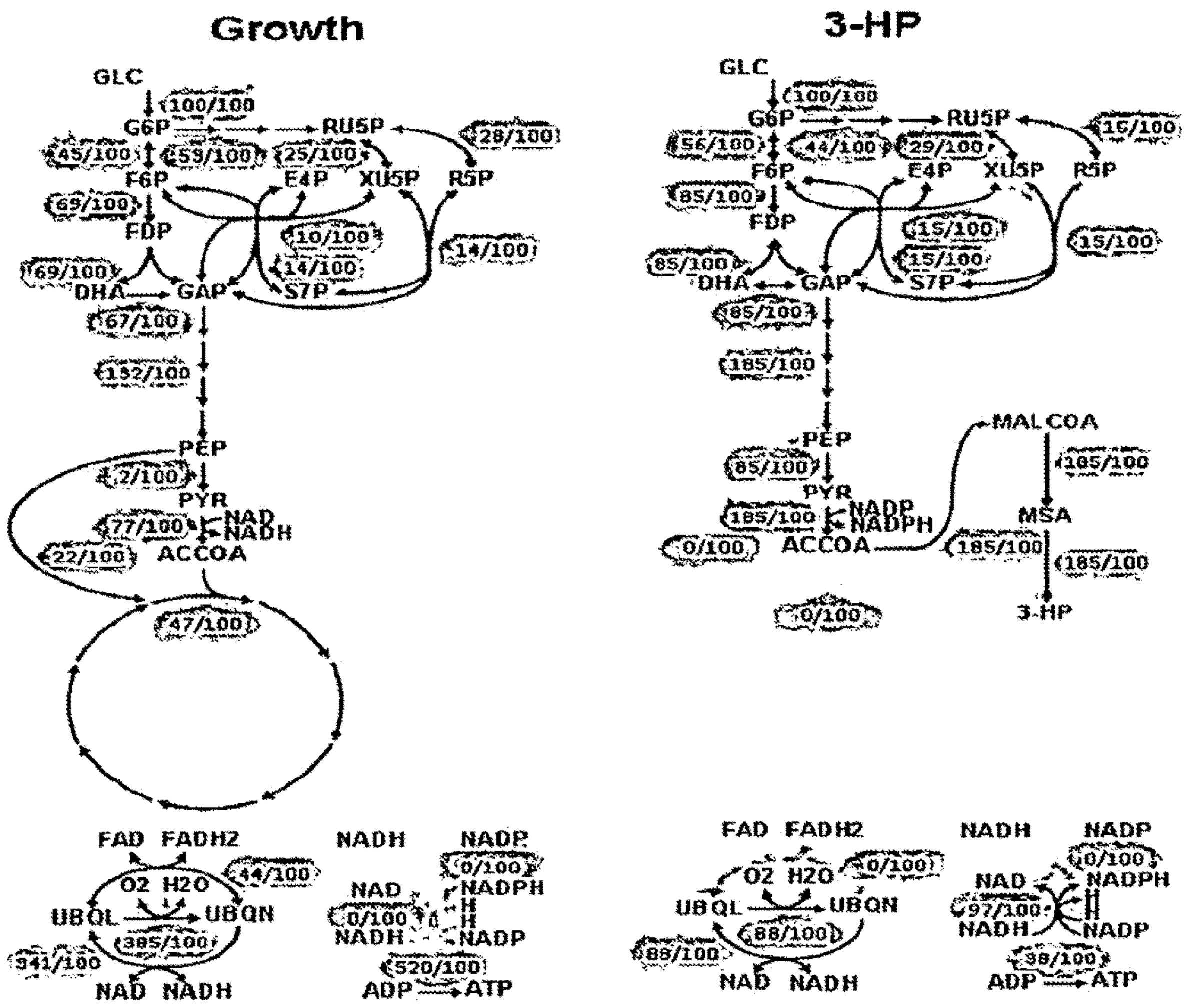

Growth
GLC
100/100
G6P
RU5P
28/100
45/100
59/100
25/100
F6P
E4P
XU5P
R5P
69/100
FDP
10/100
14/100
14/100
69/100
DHA
GAP
S7P
67/100
152/100
PEP
2/100
PYR
NAD
NADH
77/100
22/100
ACCOA
47/100
FAD
FADH2
NADH
NADP
44/100
0/100
O2
H2O
NAD
NADPH
UBQL
UBQN
0/100
NADH
NADP
385/100
341/100
520/100
NAD
NADH
ADP
ATP
3-HP
GLC
100/100
G6P
RU5P
16/100
56/100
44/100
29/100
F6P
E4P
XU5P
R5P
85/100
FDP
15/100
15/100
15/100
85/100
DHA
GAP
S7P
85/100
185/100
MALCOA
PEP
185/100
85/100
PYR
185/100
NADP
NADPH
MSA
0/100
ACCOA
185/100
185/100
3-HP
0/100
FAD
FADH2
NADH
NADP
0/100
0/100
O2
H2O
NAD
NADPH
UBQL
UBQN
97/100
88/100
NADH
NADP
88/100
38/100
NAD
NADH
ADP
ATP

FIGURE 10

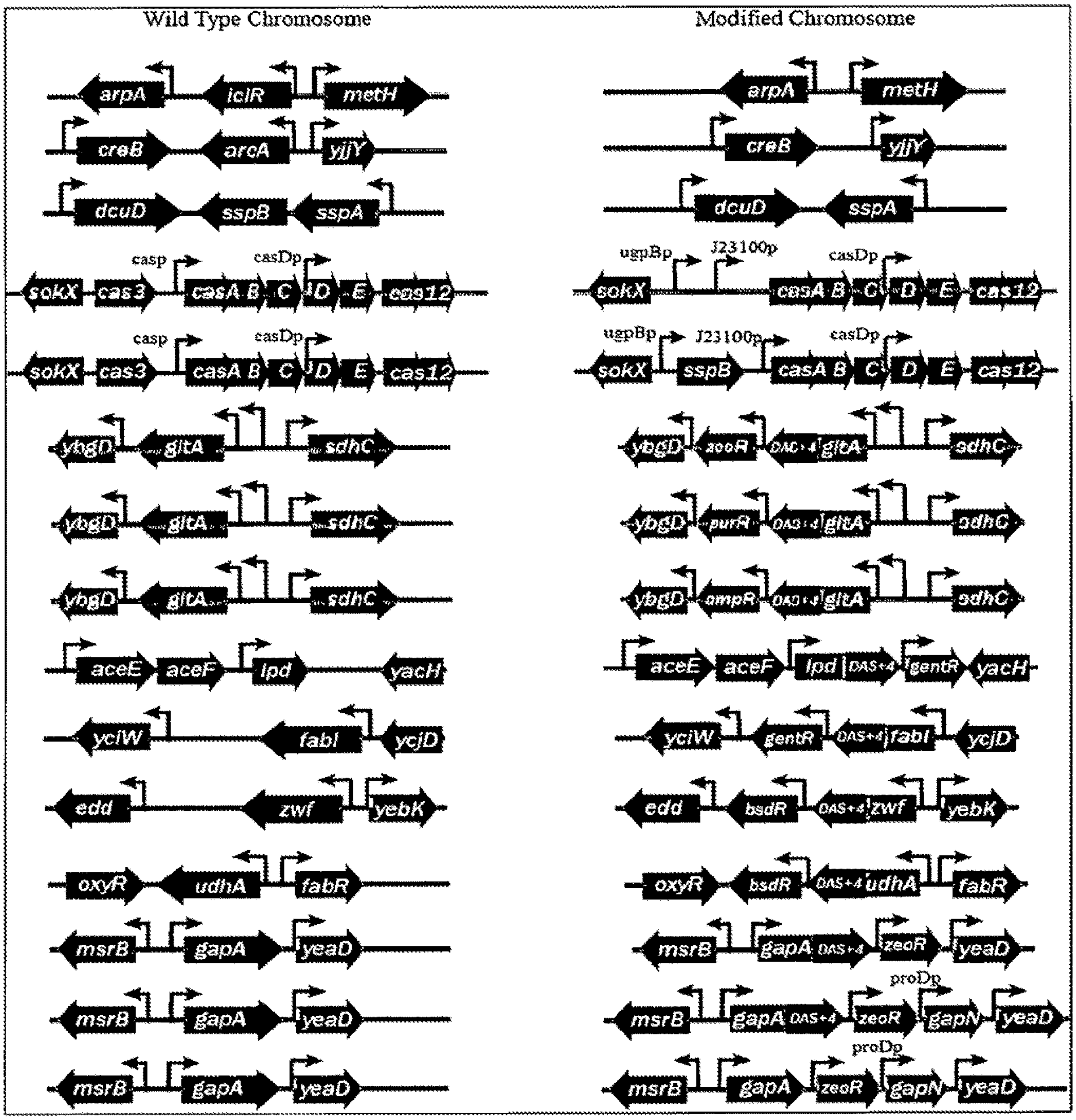

Wild Type Chromosome
Modified Chromosome
arpA
iclR
metH
creB
arcA
yjjY
dcuD
sspB
sspA
casp
casDp
ugpBp
J23100p
sokX
cas3
casA
B
C
D
E
cas12
ybgD
gltA
sdhC
zeoR
purR
ampR
aceE
aceF
lpd
yacH
gentR
yciW
fabI
ycjD
edd
zwf
yebK
bsdR
oxyR
udhA
fabR
msrB
gapA
yeaD
proDp
gapN

FIGURE 11

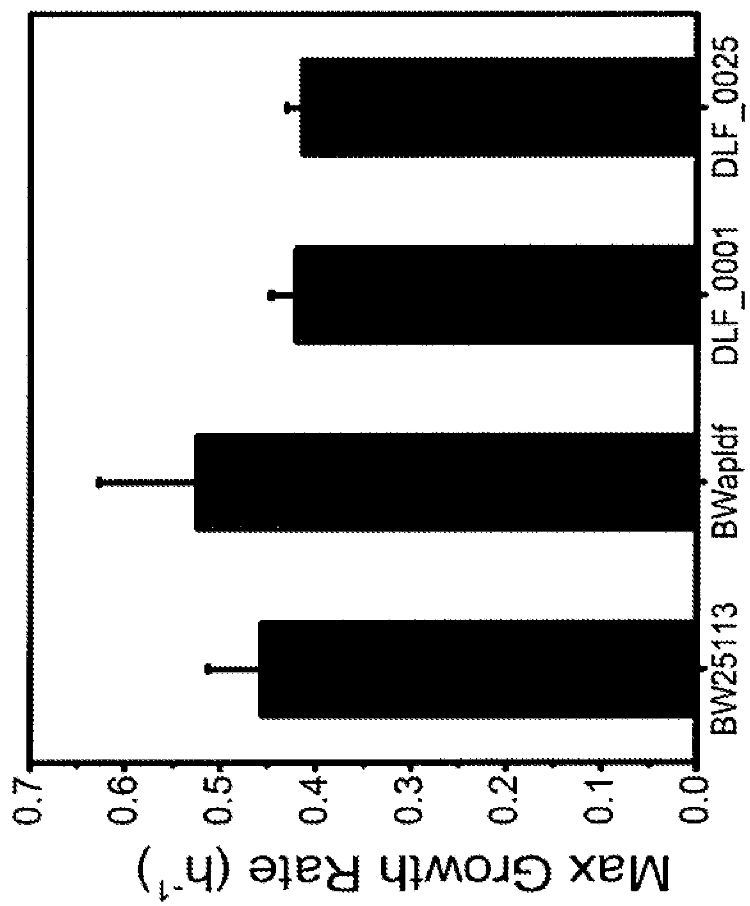

Max Growth Rate (h-1)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
BW25113
BWapldf
DLF_0001
DLF_0025

FIGURE 12

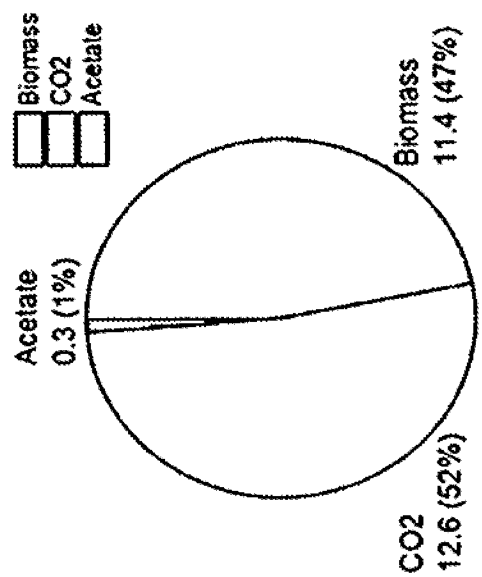


FIGURE 13B

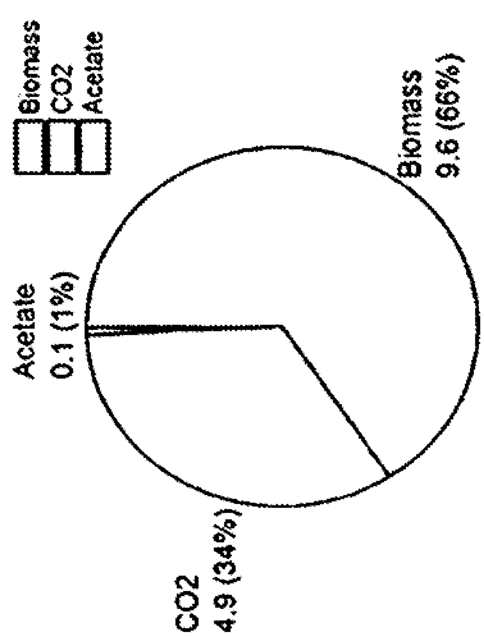


FIGURE 13A

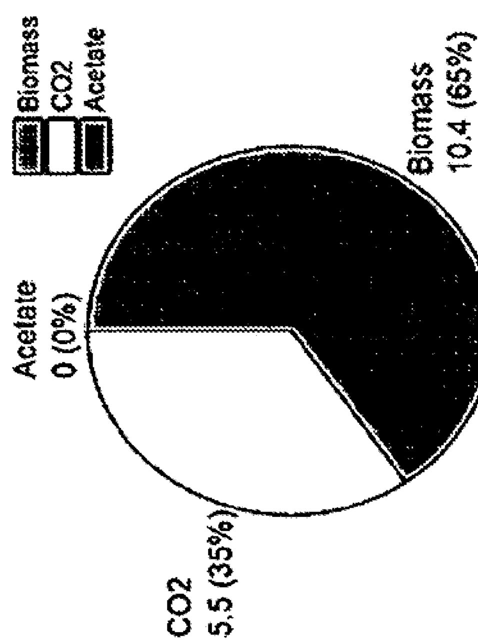


FIGURE 13C

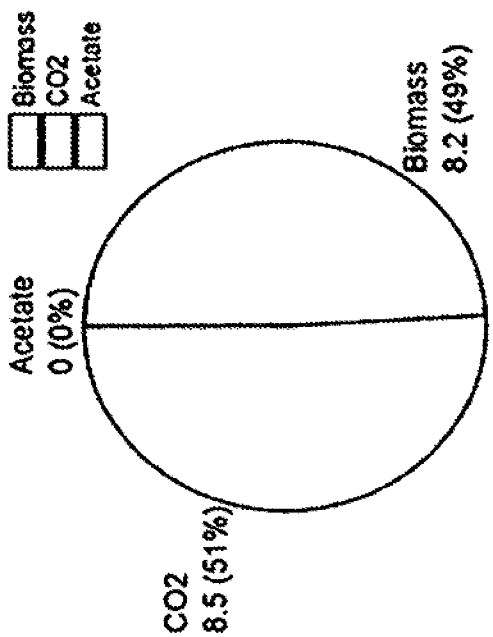


FIGURE 13D

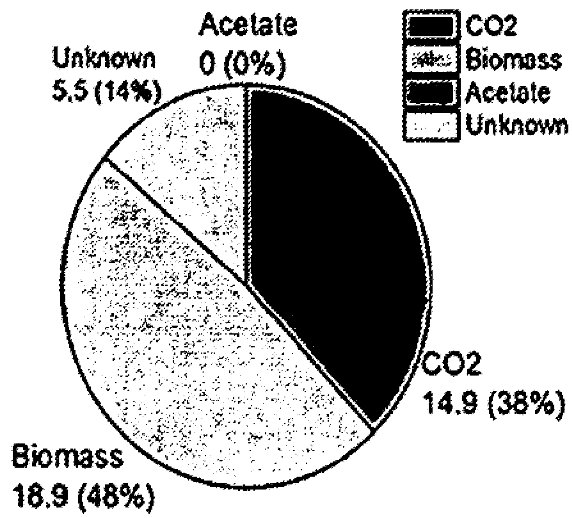

CO2
Biomass
Acetate
Unknown
Acetate
0 (0%)
Unknown
5.5 (14%)
CO2
14.9 (38%)
Biomass
18.9 (48%)

FIGURE 13E

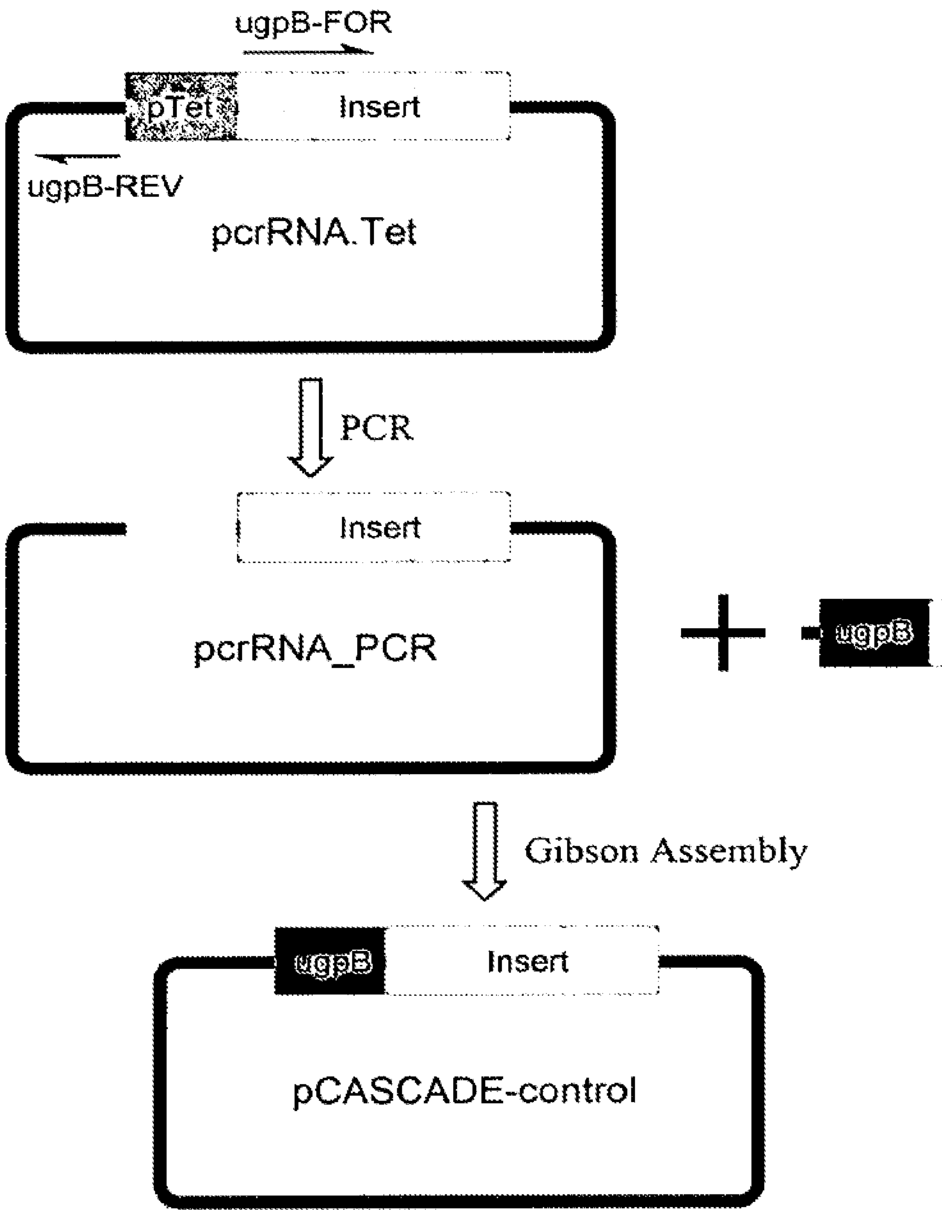

ugpB-FOR
pTet
Insert
ugpB-REV
pcrRNA.Tet
PCR
Insert
pcrRNA_PCR
ugpB
Gibson Assembly
ugpB
Insert
pCASCADE-control

FIGURE 14

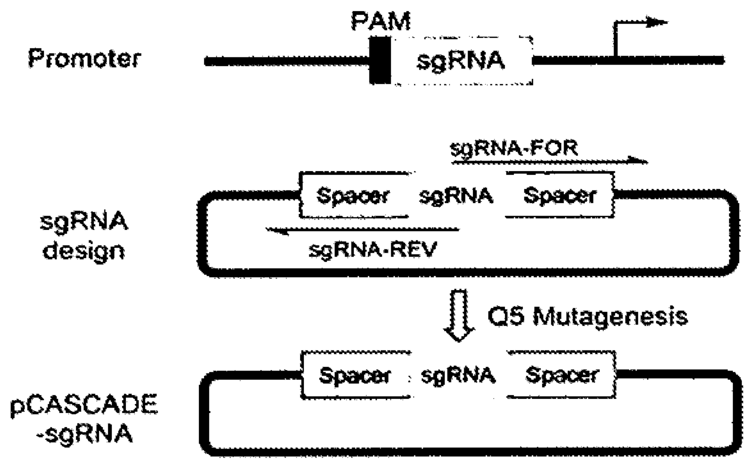


FIGURE 15A

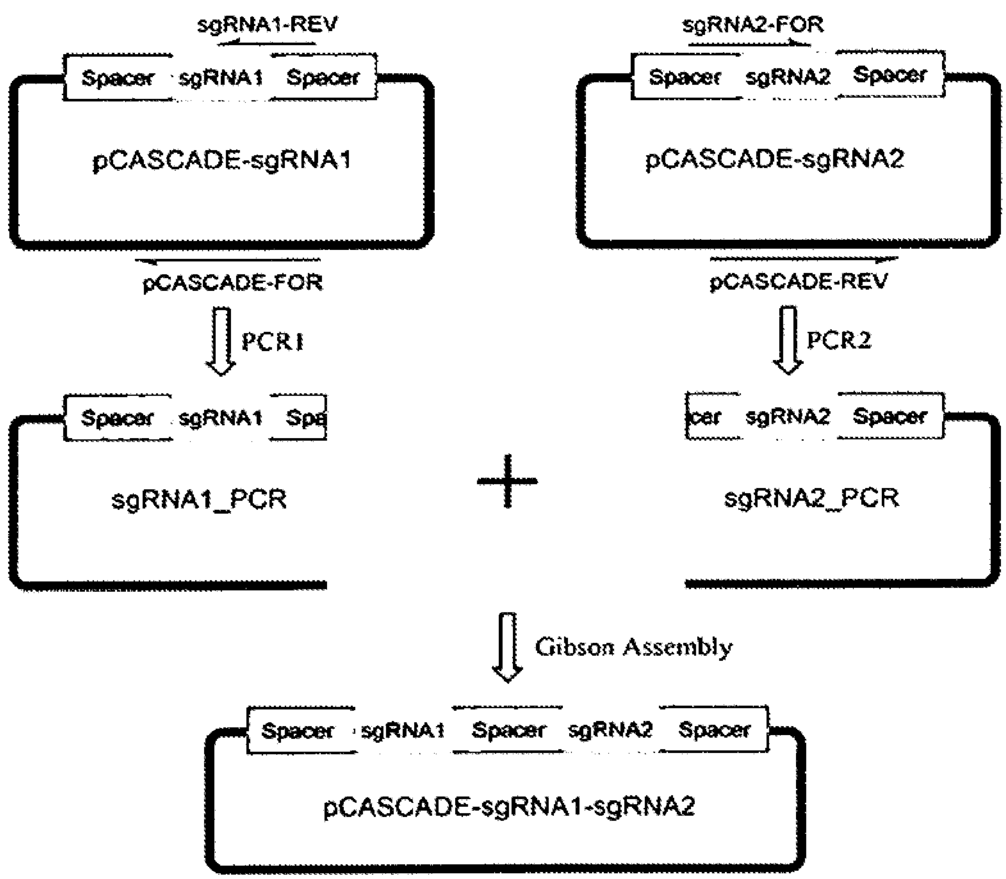


FIGURE 15B

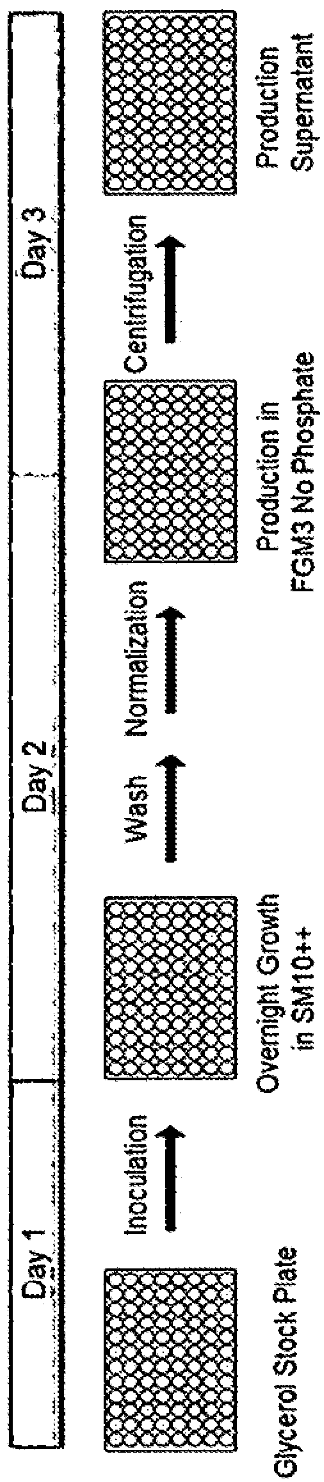

Day 1
Day 2
Day 3
Glycerol Stock Plate
Inoculation
Overnight Growth in SM10++
Wash
Normalization
Production in FGM3 No Phosphate
Centrifugation
Production Supernatant

FIGURE 16A

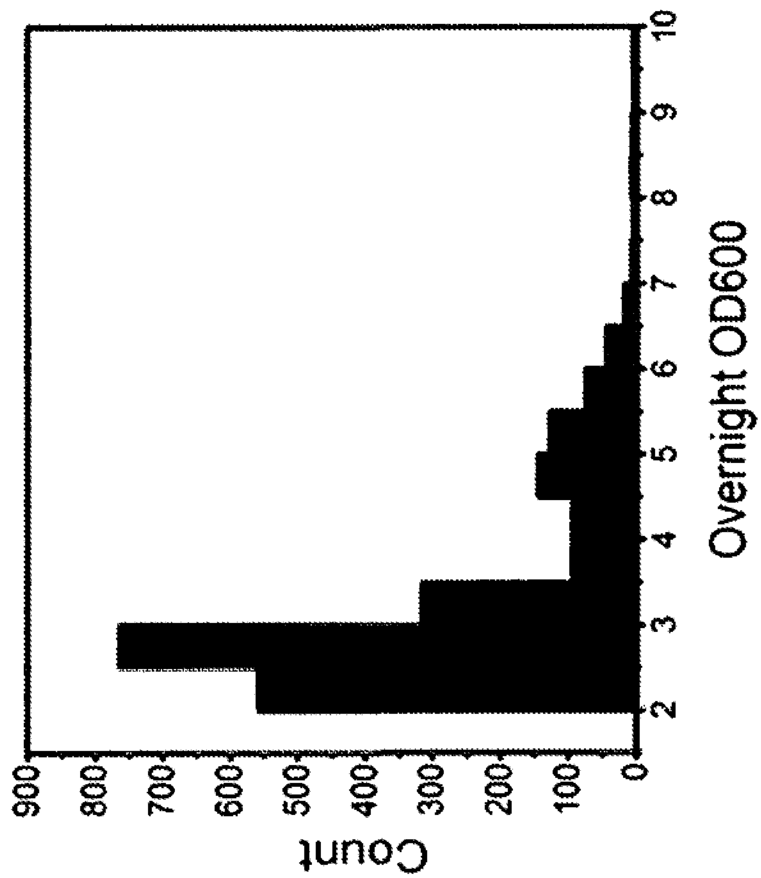

Count
0
100
200
300
400
500
600
700
800
900
2
3
4
5
6
7
8
9
10
Overnight OD600

FIGURE 16B

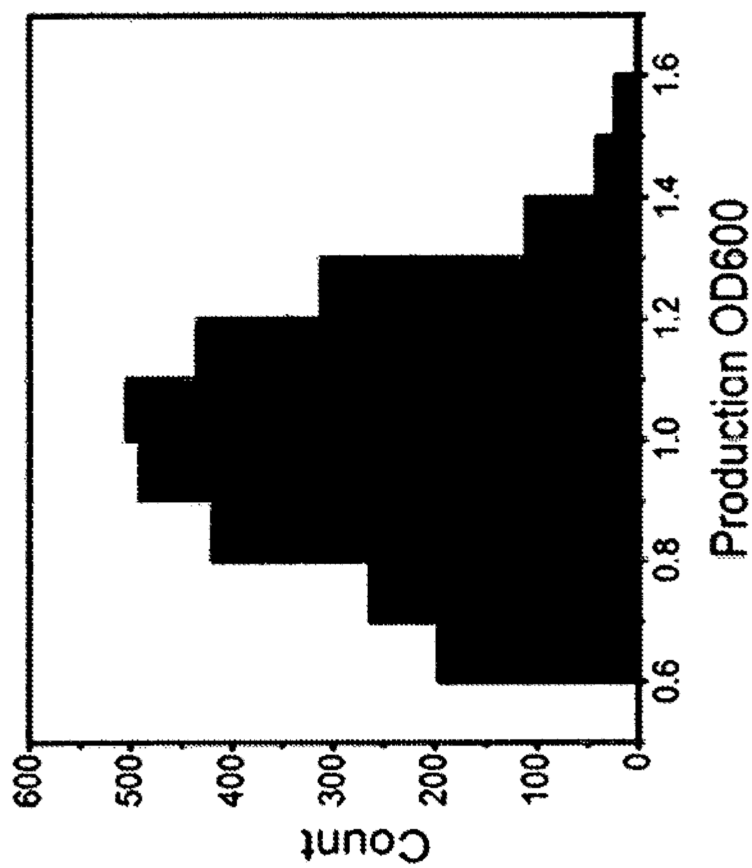

Count
600
500
400
300
200
100
0
Production OD600
0.6
0.8
1.0
1.2
1.4
1.6

FIGURE 16C

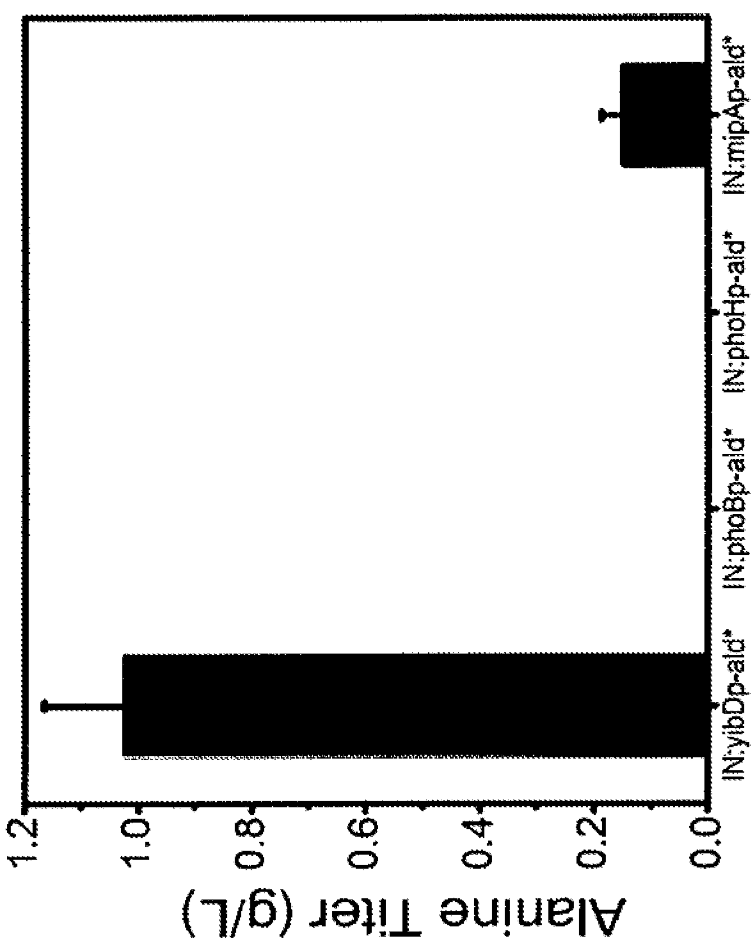

Alanine Titer (g/L)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
IN:yibDp-ald*
IN:phoBp-ald*
IN:phoHp-ald*
IN:mipAp-ald*

FIGURE 17

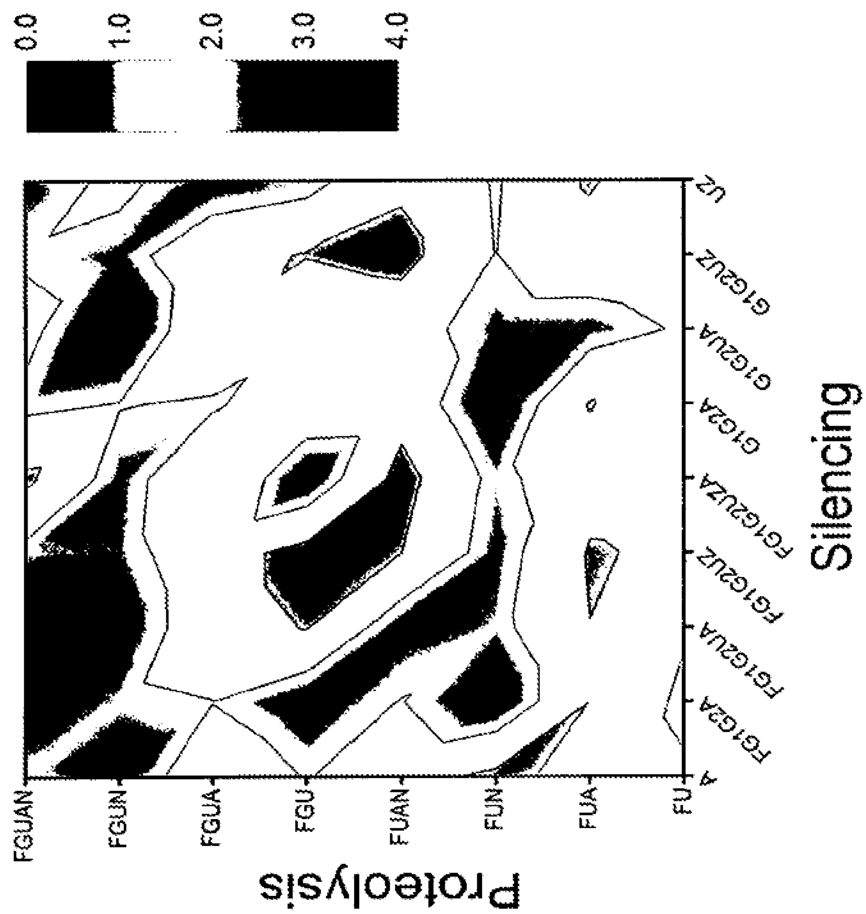

0.0
1.0
2.0
3.0
4.0
Proteolysis
FGUAN
FGUN
FGUA
FGU
FUAN
FUN
FUA
FU
Silencing
A
FG1G2A
FG1G2UA
FG1G2UZ
FG1G2UZA
G1G2A
G1G2UA
G1G2UZ
UZ

FIGURE 18

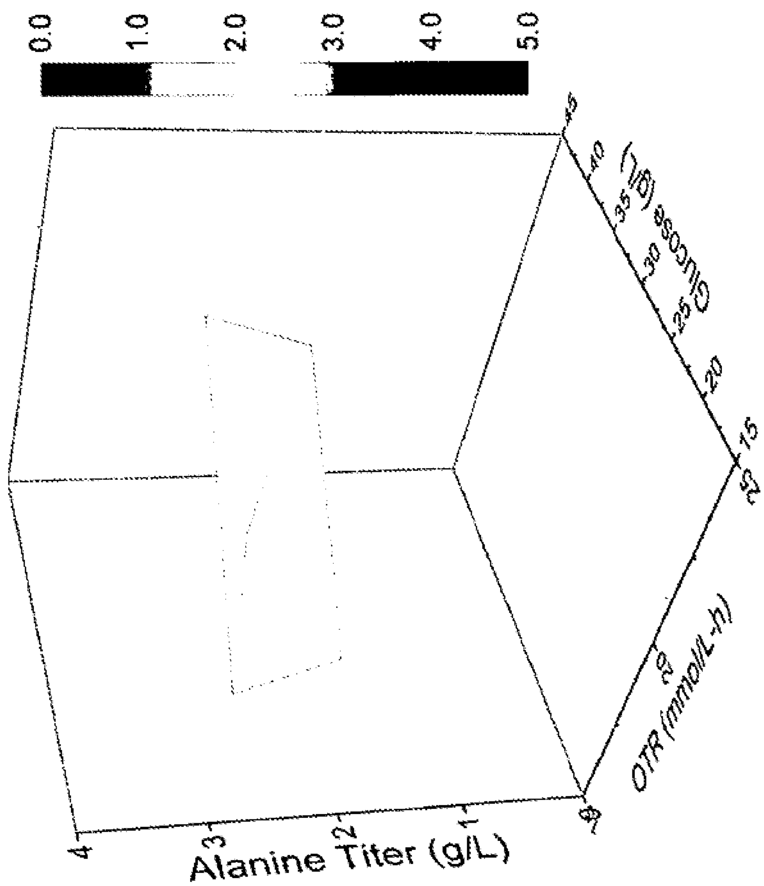


FIGURE 19A

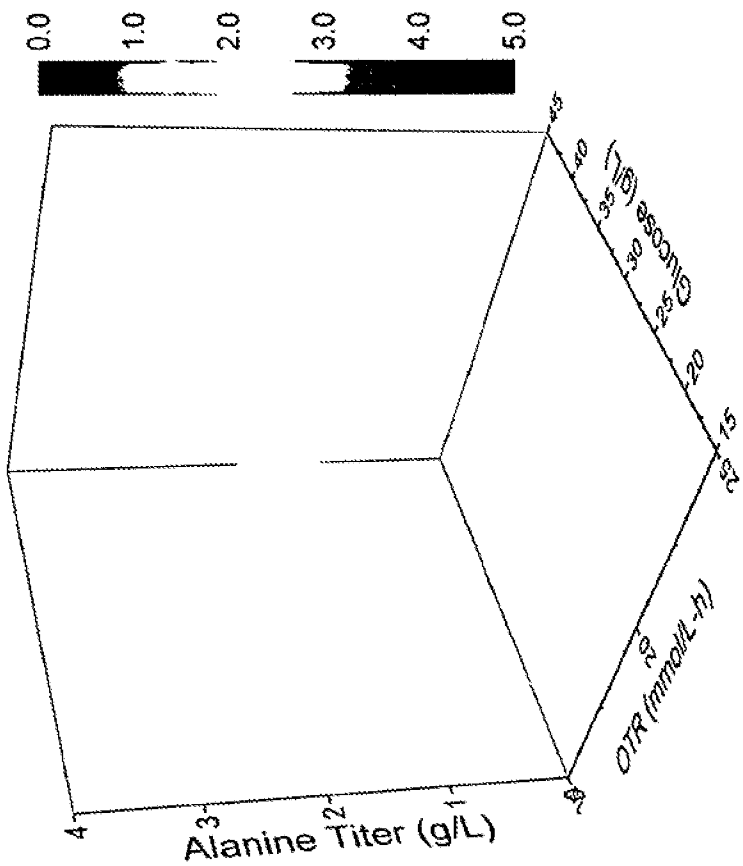

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
Alanine Titer (g/L)
4
3
2
1

FIGURE 19B

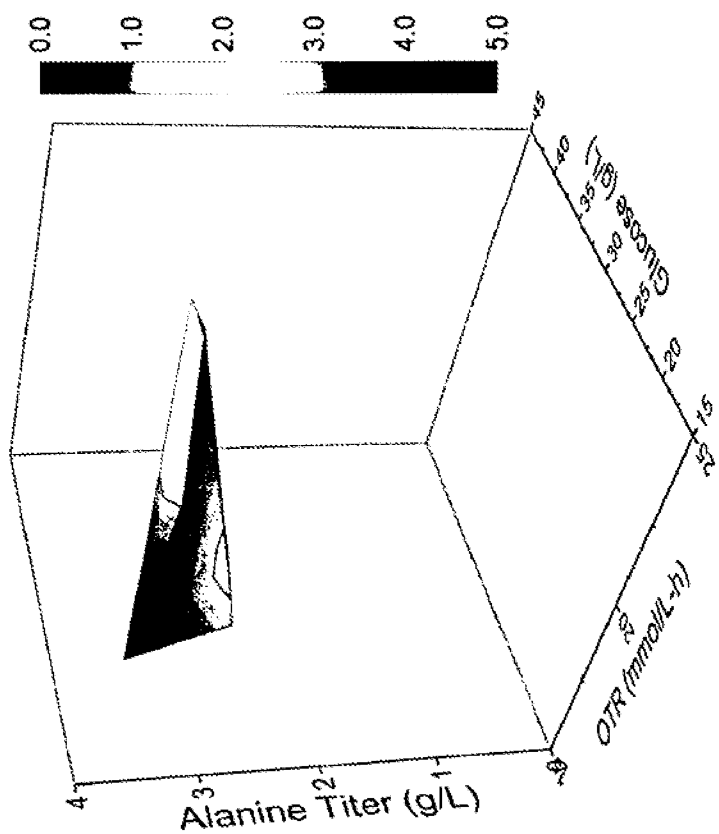

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
OTR (mmol/L-h)
Glucose (g/L)
15
20
25
30
35
40
45

FIGURE 19C

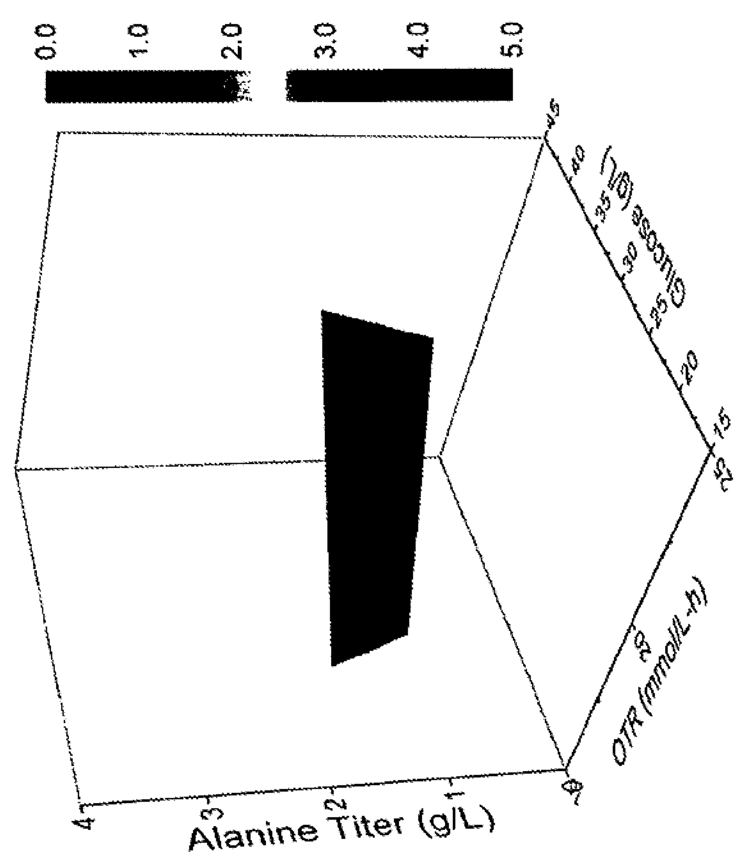


FIGURE 19D

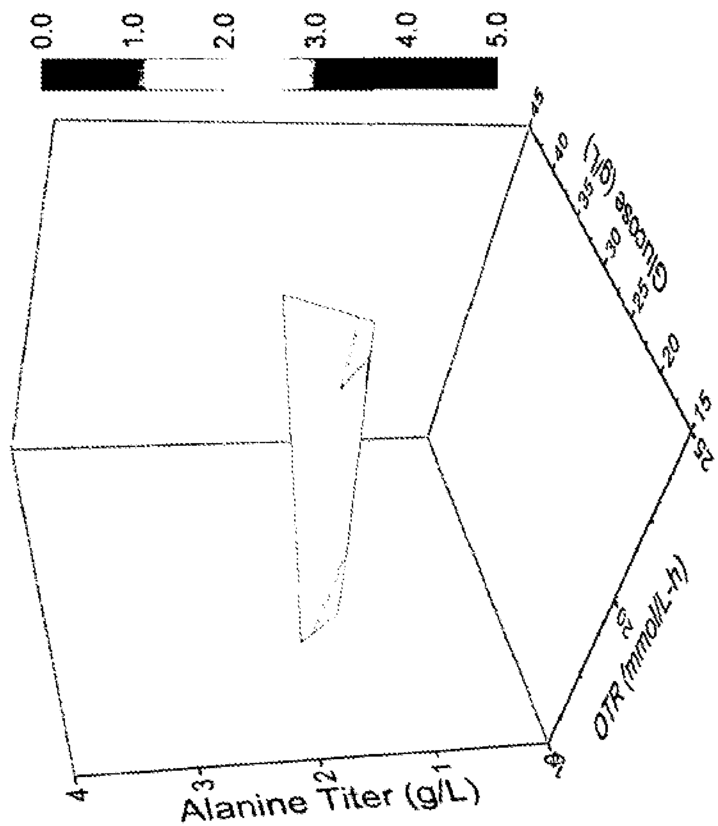

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
4
3
2
1

FIGURE 20A

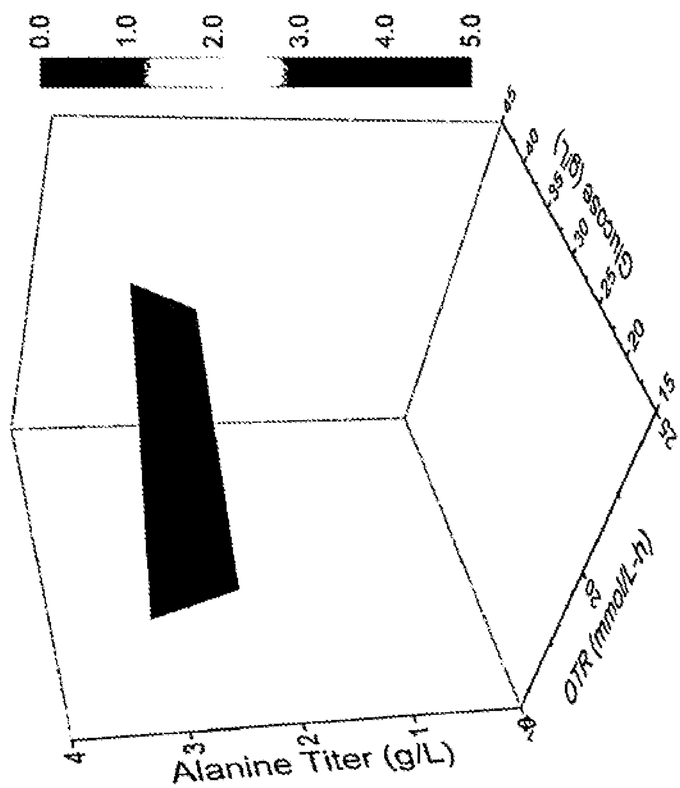

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
OTR (mmol/L-h)
Glucose (g/L)
15
20
25
30
35
40
45

FIGURE 20B

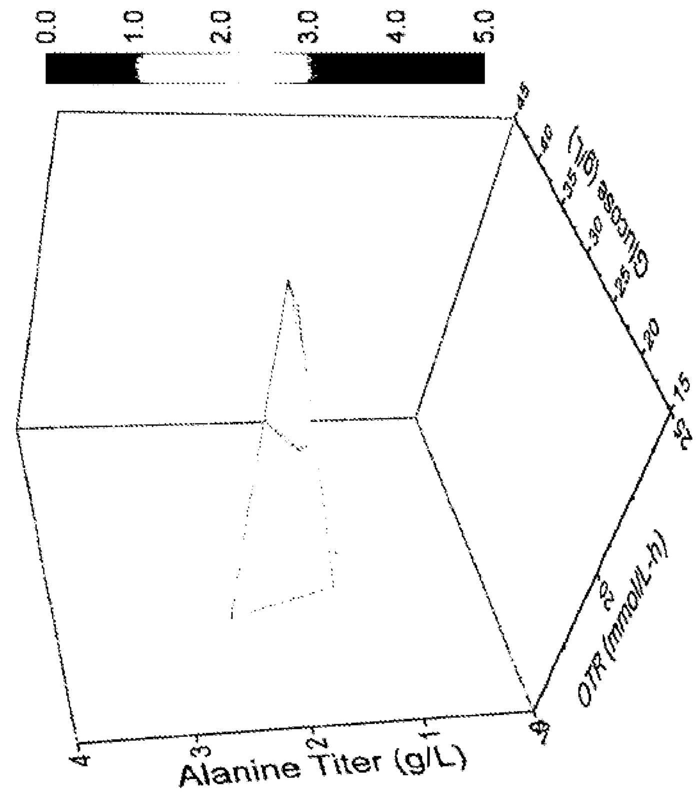

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
20
Alanine Titer (g/L)
4
3
2
1

FIGURE 20C

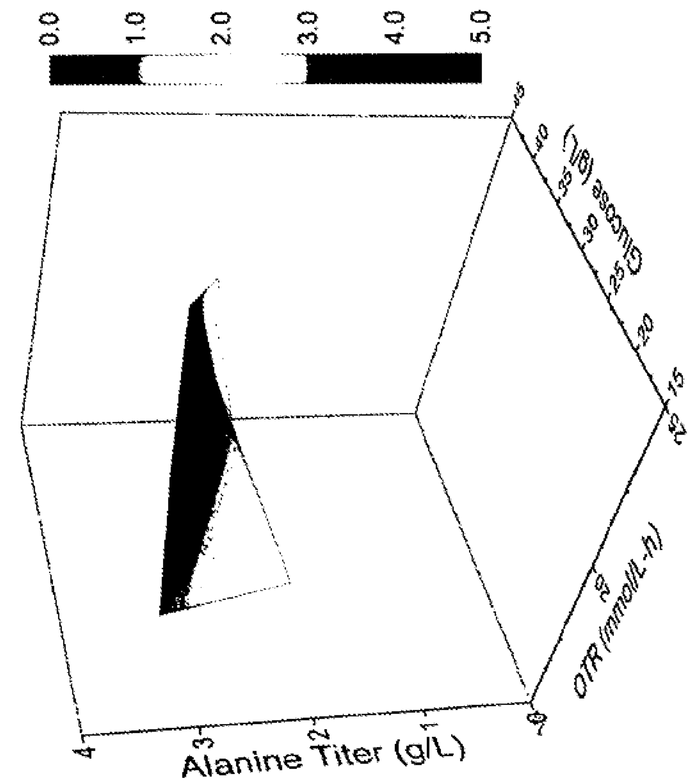

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
OTR (mmol/L.h)
Alanine Titer (g/L)
4
3
2
1
20
25
30
35
40

FIGURE 20D

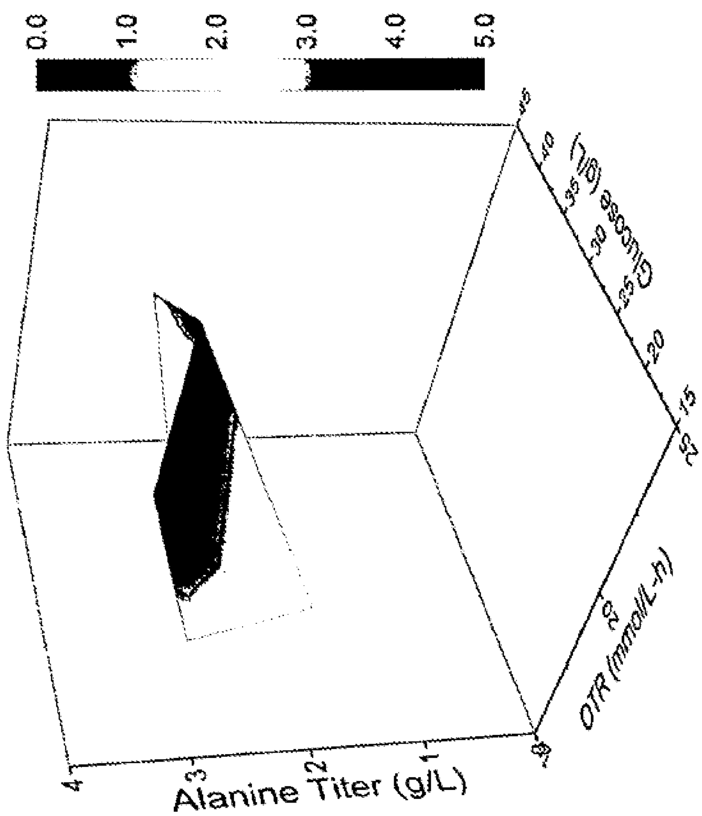


FIGURE 21A

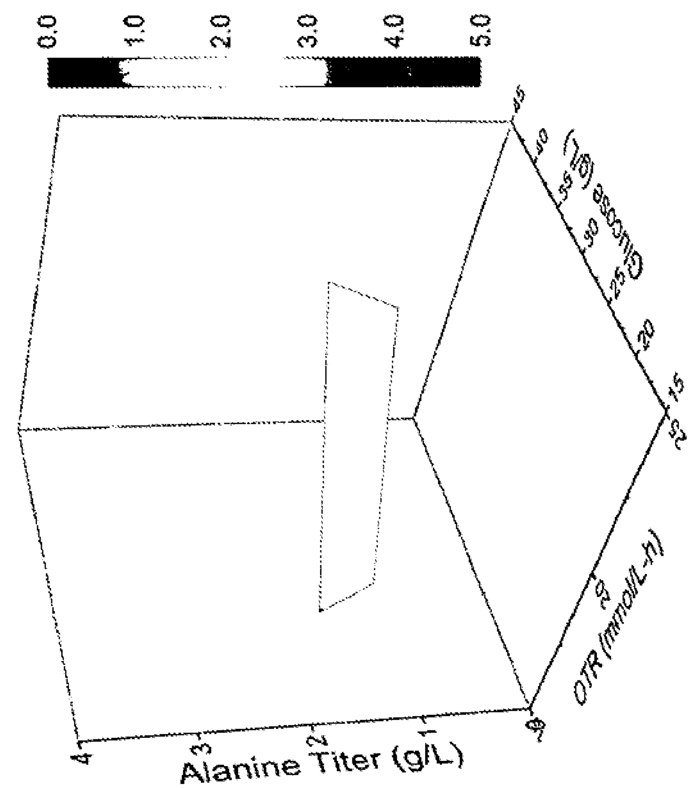


FIGURE 21B

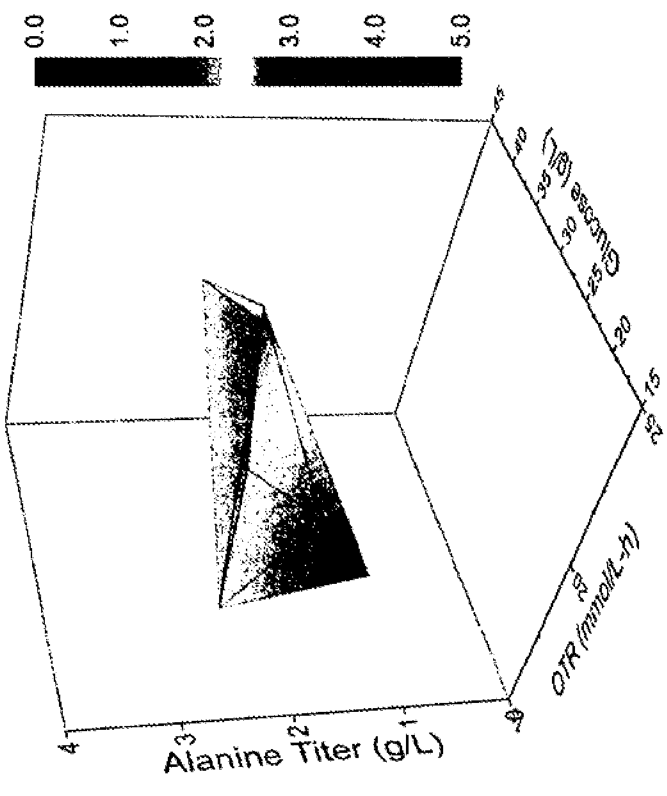


FIGURE 21C

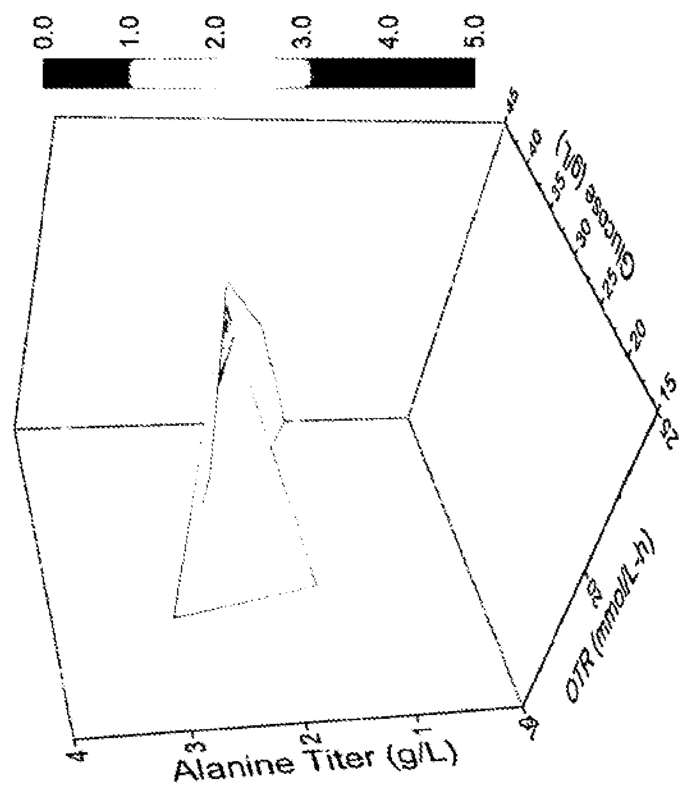


FIGURE 21D

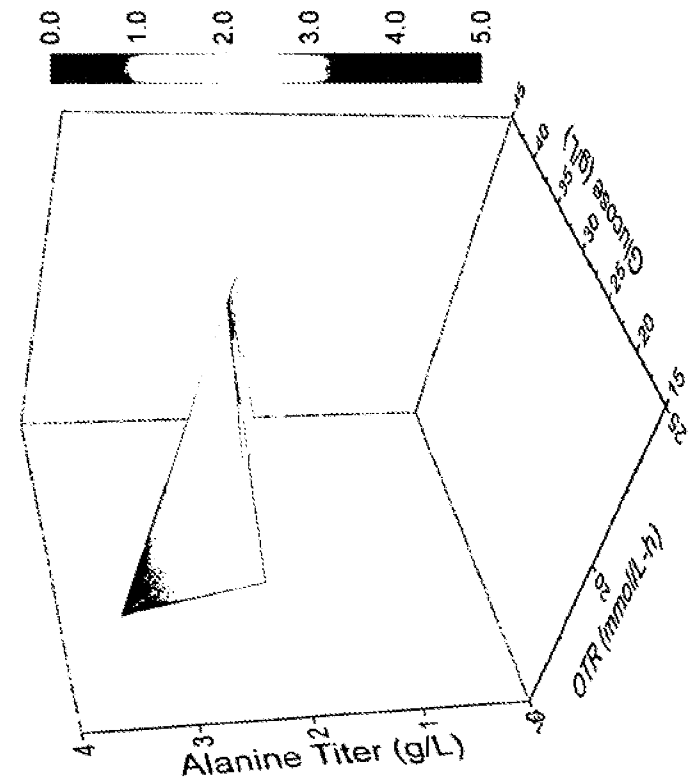


FIGURE 22A

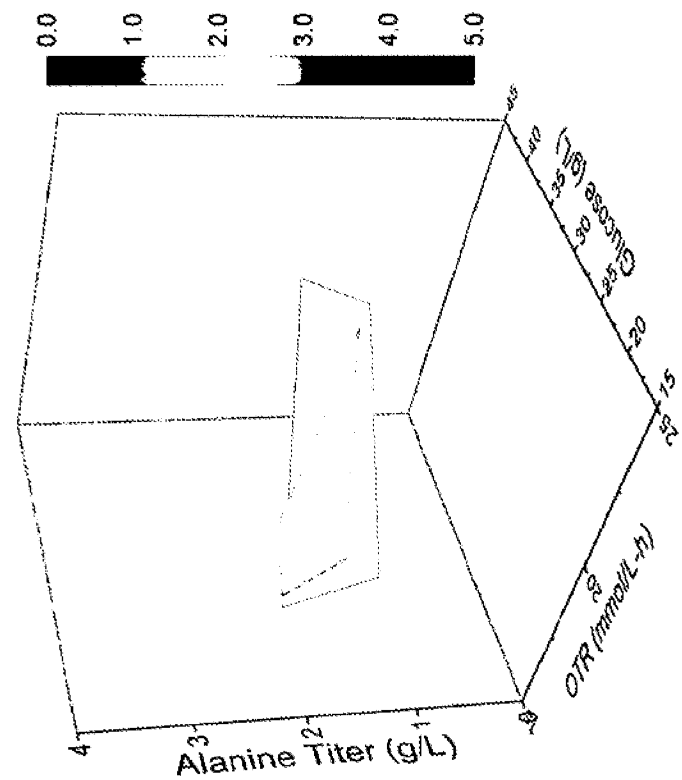


FIGURE 22B

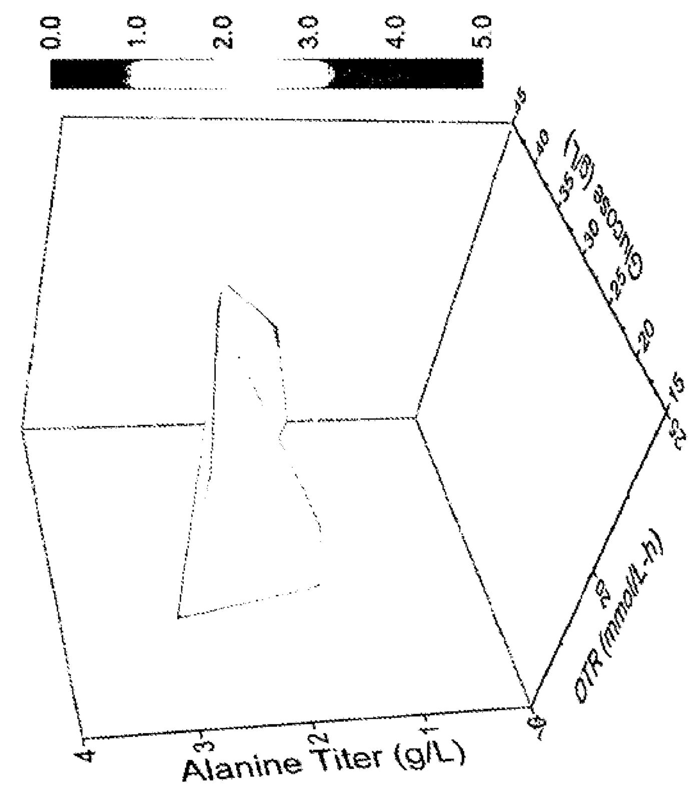

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
0
1
2
3
4

FIGURE 22C

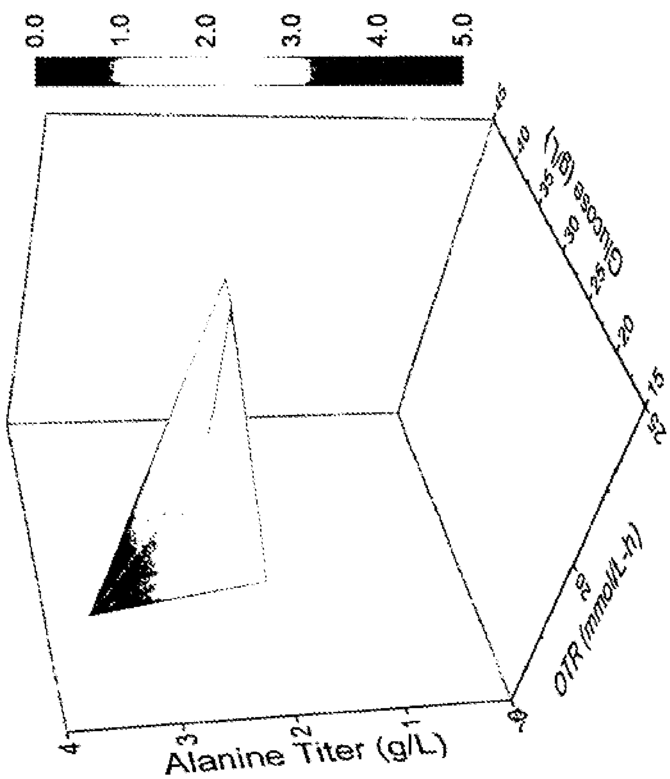

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)

FIGURE 22D

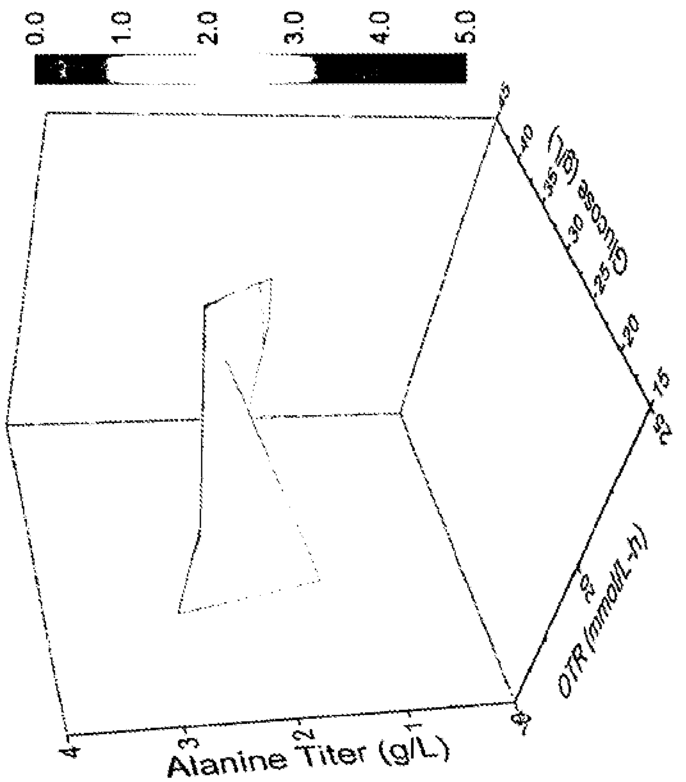

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
OTR (mmol/L-h)
20
Alanine Titer (g/L)
4
3
2
1

FIGURE 23A

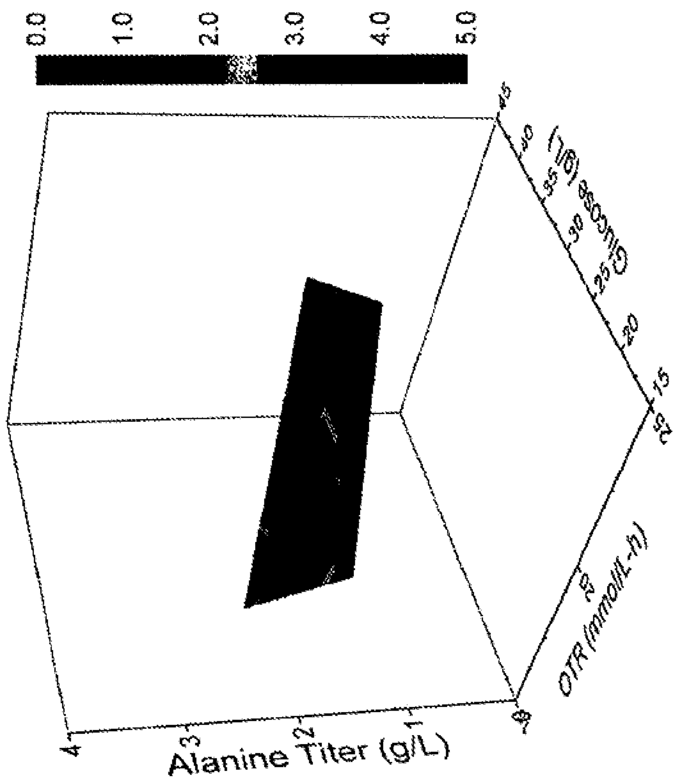


FIGURE 23B

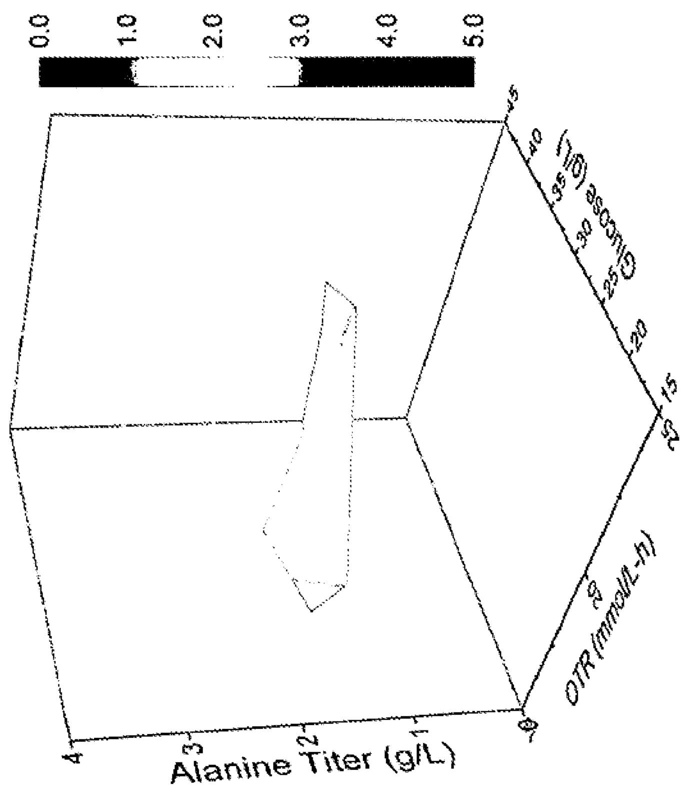


FIGURE 23C

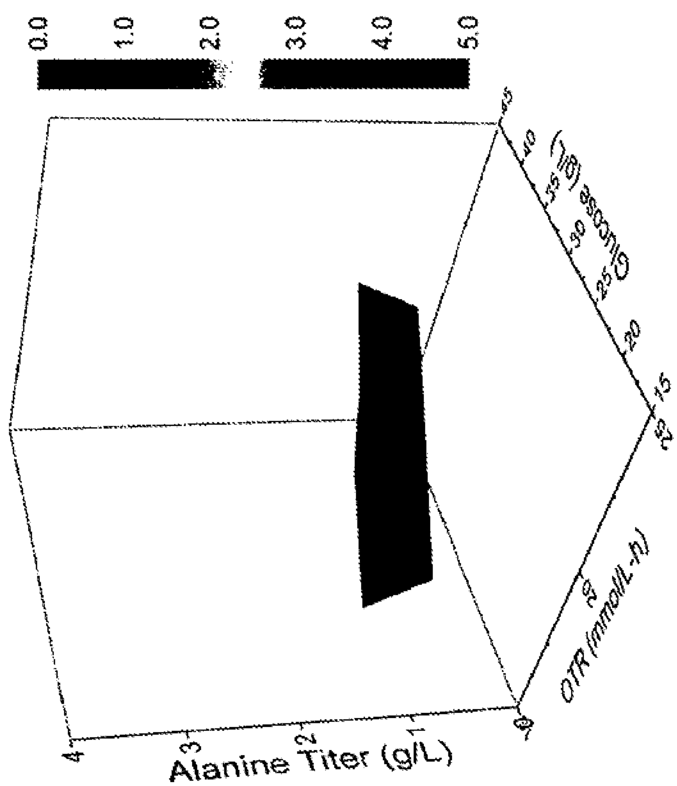


FIGURE 23D

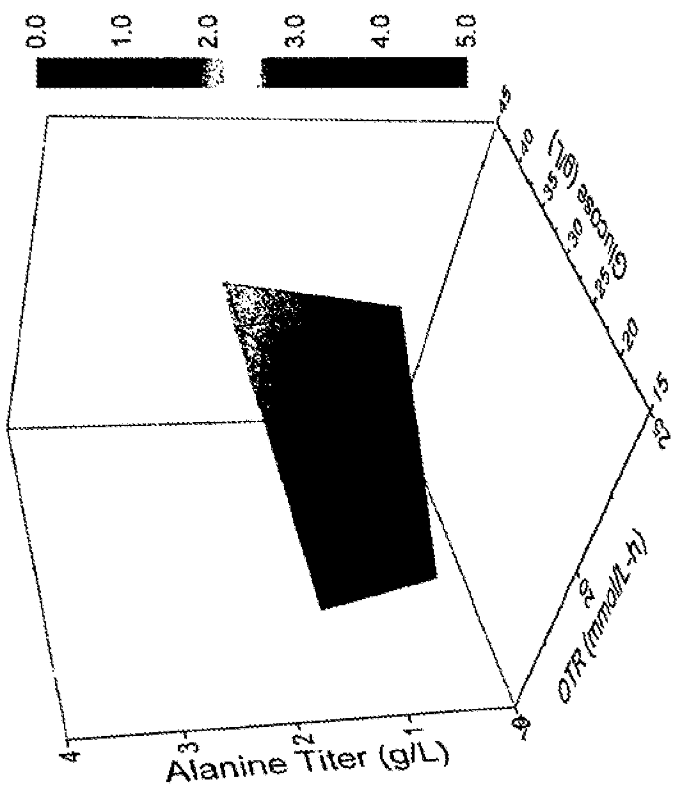


FIGURE 24A

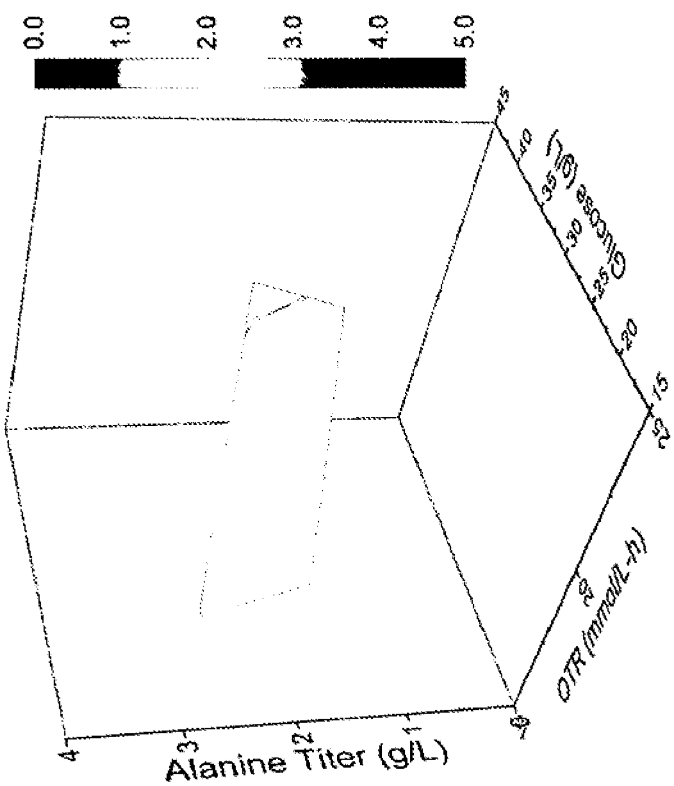


FIGURE 24B

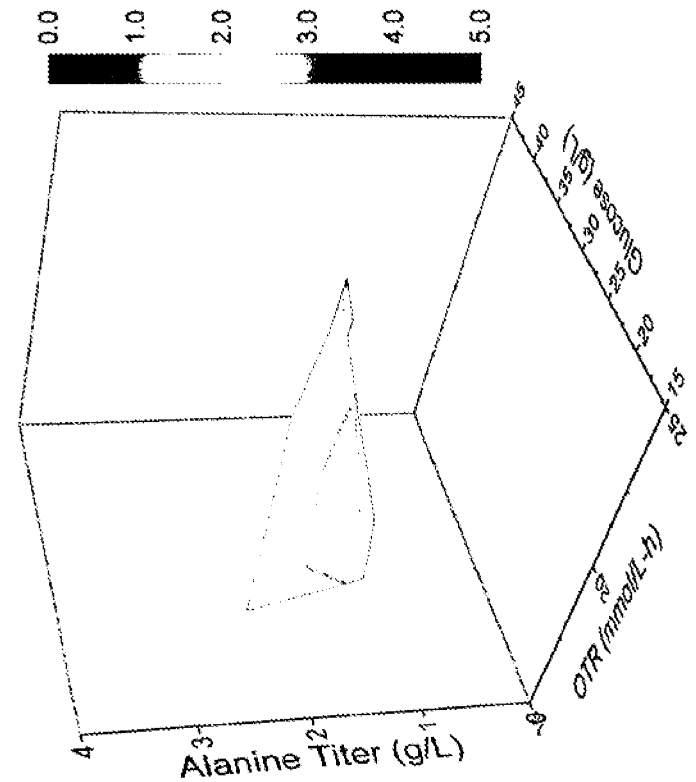

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)

FIGURE 24C

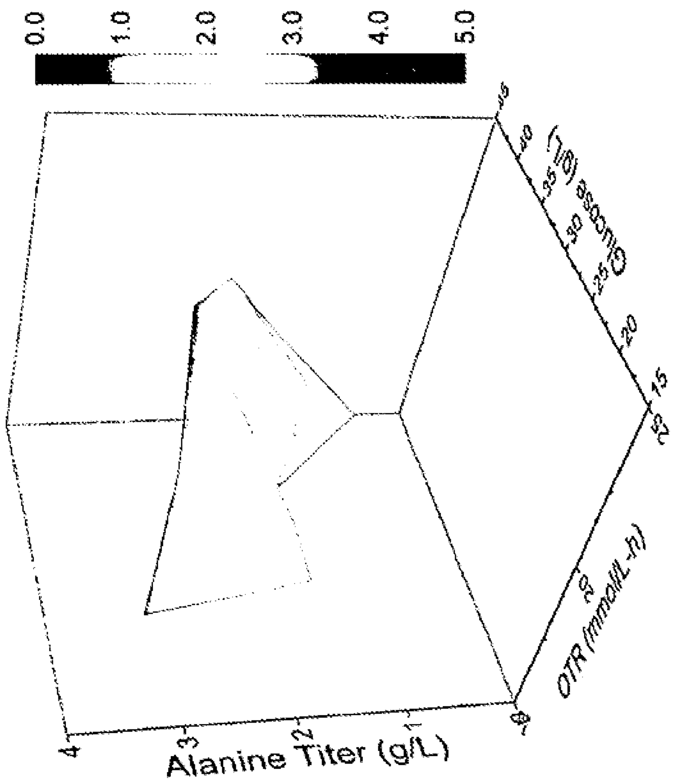

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
OTR (mmol/L-h)
Glucose (g/L)
4
3
2
1
0
20
25
15
20
25
30
35
40
45

FIGURE 24D

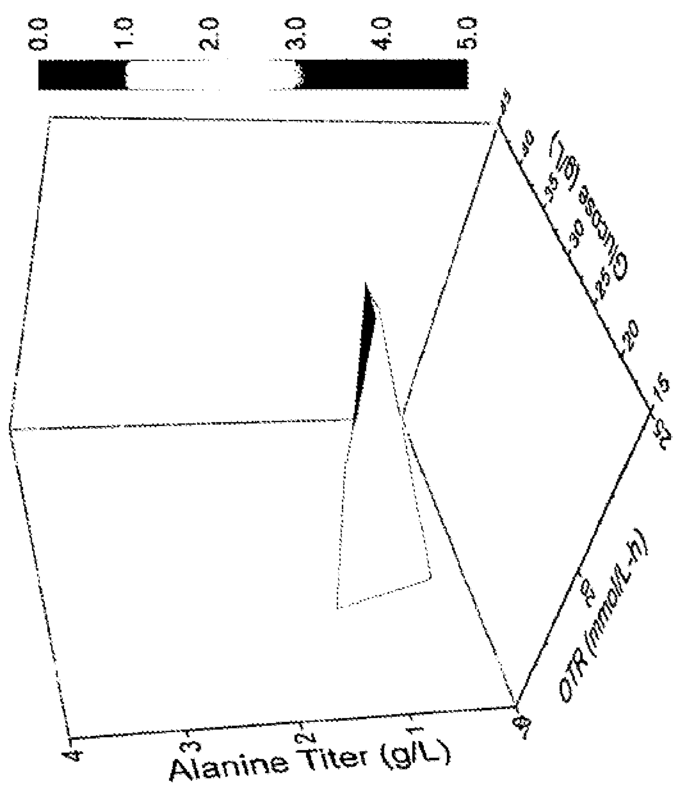

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
1
2
3
4

FIGURE 25A

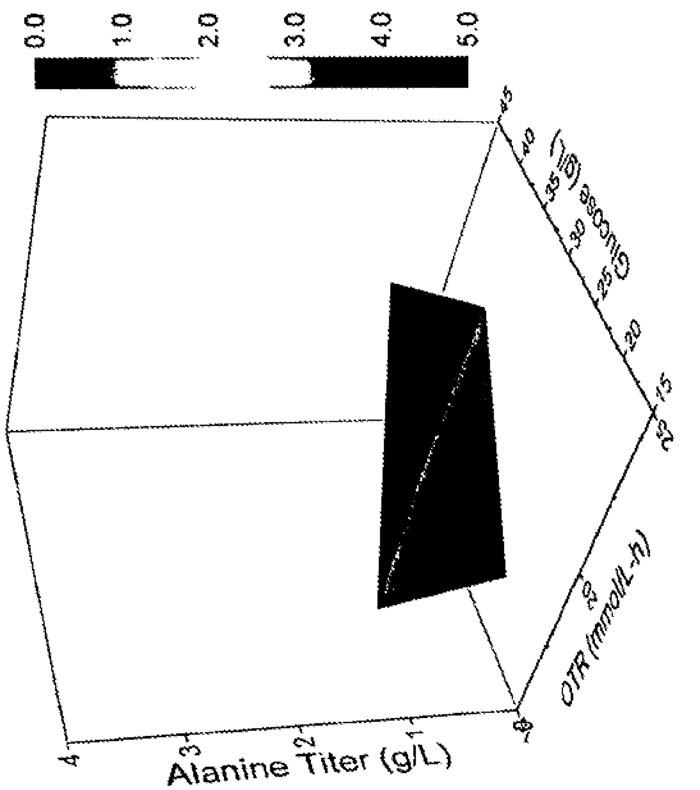


FIGURE 25B

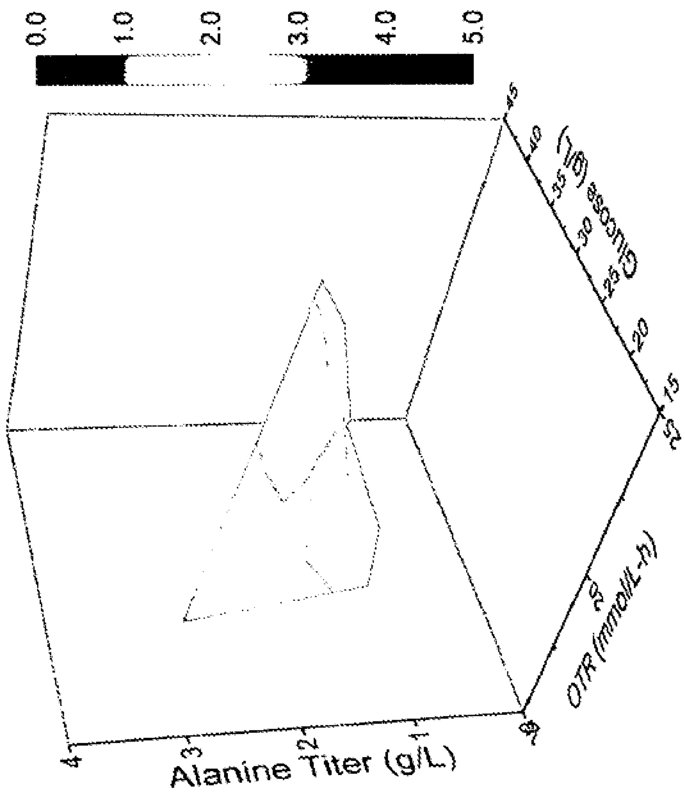


FIGURE 25C

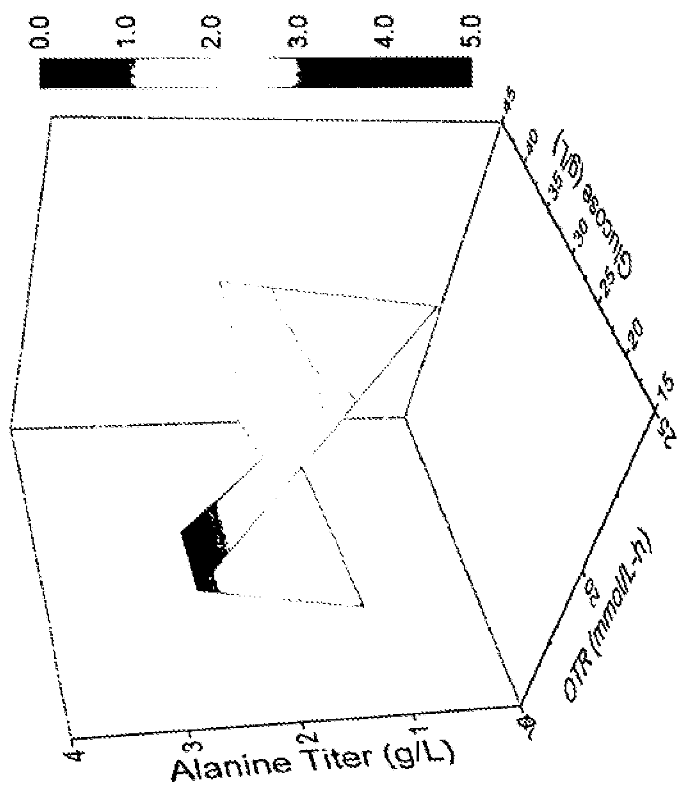


FIGURE 25D

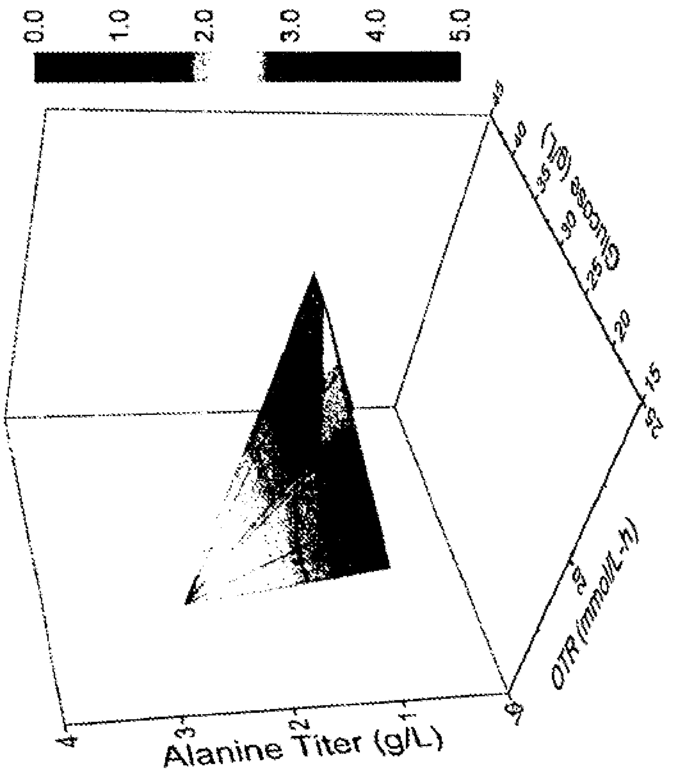

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
OTR (mmol/L-h)
Glucose (g/L)
15
20
25
30
35
40

FIGURE 26A

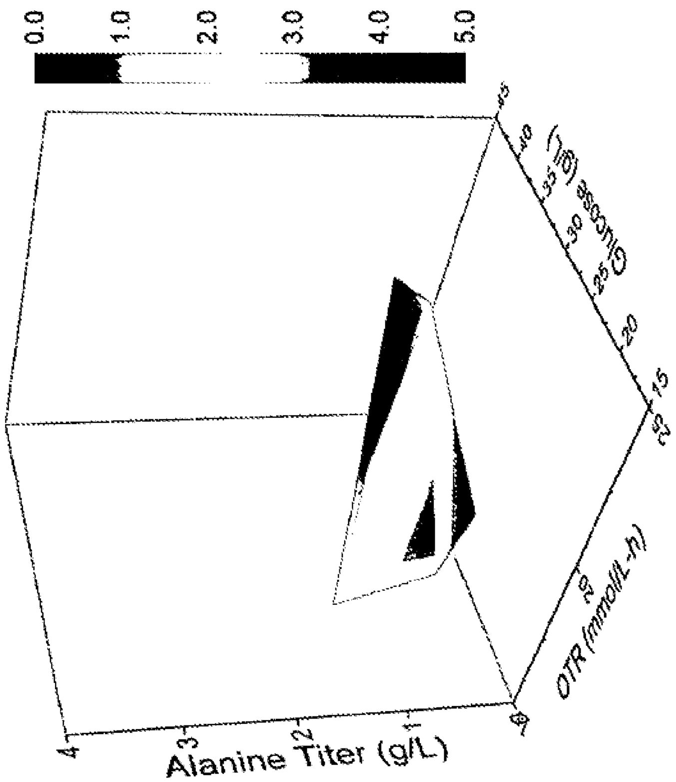


FIGURE 26B

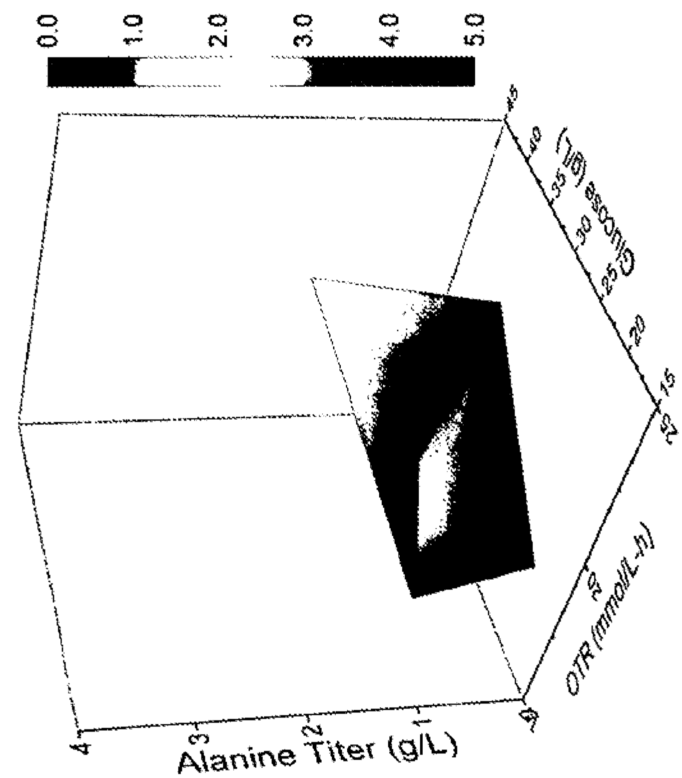

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
OTR (mmol/L-h)
20
Glucose (g/L)
15
20
25
30
35
40
45

FIGURE 26C

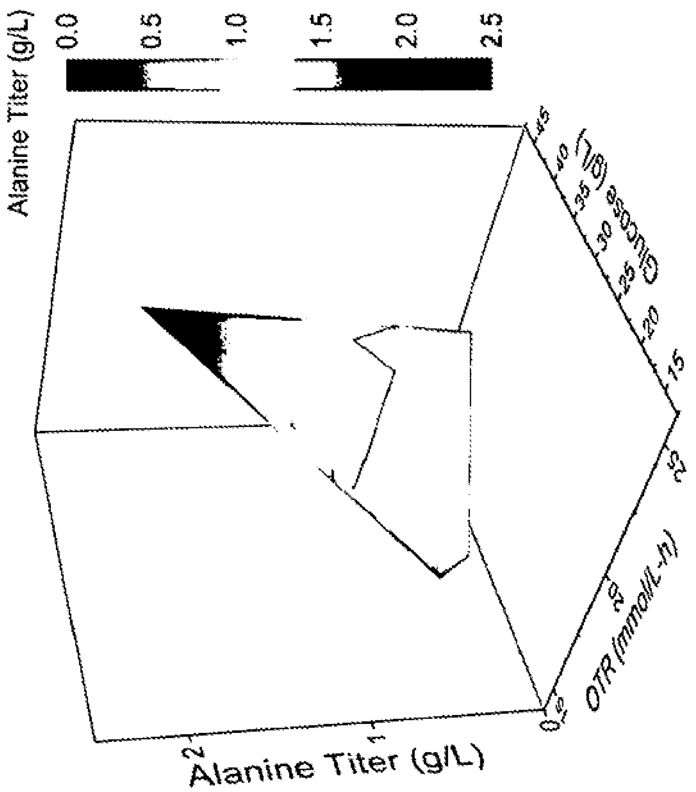

Alanine Titer (g/L)
0.0
0.5
1.0
1.5
2.0
2.5
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
0
1
2

FIGURE 26D

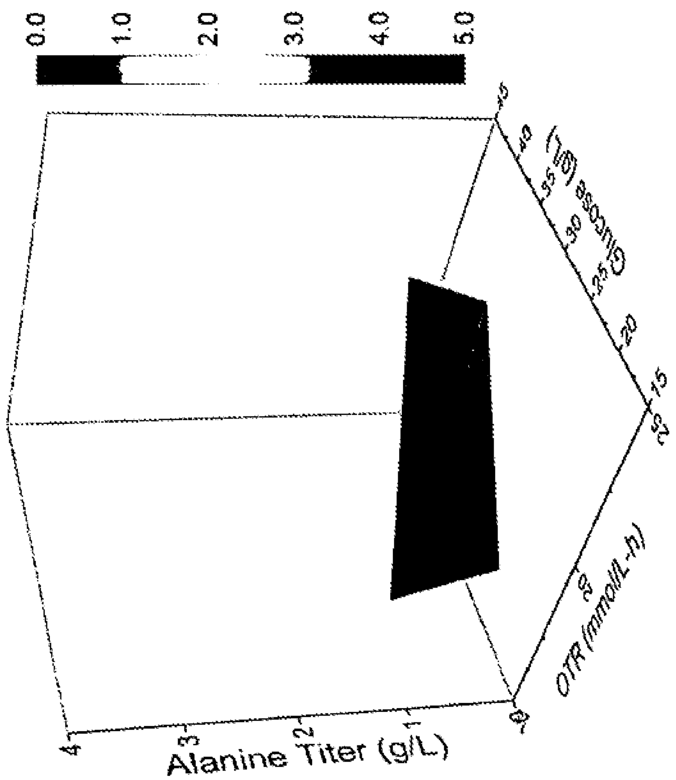


FIGURE 27A

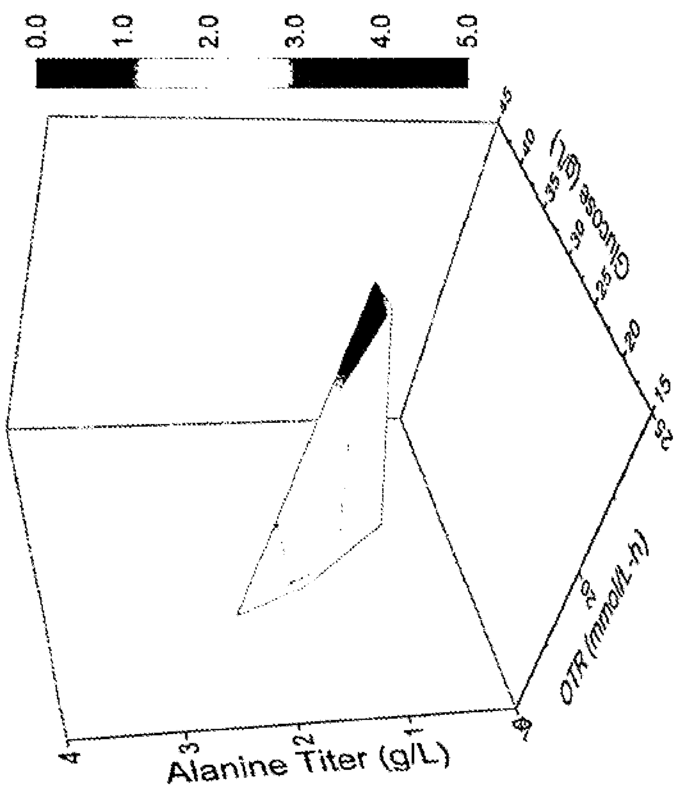


FIGURE 27B

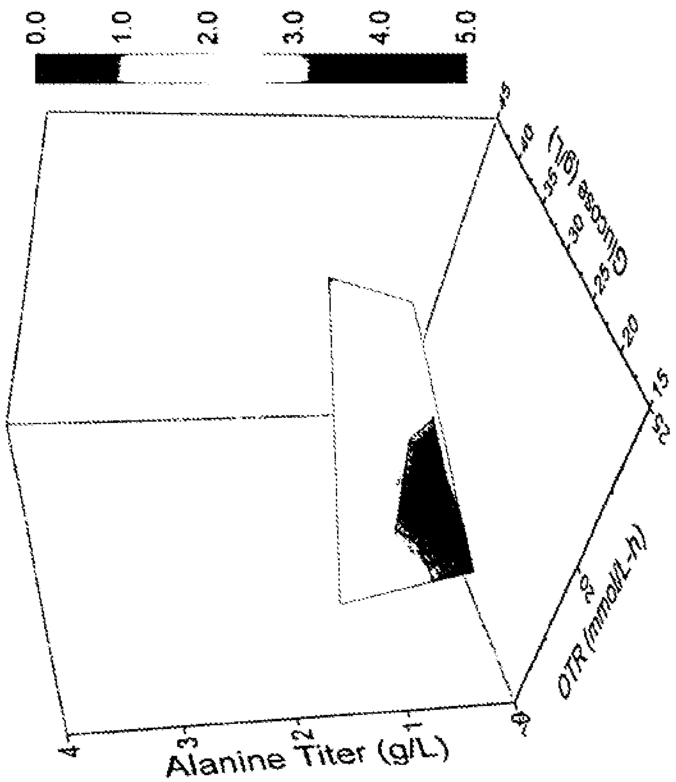

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
15
20
25
30
35
40
OTR (mmol/L-h)
Alanine Titer (g/L)
1
2
3
4

FIGURE 27C

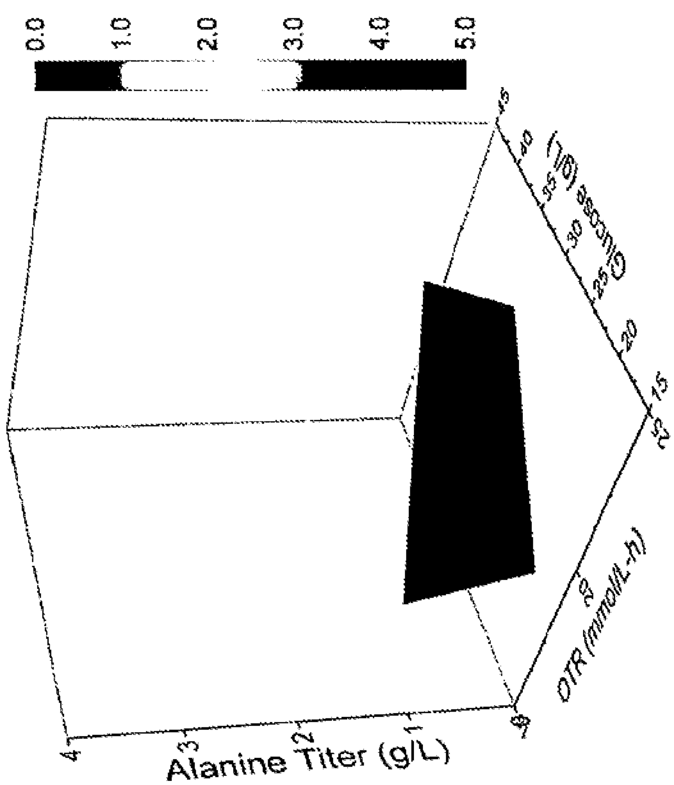


FIGURE 27D

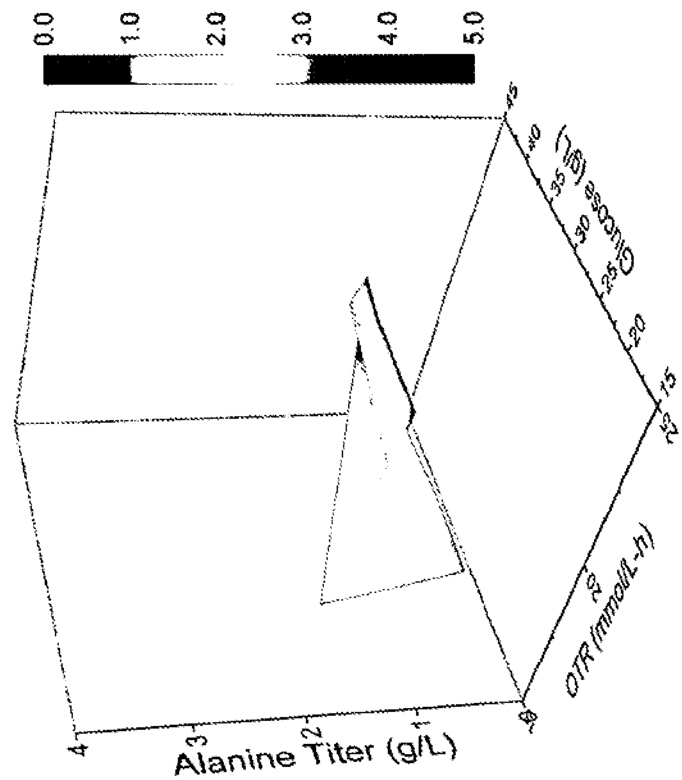

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
Alanine Titer (g/L)
4
3
2
1

FIGURE 28A

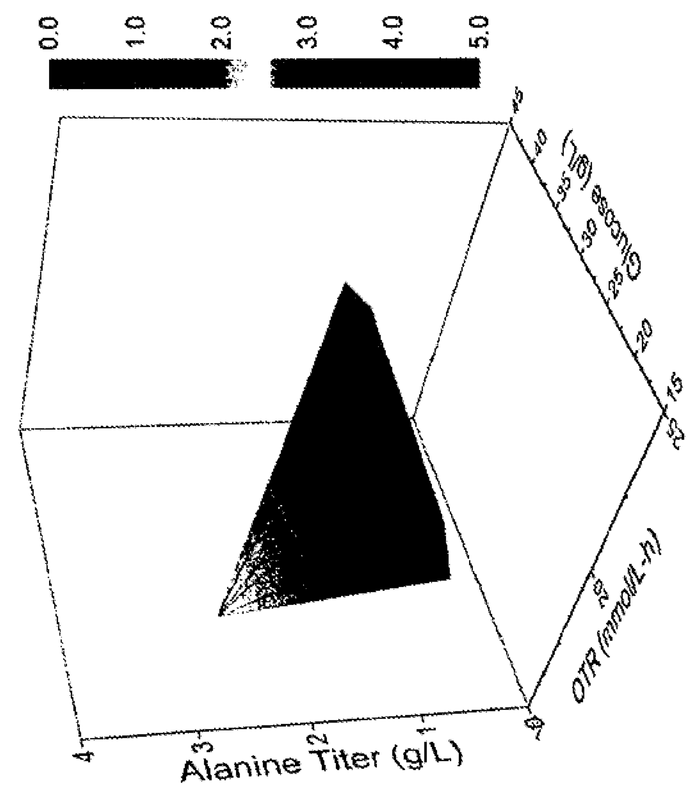

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)

FIGURE 28B

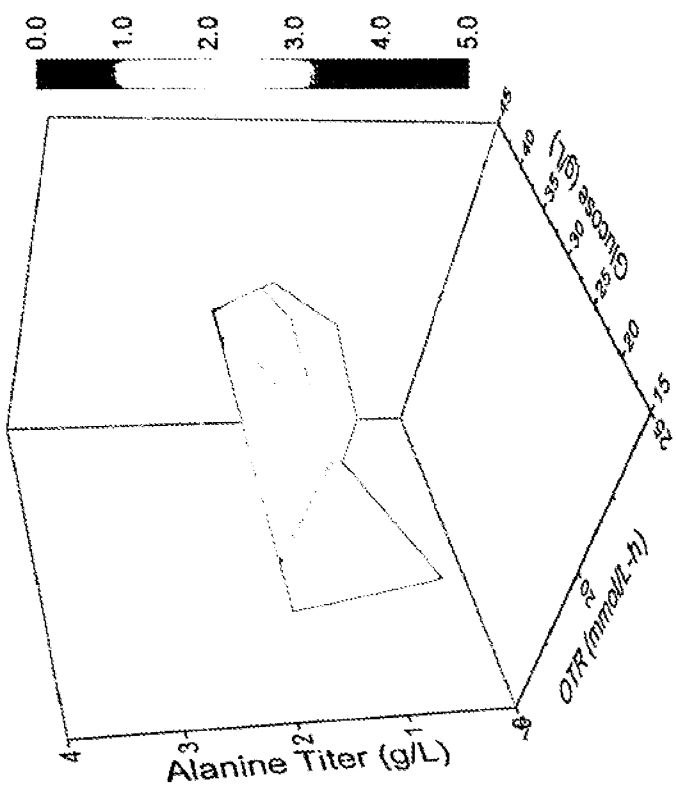

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
OTR (mmol/L-h)
Glucose (g/L)
40
35
30
25
20
15

FIGURE 28C

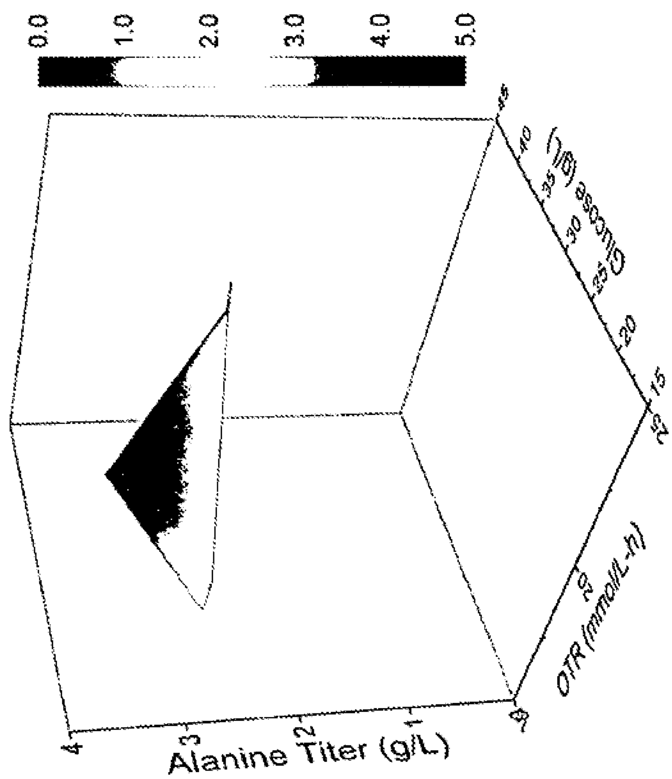


FIGURE 28D

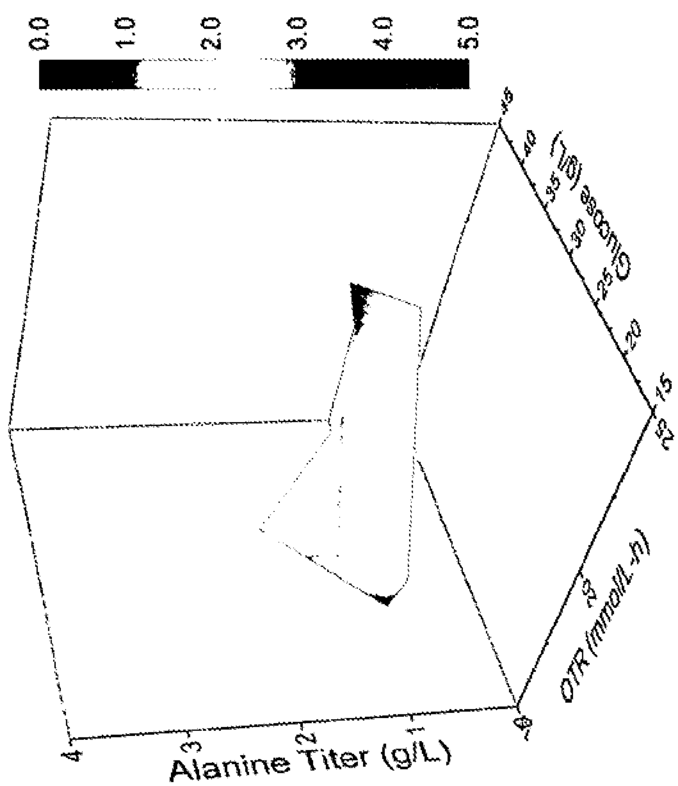

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
OTR (mmol/L-h)
Glucose (g/L)
15
20
25
30
35
40
45

FIGURE 29A

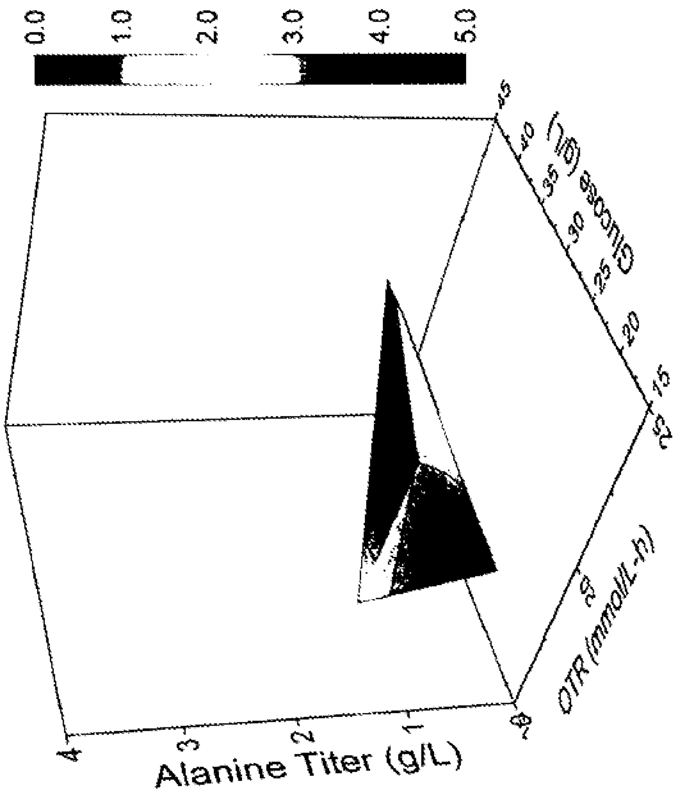

0.0
1.0
2.0
3.0
4.0
5.0
Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
Alanine Titer (g/L)
4
3
2
1

FIGURE 29B

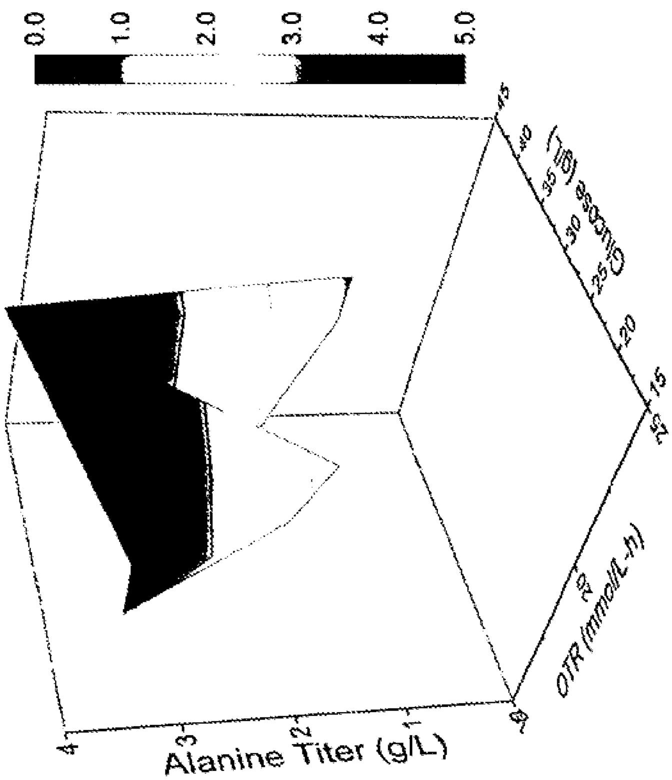


FIGURE 29C

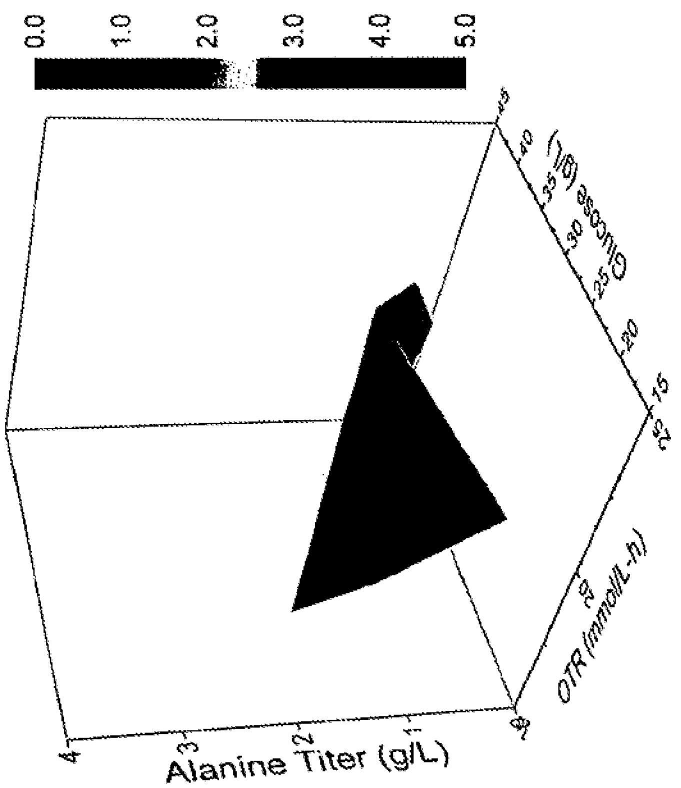


FIGURE 29D

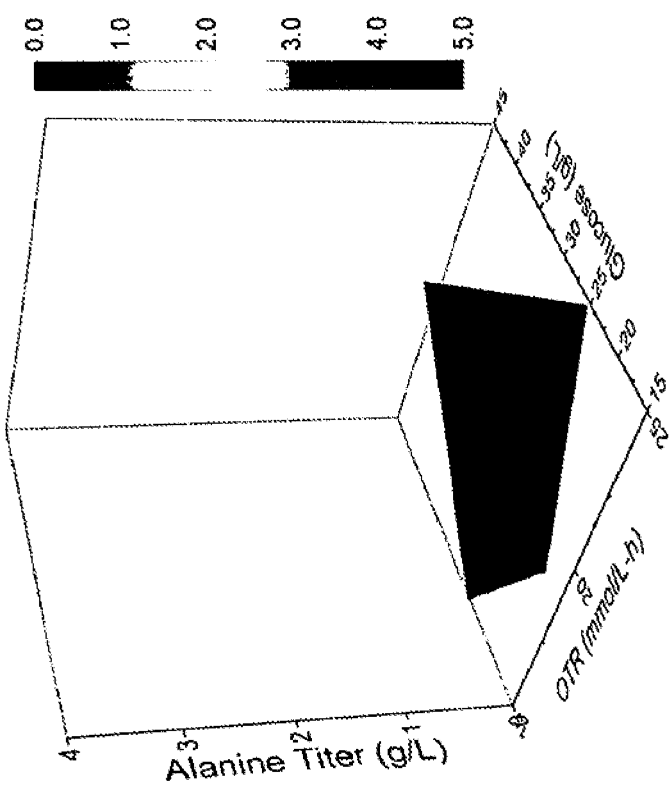


FIGURE 30A

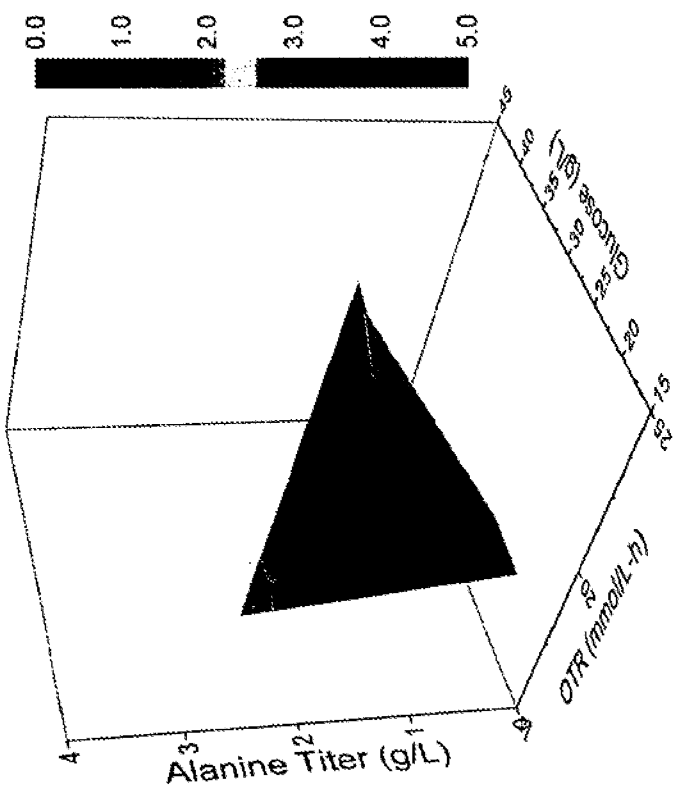

0.0
1.0
2.0
3.0
4.0
5.0
Alanine Titer (g/L)
4
3
2
1
0
OTR (mmol/L-h)
Glucose (g/L)
15
20
25
30
35
40
45

FIGURE 30B

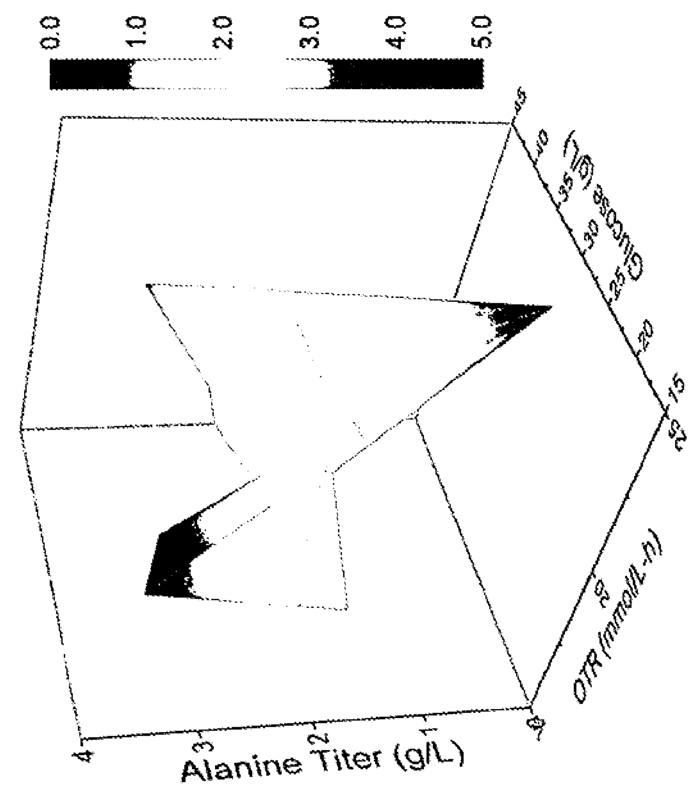


FIGURE 30C

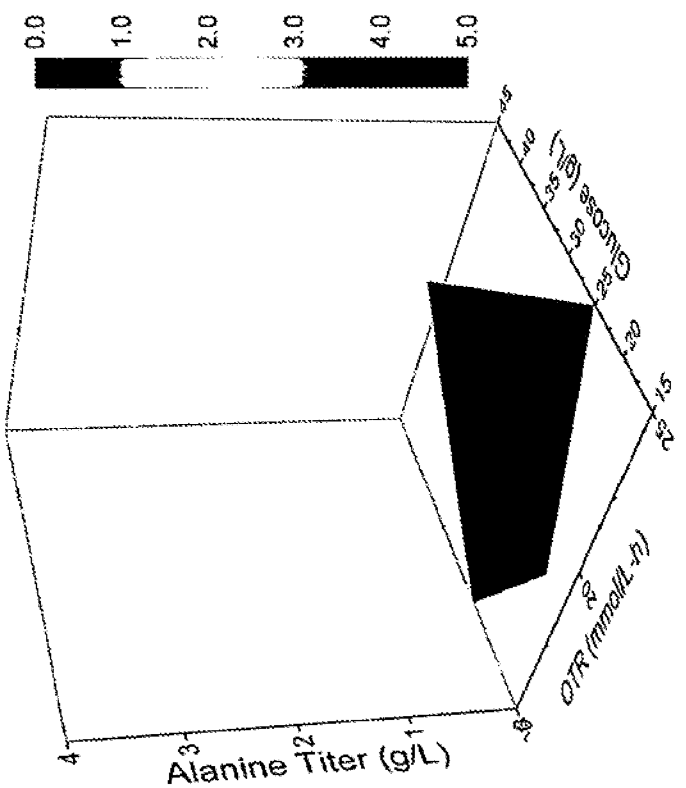


FIGURE 30D

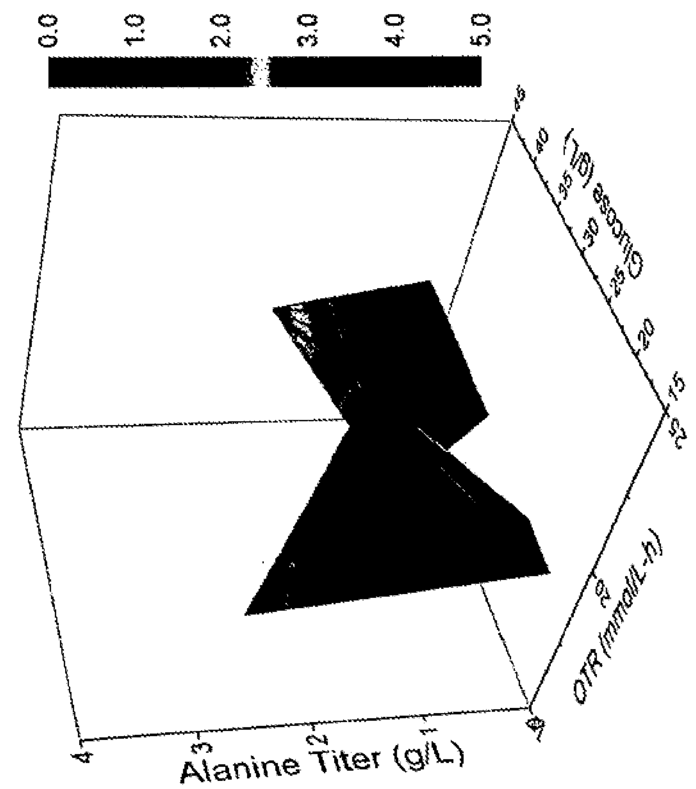
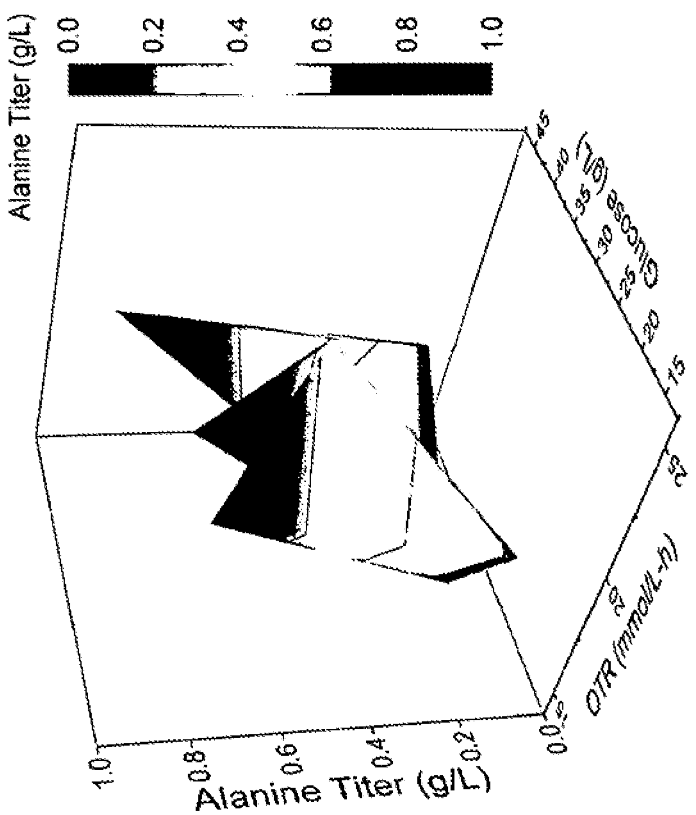


FIGURE 31A



Alanine Titer (g/L)
0.0
0.2
0.4
0.6
0.8
1.0
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
1.0
0.8
0.6
0.4
0.2
0.0

FIGURE 31B

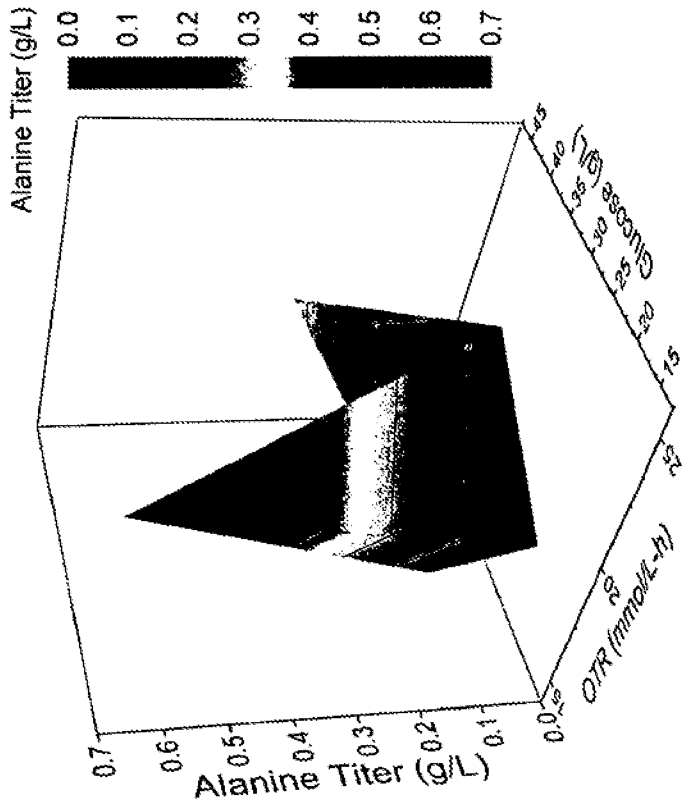

Alanine Titer (g/L)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
15
20
25
Alanine Titer (g/L)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

FIGURE 31C

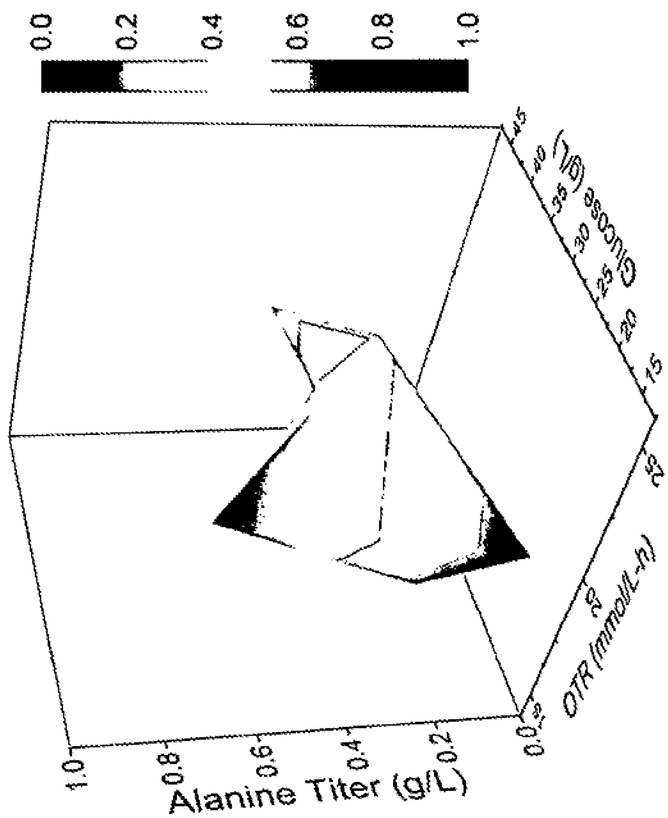

0.0
0.2
0.4
0.6
0.8
1.0
Glucose (g/L)
45
40
35
30
25
20
15
OTR (mmol/L-h)
Alanine Titer (g/L)
1.0
0.8
0.6
0.4
0.2
0.0

FIGURE 31D

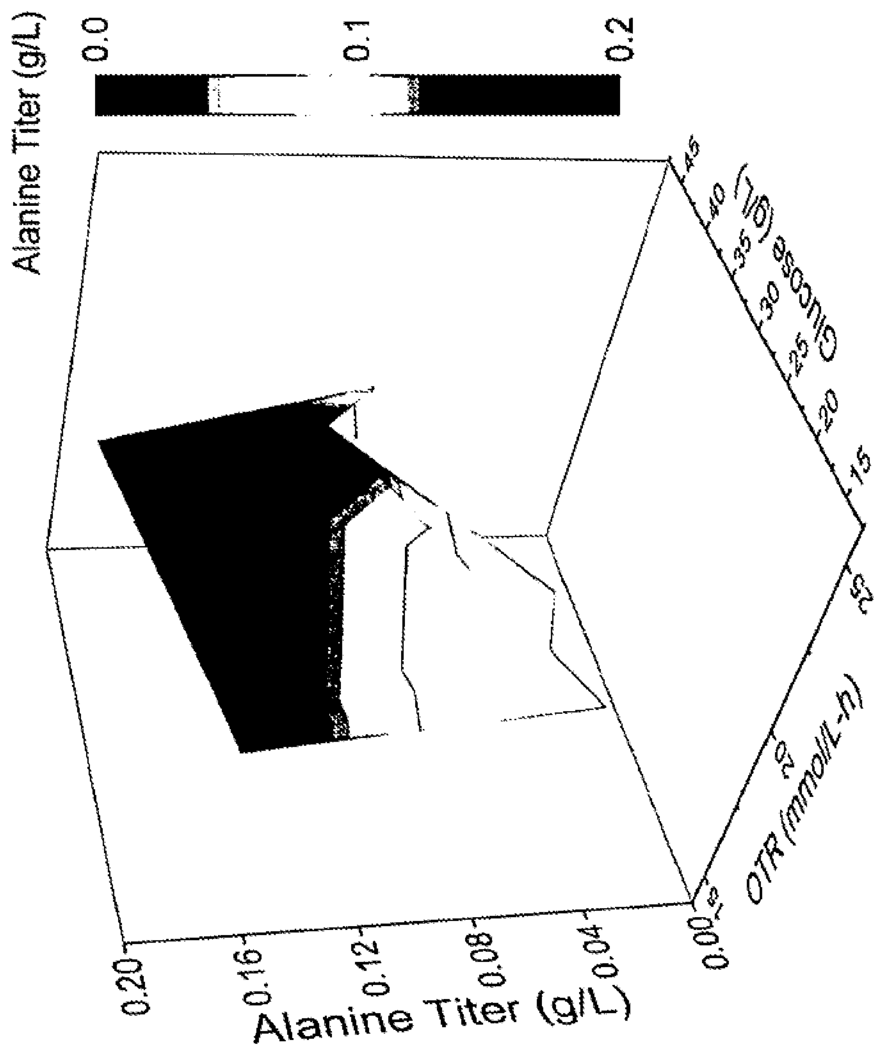

Alanine Titer (g/L)
0.0
0.1
0.2
Glucose (g/L)
15
20
25
30
35
40
45
OTR (mmol/L-h)
Alanine Titer (g/L)
0.20
0.16
0.12
0.08
0.04
0.00

FIGURE 32

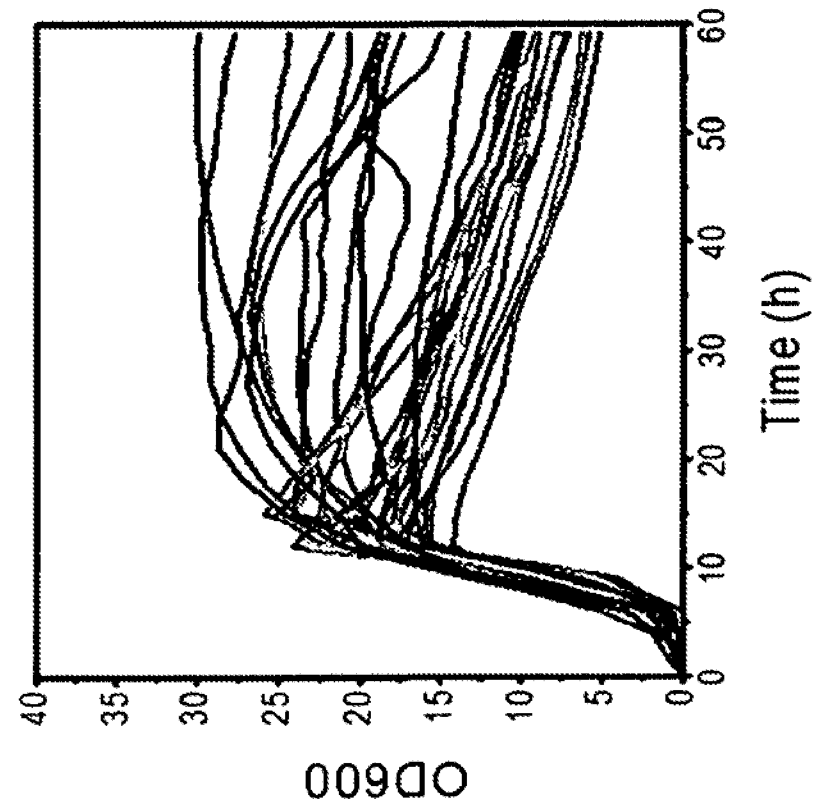


FIGURE 33A

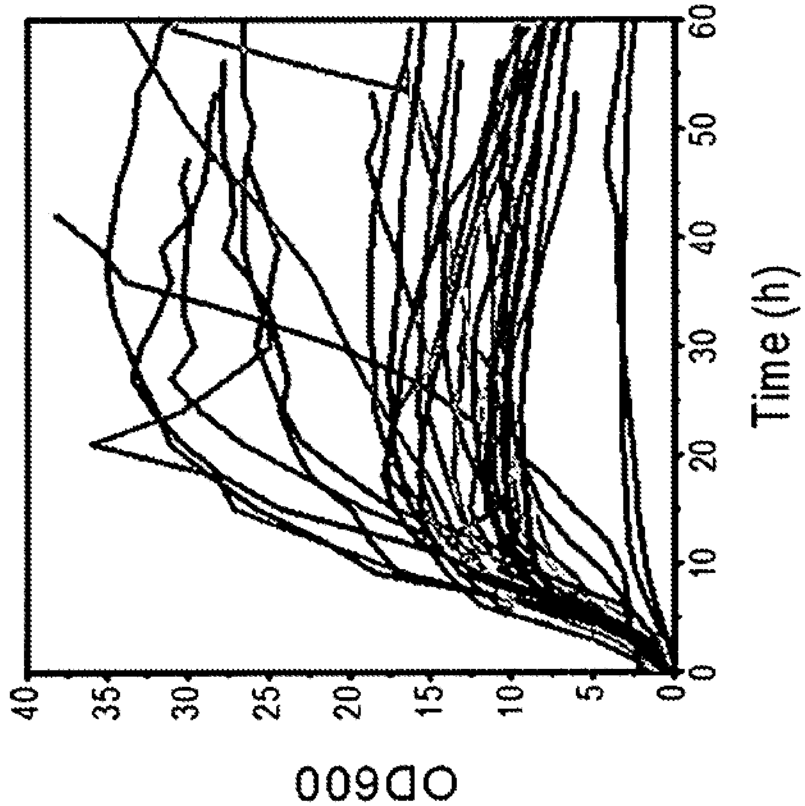


FIGURE 33B

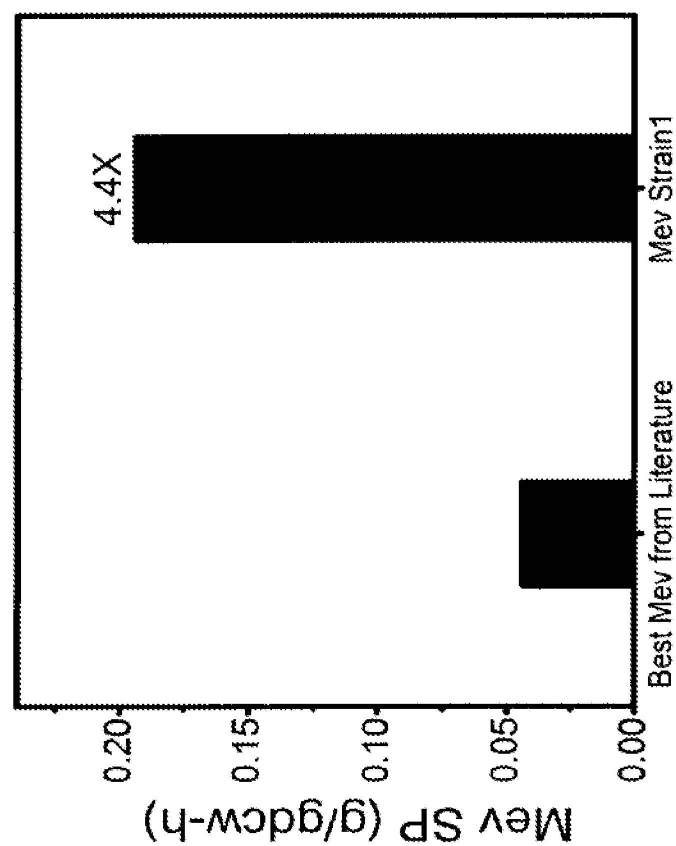

Mev SP (g/gdcw-h)
0.00
0.05
0.10
0.15
0.20
4.4X
Best Mev from Literature
Mev Strain1

FIGURE 34

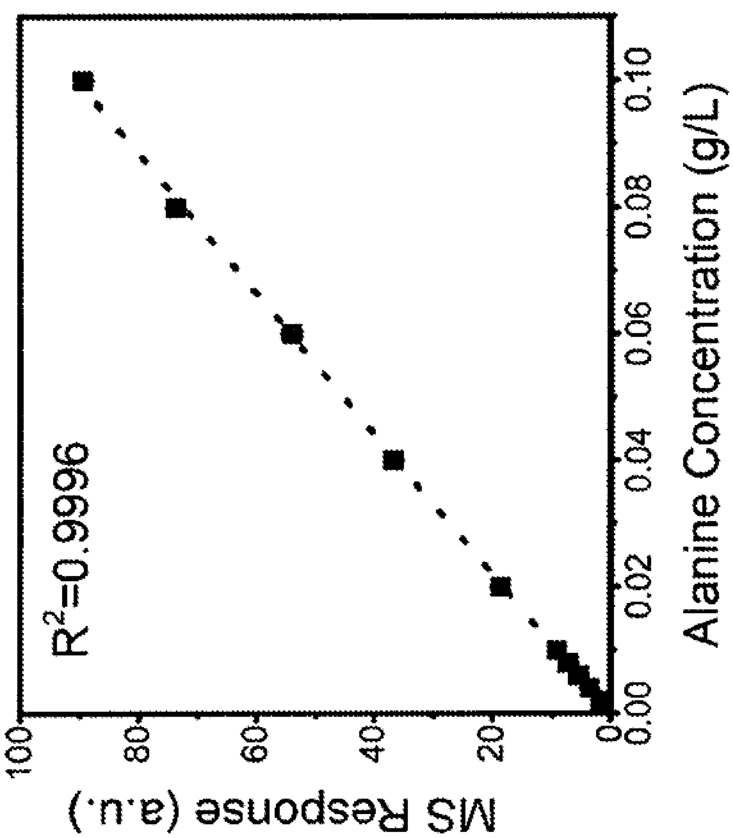

R^2=0.9996
MS Response (a.u.)
100
80
60
40
20
0
0.00
0.02
0.04
0.06
0.08
0.10
Alanine Concentration (g/L)

FIGURE 35

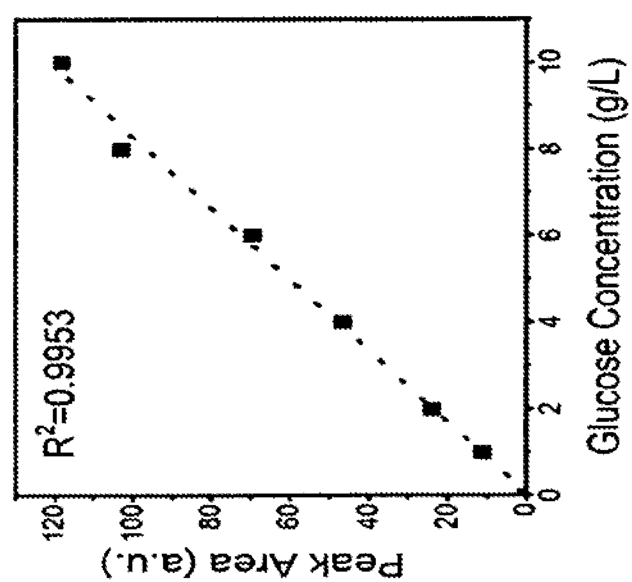


FIGURE 36A

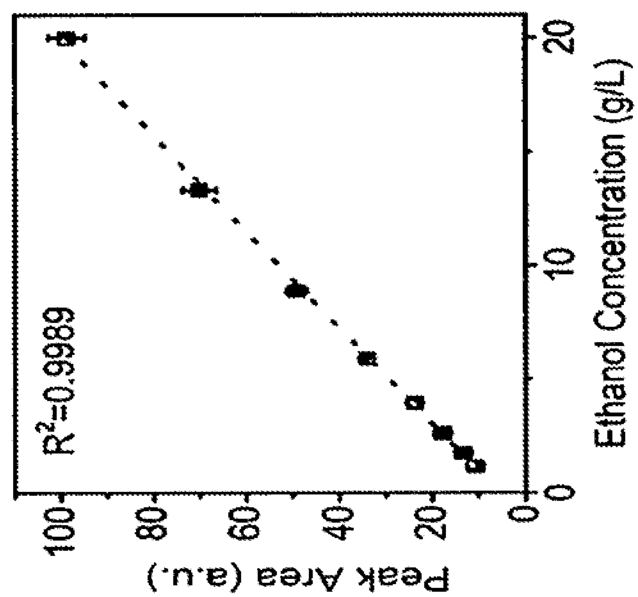


FIGURE 36B

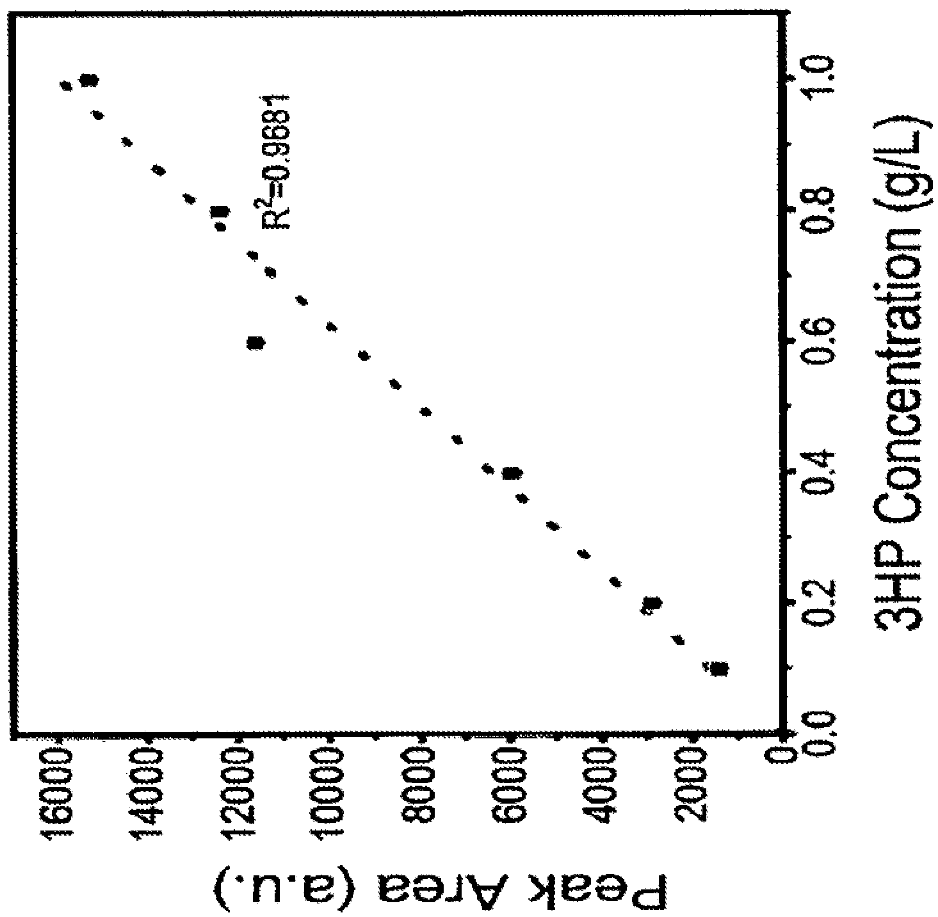

Peak Area (a.u.)
16000
14000
12000
10000
8000
6000
4000
2000
0
0.0
0.2
0.4
0.6
0.8
1.0
3HP Concentration (g/L)
R2=0.9681

FIGURE 37

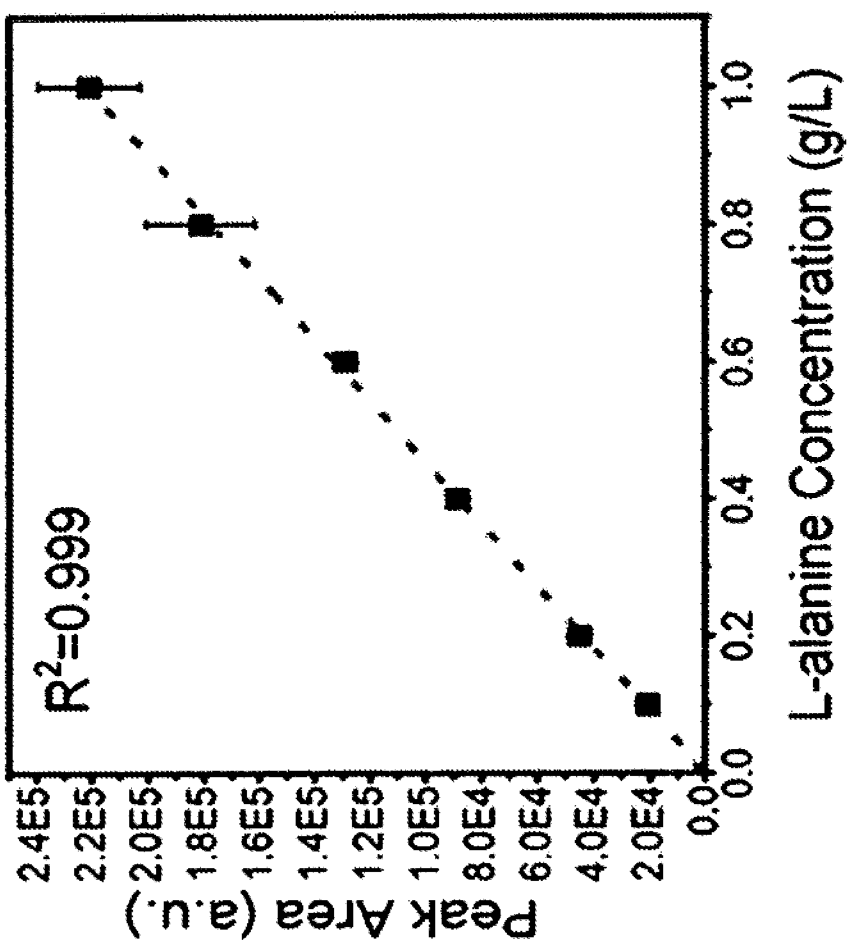
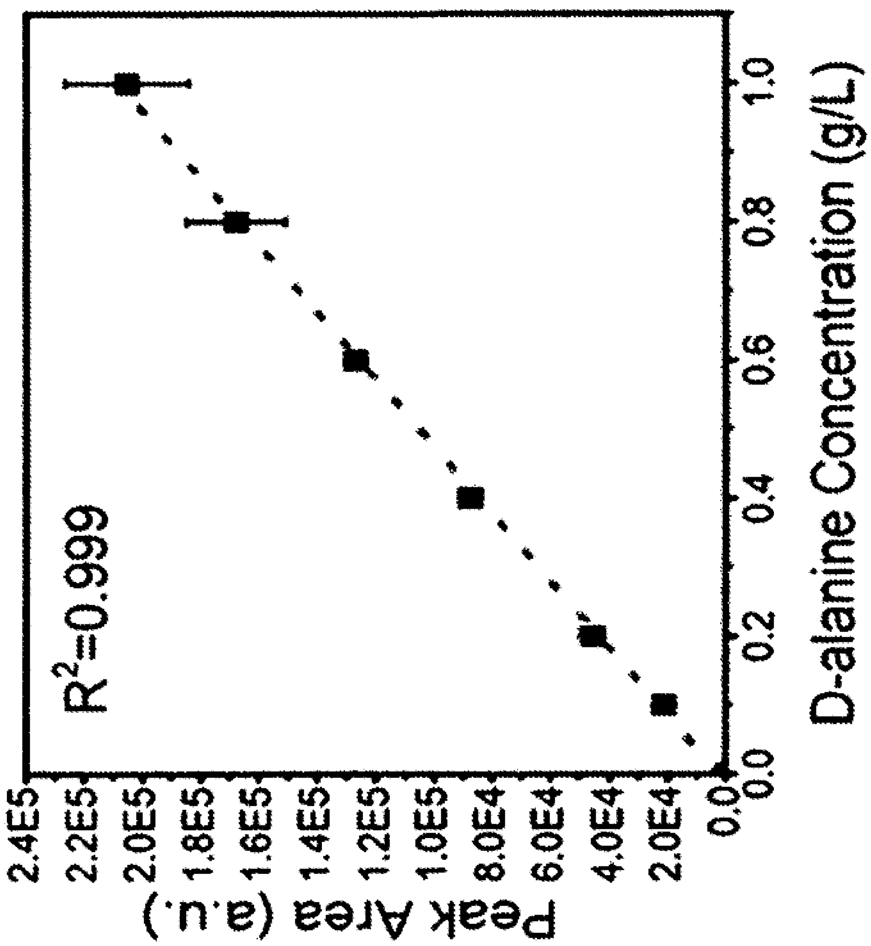

R^2=0.999
Peak Area (a.u.)
2.4E5
2.2E5
2.0E5
1.8E5
1.6E5
1.4E5
1.2E5
1.0E5
8.0E4
6.0E4
4.0E4
2.0E4
0.0
0.0
0.2
0.4
0.6
0.8
1.0
L-alanine Concentration (g/L)

FIGURE 38A



R^2=0.999
Peak Area (a.u.)
2.4E5
2.2E5
2.0E5
1.8E5
1.6E5
1.4E5
1.2E5
1.0E5
8.0E4
6.0E4
4.0E4
2.0E4
0.0
0.0
0.2
0.4
0.6
0.8
1.0
D-alanine Concentration (g/L)

FIGURE 38B

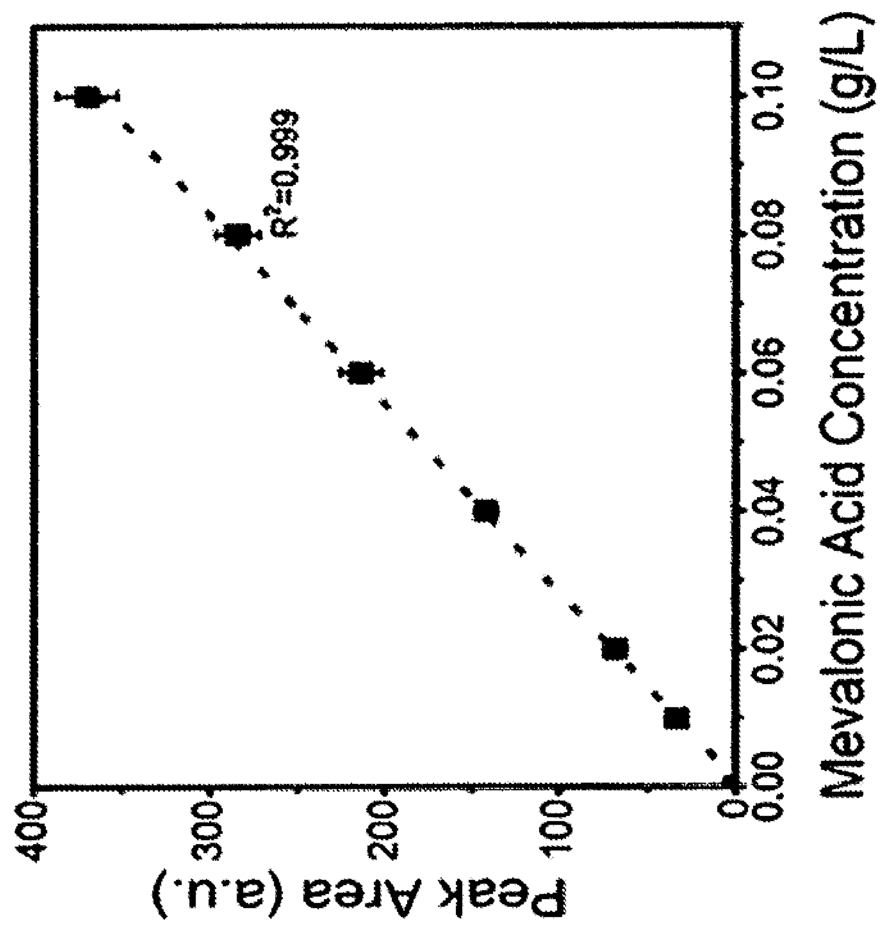

Peak Area (a.u.)
400
300
200
100
0
0.00
0.02
0.04
0.06
0.08
0.10
Mevalonic Acid Concentration (g/L)
R^2=0.999

FIGURE 38C

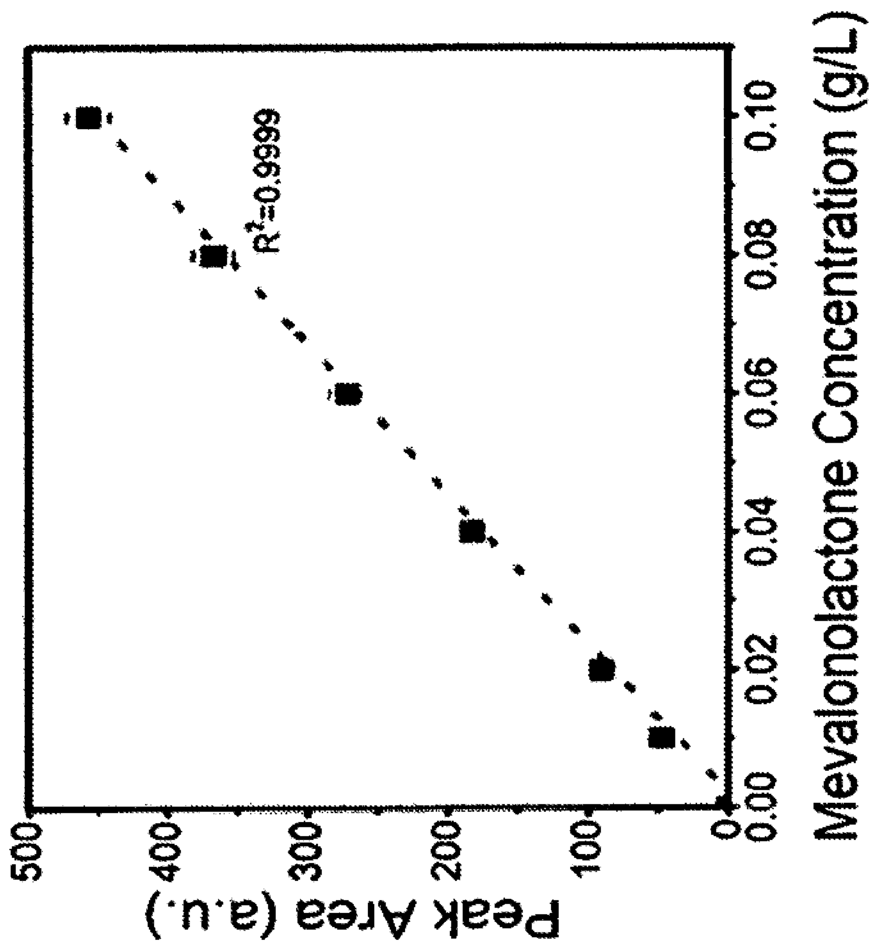

Peak Area (a.u.)
0
100
200
300
400
500
Mevalonolactone Concentration (g/L)
0.00
0.02
0.04
0.06
0.08
0.10
R²=0.9999

FIGURE 38D

COMPOSITIONS AND METHODS FOR METABOLIC CONTROL OF A BIOFERMENTATION PROCESS WITH SYNTHETIC METABOLIC VALVES

CROSS-REFERENCE

This application is a continuation of U.S. application Ser. No. 16/487,542, filed Aug. 21, 2019, which is a National Stage Entry of PCT/US 18/19040. filed Feb. 21, 2018 which claims the benefit of U.S. Provisional Application No. 62/461,436, filed Feb. 21, 2017, which application is incorporated herein by reference in its entirety.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

This invention was made with Government support under Federal Grant Nos. HR0011-14-C-0075 awarded by DOD/DARPA, 12043956 and N00014-16-1-2558 awarded by NAVY/ONR, and 1445726 awarded by NSF. The Government has certain rights to this invention.

REFERENCE TO A SEQUENCE LISTING

The instant application contains a Sequence Listing which has been filed electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Feb. 21, 2018, is named 52240_702_601_SL.txt and is 81,697 bytes in size.

BACKGROUND OF THE INVENTION

Biotechnology-based fermentation processes have been successfully developed to produce everything from biologics and small molecule therapies to specialty, bulk and commodity chemicals, and even next generation biofuels. These processes have made rapid advancements in recent years due to technology developments in the fields of fermentation science and synthetic biology, as well as metabolic and enzyme engineering. Despite these substantial advances, most successful examples of rational and directed engineering approaches have also greatly relied on numerous and often lengthy cycles of trial and error. The present disclosure provides a strategy that simultaneously reduces the complexity of the problem (as well as the size of the relevant design space), while also minimizing metabolic responses to environmental conditions, increasing robustness and scalability of engineered strains.

SUMMARY OF THE INVENTION

The present disclosure provides, in part, a high-throughput engineering platform that enables the rapid development of microbial production strains.

In one aspect, the present disclosure provides a cell for generating a product, wherein the cell comprises: a heterologous polynucleotide for controlled reduction of expression of an enzyme of a metabolic pathway, wherein the controlled reduction of expression of the enzyme induces a stationary phase of the cell; and a heterologous production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of the product; wherein a rate of production of the product during the stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the enzyme.

In some embodiments, the heterologous polynucleotide reduces flux through the metabolic pathway. In some embodiments, the enzyme is selected from the group consisting of enoyl-ACP/CoA reductase, glucose-6-phosphate dehydrogenase, lipoamide dehydrogenase, citrate synthase, soluble transhydrogenase, and NADH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the production enzyme is selected from the group consisting of NADPH-dependent alanine dehydrogenase, an alanine exporter, and NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the change of an environmental condition comprises increasing or decreasing a concentration of a sugar in a culture medium contacting the cell. In some embodiments, the sugar is glucose. In some embodiments, the change of an environmental condition comprises increasing or decreasing oxygenation of a culture medium contacting the cell. In some embodiments, the product comprises 3-hydroxypropionic acid.

In some embodiments, the product comprises an amino acid. In some aspects, the amino acid comprises alanine. In some aspects, the cell is grown in a culture, and a rate of production of the alanine by the culture is at least 0.5 g/L/hour. In some aspects, the rate of production of the alanine is at least 1.0 g/L/hour. In some aspects, the rate of production of the alanine is at least 1.5 g/L/hour. In some aspects, the rate of production of the alanine is at least 1.6 g/L/hour. In some aspects, the culture produces at least 80 g/L of the alanine. In some aspects, the culture produces at least 100 g/L of the alanine. In some aspects, the culture produces at least 120 g/L of the alanine. In some aspects, the culture produces at least 140 g/L of the alanine. In some aspects, the production polynucleotide encodes an alanine exporter. In some aspects, the alanine exporter is alaE.

In some embodiments, the product comprises mevalonic acid. In some embodiments, the cell is grown in a culture, and a rate of production of the mevalonic acid by the culture is at least 0.5 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.0 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.2 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.25 g/L/hour. In some aspects, the cell is grown in a culture, and the culture produces at least 50 g/L of the mevalonic acid. In some embodiments, the culture produces at least 70 g/L of the mevalonic acid. In some embodiments, the culture produces at least 90 g/L of the mevalonic acid. In some embodiments, the culture produces at least 95 g/L of the mevalonic acid. In some embodiments, the heterologous polynucleotide is selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding the enzyme; and a degradation polynucleotide for mediating cellular degradation of the enzyme.

In some aspects, the heterologous polynucleotide comprises a silencing polynucleotide, and the silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter of a gene encoding the enzyme. In some aspects, the heterologous polynucleotide encodes a CRISPR enzyme, and the CRISPR enzyme specifically binds to the promoter sequence when bound to the gRNA. In some aspects, the CRISPR enzyme is catalytically inactive. In some aspects, the heterologous polynucleotide comprises a degradation polynucleotide, wherein the degradation polynucleotide comprises a sequence encoding a degradation tag, wherein the degradation tag mediates degradation of the enzyme. In some embodiments, expression of the heterologous polynucleotide is regulated by phosphate availability in the cell. In some embodiments, expression of the production polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the cell is an *E. coli* cell.

In another aspect, disclosed herein is a method comprising: culturing independently a plurality of strains of a cell, wherein each strain comprises (i) a heterologous polynucleotide for mediating controlled reduction of expression of an enzyme of a metabolic pathway, wherein the controlled reduction of expression of the enzyme induces a stationary phase of the cell; and (ii) a heterologous production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of the product; wherein each strain of the plurality of strains differs from another strain in a sequence of at least one of the heterologous polynucleotide or the heterologous production polynucleotide; growing the plurality of strains to stationary phase; and selecting a strain of the plurality of strains based on a level of the product produced by the selected strain during the stationary phase.

In some embodiments, the method comprises determining the level of the product. In some embodiments, the method comprises growing the selected strain. In some embodiments, the selected strain is grown in a bioreactor. In some embodiments, a culture medium comprising the selected strain has a volume of at least 500 ml. In some embodiments, the culture medium has a volume of at least 1 L. In some embodiments, the heterologous polynucleotide is selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding the enzyme; and a degradation polynucleotide for mediating cellular degradation of the enzyme. In some embodiments, a first and second strain of the plurality of strains comprises a silencing polynucleotide. In some embodiments, the silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter sequence of a gene encoding the enzyme. In some embodiments, the gRNA sequence differs between the first and second strains. In some embodiments, the first and second strain of the plurality of strains comprise a degradation polynucleotide. In some embodiments, the degradation polynucleotide differs between the first and second strains. In some embodiments, the enzyme is selected from the group consisting of enoyl-ACP/CoA reductase, glucose-6-phosphate dehydrogenase, lipoamide dehydrogenase, citrate synthase, soluble transhydrogenase, and NADH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the production enzyme is selected from the group consisting of NADPH-dependent alanine dehydrogenase, an alanine exporter, and NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the product is selected from the group consisting of mevalonic acid, 3-hydroxypropionic acid, and an amino acid.

In some embodiments, the product is an amino acid and the amino acid is alanine. In some embodiments, the cell of the selected strain a rate of production of the product during the stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the heterologous polynucleotide. In some embodiments, the change of an environmental condition comprises a change in concentration of a sugar of a culture medium contacting the cell. In some embodiments, the change of an environmental condition comprises a change in oxygenation of a culture medium contacting the cell.

In another aspect, disclosed herein is a method of generating a cellular product comprising: culturing a heterologous cell in a culture medium, wherein the heterologous cell comprises: (i) a heterologous polynucleotide for mediating controlled reduction of expression of an enzyme of a metabolic pathway, wherein the controlled reduction of expression of the enzyme induces a stationary phase of the cell; and (ii) a heterologous production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of the product; wherein a rate of production of the product during the stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the enzyme.

In one embodiment, the method further comprises changing the environmental condition. In one embodiment, the environmental condition comprises a concentration of a sugar of the culture medium, and changing the environmental condition comprises increasing or decreasing the concentration. In some embodiments, the sugar is glucose. In some embodiments, the environmental condition comprises an oxygen concentration of the culture medium, and changing the environmental condition comprises increasing or decreasing the oxygen concentration. In some embodiments, the culturing is performed in a bioreactor. In some embodiments, the culture medium has a volume of at least 500 ml. In some embodiments, the culture medium has a volume of at least 1 L. In some embodiments, the product comprises 3-hydroxypropionic acid. In some embodiments, the product comprises an amino acid. In some embodiments, the amino acid comprises alanine. In some embodiments, the rate of production of the alanine is at least 0.5 g/L/hour. In some embodiments, the rate of production of the alanine is at least 1.0 g/L/hour. In some embodiments, the rate of production of the alanine is at least 1.5 g/L/hour. In some embodiments, the rate of production of the alanine is at least 1.6 g/L/hour. In some embodiments, the production polynucleotide encodes an alanine exporter. In some embodiments, the alanine exporter is alaE.

In some embodiments, the product comprises mevalonic acid. In some embodiments, the rate of production of the mevalonic acid is at least 0.5 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.0 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.2 g/L/hour. In some embodiments, the rate of production of the mevalonic acid is at least 1.25 g/L/hour. In some embodiments, the heterologous polynucleotide is selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding the enzyme; and a degradation polynucleotide for mediating cellular degradation of the enzyme. In some embodiments, the heterologous polynucleotide comprises a silencing polynucleotide, and the silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter sequence of a gene encoding the enzyme. In some embodiments, the heterologous polynucleotide encodes a CRISPR enzyme, wherein the CRISPR enzyme specifically binds to the promoter sequence when bound to the gRNA. In some embodiments, the CRISPR enzyme is catalytically inactive. In some embodiments, the heterologous polynucleotide comprises a degradation polynucleotide, wherein the degradation polynucleotide comprises a sequence encoding a degradation tag, wherein the degradation tag mediates degradation of the enzyme. In some embodiments, the expression of the heterologous polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the expression of the production polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the cell is an *E. coli* cell.

In another aspect, disclosed herein is a cell for production of alanine, wherein the cell comprises: (i) a heterologous polynucleotide for controlled reduction of expression of an enzyme of a metabolic pathway, wherein the enzyme is selected from the group consisting of enoyl-ACP/CoA reductase, glucose-6-phosphate dehydrogenase, lipoamide dehydrogenase (lpd), citrate synthase (gltA), soluble transhydrogenase, and NADH-dependent glyceraldehyde-3-phosphate dehydrogenase; and (ii) an alanine exporter, wherein the alanine exporter is expressed at increased levels as compared to a wildtype cell.

In some embodiments, the alanine exporter is encoded by an alaE gene. In some embodiments, the controlled reduction of expression of the enzyme induces a stationary phase of the cell. In some embodiments, the cell further comprises a heterologous production polynucleotide for controlled increase in expression of a production enzyme for generation of the alanine. In some embodiments, the production enzyme is selected from the group consisting of NADPH-dependent alanine dehydrogenase and NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the heterologous polynucleotide is selected from the group consisting of: a silencing polynucleotide for mediating transcriptional repression of a gene encoding the enzyme; and a degradation polynucleotide for mediating cellular degradation of the enzyme. In some embodiments, the heterologous polynucleotide comprises a silencing polynucleotide, and the silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter sequence of a gene encoding the enzyme. In some embodiments, the polynucleotide further encodes a CRISPR enzyme, wherein the CRISPR enzyme specifically binds to the promoter sequence when bound to the gRNA. In some embodiments, the CRISPR enzyme is catalytically inactive. In some embodiments, the heterologous polynucleotide comprises a degradation polynucleotide, wherein the degradation polynucleotide comprises a sequence encoding a degradation tag, wherein the degradation tag mediates degradation of the enzyme. In some embodiments, the polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the production polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the cell is an *E. coli* cell.

In some embodiments, a culture comprises the cell. In some embodiments, a rate of production of the alanine by the culture is at least 0.5 g/L/hour. In some embodiments, a rate of production of the alanine by the culture is at least 1.0 g/L/hour. In some embodiments, a rate of production of the alanine by the culture is at least 1.5 g/L/hour. In some embodiments, a rate of production of the alanine by the culture is at least 1.6 g/L/hour. In some embodiments, the culture produces at least 100 g/L of the alanine. In some embodiments, the culture produces at least 120 g/L of the alanine. In some embodiments, the culture produces at least 140 g/L of the alanine.

In some aspects, disclosed herein is a method of production of alanine comprising growing in a culture medium a cell comprising (i) a heterologous polynucleotide for controlled reduction of expression of a enzyme of a metabolic pathway, wherein the enzyme is selected from the group consisting of enoyl-ACP/CoA reductase, glucose-6-phosphate dehydrogenase, lipoamide dehydrogenase, citrate synthase, soluble transhydrogenase, and NADH-dependent glyceraldehyde-3-phosphate dehydrogenase; and (ii) an alanine exporter, wherein the alanine exporter is expressed at increased levels as compared to a wildtype cell.

In some embodiments, the controlled reduction of expression of the enzyme induces a stationary phase of the cell. In some embodiments, the method further comprises decreasing an oxygenation level or a sugar concentration of the culture medium during the stationary phase, wherein a rate of production of the cellular product is reduced less in response to the decreasing as compared to a cell lacking the heterologous polynucleotide. In some embodiments, the sugar is glucose. In some embodiments, the alanine exporter is encoded by an alaE gene. In some embodiments, the cell further comprises a heterologous production polynucleotide for controlled increase in expression of a production enzyme for generation of the alanine. In some embodiments, the production enzyme is selected from the group consisting of: NADPH-dependent alanine dehydrogenase and NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase. In some embodiments, the heterologous polynucleotide is selected from the group consisting of: a silencing polynucleotide for mediating transcriptional repression of a gene encoding the enzyme; and a degradation polynucleotide for mediating cellular degradation of the enzyme. In some embodiments, the heterologous polynucleotide comprises a silencing polynucleotide, and the silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter sequence of a gene encoding the enzyme. In some embodiments, the heterologous polynucleotide encodes a CRISPR enzyme, wherein the CRISPR enzyme specifically binds to the promoter sequence when bound to the gRNA. In some embodiments, the CRISPR enzyme is catalytically inactive. In some embodiments, the heterologous polynucleotide comprises a degradation polynucleotide, wherein the degradation polynucleotide comprises a sequence encoding a degradation tag, wherein the degradation tag mediates degradation of the enzyme.

In some embodiments, the expression of the heterologous polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the production polynucleotide is regulated by phosphate availability in the cell. In some embodiments, the cell is an *E. coli* cell. In some embodiments, a rate of production of the alanine is at least 0.5 g/L/hour. In some embodiments, a rate of production of the alanine is at least 1.0 g/L/hour. In some embodiments, a rate of production of the alanine is at least 1.5 g/L/hour. In some embodiments, a rate of production of the alanine is at least 1.6 g/L/hour.

INCORPORATION BY REFERENCE

All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

FIG. **1**A depicts an overview of dynamic metabolic control in 2-stage fermentations.

FIG. **1**B depicts strain and bioprocess optimization.

FIGS. **2**A-D depict an example of implementation of 2-stage Synthetic Metabolic Valves (SMVs) in *E. coli.*

FIGS. **3**A-K depict an example of alanine production in *E. coli* utilizing 2-stage dynamic control.

FIGS. **4**A-F depict example robustness comparison between 2-stage and growth associated approaches.

FIGS. **5**A-J depict example comparisons of "Valve" and growth associated alanine production in micro-fermentations and 1 L fermentation.

FIG. **6**A-H depict an example of mevalonate production in *E. coli* utilizing 2-stage dynamic control.

FIG. **7** depicts an example of phosphate depletion promoter characterization.

FIG. **8** depicts an example of insulated phosphate depletion promoter characterization.

FIG. **9** depicts an example of insulated constitutive promoter characterization.

FIG. **10** depicts an example of metabolic modeling results for optimal 3-HP flux in two stage fermentations.

FIG. **11** depicts examples of chromosomal modifications.

FIG. **12** depicts an example of average maximal growth rates of starting host strains in 1 L FGM10 minimal medium fermentations, n=2.

FIG. **13**A-E depict examples of distribution of glucose utilized during the growth phase of starting host strains in 1 L standard minimal medium fermentations.

FIG. **14** depicts pCASCADE-control plasmid construction scheme.

FIGS. **15**A-B depict pCASCADE construction scheme.

FIGS. **16**A-C depict an overview of micro-fermentation process.

FIG. **17** depicts micro-fermentation for L-alanine production using different insulated phosphate promoters in DLF_0025 strain.

FIG. **18** depicts Heatmap for L-alanine production by gapN/gapA strains.

FIGS. **19**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **20**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **21**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **22**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **23**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **24**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **25**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **26**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **27**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **28**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **29**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **30**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **31**A-D depict alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIG. **32** depicts alanine production in response to different OTR and glucose concentration in micro-fermentation for one strain evaluated for robustness.

FIGS. **33**A-B depict growth profile for all valve and growth associated strains at 1 L scale evaluated in this paper.

FIG. **34** depicts specific Productivity (SP) comparison for strain with highest mevalonate titer from literature and mevalonate strain 1 evaluated in this work.

FIG. **35** depicts alanine standard curve from MS measurement. Average and standard deviation for mass spec response from triplicate standard measurement were plotted.

FIGS. **36**A-B depict glucose and ethanol standard curves from RI measurement.

FIG. **37** depicts 3-Hydroxypropionic acid standard curve from TUV measurement.

FIGS. **38**A-D depict TUV standard curves for L-alanine, D-alanine, mevalonic acid, and mevalonolactone.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used in the specification and the claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to an "expression vector" includes a single expression vector as well as a plurality of expression vectors, either the same (e.g., the same operon) or different; reference to "microorganism" includes a single microorganism as well as a plurality of microorganisms; and the like.

As used herein, "reduced enzymatic activity," "reducing enzymatic activity," and the like is meant to indicate that a microorganism cell's, or an isolated enzyme, exhibits a lower level of activity than that measured in a comparable cell of the same species or its native enzyme. That is, enzymatic conversion of the indicated substrate(s) to indicated product(s) under known standard conditions for that enzyme is at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, or at least 90 percent less than the enzymatic activity for the same biochemical conversion by a native (non-modified) enzyme under a standard specified condition. This term also can include elimination of that enzymatic activity. A cell having reduced enzymatic activity of an enzyme can be identified using any method known in the art. For example, enzyme activity assays can be used to identify cells having reduced enzyme activity. See, for example, *Enzyme Nomenclature*, Academic Press, Inc., New York 2007.

The term "heterologous DNA," "heterologous nucleic acid sequence," and the like as used herein refers to a nucleic acid sequence wherein at least one of the following is true: (a) the sequence of nucleic acids foreign to (i.e., not naturally found in) a given host microorganism; (b) the sequence may be naturally found in a given host microorganism, but in an unnatural (e.g., greater than expected) amount; or (c) the sequence of nucleic acids comprises two or more subsequences that are not found in the same relationship to each other in nature. For example, regarding instance (c), a heterologous nucleic acid sequence that is recombinantly produced will have two or more sequences from unrelated genes arranged to make a new functional nucleic acid, such as a nonnative promoter driving gene expression.

The term "synthetic metabolic valve," and the like as used herein refers to either the use of controlled proteolysis, gene silencing or the combination of both proteolysis and gene silencing to alter metabolic fluxes.

The term "heterologous" is intended to include the term "exogenous" as the latter term is generally used in the art. With reference to the host microorganism's genome prior to the introduction of a heterologous nucleic acid sequence, the nucleic acid sequence that codes for the enzyme is heterologous (whether or not the heterologous nucleic acid sequence is introduced into that genome).

As used herein, the term "gene disruption," or grammatical equivalents thereof (and including "to disrupt enzymatic function," "disruption of enzymatic function," and the like), is intended to mean a genetic modification to a microorganism that renders the encoded gene product as having a reduced polypeptide activity compared with polypeptide activity in or from a microorganism cell not so modified. The genetic modification can be, for example, deletion of the entire gene, deletion or other modification of a regulatory sequence required for transcription or translation, deletion of a portion of the gene which results in a truncated gene product (e.g., enzyme) or by any of various mutation strategies that reduces activity (including reducing activities to no detectable activity level) the encoded gene product. A disruption may broadly include a deletion of all or part of the nucleic acid sequence encoding the enzyme, and also includes, but is not limited to other types of genetic modifications, e.g., introduction of stop codons, frame shift mutations, introduction or removal of portions of the gene, and introduction of a degradation signal, those genetic modifications affecting mRNA transcription levels and/or stability, and altering the promoter or repressor upstream of the gene encoding the enzyme.

Bio-production or fermentation, as used herein, may be aerobic, microaerobic, or anaerobic.

When the genetic modification of a gene product, e.g., an enzyme, is referred to herein, including the claims, it is understood that the genetic modification is of a nucleic acid sequence, such as or including the gene, that normally encodes the stated gene product, e.g., the enzyme.

As used herein, the term "metabolic flux" and the like refers to changes in metabolism that lead to changes in product and/or byproduct formation, including production rates, production titers and production yields from a given substrate.

Species and other phylogenic identifications are according to the classification known to a person skilled in the art of microbiology.

Enzymes are listed here within, with reference to a Universal Protein Resource (Uniprot) identification number, which would be well known to one skilled in the art (Uniprot is maintained by and available through the UniProt Consortium).

Where methods and steps described herein indicate certain events occurring in certain order, those of ordinary skill in the art will recognize that the ordering of certain steps may be modified and that such modifications are in accordance with the variations of the invention. Additionally, certain steps may be performed concurrently in a parallel process when possible, as well as performed sequentially.

The meaning of abbreviations is as follows: "C" means Celsius or degrees Celsius, as is clear from its usage, DCW means dry cell weight, "s" means second(s), "min" means minute(s), "h," "hr," or "hrs" means hour(s), "psi" means pounds per square inch, "nm" means nanometers, "d" means day(s), "μL" or "uL" or "ul" means microliter(s), "mL" means milliliter(s), "L" means liter(s), "mm" means millimeter(s), "nm" means nanometers, "mM" means millimolar, "μM" or "uM" means micromolar, "M" means molar, "mmol" means millimole(s), "μmol" or "uMol" means micromole(s), "g" means gram(s), "μg" or "ug" means microgram(s) and "ng" means nanogram(s), "PCR" means polymerase chain reaction, "OD" means optical density, "OD_{600}" means the optical density measured at a photon wavelength of 600 nm, "kDa" means kilodaltons, "g" means the gravitation constant, "bp" means base pair(s), "kbp" means kilobase pair(s), "% w/v" means weight/volume percent, "% v/v" means volume/volume percent, "IPTG" means isopropyl-μ-D-thiogalactopyranoiside, "aTc" means anhydrotetracycline, "RBS" means ribosome binding site, "rpm" means revolutions per minute, "HPLC" means high performance liquid chromatography, and "GC" means gas chromatography.

Overview

Provided herein is a high-throughput metabolic engineering platform enabling the rapid optimization of microbial production strains. The platform, which bridges a gap between current in vivo and in vitro bio-production approaches, relies on dynamic minimization of the active metabolic network. Dynamic metabolic network minimization can be accomplished using combinations of CRISPR interference and controlled proteolysis to reduce the activity of multiple enzymes in essential central metabolism. Minimization can be implemented in the context of standardized 2-stage bio-processes. This approach not only can result in a design space with greatly reduced complexity, but also in increased metabolic fluxes and production rates as well as in strains which are robust to environmental conditions. Robustness can lead to predictable scalability from high-throughput small-scale screens, or "micro-fermentations", to fully instrumented bioreactors. Predictive high-throughput approaches may be critical for metabolic engineering programs to truly take advantage of the rapidly increasing throughput and decreasing costs of synthetic biology. The examples provided herein have not only demonstrated proof of principle for this approach in the common industrial microbe: *E. coli*, and has validated this approach with the rapid optimization of *E. coli* strains producing two important industrial chemicals: alanine and mevalonic acid, at commercially meaningful rates, titers (147 g/L and 97 g/L, respectively), and yields.

Also provided herein are systems and methods to rapidly optimize a microorganism for chemical productions in a high-throughput fashion.

Also provided herein are microorganisms that can be used with the disclosed platform and/or methods for chemical productions.

Synthetic Metabolic Valves (SMVs)

The current disclosure describes the construction of synthetic metabolic valves (SMVs) comprising one or more or a combination of the following: controlled gene silencing and controlled proteolysis. It is appreciated that one well skilled in the art is aware of several methodologies for gene silencing and controlled proteolysis.

The development of platform microbial strains that utilize SMVs can decouple growth from product formation. These strains enable the dynamic control of metabolic pathways, including those that when altered have negative effects on microorganism growth. Dynamic control over metabolism is accomplished via a combination of methodologies including but not limited to transcriptional silencing and controlled enzyme proteolysis. These microbial strains are utilized in a multi-stage bioprocess encompassing as least two stages, the first stage in which microorganisms are grown and metabolism can be optimized for microbial growth and at least one other stage in which growth can be slowed or stopped, and dynamic changes can be made to metabolism to improve production of desired product, such as a chemical or fuel. The transition of growing cultures between stages and the manipulation of metabolic fluxes can be controlled by artificial chemical inducers or preferably by controlling the level of key limiting nutrients. In addition, genetic modifications may be made to provide metabolic pathways for the biosynthesis of one or more chemical or fuel products. Also, genetic modifications may be made to enable the utilization of a variety of carbon feedstocks including but not limited sugars such as glucose, sucrose, xylose, arabinose, mannose, and lactose, oils, carbon dioxide, carbon monoxide, methane, methanol and formaldehyde.

This approach allows for simpler models of metabolic fluxes and physiological demands during a production phase, turning a growing cell into a stationary phase biocatalyst. These synthetic metabolic valves can be used to turn off essential genes and redirect carbon, electrons and energy flux to product formation in a multi-stage fermentation process. One or more of the following enables these synthetic valves: 1) transcriptional gene silencing or repression technologies in combination with 2) inducible enzyme degradation and 3) nutrient limitation to induce a stationary or non-dividing cellular state. SMVs are generalizable to any pathway and microbial host. These synthetic metabolic valves allow for novel rapid metabolic engineering strategies useful for the production of renewable chemicals and fuels and any product that can be produced via whole cell catalysis.

In various cases, one SMV can refer to the manipulation of one gene (or its protein product). The manipulation can be controlled silencing of the gene and/or controlled degradation of its protein product. In certain cases, combination of SMVs can lead to improved production in yields, rate and/or robustness, which includes manipulation of two genes (or their protein products). In some cases, an engineered microorganism comprises at least one SMV. In some cases, an engineered microorganism comprises more than one SMV. In some cases, an engineered microorganism comprises two, three, four, five, six, seven, eight, nine, or ten, or more SMVs.

Method and Systems for Bio-Production

Provided herein are methods or systems for robust large scale production of molecules from biologics and small molecule therapeutics to specialty, bulk and commodity chemicals, and biofuels. The methods or systems provided herein comprise using engineered microorganism which comprises a limited set of metabolic enzymes. In some embodiments, the engineered microorganism comprises at least one metabolic enzyme that has reduced level or activity. In some embodiments, the engineered microorganism comprises two, three, four, five, six, seven, eight, nine, or ten, or more metabolic enzymes that have reduced level or activity. The methods and systems provided herein can reduce metabolic responses to environmental conditions and can be easily transferred from small scale (e.g. mgs) production to large scale (e.g. kgs) production. The methods and systems provided herein can reduce the time and costs associated with transitioning from small scale (e.g. mgs) to large scale (e.g. kgs) production.

Within the scope of the current disclosure are genetically modified microorganism, wherein the microorganism is capable of producing a product derived from any key metabolic intermediate including but not limited to malonyl-CoA, pyruvate, oxaloacetate, erthyrose-4-phosphate, xylulose-5-phosphate, alpha-ketoglutarate and citrate at a specific rate selected from the rates of greater than 0.05 g/gDCW-hr, 0.08 g/gDCW-hr, greater than 0.1 g/gDCW-hr, greater than 0.13 g/gDCW-hr, greater than 0.15 g/gDCW-hr, greater than 0.175 g/gDCW-hr, greater than 0.2 g/gDCW-hr, greater than 0.25 g/gDCW-hr, greater than 0.3 g/gDCW-hr, greater than 0.35 g/gDCW-hr, greater than 0.4 g/gDCW-hr, greater than 0.45 g/gDCW-hr, or greater than 0.5 g/gDCW-hr.

In various embodiments, the invention includes a culture system comprising a carbon source in an aqueous medium and a genetically modified microorganism, wherein said genetically modified organism is present in an amount selected from greater than 0.05 gDCW/L, 0.1 gDCW/L, greater than 1 gDCW/L, greater than 5 gDCW/L, greater than 10 gDCW/L, greater than 15 gDCW/L or greater than 20 gDCW/L, such as when the volume of the aqueous medium is selected from greater than 5 mL, greater than 100 mL, greater than 0.5 L, greater than 1 L, greater than 2 L, greater than 10 L, greater than 250 L, greater than 1000 L, greater than 10,000 L, greater than 50,000 L, greater than 100,000 L or greater than 200,000 L, and such as when the volume of the aqueous medium is greater than 250 L and contained within a steel vessel.

Carbon Sources

Bio-production media, which is used in the present invention with recombinant microorganisms must contain suitable carbon sources or substrates for both growth and production stages. Suitable substrates may include, but are not limited to glucose, sucrose, xylose, mannose, arabinose, oils, carbon dioxide, carbon monoxide, methane, methanol, formaldehyde and glycerol. It is contemplated that all of the above mentioned carbon substrates and mixtures thereof are suitable in the present invention as a carbon source(s).

Microorganisms

Features as described and claimed herein may be provided in a microorganism selected from the listing herein, or another suitable microorganism, that also comprises one or more natural, introduced, or enhanced product bio-production pathways. Thus, in some embodiments the microorganism(s) comprise an endogenous product production pathway (which may, in some such embodiments, be enhanced), whereas in other embodiments the microorganism does not comprise an endogenous product production pathway.

The examples describe specific modifications and evaluations to certain bacterial and fungal microorganisms. The scope of the invention is not meant to be limited to such species, but to be generally applicable to a wide range of suitable microorganisms.

Suitable host cells or host microorganisms for bio-production can be either prokaryotic or eukaryotic. Suitable host cells or host microorganisms can be bacteria such as *Citrobacter, Enterobacter, Clostridium, Klebsiella, Aerobacter, Lactobacillus, Aspergillus, Saccharomyces, Schizosaccharomyces, Zygosaccharomyces, Pichia, Kluyveromyces, Candida, Hansenula, Debaryomyces, Mucor, Torulopsis, Methylobacter, Escherichia, Salmonella, Bacillus, Streptomyces*, and *Pseudomonas*. In some embodiments, a host cell or an engineered cell is *E. coli*. In some embodiments, a host cell or an engineered cell is *S. cerevisiae*.

In certain aspects, provided herein is a microorganism genetically modified to comprise: a production pathway comprising at least one enzyme for the biosynthesis of a product, and a combination of multiple synthetic metabolic valves to controllably reduce or eliminate flux through multiple metabolic pathways. In some embodiments, each of the multiple synthetic metabolic valves comprises one or more genes for (i) controlled silencing of gene expression of at least one gene or (ii) the controlled proteolytic inactivation of at least one protein. In some embodiments, a rate of the biosynthesis of the product is increased in a productive stationary phase upon a depletion of a nutrient, wherein the depletion of the nutrient induces the multiple synthetic metabolic valves. In some cases, the controlled silencing of gene expression is accomplished by RNA interference, CRISPR interference or transcriptional repression. In some cases, the controlled proteolytic inactivation is accomplished by protein cleavage by a specific protease or targeted degradation by specific peptide tags. In some cases, the nutrient is phosphate, nitrogen, sulfur, magnesium, or a combination thereof.

In certain aspects, provided herein is a genetically modified microorganism comprising: a production pathway comprising at least one enzyme for the biosynthesis of a product from one of the following metabolites: pyruvate, acetolactate, acetyl-CoA, acetoacetyl-CoA or malonyl-CoA; and a combination of multiple synthetic metabolic valves, wherein each of the multiple synthetic metabolic valves comprises one of a fabI, gltA, lpd, zwf or udhA gene for (i) controlled silencing of gene expression of a corresponding one of said fabI, gltA, lpd, zwf or udhA genes or (ii) controlled proteolytic inactivation of a protein encoded by a corresponding one of said fabI, gltA, lpd, zwf or udhA genes. In some embodiments, a rate of the biosynthesis of the product is increased in a productive stationary phase upon a depletion of a nutrient, wherein the depletion of the nutrient induces the multiple synthetic metabolic valves. In some embodiments, the product is alanine or a derivative thereof. In some embodiments, the product is mevalonate or a derivative thereof. In some embodiments, the product is malonic acid or a derivative thereof. In some embodiments, the nutrient is phosphate, nitrogen, sulfur, magnesium, or a combination thereof.

In certain aspects, provided herein is a genetically modified microorganism comprising: a production pathway to produce alanine from pyruvate; and a combination of multiple synthetic metabolic valves, wherein each of the multiple synthetic metabolic valves comprises one of a fabI, gltA, lpd, zwf or udhA gene for (i) controlled silencing of gene expression of a corresponding one of said fabI, gltA, lpd, zwf or udhA genes or (ii) controlled proteolytic inactivation of a protein encoded by one of said fabI, gltA, lpd, zwf or udhA genes. In some embodiments, a rate of the biosynthesis of alanine is increased in a productive stationary phase upon a depletion of a nutrient, wherein the depletion of the nutrient induces the multiple synthetic metabolic valves. In some embodiments, the nutrient is phosphate, nitrogen, sulfur, magnesium, or a combination thereof.

In some cases, a genetically modified microorganism is a heterologous cell. In some cases, provided herein is a heterologous cell for generating a product. In some cases, a heterologous cell comprises an engineered valve polynucleotide for mediating controlled reduction of expression of a valve enzyme acting in a metabolic pathway. In certain cases, a controlled reduction of expression of a valve enzyme reduces flux through a metabolic pathway, wherein the controlled reduction of expression of the valve enzyme induces a stationary phase of the heterologous cell. In some cases, a heterologous cell further comprises an engineered production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of the product. In some situations, a heterologous cell comprises an engineered valve polynucleotide for mediating controlled reduction of expression of a valve enzyme acting in a metabolic pathway, wherein a rate of production of a product during a stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the controlled reduction of expression of the valve enzyme.

In some cases, provided herein is a heterologous cell for generating a product, wherein said cell comprises: an engineered valve polynucleotide for mediating controlled reduction of expression of a valve enzyme acting in a metabolic pathway, wherein said controlled reduction of expression of said valve enzyme reduces flux through said metabolic pathway, wherein said controlled reduction of expression of said valve enzyme induces a stationary phase of said cell; and an engineered production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of said product; wherein a rate of production of said product during said stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking said controlled reduction of expression of said valve enzyme.

In some cases, provided herein is a cell comprising a reduced expression or activity of a valve enzyme, wherein the valve enzyme comprises an enzyme selected from the group consisting of enoyl-ACP/CoA reductase (fabI), glucose-6-phosphate dehydrogenase (zwf), lipoamide dehydrogenase (lpd), citrate synthase (gltA), soluble transhydrogenase (udhA), NADH-dependent glyceraldehyde-3-phosphate dehydrogenase (gapA), and a combination thereof.

In some cases, provided herein is a cell comprising a production enzyme, wherein the production enzyme comprises an enzyme selected from the group consisting of NADPH-dependent alanine dehydrogenase (ald), alanine exporter (alaE), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (gapN), and a combination thereof.

Environmental Conditions

Environmental conditions can comprise medium and culture conditions. Environmental factors that may influence production can be temperature, pH, acidity, ethanol, sulfite, and availability of nutrients.

In addition to an appropriate carbon source, such as selected from one of the herein disclosed types, bio-production media may contain suitable minerals, salts, cofactors, buffers and other components, known to those skilled in the art, suitable for the growth of the cultures and promotion of the enzymatic pathway necessary for chemical product bio-production under the present disclosure. Another aspect of the invention regards media and culture conditions that comprise genetically modified microorganisms of the invention and optionally supplements.

Typically cells are grown at a temperature in the range of about 25° C. to about 40° C. in an appropriate medium, as well as up to 70° C. for thermophilic microorganisms. Suitable growth media are well characterized and known in the art.

Suitable pH ranges for the bio-production are between pH 2.0 to pH 10.0, where pH 6.0 to pH 8.0 is a typical pH range for the initial condition. However, the actual culture conditions for a particular embodiment are not meant to be limited by these pH ranges.

Bio-productions may be performed under aerobic, microaerobic or anaerobic conditions with or without agitation.

In some cases, a change of an environmental condition comprises a change in sugar concentration of a culture medium contacting a cell. In some cases, a change in sugar concentration of a culture medium is an increase of sugar concentration. In some other cases, a change in sugar concentration is a decrease of sugar concentration. In some situations, an increase of sugar concentration is from 1% to 2%, from 2% to 3%, from 3% to 4%, from 4% to 5%, from 5% to 10%, from 10% to 15%, from 15% to 20%, from 20% to 30%, from 30% to 40%, from 40% to 50%, from 50% to 60%, from 60% to 70%, from 70% to 80%, from 80% to 90%, or from 90% to 100% more sugar compared with the original sugar concentration in the culture medium. In some situations, a decrease of sugar concentration is from 1% to 2%, from 2% to 3%, from 3% to 4%, from 4% to 5%, from 5% to 10%, from 10% to 15%, from 15% to 20%, from 20% to 30%, from 30% to 40%, from 40% to 50%, from 50% to 60%, from 60% to 70%, from 70% to 80%, from 80% to 90%, or from 90% to 100% less sugar compared with the original sugar concentration in the culture medium.

In some cases, a change of an environmental condition comprises a change in oxygenation of a culture medium contacting a cell. In some cases, a change in oxygenation of a culture medium is an increase of oxygenation. In some other cases, a change in oxygenation of a culture medium is a decrease of oxygenation. In some situations, an increase of oxygenation is the addition of oxygen from 1% to 2%, from 2% to 3%, from 3% to 4%, from 4% to 5%, from 5% to 10%, from 10% to 15%, from 15% to 20%, from 20% to 30%, from 30% to 40%, from 40% to 50%, from 50% to 60%, from 60% to 70%, from 70% to 80%, from 80% to 90%, or from 90% to 100% more than the original amount of oxygen added in a culture medium. In some situations, a decrease of oxygenation is the addition of oxygen from 1% to 2%, from 2% to 3%, from 3% to 4%, from 4% to 5%, from 5% to 10%, from 10% to 15%, from 15% to 20%, from 20% to 30%, from 30% to 40%, from 40% to 50%, from 50% to 60%, from 60% to 70%, from 70% to 80%, from 80% to 90%, or from 90% to 100% less than the original amount of oxygen added in a culture medium.

Bio-Production Reactors and Systems

Fermentation systems utilizing methods and/or compositions according to the invention are also within the scope of the invention.

Any of the recombinant microorganisms as described and/or referred to herein may be introduced into an industrial bio-production system where the microorganisms convert a carbon source into a product in a commercially viable operation. The bio-production system includes the introduction of such a recombinant microorganism into a bioreactor vessel, with a carbon source substrate and bio-production media suitable for growing the recombinant microorganism, and maintaining the bio-production system within a suitable temperature range (and dissolved oxygen concentration range if the reaction is aerobic or microaerobic) for a suitable time to obtain a desired conversion of a portion of the substrate molecules to a selected chemical product. Bio-productions may be performed under aerobic, microaerobic, or anaerobic conditions, with or without agitation. Industrial bio-production systems and their operation are well-known to those skilled in the arts of chemical engineering and bioprocess engineering. The amount of a product produced in a bio-production media generally can be determined using a number of methods known in the art, for example, high performance liquid chromatography (HPLC), gas chromatography (GC), or GC/Mass Spectroscopy (MS).

Genetic Modifications, Nucleotide Sequences, and Amino Acid Sequences

Embodiments of the present disclosure may result from introduction of an expression vector into a host microorganism, wherein the expression vector contains a nucleic acid sequence coding for an enzyme that is, or is not, normally found in a host microorganism.

The ability to genetically modify a host cell is essential for the production of any genetically modified (recombinant) microorganism. The mode of gene transfer technology may be by electroporation, conjugation, transduction, or natural transformation. A broad range of host conjugative plasmids and drug resistance markers are available. The cloning vectors are tailored to the host organisms based on the nature of antibiotic resistance markers that can function in that host. Also, as disclosed herein, a genetically modified (recombinant) microorganism may comprise modifications other than via plasmid introduction, including modifications to its genomic DNA.

More generally, nucleic acid constructs can be prepared comprising an isolated polynucleotide encoding a polypeptide having enzyme activity operably linked to one or more (several) control sequences that direct the expression of the coding sequence in a microorganism, such as *E. coli*, under conditions compatible with the control sequences. The isolated polynucleotide may be manipulated to provide for expression of the polypeptide. Manipulation of the polynucleotide's sequence prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotide sequences utilizing recombinant DNA methods are well established in the art.

The control sequence may be an appropriate promoter sequence, a nucleotide sequence that is recognized by a host cell for expression of a polynucleotide encoding a polypeptide of the present disclosure. The promoter sequence may contain transcriptional control sequences that mediate the expression of the polypeptide. The promoter may be any nucleotide sequence that shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell. The techniques for modifying and utilizing recombinant DNA promoter sequences are well established in the art.

For various embodiments of the invention the genetic manipulations may be described to include various genetic manipulations, including those directed to change regulation of, and therefore ultimate activity of, an enzyme or enzymatic activity of an enzyme identified in any of the respective pathways. Such genetic modifications may be directed to transcriptional, translational, and post-translational modifications that result in a change of enzyme activity and/or selectivity under selected and/or identified culture conditions and/or to provision of additional nucleic acid sequences such as to increase copy number and/or mutants of an enzyme related to product production. Specific methodologies and approaches to achieve such genetic modification are well known to one skilled in the art.

In various embodiments, to function more efficiently, a microorganism may comprise one or more gene deletions.

For example, in *E. coli*, the genes encoding the lactate dehydrogenase (ldhA), phosphate acetyltransferase (pta), pyruvate oxidase (poxB), pyruvateformate lyase (pflB), methylglyoxal synthase (mgsA), acetate kinase (ackA), alcohol dehydrogenase (adhE), the clpXP protease specificity enhancing factor (sspB), the ATPdependent Lon protease (lon), the outer membrane protease (ompT), the arcA transcriptional dual regulator (arcA), and the iclR transcriptional regulator (iclR) may be disrupted, including deleted. Such gene disruptions, including deletions, are not meant to be limiting, and may be implemented in various combinations in various embodiments. Gene deletions may be accomplished by numerous strategies well known in the art, as are methods to incorporate foreign DNA into a host chromosome.

In various embodiments, to function more efficiently, a microorganism may comprise one or more synthetic metabolic valves, composed of enzymes targeted for controlled proteolysis, expression silencing or a combination of both controlled proteolysis and expression silencing. In some embodiments, a microorganism may comprise two, three, four, five, six, seven, eight, nine, or ten, or more synthetic metabolic valves. For example, one enzyme encoded by one gene or a combination of numerous enzymes encoded by numerous genes in *E. coli* may be designed as synthetic metabolic valves to alter metabolism and improve product formation. Representative genes in *E. coli* may include but are not limited to the following: fabl, zwf gltA, ppc, udhA, lpd, sucD, aceA, pfkA, lon, rpoS, tktA or tktB. It is appreciated that it is well known to one skilled in the art how to identify homologues of these genes and or other genes in additional microbial species.

For all nucleic acid and amino acid sequences provided herein, it is appreciated that conservatively modified variants of these sequences are included, and are within the scope of the invention in its various embodiments. Functionally equivalent nucleic acid and amino acid sequences (functional variants), which may include conservatively modified variants as well as more extensively varied sequences, which are well within the skill of the person of ordinary skill in the art, and microorganisms comprising these, also are within the scope of various embodiments of the invention, as are methods and systems comprising such sequences and/or microorganisms.

Accordingly, as described in various sections above, some compositions, methods and systems of the present disclosure comprise providing a genetically modified microorganism that comprises both a production pathway to make a desired product from a central intermediate in combination with synthetic metabolic valves to redistribute flux.

Aspects of the invention also regard provision of multiple genetic modifications to improve microorganism overall effectiveness in converting a selected carbon source into a selected product. Particular combinations are shown, such as in the Examples, to increase specific productivity, volumetric productivity, titer and yield substantially over more basic combinations of genetic modifications. In addition to the above-described genetic modifications, in various embodiments genetic modifications, including synthetic metabolic valves also are provided to increase the pool and availability of the cofactor NADPH and/or NADH which may be consumed in the production of a product.

More generally, and depending on the particular metabolic pathways of a microorganism selected for genetic modification, any subgroup of genetic modifications may be made to decrease cellular production of fermentation product(s) other than the desired fermentation product, selected from the group consisting of acetate, acetoin, acetone, acrylic, malate, fatty acid ethyl esters, isoprenoids, glycerol, ethylene glycol, ethylene, propylene. butylene, isobutylene, ethyl acetate, vinyl acetate, other acetates, 1,4-butanediol, 2,3-butanediol, butanol, isobutanol, sec-butanol, butyrate, isobutyrate, 2-OH-isobutyrate, 3-OHbutyrate, ethanol, isopropanol, D-lactate, L-lactate, pyruvate, itaconate, levulinate, glucarate, glutarate, caprolactam, adipic acid, propanol, isopropanol, fusel alcohols, and 1,2-propanediol, 1,3-propanediol, formate, fumaric acid, propionic acid, succinic acid, valeric acid, maleic acid and poly-hydroxybutyrate. Gene deletions may be made as disclosed generally herein, and other approaches may also be used to achieve a desired decreased cellular production of selected fermentation products other than the desired products.

VI.A Gene Silencing

In particular the invention describes the use of controlled gene silencing to help enable the control over metabolic fluxes in controlled multi-stage fermentation processes. There are several methodologies known in the art for controlled gene silencing, including but not limited to mRNA silencing or RNA interference, silencing via transcriptional repressors and CRISPR interference.

In some cases, a valve polynucleotide comprises a polynucleotide selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding said valve enzyme; a degradation polynucleotide for mediating cellular degradation of said valve enzyme; and a combination thereof.

In some cases, a valve polynucleotide comprises a silencing polynucleotide, and said silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter of a gene encoding said valve enzyme.

In some cases, a valve polynucleotide further encodes a CRISPR enzyme, wherein said CRISPR enzyme specifically binds to said promoter sequence when bound to said gRNA. In some cases, a CRISPR enzyme is catalytically inactive.

In some cases, a valve polynucleotide comprises a degradation polynucleotide, wherein said degradation polynucleotide comprises a sequence encoding a degradation tag, wherein said degradation tag mediates degradation of said valve enzyme. In some cases, the expression of a valve polynucleotide is regulated by phosphate availability in a cell. In some cases, the expression of a production polynucleotide is regulated by phosphate availability in a cell. In certain cases, the cell is an *E. coli* cell.

Controlled Proteolysis

In particular the current disclosure describes the use of controlled protein degradation or proteolysis to help enable the control over metabolic fluxes in controlled multi-stage fermentation processes. There are several methodologies known in the art for controlled protein degradation, including but not limited to targeted protein cleavage by a specific protease and controlled targeting of proteins for degradation by specific peptide tags. Systems for the use of the *E. coli* clpXP protease for controlled protein degradation can be used. This methodology relies upon adding a specific C-terminal peptide tag such as a DAS4 (or DAS+4) tag. Proteins with this tag are not degraded by the clpXP protease until the specificity enhancing chaperone sspB is expressed. sspB induces degradation of DAS4 tagged proteins by the clpXP protease. In additional numerous site specific protease systems are well known in the art. Proteins can be engineered to contain a specific target site of a given protease and then cleaved after the controlled expression of the protease. In some embodiments the cleavage can be expected lead to protein inactivation or degradation. For example, an N-terminal sequence can be added to a protein of interest to enable clpS dependent clpAP degradation. In addition, this sequence can further be masked by an additional N-terminal sequence, which can be controllable cleaved such as by a ULP hydrolase. This allows for controlled N-rule degradation dependent on hydrolase expression. It is therefore possible to tag proteins for controlled proteolysis either at the N-terminus or C-terminus.

The preference of using an N-terminal vs. C-terminal tag will largely depend on whether either tag affects protein function prior to the controlled onset of degradation. The invention describes the use of controlled protein degradation or proteolysis to help enable the control over metabolic fluxes in controlled multi-stage fermentation processes, in *E. coli*. There are several methodologies known in the art for controlled protein degradation in other microbial hosts, including a wide range of gram-negative as well as gram-positive bacteria, yeast and even archaea. In particular, systems for controlled proteolysis can be transferred from a native microbial host and used in a non-native host.

Synthetic Metabolic Valve Control

In particular the current disclosure describes the use of synthetic metabolic valves to control metabolic fluxes in multi-stage fermentation processes. There are numerous methodologies known in the art to induce expression that can be used at the transition between stages in multistage fermentations. These include but are not limited to artificial chemical inducers including: tetracycline, anhydrotetracycline, lactose, IPTG (isopropyl-beta-D-1-thiogalactopyranoside), arabinose, raffinose, tryptophan and numerous others. Systems linking the use of these well known inducers to the control of gene expression silencing and/or controlled proteolysis can be integrated into genetically modified microbial systems to control the transition between growth and production phases in multi-stage fermentation processes.

In addition, it may be desirable to control the transition between growth and production in multi-stage fermentations by the depletion of one or more limiting nutrients that are consumed during growth. Limiting nutrients can include but are not limited to: phosphate, nitrogen, sulfur and magnesium. Natural gene expression systems that respond to these nutrient limitations can be used to operably link the control of gene expression silencing and/or controlled proteolysis to the transition between growth and production phases in multi-stage fermentation processes.

Products

In some embodiments, provided herein is a microorganism or a cell for producing a product. In some cases, the product comprises 3-hydroxypropionic acid. In some cases, the product comprises an amino acid. In some cases, the amino acid comprises alanine. In some cases, the alanine is L-alanine. In some cases, the alanine is D-alanine. In some cases, a rate of production of alanine is at least 0.1 g/L/hr, 0.2 g/L/hr, 0.3 g/L/hr, 0.4 g/L/hr, 0.5 g/L/hr, 0.6 g/L/hr, 0.7 g/L/hr, 0.8 g/L/hr, 0.9 g/L/hr, 1.0 g/L/hr, 1.1 g/L/hr, 1.2 g/L/hr, 1.3 g/L/hr, 1.4 g/L/hr, 1.5 g/L/hr, 1.6 g/L/hr, 1.7 g/L/hr, 1.8 g/L/hr, 1.9 g/L/hr, 2.0 g/L/hr, 2.5 g/L/hr, 3.0 g/L/hr, 3.5 g/L/hr, 4.0 g/L/hr, 4.5 g/L/hr, 5.0 g/L/hr, 5.5 g/L/hr, 6.0 g/L/hr, 7.0 g/L/hr, 8.0 g/L/hr, 9.0 g/L/hr, or at least 10 g/L/hr.

In some cases, the alanine titers after 24 hours can be from 0 to 0.5 g/L, 0.5 g/L to 1 g/L, 1 g/L to 1.5 g/L, 1.5 g/L to 2 g/L, 2 g/L to 2.5 g/L, 2.5 g/L to 3 g/L, 3 g/L to 3.5 g/L, 3.5 g/L to 4 g/L, 4 g/L to 4.5 g/L, 4.5 g/L to 5 g/L, or from 5 g/L to 10 g/L. The dynamic range of alanine production offered by SMVs can be up to a 4-fold increase compared to that offered by solely altering the expression level of the production pathway enzymes (by changing the promoter). In some cases, the dynamic range of alanine production offered by SMVs can be up to a 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold increase compared to that offered by solely altering the expression level of the production pathway enzymes.

In some cases, a production polynucleotide in the microorganism encodes an alanine exporter. In some cases, the alanine exporter is alaE.

In some cases, the product comprises mevalonic acid. In some cases, a rate of production of mevalonic acid is at least 0.1 g/L/hr, 0.2 g/L/hr, 0.3 g/L/hr, 0.4 g/L/hr, 0.5 g/L/hr, 0.6 g/L/hr, 0.7 g/L/hr, 0.8 g/L/hr, 0.9 g/L/hr, 1.0 g/L/hr, 1.1 g/L/hr, 1.2 g/L/hr, 1.3 g/L/hr, 1.4 g/L/hr, 1.5 g/L/hr, 1.6 g/L/hr, 1.7 g/L/hr, 1.8 g/L/hr, 1.9 g/L/hr, 2.0 g/L/hr, 2.5 g/L/hr, 3.0 g/L/hr, 3.5 g/L/hr, 4.0 g/L/hr, 4.5 g/L/hr, 5.0 g/L/hr, 5.5 g/L/hr, 6.0 g/L/hr, 7.0 g/L/hr, 8.0 g/L/hr, 9.0 g/L/hr, or at least 10 g/L/hr.

Methods

Provided herein are methods for producing a product in an engineered microorganism in a large scale. Also provided herein are methods for engineering microorganisms for large-scale production of a product in a high-throughput fashion.

In some cases, provided herein is a method, comprising: culturing a plurality of strains of a cell, wherein each strain of said plurality of strains comprises (i) an engineered valve polynucleotide for mediating controlled reduction of expression of a valve enzyme acting in a metabolic pathway, wherein said controlled reduction of expression of said valve enzyme reduces flux through said metabolic pathway; and (ii) an engineered production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of said product; wherein each strain of said plurality of strains differs from another strain in a sequence of at least one of said engineered valve polynucleotide or said engineered production polynucleotide; measuring a level of said product generated by each of said plurality of strains; and selecting a strain based on said level of said product. In some embodiments, the method further comprises growing said selected strain in a bioreactor. In some embodiments, a culture medium comprising said selected strain has a volume of at least 100 ml, 200 ml, 300 ml, 400 ml, 500 ml, 600 ml, 700 ml, 800 ml, 900 ml, or at least 1000 ml. In some embodiments, a culture medium has a volume of at least 1 L.

In some embodiments, a valve polynucleotide comprises a polynucleotide selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding said valve enzyme; a degradation polynucleotide for mediating cellular degradation of said valve enzyme; and a combination thereof. In some embodiments, a first and a second strain of said plurality of strains comprise a silencing polynucleotide. In some embodiments, a silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter of a gene encoding said valve enzyme. In some embodiments, a gRNA sequence differs between said first and second strains. In some embodiments, a promoter recognized by said gRNA differs between said first and second strains. In some embodiments, a first strain comprises said silencing polynucleotide and said degradation polynucleotide, and a second strain comprises said silencing polynucleotide but does not comprise said degradation polynucleotide. In some embodiments, a level of product is greater in said second strain than said first strain. In some embodiments, a level of product is greater in said first strain than said second strain. In some embodiments, a valve enzyme comprises an enzyme selected from the group consisting of enoyl-ACP/CoA reductase (fabI), glucose-6-phosphate dehydrogenase (zwf), lipoamide dehydrogenase (lpd), citrate synthase (gltA), soluble transhydrogenase (udhA), NADH-dependent glyceraldehyde-3-phosphate dehydrogenase (gapA), and a combination thereof. In some embodiments, a production enzyme comprises an enzyme selected from the group consisting of NADPH-dependent alanine dehydrogenase (ald), alanine exporter (alaE), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (gapN), and a combination thereof.

In some embodiments, a product is selected from the group consisting of mevalonic acid, 3-hydroxypropionic acid, an amino acid, and a combination thereof. In some embodiments, the amino acid is alanine. In some embodiments, the alanine is L-alanine. In some embodiments, the alanine is D-alanine.

In some embodiments, a rate of production of the product during said stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking said controlled reduction of expression of said valve enzyme.

In some embodiments, a change of an environmental condition comprises a change in a sugar concentration of a culture medium contacting said cell.

In some embodiments, a change of an environmental condition comprises a change in oxygenation of a culture medium contacting said cell.

In some cases, provided herein is a method of generating a cellular product comprising: culturing a heterologous cell in a culture medium, wherein said heterologous cell comprises: (i) an engineered valve polynucleotide for mediating controlled reduction of expression of a valve enzyme acting in a metabolic pathway, wherein said controlled reduction of expression of said valve enzyme reduces flux through said metabolic pathway, wherein said controlled reduction of expression of said valve enzyme induces a stationary phase of said cell; and (ii) an engineered production polynucleotide for mediating controlled increase in expression of a production enzyme for generation of said product; wherein a rate of production of said product during said stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking said controlled reduction of expression of said valve enzyme. In some embodiments, the method further comprises changing said environmental condition. In some embodiments, the environmental condition comprises a sugar concentration of said culture medium, and changing said environmental condition comprises increasing or decreasing said sugar concentration. In some cases, said sugar is glucose, sucrose, lactose, maltose, xylose, mannitol, or a combination thereof. In some cases, said sugar is glucose. In some cases, the environmental condition comprises an oxygen concentration of said culture medium, and changing said environmental condition comprises increasing or decreasing said oxygen concentration. In some cases, said culturing is performed in a bioreactor.

In some cases, said culture medium has a volume of at least 100 ml, 200 ml, 300 ml, 400 ml, 500 ml, 600 ml, 700 ml, 800 ml, 900 ml, or at least 1000. In some cases, said culture medium has a volume of at least 1 L. In some case, said product comprises 3-hydroxypropionic acid. In some cases, said product comprises an amino acid. In some cases, said amino acid comprises alanine.

In some cases, a rate of production of said alanine is at least 0.1 g/L/hr, 0.2 g/L/hr, 0.3 g/L/hr, 0.4 g/L/hr, 0.5 g/L/hr, 0.6 g/L/hr, 0.7 g/L/hr, 0.8 g/L/hr, 0.9 g/L/hr, 1.0 g/L/hr, 1.1 g/L/hr, 1.2 g/L/hr, 1.3 g/L/hr, 1.4 g/L/hr, 1.5 g/L/hr, 1.6 g/L/hr, 1.7 g/L/hr, 1.8 g/L/hr, 1.9 g/L/hr, 2.0 g/L/hr, 2.5 g/L/hr, 3.0 g/L/hr, 3.5 g/L/hr, 4.0 g/L/hr, 4.5 g/L/hr, 5.0 g/L/hr, 5.5 g/L/hr, 6.0 g/L/hr, 7.0 g/L/hr, 8.0 g/L/hr, 9.0 g/L/hr, or at least 10 g/L/hr. In some cases, said production polynucleotide encodes an alanine exporter. In some cases, said alanine exporter is alaE. In some cases, said culturing occurs for less than 20 hours, 30 hours, 40 hours, 50 hours, 60 hours, 70 hours, 80 hours, 90 hours, or less than 100 hours. In some cases, said culturing occurs for less than 10 hours, 15 hours, 20 hours, 25 hours, 30 hours, 35 hours, 40 hours, or less than 45 hours. In some cases, said culturing occurs for less than 30 hours.

In some cases, said product comprises mevalonic acid. In some cases, a rate of production of said mevalonic acid is at least 0.1 g/L/hr, 0.2 g/L/hr, 0.3 g/L/hr, 0.4 g/L/hr, 0.5 g/L/hr, 0.6 g/L/hr, 0.7 g/L/hr, 0.8 g/L/hr, 0.9 g/L/hr, 1.0 g/L/hr, 1.1 g/L/hr, 1.2 g/L/hr, 1.3 g/L/hr, 1.4 g/L/hr, 1.5 g/L/hr, 1.6 g/L/hr, 1.7 g/L/hr, 1.8 g/L/hr, 1.9 g/L/hr, 2.0 g/L/hr, 2.5 g/L/hr, 3.0 g/L/hr, 3.5 g/L/hr, 4.0 g/L/hr, 4.5 g/L/hr, 5.0 g/L/hr, 5.5 g/L/hr, 6.0 g/L/hr, 7.0 g/L/hr, 8.0 g/L/hr, 9.0 g/L/hr, or at least 10 g/L/hr. In some cases, said culturing occurs for less than 20 hours, 30 hours, 40 hours, 50 hours, 60 hours, 70 hours, 80 hours, 90 hours, or less than 100 hours. In some cases, said culturing occurs for less than 80 hours.

In some embodiments, a valve polynucleotide comprises a polynucleotide selected from the group consisting of: a silencing polynucleotide for repressing transcription of a gene encoding said valve enzyme; a degradation polynucleotide for mediating cellular degradation of said valve enzyme; and a combination thereof. In some cases, a valve polynucleotide comprises a silencing polynucleotide, and said silencing polynucleotide comprises a guide RNA (gRNA) comprising a gRNA sequence that recognizes a promoter of a gene encoding said valve enzyme. In some cases, a valve polynucleotide further encodes a CRISPR enzyme, wherein said CRISPR enzyme specifically binds to said promoter sequence when bound to said gRNA. In some cases, a CRISPR enzyme is catalytically inactive. In some case, a valve polynucleotide comprises a degradation polynucleotide, wherein said degradation polynucleotide comprises a sequence encoding a degradation tag, wherein said degradation tag mediates degradation of said valve enzyme. In some cases, an expression of said valve polynucleotide is regulated by phosphate. In some cases, an expression of said production polynucleotide is regulated by phosphate. In some cases, said cell is an *E. coli* cell.

Optimization of Bio-Production

Biotechnology based fermentation processes have been successfully developed to produce everything from biologics and small molecule therapeutics to specialty, bulk and commodity chemicals, and even next generation biofuels[1-3]. These processes have made rapid advancements in recent years due to numerous technology developments[4, 5]. It has never been easier to produce new molecules using synthetic biology. Despite these advances, a major challenge remains in taking molecules from proof of concept (POC) to commercially meaningful levels. Strain optimization, or overcoming the "mg" to "kg" hurdle has remained a key barrier to the successful commercialization of bio-processes. After the demonstration of POC, successful bio-process development routinely requires lengthy iterations of both microbial strain and fermentation optimization[6-8] (FIG. 1B). These optimization efforts are often specific to the product or host strain of interest. The throughput of synthetic biology has outpaced that of metabolic engineering, partly due to a lack of broadly useful tools to perform meaningful and standardized optimization of engineered microbial strains in a high-throughput manner[9].

There are numerous challenges in strain optimization and moving past POC levels, not the least of which are the size and complexity of the potential design space. In contrast to simpler gene circuits, amenable to electrical circuit models[10-12], metabolic networks are highly interconnected. Each metabolite and/or enzyme can interact with endless others. This combinatorial complexity results in a huge potential design space, which is intractable to the kinds of systematic experimentation required for the development of standardized design principles (Supplemental Materials, Table 1). The challenges in addressing such a large design space have persisted despite the dramatic advances in, and decreased costs of, reading and writing DNA that have led to new high-throughput DNA assembly and microbial strain construction methods[13-16]. It is not surprising that new synthetic biology technologies involving strain engineering are often demonstrated with easily screened or selected phenotypes[13, 17-19]. Most of these are limited to a focus on optimizing a limited set of pathway specific enzymes.

One approach to overcome the complexity of this challenge is the use of in vitro systems for bio-production, which comprise a limited set of metabolic enzymes. However, these approaches have challenges in replicating key advantages of in vivo systems, including cofactor recycling and energy generation[20, 21]. Another approach to deal with this complexity is to develop faster screening methods for strain evaluation[22]. However, increased throughput alone can never evaluate the full complexity of the potential design space. In addition, results obtained from high-throughput studies often do not translate, even in the same microbe, to a different environment[20, 23, 24]. Small scale screens do not readily translate to larger scale production processes, leading to iterations of process optimization on top of strain optimization (FIG. **1**B). This is because metabolism is highly regulated and can respond, sometimes dramatically, to changes in environmental conditions[25 20, 26-28]. A lack of environmental robustness is traditionally one factor making the scale up of fermentation based processes difficult. This issue has led to the development of specialized complex micro-reactor systems for scale down offering only modest improvements in throughput[20, 29-31].

There remains a significant need for broadly applicable, rapid and robust approaches to greatly reduce the time and costs transitioning from "mgs" to "kgs". Ideally, approaches should be amenable to multiple products and production hosts. Provided herein is the development of a generalizable, high-throughput strain optimization approach that enables the use of truly scalable, standardized fermentation processes. This approach, as outlined in FIG. **1**B, panel b, involves the dynamic minimization of the active metabolic network[32], which combines the benefits of a smaller design space common to in vitro approaches while maintaining the benefits of in vivo biosynthesis[20]. We can isolate and focus on the minimal metabolic networks required for production. Utilizing combinations of synthetic metabolic valves (SMVs)[32, 33] (FIGS. **2**A-D) we can dynamically minimize the metabolic network and redirect metabolic flux in the context of a standardized 2-stage fermentation process[20].

This approach can reduce the complexity of the problem and the size of the relevant design space, greatly speeding up optimization. In various embodiments, it is demonstrated herein that dynamic metabolic network minimization can improve pathway fluxes beyond those achievable with production pathway modifications alone (FIGS. **3**A-K and **6**A-H).

Simultaneously, we demonstrate that dynamic network minimization reduces metabolic responses to environmental conditions, which increases the robustness and scalability of engineered strains (FIGS. **3**A-K and **5**A-J).

EXAMPLES

2-Stage Synthetic Metabolic Valves in *E. coli*

We first developed improved synthetic metabolic valves (SMVs) in *E. coli* that are capable of the dynamic reduction of protein levels in a 2-stage process. These SMVs can be used to reduce levels of key metabolic enzymes (or reduce enzymatic activities of key metabolic enzymes) and rely on controlled proteolysis or CRISPR-based gene silencing or both proteolysis and silencing in combination (FIGS. **2**A-D)[32-35]. Cell growth and dynamic metabolic control can be implemented using phosphate depletion as an environmental trigger. Phosphate can be an ideal candidate as a trigger, as one of the costliest components of minimal media. In addition, stationary phases induced in *E. coli* by phosphate depletion have retained glycolytic uptake as well as increased protein expression[31, 36]. Numerous promoter systems responding to phosphate are well characterized in *E. coli* as well as other microbes including *S. cerevisiae*[37]. Phosphate responsive promoter variants were evaluated (Supplemental Materials, Section 1) and subsequently used for 2-stage control.

SMVs were implemented in *E. coli* using the native Type I-E Cascade CRISPR system for induced gene silencing[34, 38], while controlled proteolysis was induced by incorporating C-terminal degron tags on target proteins, both as previously demonstrated[63, 33] (FIG. **2**A). These systems were introduced into a host strain initially engineered for minimal byproduct formation and high biomass yields and growth rates (*E. coli* strain DLF_0025, Supplemental Materials, Section 3)[24, 27, 28 39]. Using this approach, as FIGS. **2**A-D demonstrate, protein levels can be controlled in 2-stage processes, as exemplified by turning "ON" GFPuv and "OFF" mCherry fluorescent proteins with phosphate depletion in minimal medium. The combination of gene silencing with proteolysis results in the largest rates of protein degradation (FIGS. **2**C-D). The specific impact of gene silencing and proteolysis on decay rates will likely vary depending on the host, target gene/enzyme, and its specific natural turnover rates and expression levels[40, 41].

Metabolic Network Minimization Leads to Improved Fluxes

With the successful demonstration of dynamic control of protein levels in a 2-stage process, we turned to investigate the dynamic control of metabolic fluxes in *E. coli* through controlled reduction of key central metabolic enzymes alone and in combination. Reducing fluxes through thermodynamically favored "committed" reactions in the network is expected to lead to increases in network metabolite pools (Supplemental Materials Section 5), and as a result, changes in pathway fluxes. Enzymes in key committed steps in central metabolic pathways were identified and chosen as initial SMV targets and alanine was chosen as an initial test product (FIGS. **3**A-K). A set of strains were constructed for alanine production (FIG. **3**A), comprising an NADPH-dependent alanine dehydrogenase (ald*)[42]. Variants with multiple combinations of SMVs in central metabolic enzymes were made, with either modifications to induce proteolysis or gene silencing or both in combination.

(Supplemental Materials, Section 3). Together the set of strains having SMVs evaluated in 2-stage processes are identified as "Valve" strains. A panel of alanine "Valve" strains (~500 strains in total) were evaluated for alanine production in standardized, 2-stage, 96-well plate based micro-fermentations (Supplemental Materials, Section 7). Alanine titers after 24 hours of production are given in FIGS. **3**B-C. Briefly, alanine titers after 24 hours ranged from ~0 g/L to ~4.7 g/L, and as expected, varied significantly with respect to the number and combination of SMVs; most SMV combinations lead to improved performance when compared to the control with no SMVs and the alanine pathway alone. In some cases, the alanine titers after 24 hours can be from 0 to 0.5 g/L, 0.5 g/L to 1 g/L, 1 g/L to 1.5 g/L, 1.5 g/L to 2 g/L, 2 g/L to 2.5 g/L, 2.5 g/L to 3 g/L, 3 g/L to 3.5 g/L, 3.5 g/L to 4 g/L, 4 g/L to 4.5 g/L, 4.5 g/L to 5 g/L, or from 5 g/L to 10 g/L. The dynamic range of alanine production offered by SMVs can be up to a 4-fold increase compared to that offered by solely altering the expression level of the production pathway enzymes (by changing the promoter) (Supplemental Materials, Section 7). In some cases, the dynamic range of alanine production offered by SMVs can be up to a 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold increase compared to that offered by solely altering the expression level of the production pathway enzymes. Importantly, the use of proteolysis or silencing alone and/or in combination had significant impacts on production, indicating that for each enzyme the fine tuning of activity using SMVs is critical. One of the best performing strains from the micro-fermentations was then evaluated in a minimal medium, 2-stage, 1 L fermentation with 10 gdcw/L of biomass (FIG. **3**F), which resulted in 80 g/L 100% L-alanine after 48 hours of production with a yield of 0.8 g/g. Further engineering of this strain by overexpressing an alanine exporter (encoded by the *E. coli* alaE gene[43]) resulted in 147 g/L 100% L-alanine after 27 hours of production with a yield within error of theoretical yield~1 g/g, (FIG. **3**G).

Micro-Fermentation Robustness

A central hypothesis was that by restricting metabolism in the production stage, strain performance could not only be improved, but would be more robust to environmental (process) conditions. Simply put, carbon flow is restricted through a minimized metabolic network, which can no longer adapt via cellular responses to the environment. To test this hypothesis, strains were evaluated under different "micro-fermentation" process conditions. Glucose concentration and oxygen transfer rate (key process variables impacting strain performance in traditional fermentations[26]) were varied (FIG. **3**D, Supplemental Materials, Section 8), and alanine production measured. A robustness score (RS) was developed to quantify environmental robustness. Larger RS scores indicate more robust strains. Whereas relative standard deviation (RSD) is one metric for robustness, we wanted to incorporate a stricter measure of robustness which also incorporates the maximal deviation (Max Dev) a strain has under all process conditions (RS, Equation (1)).

$$RS = 100 - \frac{\text{average}(RSD) + \max(Dev)}{2} * 100 \qquad \text{Equation (1)}$$

Robustness scores for a subset of 48 alanine "Valve" strains are given in FIG. **3**E. Results from these experiments studies are tabulated in Supplemental Materials, Section 8. A Chi^2 analysis using a cutoff of RS>0.6 for robustness was used to identify key SMVs which statistically contribute to process robustness. The proteolytic degradation of fabI was a primary contributor to robustness ($Chi^2=13.85$, $P_{value}<0.001$) and as a result, "Valve" strains with proteolytic degradation of fabI were used in further studies. In addition, the "Valve" strains with proteolytic degradation of gltA and/or the combination of the proteolytic degradation of fabI and gltA were found to also be significant contributers of robustness, albeit with a large P_{value}.

2-Stage "Valve" Strains Compared to Traditional Growth Associated Strains

To compare the 2-stage approach enabled by SMVs to more traditional growth associated processes, we constructed 5 strains, with constitutively expressed alanine dehydrogenase (ald*), capable of the growth associated production of alanine. These growth associated strains varied in the strength of the promoter used to drive ald* expression[44] (Supplemental Materials, Section 2), yet utilized the same common no-valve control host strain. FIG. **5** illustrates the results of a direct comparison of "Valve" strains in a 2-stage process compared to "Growth Associated (GA)" strains in a traditional fermentation at the microtiter (FIGS. **5**A-D) and 1 L (FIGS. **5**E-J) scales. In micro-fermentations, 2-stage "Valve" strains outperformed GA strains with respect to titer and process robustness. The most robust GA strain from the micro-fermentation analysis (also with the highest production level) was compared to a robust "Valve" strain in 1 L fermentations with varied process conditions. The "Valve" strains showed consistent performance in all process conditions evaluated (FIG. **5**E), consistent with results from micro-fermentations, where the GA strain had significant performance variability dependent on process. We hypothesized that the increased environmental robustness observed in both "micro-" and 1 L scale fermentations for "Valve" strains would lead to predictable scale up, where strains with improved performance in high-throughput micro-fermentations would reliably have improved performance in controlled bioreactors. To evaluate the scalability of the system, "Valve" alanine strains with statistically differentiated performance in micro-fermentations (P-value<0.001) were evaluated in standardized 2-stage 1 L fermentations and compared to all GA strains. Statistically different performances observed in "micro-fermentations" have scaled predictably to 1 L fermentations for 2-stage "Valve" strains. This contrasts with results obtained with GA strains where no correlation between micro-fermentation and 1 L performance was observed (FIGS. **5**G-H).

Product Flexibility

With the successful and predictable scale-up of alanine strains into 1 L fully instrumented fermentations, we moved to validate the technology platform for an additional product: mevalonic acid. To this end, additional dynamic production pathways were constructed for mevalonic acid biosynthesis (FIG. **6**A). A set of two-gene production pathway plasmids encoding three enzymatic functions was constructed for mevalonic acid production, consisting of the *E. faecalis* mvaE and mvaS genes encoding a bifunctional acetyl-CoA acetyltransferase, NADPH dependent HMG-CoA reductase, and HMG-CoA synthase respectively. A mutant mvaS gene, mvaS(A110G) with higher activity was used[45, 46]. Production plasmids were initially evaluated for mevalonate production in the control strain (FIG. **6**B). The best producing plasmid was then introduced into a variety of engineered "Valve" strains and evaluated in micro-fermentations (FIG. **6**C). A subset of statistically differentiated strains were then evaluated in 1 L fermentations to assess scalability (FIG. 6D), which, as in the case of alanine, was predictive. In some cases, a performing strain produced meaningful titers and yields, 97 g/L in 78 hrs of production with a yield of 0.46 g/g (84% of theoretical yield) (FIG. 6E). Specific productivity for this mevalonate strain is over 4-fold higher than the best previously reported results[47] (Supplemental Materials, Section 9).

Discussion

Historically some of the most successful efforts to metabolically engineer the production of small molecules have leveraged the power of anaerobic metabolism to couple product formation with growth. This has allowed for the classical design and selection of industrial strains to produce many products including ethanol, succinic acid, lactate and isobutanol, which have leveraged the power of evolution and selection to reach optimal metabolic fluxes in engineered networks[48, 49]. While growth associated production is not strictly linked to anaerobic metabolism, growth association greatly limits the number and variety of different molecules that can be made using synthetic biology. A generic, robust and accessible non-growth associated platform would greatly simplify the optimization and scale up of a diverse number of products.

In contrast to most existing 2-stage processes, which have relied on natural metabolic responses to environmental triggers for production improvement, we have taken the next step in actively minimizing the essential metabolic network and redirecting metabolites to products of interest. Many of the targeted essential central metabolic pathways in this work have traditionally been off limits to engineering strategies, as deleting essential enzymes is incompatible with growth and growth associated production in traditional fermentation. The dynamically minimized metabolic network also results in enhanced robustness to environmental variables enabling the faithful translation of high-throughput small-scale studies to larger instrumented fermentations. A current paradigm in the field is to improve the throughput of relevant strain evaluations by developing small-scale, custom-designed micro-reactors for enhanced process control. In contrast, our approach is a move in a new direction involving engineering microbial metabolism to be less sensitive to process changes, simplifying high-throughput experimentation.

Beyond robustness, we have demonstrated that combinatorial modifications to essential enzymes in minimal metabolic networks can lead to significant improvements in production, particularly when compared to altering production pathway expression levels alone. These large variations in performance are due to changes in a limited subset of key central metabolic nodes, likely resulting in altered metabolite levels. Compared to previous approaches to dynamically control enzyme levels, we demonstrate improved potential for fine tuning of protein levels with a combination of gene silencing and proteolysis[50]. As stationary phase cells cannot dilute existing proteins with cell division, this dual approach makes sense. The specific control of the level of any given enzyme will of course also depend on natural turnover mechanisms. At first glance, it may still be surprising that the combination of both gene silencing and proteolysis together does not always result in improved performance, i.e. "more is not always better". Future efforts may be needed to explain these results, which could either be due to a requirement of maintaining minimal fluxes in the larger network or a consequence of changes in the levels of key regulatory metabolites that are not part of the minimal network, yet influence network activity.

While the approach as demonstrated can address many issues common to most bio-production processes, many product specific challenges remain. The toxicity of a product or pathway metabolite may limit titers or production rates. A minimal network that may be optimal at a low titer, may not be optimal at elevated titers. In addition, the engineering of improved enzymes is often a challenge in many "mg" to "kg" projects.

Feasibility of adapting this approach to other microbial hosts is expected. Key requirements for new hosts include a rapid and robust growth phase, the ability to engineer dynamic control over protein levels, and a metabolically active stationary phase. Numerous microbes have well characterized nutrient triggers for productive stationary phase metabolism[36], for example nitrogen limitation in *Ralstonia* species, *Yarrowia* species and others[51 52]. Even when these requirements are not naturally met, they can be engineered into the host such as *S. cerevisiae* or other microbes, with each potential host presenting unique challenges and corresponding solutions.

Future efforts can be aimed at applying this platform for molecules with more complex production pathways. This approach can offer a tractable route for rapid optimization to metabolic engineers and synthetic biologists, who wish to move past POC levels and begin to tackle problems at more industrially relevant rates, titers and yields.

Methods

Reagents and Media

Unless otherwise stated, all materials and reagents were of the highest grade possible and purchased from Sigma (St. Louis, Mo.). C13 labeled Alanine (2,3-13C2, 99%) (Item #CLM-2734-PK) was purchased from Cambridge Isotope Laboratories, Inc. (Tewksbury, Mass.). Luria Broth was used for routine strain and plasmid propagation and construction. Working antibiotic concentrations were as follows: ampicillin (100 μg/mL), kanamycin (35 μg/mL), chloramphenicol (35 μg/mL), spectinomycin (100 μg/mL), zeocin (50 μg/mL), gentamicin (10 μg/mL), blasticidin (100 μg/mL), puromycin (150 μg/mL), tetracycline (5 μg/mL). Luria broth with low salt (Lennox formulation) was used to select for zeocin, blasticidin and puromycin resistant clones. In addition, for puromycin selection, phosphate buffer (pH=8.0) was added to LB Lennox to a final concentration of 50 mM. Media formulations including stock solutions are described in Supplemental Materials, Section 7.

E. coli Strain Construction

Oligonucleotides and synthetic linear DNA (Gblocks™) used for strain construction and confirmation are all given in Supplemental Materials, Section 3, and they were obtained from Integrated DNA Technologies (IDT, Coralville, Iowa). Strain BW25113 was obtained from the Yale Genetic Stock Center (CGSC http://cgsc.biology.yale.edu/). Strain BWapldf was a kind gift from George Chen (Tsinghua University)[62]. Chromosomal modifications were made using standard recombineering methodologies[63] either with direct antibiotic cassette integration in the case of C-terminal DAS+4 tags carrying antibiotic resistance cassettes, or through scarless tet-sacB selection and counterselection, strictly following the protocols of Li et al[64]. The recombineering plasmid pSIM5 and the tet-sacB selection/counterselection marker cassette were kind gifts from Donald Court (NCI, https://redrecombineering.ncifcrf.gov/court-lab.html). Briefly, the tet-sacB selection/counterselection cassette was amplified using the appropriate oligos supplying~50 bp flanking homology sequences using Econotaq (Lucigen Middleton, Wis.) according to manufacturer's instructions, with an initial 10 minutes denaturation at 94°

C., followed by 35 cycles of 94° C., for 15 seconds, 52° C. for 15 seconds, and 72° C. for 5 minutes. Cassettes used for "curing" of the tet-sacB cassette or direct integration (when an antibiotic marker is present) were obtained as gBlocks from IDT. In the case of the sspB gene deletion, the open reading frame deletion replaced with a kanamycin resistance was amplified from the Keio Collection strain, JW3197-1[65], and moved to the appropriate background strain using standard methodologies. The kanamycin resistance cassette was cured using the pCP20 plasmid, leaving an frt scar[63, 65]. Chromosomal modifications were confirmed by PCR amplification and sequencing (Eton Biosciences) using paired oligonucleotides, either flanking the entire region, or in the case of DAS+4 tag insertions an oligo 5' of the insertion and one internal to the resistance cassette.

E. coli Plasmid Construction

Primers used for the design and construction of CASCADE guides arrays were listed in Supplemental Materials, Section 6. Gene silencing guide arrays were expressed from a series of pCASCADE plasmids. The pCASCADE-control plasmid was prepared by swapping the pTet promoter in pcrRNA.Tet[73] with an insulated low phosphate induced ugpB promoter[74]. Promoter sequences for all genes were obtained from EcoCyc database (https://ecocyc.org/). In order to design CASCADE guide array, CASCADE PAM sites near the −35 or −10 box of the promoter of interest were identified, 30 bp at the 3' end of PAM site was selected as the guide sequence and cloned into pCASCADE plasmid using Q5 site-directed mutagenesis (NEB, MA) following manufacturer's protocol, with the modification that 5% v/v DMSO was added to the Q5 PCR reaction. PCR cycles were as follows: amplification involved an initial denaturation step at 98° C. for 30 second followed by cycling at 98° C. for 10 second, 72° C. for 30 second, and 72° C. for 1.5 min (the extension rate was 30 second/kb) for 25 cycles, then a final extension for 2 min at 72° C. 2 μL of PCR mixture was used for 10 μL KLD reaction, which proceeded under room temperature for 1 hour, after which, 1 μL KLD mixture was used for electroporation.

The pCASCADE guide array plasmids were prepared by sequentially amplifying complementary halves of each smaller guide plasmid by PCR, followed by subsequent DNA assembly. The pCASCADE-control vector was used as template. pCASCADE plasmids with arrays of two or more guides were prepared using Q5 High-Fidelity 2×Master Mix (NEB, MA). PCR cycles were as follows: amplification involved an initial denaturation step at 98° C. for 30 second followed by cycling at 98° C. for 10 second, 66° C. for 30 second, and 72° C. for 45 second (the extension rate was 30 second/kb) for 35 cycles, then a final extension for 2 min at 72° C. PCR product was purified by gel-extraction, 20 μL ultrapure water was used to elute 50 μL PCR reaction purification. 1 μL of each eluted PCR product was used for 10 μL of Gibson Assembly (NEB, MA), which was completed by incubation at 50° C. for 15 min. 1 μL Gibson Assembly mix was used for electroporation.

Production pathways enzymes were expressed from high copy plasmids via low phosphate inducible promoters. Production pathway gene sequences were codon optimized using the Codon Optimization Tool from the IDT website, phosphorylated G-blocks™ were designed and purchased from IDT for each pathway. Plasmids were assembled using NEBuilder® HiFi DNA Assembly Master Mix following manufacturer's protocol (NEB, MA). pSMART-HC-Kan (Lucigen, WI) was used as backbone for all pathway plasmids. All plasmid sequences were confirmed by DNA sequencing (Eton Bioscience, NC) and deposited with Addgene.

E. coli BioLector

Single colonies of each strain were inoculated into 5 mL LB with appropriate antibiotics and cultured at 37° C., 220 rpm for 9 hours or until OD600 reached>2. 500 μL of the culture was inoculated into 10 mL SM10 medium with appropriate antibiotics, and cultured in a square shake flask (CAT #: 25-212, Genesee Scientific, Inc. San Diego, Calif.) at 37° C., 220 rpm for 16 hours. Cells were pelleted by centrifugation and the culture density was normalized to OD600=5 using FGM3 media. Growth and fluorescence measurements were obtained in a Biolector (m2p labs, Baesweiler, Germany) using a high mass transfer FlowerPlate (CAT #: MTP-48-B, m2p-labs, Germany). 40 μL of the OD normalized culture was inoculated into 760 μL of FGM3 medium with appropriate antibiotics. Biolector settings were as follows: RFP gain=100, GFP gain=20, Biomass gain=20, shaking speed=1300 rpm, temperature=37° C., humidity=85%. Every strain was analyzed in triplicate.

E. coli Micro-Fermentations

Plasmids were transformed into host strains by electroporation using ECM 630 High Throughput Electroporation System (Harvard Apparatus, Inc. Holliston, Mass.) following manufacturer's protocol or using individual electroporation cuvettes. Glycerol stocks were prepared for each transformation plate by adding equal volume of sterile 20% glycerol, and 3 μL were used to inoculate overnight culture in 150 μL SM10++ medium with appropriate antibiotics. Plates were covered with sandwich covers (Model #CR1596 obtained from EnzyScreen, Haarlam, The Netherlands). These covers ensured minimal evaporative loss during incubation. Unless otherwise stated, 96 well plates were cultured at 37° C., 400 rpm for 16 hours, shaker orbit is 25 mm. This combination of orbit and minimal shaking speed is required to obtain needed mass transfer coefficient and enable adequate culture oxygenation.

After 16 hours of growth, cells were pelleted by centrifugation, excess media was removed and cells were resuspended in 150 μL of FGM3 Wash solution. Subsequently cells were once again pelleted and again excess media was removed, pellet was resuspended in 50 μL FGM3 No Phosphate media containing appropriate antibiotics. 5 μL of the resuspended culture was added to 195 μL of water for OD600 measurement using standard flat bottom 96 well plate. OD600 for production was normalized to OD600=1, using FGM3 No Phosphate media containing appropriate antibiotics, in a total volume of 150 μL using standard 96 well plate. Plates were covered with sandwich covers (Model #CR1596 obtained from EnzyScreen, Haarlam, The Netherlands) and 96 well plate cultures were incubated at 37° C., 400 rpm for 24 hours. After 24 hours of production, all samples from each well were pelleted by centrifugation and the supernatant collected for subsequent analytical measurement. Triplicate micro-fermentations were performed for each strain.

For growth associated alanine micro-fermentations, glycerol stock preparation and 16 hour overnight culture in SM10++ proceeded as described above. After 16 hours of growth in SM10++ medium, 5 μL of overnight culture was inoculated into 150 μL FGM3 with 40 mM phosphate containing appropriate antibiotic. Plates were covered with sandwich covers (Model #CR1596 obtained from EnzyScreen, Haarlam, The Netherlands) and 96 well plate cultures were incubated at 37° C., 400 rpm for 24 hours. After 24 hours of production, OD600 was recorded, all samples from each well were then pelleted by centrifugation and the supernatant collected for subsequent analytical measurement. Triplicate micro-fermentations were performed for each strain.

Micro-fermentation robustness evaluations were conducted as described in Supplemental Materials, Section 8.

1 L Fermentation Seeds

Single colony from transformation plate was inoculated into 5 mL LB with appropriate antibiotics and cultured at 37° C., 220 rpm for 16 hours. 500 μL of the LB culture was inoculated into 50 mL SM10 media with appropriate antibiotics in square shake flask (CAT #: 25-214, Genesee Scientific, Inc. San Diego, Calif.), the culture was incubated at 37° C. with a shaking speed of 220 rpm for 24 hours, at which time OD600 is usually between 3 and 10, the culture was harvested by centrifugation at 4000 rpm for 15 min, supernatant was discarded and cell culture was normalized to OD600=10 using SM10 media. For 1 L fermentation seed, 6 mL of normalized OD600=10 culture was added to 1.5 mL of 50% glycerol in cryovials, and stored at −80° C.

1 L Fermentations

An Infors-HT Multifors (Laurel, Md., USA) parallel bioreactor system was used to perform 1 L fermentations, including three gas connection mass flow controllers configured for air, oxygen and nitrogen gases. Vessels used had a total volume of 1400 mL and a working volume of up to 1 L. Online pH and pO2 monitoring and control were accomplished with Hamilton probes. Offgas analysis was accomplished with a multiplexed Blue-in-One BlueSens gas analyzer (BlueSens. Northbrook, Ill., USA). Culture densities were continually monitored using Optek 225 mm OD probes, (Optek, Germantown, Wis., USA). The system used was running IrisV6.0 command and control software and integrated with a Seg-flow automated sampling system (Flownamics, Rodeo, Calif., USA), including FISP cell free sampling probes, a Segmod 4800 and FlowFraction 96 well plate fraction collector.

For the standardized 2-stage process with ~10 gcdw/L biomass, tanks were filled with 800 mL of FGM10 medium, with enough phosphate to target a final *E. coli* biomass concentration~10 gcdw/L. Antibiotics were added as appropriate. Frozen seed vials were thawed on ice and 7.5 mL of seed culture was used to inoculate the tanks. After inoculation, tanks were controlled at 37° C. and pH 6.8 using 5 M ammonium hydroxide and 1 M hydrochloric acid as titrants. 10 M ammonium hydroxide was used for FIG. **3**G fermentation run. The following oxygen control scheme was used to maintain the desired dissolved oxygen set point. First gas flow rate was increased from a minimum of 0.3 L/min of air to 0.8 L/min of air, subsequently, if more aeration was needed, agitation was increased from a minimum of 300 rpm to a maximum of 1000 rpm. Finally, if more oxygen was required to achieve the set point, oxygen supplementation was included using the integrated mass flow controllers. Starting glucose concentration was 25 g/L. A constant concentrated sterile filtered glucose feed (500 g/L) was added to the tanks at specified rate, i.e. 2 g/h, once agitation reached 800 rpm. In cases where feed rate or dissolved oxygen content needed to be varied for robustness study, changes were made after cells entered stationary phase. Fermentation runs were extended for up to ~50 hours after entry into stationary phase and samples automatically withdrawn every 3 hours. Samples were saved for subsequent analytical measurement.

In the case of growth associated fermentation processes, tanks were filled with 800 mL of FGM10 medium with 40 mM phosphate, which was in great excess and ensured phosphate depletion doesn't happen for growth associated fermentation processes. Antibiotics were added as appropriate. Frozen seed vials were thawed on ice and 7.5 mL of seed culture was used to inoculate the tanks. After inoculation, tanks were controlled at 37° C. and pH 6.8 using 5 M ammonium hydroxide and 1 M hydrochloric acid as titrants. The following oxygen control scheme was used to maintain the desired dissolved oxygen set point. First gas flow rate was increased from a minimum of 0.3 L/min of air to 0.8 L/min of air, subsequently, if more aeration was needed, agitation was increased from a minimum of 300 rpm to a maximum of 1000 rpm. Finally, if more oxygen was required to achieve the set point, oxygen supplementation was included using the integrated mass flow controllers. Starting glucose concentration was 25 g/L. A constant concentrated sterile filtered glucose feed (500 g/L) was added to the tanks at specified rate, i.e. 2 g/h, once agitation reached 800 rpm. Feed rate and dissolved oxygen concentration was set to desired values in the beginning, and maintained throughout the fermentation process. Fermentation runs were continued for up to ~50 hours and samples automatically withdrawn every 3 hours. Samples were saved for subsequent analytical analysis.

Analytical Methods

Sample standard curves for all compounds quantified are shown in Supplemental Materials, Section 10.

Glucose and Ethanol Quantification: A UPLC-RI method was developed for the simultaneous quantification of glucose and ethanol concentrations, using an Acquity H-Class UPLC integrated with a Waters 2414 Refractive Index (RI) detector (Waters Corp., Milford, Mass. USA). Chromatographic separation was performed using a Bio-Rad Fast Acid Analysis HPLC Column (100×7.8 mm, 9 μm particle size; CAT #: #1250100, Bio-Rad Laboratories, Inc., Hercules, Calif.) at 65° C. 5 mM sulfuric acid was used as the eluent. The isocratic elution was as follows: 0-0.1 min, flow rate increased from 0.4 mL/min to 0.42 mL/min, 0.1-12 min flow rate at 0.48 mL/min. Sample injection volume was 10 μL. UPLC method development was carried out using standard aqueous stock solutions of analytes. Peak integration and further analysis was performed using MassLynx v4.1 software. The linear range used for glucose was 1-10 g/L, for ethanol was 1-20 g/L. Samples were diluted as needed to be within the accurate linear range. Dilution was performed using ultrapure water.

Alanine Quantification: A reverse phase UPLC-MS/MS method was developed for alanine. Chromatographic separation was performed using a Restek Ultra AQ C18 column (150 mm×2.1 i.d., 3 μm; CAT #: 9178362, Restek Corporation, Bellefonte, Pa.) at 70° C. The following eluents were used: solvent A: H_2O, 0.2% formic acid and 0.05% ammonium (v/v); solvent B: MeOH, 0.2% formic acid and 0.05% ammonium (v/v). The gradient elution was as follows: 0-0.1 min isocratic 5% B, flow rate increased from 0.65 mL/min to 0.75 mL/min; 0.1-0.3 min, linear from 5% to 95% B at 0.75 mL/min; 0.3-0.9 min isocratic 95% B at 0.75 mL/min; and 0.9-1.2 min linear from 95% to 5% B at 0.75 mL/min; 1.2-1.3 min isocratic 5% B at 0.75 mL/min. Sample injection volume was 5 μL. UPLC method development was carried out using standard aqueous stock solutions of analyte. Separations were performed using an Acquity H-Class UPLC integrated with a Xevo™ TQD Mass spectrometer (Waters Corp., Milford, Mass. USA). MS/MS parameters including MRM transitions were tuned for each analyte and are listed in Table 22. Alanine (2,3-13C2, 99%) was used as internal standard for alanine at a concentration of 5 mg/L. Peak integration and further analysis was performed using

MassLynx v4.1 software. The linear range for alanine was 1-100 mg/L. Samples were diluted as needed to be within the accurate linear range. Dilution was performed using ultrapure water, and the final 10-fold dilution was performed using solvent A, with 5 mg/L of C13 alanine (2,3-13C2, 99%).

Mevalonic Acid Quantification: A reverse phase UPLC-TUV method was developed for the simultaneous quantification of mevalonic acid and mevalonolactone. Chromatographic separation was performed using a Restek Ultra AQ C18 column (150 mm×2.1 i.d., 3 μm; CAT #: 9178362, Restek Corporation, Bellefonte, Pa.) at 30° C. 20 mM phosphoric acid was used as the eluent. The isocratic elution was as follows: 0-3 min isocratic at 1 mL/min. Sample injection volume was 10 μL. Absorbance was monitored at 210 nm. UPLC method development was carried out using standard aqueous stock solutions of analytes. Separations were performed using an Acquity H-Class UPLC (Waters Corp., Milford, Mass. USA). Peak integration and further analysis was performed using MassLynx v4.1 software. The linear range for mevalonic acid and mevalonolactone were 0.01-0.1 g/L. Samples were diluted as needed to be within the accurate linear range. Mevalonic acid diluted in 20 mM phosphoric acid would spontaneously convert to mevalonolactone[80], thus, quantification of both mevalonic acid and mevalonolactone was necessary for fermentation samples. Mevalonic acid and mevalonolactone standards were prepared fresh each time, and ran immediately on UPLC. Dilution was performed using ultrapure water, and the final 10-fold dilution was performed using 20 mM phosphoric acid.

Alanine Stereoisomer Quantification: A reverse phase UPLC-TUV method was developed for the simultaneous quantification and differentiation of L-/D-alanine. Chromatographic separation was performed using a Chirex 3126 (D)-penicillamine column (150×4.6 mm, 5 μm; Phenomenex Inc., Torrance, Calif.) at 50° C. 2 mM Copper Sulfate was used as the eluent. The isocratic elution was as follows: 0-10 min at 0.75 mL/min. Sample injection volume was 10 μL. Absorbance was monitored at 254 nm. UPLC method development was carried out using standard aqueous stock solutions of analytes. Separations were performed using an Acquity H-Class UPLC (Waters Corp., Milford, Mass. USA). Peak integration and further analysis was performed using MassLynx v4.1 software. The linear range for L-/D-alanine was 0.1-1 g/L. Samples were diluted as needed to be within the accurate linear range. Dilution was performed using ultrapure water.

Supplemental Materials

TABLE 1

Combinatorial complexity of metabolic networks.

Combination #	Number of Experiments Entire *E. coli* Gene Network	Reduced Central Metabolism Network
1	4500	~45 (Glycolysis, TCA, PPP and ETC genes only)
2	1.0×10^{6}	990
3	1.5×10^{10}	14,190
4	1.7×10^{13}	148,995
5	1.5×10^{16}	1.2×10^{6}

Section 1: Phosphate Promoters

Phosphate promoter sequences were obtained from the EcoCyc database[81] for PhoB regulated promoters (https://ecocyc.org/, Table 2). We sought to evaluate not only the relative strength of promoters previously characterized to respond to phosphate depletion, but in addition the relative leakiness in phosphate rich conditions. To this aim we constructed a set of fluorescent reporter plasmids. We cloned the ultraviolet excitable GFPuv gene behind a set of 12 phosphate dependent promoters, in the pSMART-HC-Kan (Lucigen, WI) backbone. These reporter strains were evaluated in a 2-stage micro-fermentation protocol in an m2p-labs Biolector™. Results are illustrated in FIG. **7**. The ugpB gene promoter was often chosen for high level tightly controlled expression when expression cassettes were chromosomally integrated or for the inducible expression of guide arrays.

Insulators[82] were added to both 5' and 3' end of a subset of phosphate promoters (Table 3) to help with consistent performance in different sequence contexts. To reduce read-through transcription, a unique terminator was added to the 5' end of each insulated promoter. Terminator sequences were from http://parts.igem.org/Terminators/Catalog. Insulated phosphate promoters were similarly characterized using GFPuv expression in a m2p-labs Biolector™ (FIG. **8**).

TABLE 2

Phosphate inducible promoter sequences evaluated; the ribosomal binding site is underlined, and the start codon of the gene (GFPuv) is shown in green.

Promoter Name	Sequence	SEQ ID NO
ugpBp	TCTTTCTGACACCTTACTATCTTACAAATGTAACAAAAAAGTTATTTTTCTGTAATTCGA GCATGTCATGTTACCCCGCGAGCATAAAACGCGTGTGTAGGAGGATAATCTATG	1
yibDp	GTGCGTAATTGTGCTGATCTCTTATATAGCTGCTCTCATTATCTCTCTACCCTGAAGTGAC TCTCTCACCTGTAAAAATAATATCTCACAGGCTTAATAGTTTCTTAATACAAAGCCTGTA AAACGTCAGGATAACTTCTGTGTAGGAGGATAATCTATG	2
phoAp	CGATTACGTAAAGAAGTTATTGAAGCATCCTCGTCAGTAAAAAGTTAATCTTTTCAACA GCTGTCATAAAGTTGTCACGGCCGAGACTTATAGTCGCTTTGTTTTTATTTTTTAATGTAT TTGTAGTGTAGGAGGATAATCTATGGCTAGCAAAGGAGAAGAACTTTTCACATG	3
phoBp	GCCACGGAAATCAATAACCTGAAGATATGTGCGACGAGCTTTTCATAAATCTGTCATAA ATCTGACGCATAATGACGTCGCATTAATGATCGCAACCTATTTATTGTGTAGGAGGATA ATCTATGGCTAGCAAAGGAGAAGAACTTTTCACATG	4
amnp	AGACAGTCAACGCGCTTGATAGCCTGGCGAAGATCATCCGATCTTCGCCTTACACTTTTG TTTCACATTTCTGTGACATACTATCGGATGTGCGGTAATTGTATAGGAGGATAATCTATG	5
ydfHp	GCTATGCCGGACTGAATGTCCACCGTCAGTAATTTTTATACCCGGCGTAACTGCCGGGTT ATTGCTTGTCACAAAAAAGTGGTAGACTCATGCAGTTAACTCACTGTGTAGGAGGATAA TCTATG	6
mipAp	CATCCATAAATTTTGCATAATTAATGTAAAGACCAGGCTCGCCAGTAACGCTAAATTCA TTTGGCTGTAAGCGCGGTGTCATCCGCGTCAGGAAAATTAAACAGTTACTTTAAAAAAT GAAAACGTAAAAAGGTTGGGTTTCGATGTATTGACGGGTAAACTTTGTCGCCCGCTAAA CATTTGTTTGTGTAGGAGGATAATCTATG	7
phoHp	AATCCTGCTGAAAGCACACAGCTTTTTTCATCACTGTCATCACTCTGTCATCTTTCCAGT AGAAACTAATGTCACTGAAATGGTGTTTTATAGTTAAATATAAGTAAATATATTGTTGCA ATAAATGCGAGATCTGTTGTACTTATTAAGTAGCAGCGGAAGTTCGTGTAGGAGGATAA TCTAT	8
yhjCp	CTACAGAGATGACGTGTAGAAAATAGTTACCGATATAAATAGTTACAGCTAAACGCCTG AAATTACATGTCGAGGGCACTATTTAAAAACAATTTTGAGGATTTCCTTATATTGGTGGTT AGTACGCATGCAATTAAAAATGAAATTCCGCGACCACAAGCCAAAATAACAAACGGCA AGGAGACAAAAATAAGCACAAATAGCCAACACGTCCTCTGTTCACTTTAAAGGGAATCG CTGAAAAATACGCTCTGTTTAAGGGGATTCACCTTTCTCAGAAAGCTATTCCGCCCTTTT CCTGCTGAGAAATCGCCACATTCGGCATGACAACATTGTGAAAGTGTAGGAGGATAATC TATG	9
phoUp	ACCGAACTGAAGCAGGATTACACCGTGGTGATCGTCACCCACAACATGCAGCAGGCTGC GCGTTGTTCCGACCACACGGCGTTTATGTACCTGGGCGAATTGATTGAGTTCAGCAACA CGGACGATCTGTTCACCAGTGTAGGAGGATAATCTATG	10
pstSp	AAGACTTTATCTCTCTGTCATAAAACTGTCATATTCCTTACATATAACTGTCACCTGTTTG TCCTATTTTGCTTCTCGTAGCCAACAAACAATGCTTTATGAGTGTAGGAGGATAATCTAT GGCTAGCAAAGGAGAAGAACTTTTCACATG	11
phoEp	AGCATGGCGTTTTGTTGCGCGGGATCAGCAAGCCTAGCGGCAGTTGTTTACGCTTTTATT ACAGATTTAATAAATTACCACATTTTAAGAATATTATTAATCTGTAATATATCTTTAACA ATCTCAGGTTAAAAACTTTCCTGTTTTCAACGGGACTCTCCCGCTGGTGTAGGAGGATAA TCTATG	12

TABLE 3

Insulated promoter sequences. Insulator sequences are italicized. -35 and -10 boxes are highlighted in bold and underlined.

Insulated Promoter	Sequence	SEQ ID NO
BBa_B0015_IN_yibDp	CCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTT TTATCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCT TCGGGTGGGCCTTTCTGCGTTTATA*CACAGCTAACACCACGTCGTCCCTATCTG CTGCCCTAGGTCTATGAGTGGTTGCTGGATAAC*GTGCGTAATTGTGCTGATCTC TTATATAGCTGCTCTCATTATCTCTCTACCCTGAA**GTGACT**CTCTCACCTGTA AAAATAATATCTCACAGGCT**TAATA**GTTTCTTAATACAAAGCCTGTAAAACG TCAGGATAACTTCTA*TATTCAGGGAGACCACAACGGTTTCCCTCTACAAATAATTT TGTTTAACTTT*	13

TABLE 3-continued

Insulated promoter sequences. Insulator sequences are italicized. -35 and -10 boxes are highlighted in bold and underlined.

Insulated Promoter	Sequence	SEQ ID NO
BBa_B1002_IN_phoBp	CGCAAAAAACCCCGCTTCGGCGGGGTTTTTTCGCACCGTCTCCATCGCTTGCC CAAGTTGTGAAG*CACAGCTAACACCACGTCGTCCCTATCTGCTGCCCTAGGTCT* *ATGAGTGGTTGCTGGATAAC*GCCACGGAAATCAATAACCTGAAGATATGTGCCG ACGAGCTT**TTCATA**AATCTGTCATAAATCTGACG**CATAAT**GACGTCGCATTA ATGATCGCAACCTATTTATTA*TATTCAGGGAGACCACAACGGTTTCCCTCTACCA* *ATAATTTTGTTTAACTTT*	14
BBa_B1004_IN_mipAp	CGCCGAAAACCCCGCTTCGGCGGGGTTTTGCCGCACGTCTCCATCGCTTGCC CAAGTTGTGAAG*CACAGCTAACACCACGTCGTCCCTATCTGCTGCCCTAGGTCT* *ATGAGTGGTTGCTGGATAAC*CATCCATAAATTTTGCATAATTAATGTAAAGAC CAGGCTCGCCAGTAACGCTAAATTCATTTGGCTGTAAGCGCGGTGTCATCCG CGTCAGGAAAATTAAACAGTTACTTTAAAAAATGAAAACGTAAA**AAGGTT**G GGTTTCGATGTATTGACGG**GTAAAC**TTTGTCGCCCGCTAAACATTTGTTT*ATA* *TTCAGGGAGACCACAACGGTTTCCCTCTACAAATAATTTTGTTTAACTTT*	15
BBa_B1006_IN_phoUp	AAAAAAAAACCCCGCCCCTGACAGGGCGGGGTTTTTTTACGTCTCCATCGC TTGCCCAAGTTGTGAAG*CACAGCTAACACCACGTCGTCCCTATGCTGCCCTA* *GGTCTATGAGTGGTTGCTGGATAAC*ACCGAACTGAAGCAGGATTACACCGTGG TGATCGTCACCCACAACATGCAGCAGGCTGCGCGTTGTTCCGACCACA**CGG** **CGT**TTATGTACCTGGGCGAATT**GATTGA**GTTCAGCAACACGGACGATCTGTT CACCA*ATATTCAGGGAGACCACAACGGTTTCCCTCTACAAATAATTTTGTTTAACTT* *T*	16
BBa_B1010_IN_phoHp	CGCCGCAAACCCCGCCCCTGACAGGGCGGGGTTTCGCCGCACGTCTCCATCG CTTGCCCAAGTTGTGAAG*CACAGCTAACACCACGTCGTCCCTATCTGCTGCCCT* *AGGTCTATGAGTGGTTGCTGGATAAC*AATCCTGCTGAAAGCACACAGCTTTTTT CATCACTGTCATCACT**CTGTCA**TCTTTCCAGTAGAAAC**TAATGT**CACTGAAA TGGTGTTTTATAGTTAAATATAAGTAAATATATTGTTGCAATAAATGCGAGA TCTGTTGTACTTATTAAGTAGCAGCGGAAGTTC*ATATTCAGGGAGACCACAAC* *GGTTTCCCTCTACAAATAATTTTGTTTAACTTT*	17

Section 2: Constitutive Promoters

A set of constitutive insulated promoters of varying strength were used for constitutive expression and taken directly from Davis et al., including the proA, proB, proC, proD promoters[82] and HCEp promoter[83]. Insulator was added to 5' and 3' of HCEp promoter. Similar to insulated phosphate promoters, a unique terminator was added to the 5' end of constitutive promoters. These were used to drive constitutive pathway expression in growth associated production strains as well as to make strain modifications where constitutive heterologous gene expression was appropriate. These promoter sequences are given in Table 4 below and promoter characterized using GFPuv expression (FIG. **9**).

TABLE 4

Constitutive promoter sequences.

Promoter	Sequence	SEQ ID NO
BBa_B1004_proA	CGCCGAAAACCCCGCTTCGGCGGGGTTTTGCCGCACGTC TCCATCGCTTGCCCAAGTTGTGAAGCACAGCTAACACCA CGTCGTCCCTATCTGCTGCCCTAGGTCTATGAGTGGTTG CTGGATAACTTTACGGGCATGCATAAGGCTCGTAGGCTA TATTCAGGGAGACCACAACGGTTTCCCTCTACAAATAAT TTTGTTTAACTTT	18
BBa_B1006_proB	AAAAAAAAACCCCGCCCCTGACAGGGCGGGGTTTTTTT ACGTCTCCATCGCTTGCCCAAGTTGTGAAGCACAGCTAA CACCACGTCGTCCCTATCTGCTGCCCTAGGTCTATGAGT GGTTGCTGGATAACTTTACGCGCATGCATAAGGCTCGTA ATATATATTCAGGGAGACCACAACGGTTTCCCTCTACAA ATAATTTTGTTTAACTTT	19
BBa_B1010_proC	CGCCGCAAACCCCGCCCCTGACAGGGCGGGGTTTCGCC GCACGTCTCCATCGCTTGCCCAAGTTGTGAAGCACAGCT AACACCACGTCGTCCCTATCTGCTGCCCTAGGTCTATGA GTGGTTGCTGGATAACTTTACGGGCATGCATAAGGCTCG TATGATATATTCAGGGAGACCACAACGGTTTCCCTCTAC AAATAATTTTGTTTAACTTT	20
BBa_B1002_proD	CGCAAAAAACCCCGCTTCGGCGGGGTTTTTTCGCACGTC TCCATCGCTTGCCCAAGTTGTGAAGCACAGCTAACACCA CGTCGTCCCTATCTGCTGCCCTAGGTCTATGAGTGGTTG CTGGATAACTTTACGGGCATGCATAAGGCTCGTATAATA	21

TABLE 4-continued

Constitutive promoter sequences.		
Promoter	Sequence	SEQ ID NO
	TATTCAGGGAGACCACAACGGTTTCCCTCTACAAATAAT TTTGTTTAACTTT	
BBa_B0015_IN_HCEp	CCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGAC TGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTC TCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTT TCTGCGTTTATACACAGCTAACACCACGTCGTCCCTATC TGCTGCCCTAGGTCTATGAGTGGTTGCTGGATAACCTCC TTCACAGATTCCCAATCTCTTGTTAAATAACGAAAAAGC ATCAATTAAAACCCATGTCTTTCTATATTCCAGCAATGT TTTATAGGGGACATATTGATGAAGATGGGTATCACCTTA GTGAATTGCTATAAGCTGCTCTTTTTTGTTCGTGATATAC TGATAAATTGAATTTTCACACTTCATATTCAGGGAGACC ACAACGGTTTCCCTCTACAAATAATTTTGTTTAACTTT	22

Section 3: Chromosomally Modified Host Strains

FIG. **11** depicts each chromosomal modification. Strains utilized and/or constructed for this study are listed in Table 5. Tables 6 and 7 lists oligonucleotides and synthetic DNA sequences used for strain construction and/or confirmation. FIG. **12** and FIG. **13**A-E show growth rates and glucose distribution during growth for control strains in 1 L fermentation.

TABLE 5

List of chromosomally modified strains.		
Strain	Genotype	Source
BW25113 (wt)	F-, λ-, Δ(araD-ataB)567, lacZ4787(del)(::rrnB-3), rph-1, Δ(rhaD-rhaB)568, hsdR514	CGSC
JW3197-1	BW25113, sspB756(del)::.kan	53
Bwapldf	BW25113, ΔackA-pta, ΔpoxB, ΔpflB, ΔldhA, ΔadhE	39
DLF_0001	BWapldf, ΔiclR, ΔarcA	this study
DLF_0002	BWapldf, ΔiclR, ΔarcA, ΔsspB::frt	this study
DLF_0025	DLF_0002, Δcas3::tm-ugpb-sspB-pro-casA(N2S)	this study
DLF_0028	DLF_0025, fabI-DAS + 4-gentR	this study
DLF_0031	DLF_0025, lpd-DAS + 4-gentR	this study
DLF_0038	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR	this study
DLF_0039	DLF_0025, fabI-DAS + 4-gentR, gltA-DAS + 4-zeoR	this study
DLF_0040	DLF_0025, fabI-DAS + 4-gentR, zwf-DAS + 4-bsdR	this study
DLF_0041	DLF_0025, lpd-DAS + 4-gentR, gltA-DAS + 4-zeoR	this study
DLF_0042	DLF_0025, lpd-DAS + 4-gentR, udhA-DAS + 4-bsdR	this study
DLF_0043	DLF_0025, gltA-DAS + 4-zeoR	this study
DLF_0044	DLF_0025, gltA-DAS + 4-zeoR, zwf-DAS + 4-bsdR	this study
DLF_0045	DLF_0025, gltA-DAS + 4-zeoR, udhA-DAS + 4-bsdR	this study
DLF_0046	DLF_0025, fabI-DAS + 4-gentR, gltA-DAS + 4-zeoR, zwf-DAS + 4-bsdR	this study
DLF_0047	DLF_0025, fabI-DAS + 4-aentR, gltA-DAS + 4::zeoR, udhA-DAS + 4-bsdR	this study
DLF_0048	DLF_0025, lpd-DASH + 4-gentR, gltA-DAS + 4-zeoR, zwf-DAS + 4-bsdR	this study
DLF_0049	DLF_0025, lpd-DAS + 4-gentR, gltA-DAS + 4-zeoR, udhA-DAS + 4-bsdR	this study
DLF_0165	DLF_0025, lpd-DAS + 4-gentR, zwf-DAS + 4-bsdR	this study
DLF_0763	DLF_0025, udhA-DAS + 4-bsdR	this study
DLF_01002	DLF_0025, zwf-DAS + 4-bsdR	this study
DLF_01517	DLF_0012, Δcas3::pro-casA(N2S)	this study
DLF_01530	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, zeoR-proDp-gapN-zeoR	this study
DLF_01531	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, gltA-DAS + 4-purR	this study
DLF_01532	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, gapA-DAS + 4-zeoR-proDp-gapN	this study
DLF_01533	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, gapA-DAS + 4-zeoR-proDp-gapN, gltA-DAS + 4-purR	this study
DLF_01536	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, zeoR-proDp-gapN, gltA-DAS + 4-purR	this study
DLF_01537	DLF_0025, fabI-DAS + 4-gentR, udhA-DAS + 4-bsdR, gapA-DAS + 4-zeoR	this study
DLF_01538	DLF_0025, fabI-DAS + 4-gentR, gltA-DAS + 4-zeoR, udhA-DAS + 4-bsdR, gapA-DAS + 4-zeoR	this study

TABLE 6

Oligonucleotides utilized for strain construction

Oligo	Sequence	SEQ ID NO
ilcR_tetA_F	TAACAATAAAAATGAAAATGATTTCCACGATACAGAAA AAAGAGACTGTCATCCTAATTTTTGTTGACACTCTATC	23
ilcR_sacB_R	TGCCACTCAGGTATGATGGGCAGAATATTGCCTCTGCCC GCCAGAAAAAGATCAAAGGGAAAACTGTCCATATGC	24
iclR_500up	CCCGACAGGGATTCCATCTG	25
iclR_500dn	TATGACGACCATTTTGTCTACAGTTC	26
arcA_tetA_F	GGACTTTTGTACTTCCTGTTTCGATTTAGTTGGCAATTTA GGTAGCAAACTCCTAATTTTTGTTGACACTCTATC	27
arcA_sacB_R	ATAAAAACGGCGCTAAAAAGCGCCGTTTTTTTTGACGGT GGTAAAGCCGAATCAAAGGGAAAACTGTCCATATGC	28
arcA_500up	CCTGACTGTACTAACGGTTGAG	29
arcA_500dn	TGACTTTTATGGCGTTCTTTGTTTTTG	30
sspB_kan_F	CTGGTACACGCTGATGAACACC	31
sspB_kan_R	CTGGTCATTGCCATTTGTGCC	32
sspB_conf_F	CAATCAGAGCGTTCCGACCC	33
sspB_conf_R	GTACGCAGTTTGCCAACGTG	34
cas3_tetA_F	AATAGCCCGCTGATATCATCGATAATACTAAAAAAAACAG GGAGGCTATTATCCTAATTTTTGTTGACACTCTATC	35
cas3_sacB_R	TACAGGGATCCAGTTATCAATAAGCAAATTCATTTGTTCT CCTTCATATGATCAAAGGGAAAACTGTCCATATGC	36
cas3_conf_F	CAAGACATGTGTATATCACTGTAATTC	37
cas3_500dn	GCGATTGCAGATTTATGATTTGG	38
fabl_conf_F	GCAAAATGCTGGCTCATTG	39
gapA_conf_F	GAACTGAATGGCAAACTGACTG	40
gapA_500dn	TGGGGATGATCGACCACA	41
gltA_conf_F	TATCATCCTGAAAGCGATGG	42
lpd_conf_F	ATCTCACCGTGTGATCGG	43
udhA_conf_F	CAAAAGAGATTCTGGGTATTCACT	44
zwf_conf_F	CTGCTGGAAACCATGCG	45
zwf_500dn	AGAGCATGTCGTTATAGGAGGTGAT	46
ampR_intR	AGTACTCAACCAAGTCATTCTG	47
bsdR_intR	GAGCATGGTGATCTTCTCAGT	48
gentR_intR	GCGATGAATGTCTTACTACGGA	49
purR_intR	GTCGCTGGGTAATCTGCAA	50
tetA_intR	ATCAACGCATATAGCGCTAGCAG	51
zeoR_intR	ACTGAAGCCCAGACGATC	52

TABLE 7

Synthetic DNA utilized for strain construction.	SEQ ID NO
tetA-sacB Cassette	
TCCTAATTTTTGTTGACACTCTATCATTGATAGAGTTATTTTACCACTCCCTA TCAGTGATAGAGAAAAGTGAAATGAATAGTTCGACAAAGATCGCATTGGTA ATTACGTTACTCGATGCCATGGGGATTGGCCTTATCATGCCAGTCTTGCCAA CGTTATTACGTGAATTTATTGCTTCGGAAGATATCGCTAACCACTTTGGCGT ATTGCTTGCACTTTATGCGTTAATGCAGGTTATCTTTGCTCCTTGGCTTGGAA AAATGTCTGACCGATTTGGTCGGCGCCCAGTGCTGTTGTTGTCATTAATAGG CGCATCGCTGGATTACTTATTGCTGGCTTTTTCAAGTGCGCTTTGGATGCTGT ATTTAGGCCGTTTGCTTTCAGGGATCACAGGAGCTACTGGGGCTGTCGCGGC ATCGGTCATTGCCGATACCACCTCAGCTTCTCAACGCGTGAAGTGGTTCGGT TGGTTAGGGGCAAGTTTTGGGCTTGGTTTAATAGCGGGGCCTATTATTGGTG GTTTTGCAGGAGAGATTTCACCGCATAGTCCCTTTTTTATCGCTGCGTTGCTA AATATTGTCACTTTCCTTGTGGTTATGTTTTGGTTCCGTGAAACCAAAAATAC ACGTGATAATACAGATACCGAAGTAGGGGTTGAGACGCAATCGAATTCGGT ATACATCACTTTATTTAAAACGATGCCCATTTTGTTGATTATTTATTTTTCAG CGCAATTGATAGGCCAAATTCCCGCAACGGTGTGGGTGCTATTTACCGAAA ATCGTTTTGGATGGAATAGCATGATGGTTGGCTTTTCATTAGCGGGTCTTGG TCTTTTACACTCAGTATTCCAAGCCTTTGTGGCAGGAAGAATAGCCACTAAA TGGGGCGAAAAAACGGCAGTACTGCTCGGATTTATTGCAGATAGTAGTGCA TTTGCCTTTTTAGCGTTTATATCTGAAGGTTGGTTAGTTTTCCCTGTTTTAATT TTATTGGCTGGTGGTGGGATCGCTTTACCTGCATTACAGGGAGTGATGTCTA TCCAAACAAAGAGTCATCAGCAAGGTGCTTTACAGGGATTATTGGTGAGCC TTACCAATGCAACCGGTGTTATTGGCCCATTACTGTTTGCTGTTATTTATAAT CATTCACTACCAATTTGGGATGGCTGGATTTGGATTATTGGTTTAGCGTTTTA CTGTATTATTATCCTGCTATCGATGACCTTCATGTTAACCCCTCAAGCTCAGG GGAGTAAACAGGAGACAAGTGCTTAGTTATTTCGTCACCAAATGATGTTATT CCGCGAAATATAATGACCCTCTTGATAACCCAAGAGCATCACATATACCTGC CGTTCACTATTATTTAGTGAAATGAGATATTATGATATTTTCTGAATTGTGAT TAAAAAGGCAACTTTATGCCCATGCAACAGAAACTATAAAAAATACAGAGA ATGAAAAGAAACAGATAGATTTTTTAGTTCTTTAGGCCCGTAGTCTGCAAAT CCTTTTATGATTTTCTATCAAACAAAAGAGGAAAATAGACCAGTTGCAATCC AAACGAGAGTCTAATAGAATGAGGTCGAAAAGTAAATCGCGCGGGTTTGTT ACTGATAAAGCAGGCAAGACCTAAAATGTGTAAAGGGCAAAGTGTATACTT TGGCGTCACCCCTTACATATTTTAGGTCTTTTTTTATTGTGCGTAACTAACTT GCCATCTTCAAACAGGAGGGCTGGAAGAAGCAGACCGCTAACACAGTACAT AAAAAAGGAGACATGAACGATGAACATCAAAAAGTTTGCAAAACAAGCAA CAGTATTAACCTTTACTACCGCACTGCTGGCAGGAGGCGCAACTCAACCGTT TGCGAAAGAAACGAACCAAAAGCCATATAAGGAAACATACGGCATTTCCCA TATTACACGCCATGATATGCTGCAAATCCCTGAACAGCAAAAAAATGAAAA ATATCAAGTTCCTGAGTTCGATTCGTCCACAATTAAAAATATCTCTTCTGCA AAAGGCCTGGACGTTTGGGACAGCTGGCCATTACAAAACGCTGACGGCACT GTCGCAAACTATCACGGCTACCACATCGTCTTTGCATTAGCCGGAGATCCTA AAAATGCGGATGACACATCGATTTACATGTTCTATCAAAAAGTCGGCGAAA CTTCTATTGACAGCTGGAAAAACGCTGGCCGCGTCTTTAAAGACAGCGACA AATTCGATGCAAATGATTCTATCCTAAAAGACCAAACACAAGAATGGTCAG GTTCAGCCACATTTACATCTGACGGAAAAATCCGTTTATTCTACACTGATTT CTCCGGTAAACATTACGGCAAACAAACACTGACAACTGCACAAGTTAACGT ATCAGCATCAGACAGCTCTTTGAACATCAACGGTGTAGAGGATTATAAATC AATCTTTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGA TGAAGGCAACTACAGCTCAGGCGACAACCATACGCTGAGAGATCCTCACTA CCTTAGAAGATAAAGGCCACAAATACTTAGTATTTGAAGCAAACACTGGAAC TGAAGATGGCTACCAAGGCGAAGAATCTTTATTTAACAAAGCATACTATGG CAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTCTGCAAAGCGA TAAAAAACGCACGGCTGAGTTAGCAAACGGCGCTCTCGGTATGATTGAGCT AAACGATGATTACACACTGAAAAAAGTGATGAAACCGCTGATTGCATCTAA CACAGTAACAGATGAAATTGAACGCGCGAACGTCTTTAAAATGAACGGCAA ATGGTACCTGTTCACTGACTCCCGCGGATCAAAAATGACGATTGACGGCATT ACGTCTAACGATATTTACATGCTTGGTTATGTTTCTAATTCTTTAACTGGCCC ATACAAGCCGCTGAACAAAACTGGCCTTGTGTTAAAAATGGATCTTGATCCT AACGATGTAACCTTTACTTACTCACACTTCGCTGTACCTCAAGCGAAAGGAA ACAATGTCGTGATTACAAGCTATATGACAAACAGAGGATTCTACGCACTACA AACAATCAACGTTTGCGCCAAGCTTCCTGCTGAACATCAAAGGCAAGAAAA CATCTGTTGTCAAAGACAGCATCCTTGAACAAGGACAATTAACAGTTAACA AATAAAAACGCAAAAGAAAATGCCGATATTGACTACCGCAAGCAGTGTGAC CGTGTGCTTCTCAAATGCCTGATTCAGGCTGTCTATGTGTGACTGTTGAGCT GTAACAAGTTGTCTCAGGTGTTCAATTTCATGTTCTAGTTGCTTTGTTTTACT GGTTTCACCTGTTCTATTAGGTGTTACATGCTGTTCATCTGTTACATTGTCGA TCTGTTCATGGTGAACAGCTTTAAATGCACCAAAAACTCGTAAAAGCTCTGA TGTATCTATCTTTTTTACACCGTTTTCATCTGTGCATATGGACAGTTTTCCCTT TGAT	53

TABLE 7-continued

Synthetic DNA utilized for strain construction.

	SEQ ID NO
ΔiclR-cure	
AAATGATTTCCACGATACAGAAAAAAGAGACTGTCATGGGCAGAATATTGC CTCTGCCCGCCAGAAAAAG	54
ΔarcA-cure	
CTGTTTCGATTTAGTTGGCAATTTAGGTAGCAAACTCGGCTTTACCACCGTC AAAAAAAACGGCGCTTTT	55
Δcas3-pro-casA	
CAAGACATGTGTATATCACTGTAATTCGATATTTATGAGCAGCATCGAAAAA TAGCCCGCTGATATCATCGATAATACTAAAAAAACAGGGAGGCTATTACCA GGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTA TCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCG GGTGGGCCTTTCTGCGTTTATATCTTTCTGACACCTTACTATCTTACAAATGT AACAAAAAAGTTATTTTTCTGTAATTCGAGCATGTCATGTTACCCCGCGAGC ATAAAACGCGTGTGTAGGAGGATAATCTTTGACGGCTAGCTCAGTCCTAGGT ACAGTGCTAGCCATATGAAGGAGAACAAATGAATTTGCTTATTGATAACTG GATCCCTGTACGCCCGCGAAACGGGGGGAAAGTCCAAATCATAAATCTGCA ATCGCTATAC	56
Δcas3::ugBp-sspB-pro-casA	
CAAGACATGTGTATATCACTGTAATTCGATATTTATGAGCAGCATCGAAAAA TAGCCCGCTGATATCATCGATAATACTAAAAAAACAGGGAGGCTATTACCA GGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTA TCTGTTGTTTGTCGGTGAACGCTCTCTACTAGAGTCACACTGGCTCACCTTCG GGTGGGCCTTTCTGCGTTTATATCTTTCTGACACCTTACTATCTTACAAATGT AACAAAAAAGTTATTTTTCTGTAATTCGAGCATGTCATGTTACCCCGCGAGC ATAAAACGCGTGTGTAGGAGGATAATCTATGGATTTGTCACAGCTAACACC ACGTCGTCCCTATCTGCTGCGTGCATTCTATGAGTGGTTGCTGGATAACCAG CTCACGCCGCACCTGGTGGTGGATGTGACGCTCCCTGGCGTGCAGGTTCCTA TGGAATATGCGCGTGACGGGCAAATCGTACTCAACATTGCGCCGCGTGCTGT CGGCAATCTGGAACTGGCGAATGATGAGGTGCGCTTTAACGCGCGCTTTGGT GGCATTCCGCGTCAGGTTTCTGTGCCGCTGGCTGCCGTGCTGGCTATCTACG CCCGTGAAAATGGCGCAGGCACGATGTTTGAGCCTGAAGCTGCCTACGATG AAGATACCAGCATCATGAATGATGAAGAGGCATCGGCAGACAACGAAACC GTTATGTCGGTTATTGATGGCGACAAGCCAGATCACGATGATGACACTCATC CFGACGATGAACCTCCGCAGCCACCACGCGGTGGTCGACCGGCATTACGCG TTGTGAAGTAATTGACGGCTAGCTCAGTCCTAGGTACAGTGCTAGCCATATG AAGGAGAACAAATGAATTTGCTTATTGATAACTGGATCCCTGTACGCCCGCG AAACGGGGGGAAAGTCCAAATCATAAATCTGCAATCGCTATAC	57
fabI-DAS+4-gentR	
CTATTGAAGATGTGOGTAACTCTGCGCCATTCCTGTGCTCCGATCTCTCTGC CGOTATCTCCGGTGAAGTGGTCCACGTTGACGGCGGTTTCAGCATTGCTGCA ATGAACGAACTCGAACTGAAAGCGGCCAACGATGAAAACTATTCTGAAAAC TATGCGGATGCGTCTTAATAGGAAGTTCCTATTCTCTAGAAAGTATAGGAAC TTCCGAATCCATGTGGGAGTTTATTCTTGACACAGATATTTATGATATAATA ACTGAGTAAGCTTAACATAAGGAGGAAAAACATATGTTACGCAGCAGCAAC GATGTTACGGAGCAGGGCAGTCGCCCTAAAACAAAGTTAGGTGGCTCAAGT ATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCAAGTCAAATCCATGC GGGCTGCTCTTGATCTTTTCGGTCGTGAGTTCGGAGACGTAGCCACCTACTC CCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGCTCCGTAGTAAGACA TTCATCGCGCTTGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTCGCGG CTTACGTTCTGCCCAAGTTTGAGCAGCCGCGTAGTGAGATCTATATCTATGA TCTCGCAGTCTCCGGCGAGCACCGGAGGCAGGGCATTGCCACCGCGCTCAT CAATCTCCTCAAGCATGAGGCCAACGCGCTTGGTGCTTATGTGATCTACGTG CAAGCAGATTACGGTGACGATCCCGCACTGGCTCTCTATACAAAGTTGGGC ATACGGGAAGAAGTGATGCACTTTGATATCGACCCAAGTACCGCCACCTAA GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTCCGTTCTGTTGGTAAAGAT GGGCGGCGTTCTGCCGCCCGTTATCTCTGTTATACCTTTCTGATATTTGTTAT CGCCGATCCGTCTTTCTCCCCTTCCCGCCTTGCGTCAGG	58
gapA-DAS+4-zeoR-proDp-gapN	
TCTCCAAAGCGGCCAACGATGAAAACTATTCTGAAAACTATGCGGATGCGT CTTGATTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCAACTTTAAAATT AAAGAGGTATATATTAATGACTAACCAATATAAGAATTACGTAAATGGGGA GTGGAAGCTTTCGGAGAATGAAATTAAGATCTATGAACCAGCCAGTGGGGC GGAATTGGGGTCAGTCCCGGCAATGTCCACTGAAGAAGTFGACTATGTCTAC GCCTCGGCCAAAAAAGCGCAGCCAGCATGGCGCTCGCTTTCCTATATTGAGC	59

TABLE 7-continued

Synthetic DNA utilized for strain construction.	SEQ ID NO
GTGCGGCTTATTTGCACAAAGTCGCAGACATCCTGATGCGTGACAAGGAGA	
AAATTGGAGCGGTATTGTCCAAGGAAGTAGCGAAAGGCTACAAATCCGCAG	
TATCGGAGGTCGTCCGCACCGCCGAGATTATTAATTATGCGGCCGAAGAAG	
GGCTTCGCATGGAGGGTGAGCTTCTTGGAGGGCGGCAGTTTTGAGGCGGCAT	
CCAAGAAAAAAATCGCTGTCGTCCGTCGCGAGCCGGTGGGACTTCTGCTTG	
CTATTAGTCCGTTCAATTACCCCGTGAATCTGGCCGGCTCCAAGATTCCCC	
TGCACTGATCGCGGGCAATGTAATCGCTTTTAAACCACCGACCCAAGGATCG	
ATTAGTGGACTTCTTTTAGCGGAGGCGTTTGCGGAGGCAGGTCTTCCAGCCG	
GCGTATTCAATACCATCACGGGGCGTGGAAGTGAAATCGGGGATTACATCG	
TGGAGCACCAGGCAGTAAATTTCATCAACTTCACGGGTTCCACGGGGATCG	
GGGAGCGTATCGGTAAGATGGCTGGGATGCGTCCGATCATGTTGGAACTTG	
GCGGCAAGGATAGTGCGATTGTGCTGGAAGACGCAGACTTGGAATTCACAG	
CTAAAAACATTATCGCTGGAGCCTTCGGGTATAGTGGTCAACGTTGGACGGC	
AGTTAAGCGCGTTCTTGTTATGGAAAGTGTCGCGGATGAATTGGTCGAGAA	
GATTCGCGAGAAAGTGTTAGCTCTTACGATTGGAAATCCAGAGGACGATGC	
TGACATCACTCCATTGATCGACACGAAATCCGCGGATTACGTCGAGGGGCT	
GATCAACGACGCGAACGATAAGGGAGCAGCGGCTTTGACCGAGATCAAACG	
CGAGGGGAACCTGATCTGCCCGATTCTTTTTGACAAAGTCACAACTGACATG	
CGCTTGGCATGGGAAGAACCCTTCGGCCCAGTCTTGCCTATTATCCGCGTTA	
CTAGCGTAGAGGAAGCAATTGAAATTTCCAATAAATCCGAATATGGGTTGC	
AAGCGAGTATCTTTACTAACGATTTTCCACGTGCCTTTGGTATTGCGGAACA	
GTTAGAAGTCGGGACAGTTCACATCAACAACAAGACGCAGCGCGGGACAGA	
TAACTTCCCCTTTTTGGGAGCAAAGAAGTCTGGGGCTGGAATCCAAGGGGT	
GAAATACTCCATCGAAGCCATGACGACGGTGAAGAGCGTTGTTTTTGACATC	
AAGTAAAACATAAGGAGGAAAAACAGATGGCGAAACTGACCTCGGCGGTT	
CCGGTTCTGACGGCACGTGATGTGGCGGGCGGGGTTGAATTTTGGACGGATC	
GTCTGGGCTTCAGTCGTGATTTTGTGGAAGATGACTTCGCAGGCGTGGTTCG	
CGATGACGTCACCCTGTTTATTTCCGCAGTTCAGGATCAAGTCGTGGCGGAC	
AACACGCTGGCTTGGGTGTGGGTTCGTGGCCTGGATGAACTGTATGCGGAAT	
GGAGCGAAGTTGTCTCTACCAATTTCCGTGACGCGAGCGGTCCGGCCATGAC	
GGAAATCGGCGAACAGCCGTGGGCTCGCGAATTTGCTCTGCGTGACCCGGC	
TGGCAACTGTGTCCATTTCGTGGCTGAAGAACAAGATTGAGTTGAGATGAC	
ACTGTGATCTAAAAAGAGCGACTTCGGTCGCTCTTTTTTTTACCTGA	
gapA-zeoR-proDp-gapN	
ACGAAACCGGTTACTCCAACAAAGTTCTGGACCTGATCGCTCACATCTCCAA	60
ATGATTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCAACTTTAAAATTA	
AAGAGGTATATATTAATGACTAAGCAATATAAGAATTACGTAAATGGGGAG	
TGGAAGCTTTCGGAGAATGAAATTAAGATCTATGAACCAGCCAGTGGGGCG	
GAATTGGGGTCAGTCCCGGCAATGTCCACTGAAGAAGTTGACTATGTCTACG	
CCTCGGCCAAAAAAGCGCAGCCAGCATGGCGCTCGCTTTCCTATATTGAGCG	
TGCGGCTTATTTGCACAAAGTCGCAGACATCCTGATGCGTGACAAGGAGAA	
AATTGGAGCGGTATTGTCCAAGGAAGTAGCGAAAGGCTACAAATCCGCAGT	
ATCGGAGGTCGTCCGCACCGCCGAGATTATTAATTATGCGGCCGAAGAAGG	
GCTTCGCATGGAGGGTGAGGTCTTGGAGGGCGGCAGTTTTGAGGCGGCATC	
CAAGAAAAAAATCGCTGTCGTCCGTCGCGAGCCGGTGGGACTTGTGCTTGCT	
ATTAGTCCGTTCAATTACCCCGTGAATCTGGCCGGCTCCAAGATTGCCCCTG	
CACTGATCGCGGGCAATGTAATCGCTTTTAAACCACCGACCCAAGGATCGAT	
TAGTCGACTTCTTTTAGCGGAGGCGTTTGCGGAGGCAGGTCTTCCAGCCGGC	
GTATTCAATACCATCACGGGGCGTGGAAGTGAAATCGGGGATTACATCGTG	
GAGCACCAGGCAGTAAATTTCATCAACTTCACGGGTTCCACGGGGATCGGG	
GAGCGTATCGGTAAGATGGCTGGGATGCGTCCGATCATGTTGGAACTTGGC	
GGCAAGGATAGTGCGATTGTGCTGGAAGACGCAGACTTGGAATTGACAGCT	
AAAAACATTATCGCTGGAGCCTTCGGGTATAGTGGTCAACGTTGCACGGCA	
GTTAAGCGCGTTCTTGTTATGGAAAGTGTCGCGGATGAATTGGTCGAGAAG	
ATTCGCGAGAAAGTGTTAGCTCTTACGATTGGAAATCCAGAGGACGATGCT	
GACATCACTCCATTGATCGACACGAAATCCGCGGATTACGTCGAGGGGCTG	
ATCAACGACGCGAACGATAAGGGAGCAGCGGCTTTGACCGAGATCAAACGC	
GAGGGGAACCTGATCTGCCCGATTCTTTTTGACAAAGTCACAACTGACATGC	
GCTTGGCATGGGAAGAACCCTTCGGCCCAGTCTTGCCTATTATCCGCGTTAC	
TAGCGTAGAGGAAGCAATTGAAATTTCCAATAAATCCGAATATGGGTTGCA	
AGCGAGTATCTTTACTAACGATTTTCCACGTGCCTTTGGTATTGCGGAACAG	
TTAGAAGTCGGGACAGTTCACATCAACAACAAGACGCAGCGCGGGACAGAT	
AACTTCCCCTTTTTGGGAGCAAAGAAGTCTGGGGCTGGAATCCAAGGGGTG	
AAATACTCCATCGAAGCCATGACGACGGTCAAGAGCGTTGTTTTTGACATCA	
AGTAAAACATAAGGAGGAAAAACAGATGGCGAAACTGACCTCGGCGGTTCC	
GGTTCTGACGGCACGTGATGTGGCGGCCGCCGTTGAATTTTGGACGGATCGT	
CTGGGCTTCAGTCGTGATTTTGTGGAAGATGACTTCGCAGGCGTGGTTCGCG	
ATGACGTCACCCTGTTTATTTCCGCAGTTCAGGATCAAGTCGTGCCGGACAA	
CACGCTGGCTTGGGTGTGGGTTCGTGGCCTGGATGAACTGTATGCGGAATGG	
AGCGAAGTTGTCTCTACCAATTTCCGTGACGCGAGCGGTCCGGCCATGACGG	
AAATCGGCGAACAGCCGTGGGGTCGCGAATTTGCTCTGCGTGACCCGGCTG	
GCAACTGTGTCCATTTCGTGGCTGAACAACAAGATTGAGTTGAGATGACACT	
GTGATCTAAAAAGAGCGACTTCGGTCGCTCTTTTTTTTACCTGA	

TABLE 7-continued

Synthetic DNA utilized for strain construction.

	SEQ ID NO
gapA-DAS+4-zeoR	
TCTACCGATTTCAACGGCGAAGTTTGCACTTCCGTGTTCGATGCTAAAGCTG GTATCGCTCTGAACGACAACTTCGTGAAACTGGTATCCTGGTACGACAACGA AACCGGTTACTCCAACAAAGTTCTGGACCTGATCGCTCACATCTCCAAAGCG GCCAACGATGAAAACTATTCTGAAAACTATGCGGATGCGTCTTGATCCTGAC GGATGGCCTTTTTGCGTTTCTACAAACTCTTTTTGTTTATTTTTCTAAATACAT TCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAAT ATTGAAAAAGGAAGAGTAATGGCGAAACTGACCTCGCCGGTTCCGGTTCTG ACGGCACGTGATGTGGCGGGCGCGGTTGAATTTTGGACGGATCGTCTGGGC TTGAGTCGTGATTTTGTGGAAGATGACTTCGCAGGCGTGGTTCGCGATGACG TCACCCTGTTTATTTCCGCAGTTCAGGATCAAGTCGTGCCGGACAACACGCT GGCTTGGGTGTGGGTTCGTGGCCTGGATGAACTGTATGCGGAATGGAGCGA AGTTGTCTCTACCAATTTCCGTGACTCGAGCGGTCCGGCCATGACGGAAATC GGCGAACAGCCGTGGGGTCGCGAATTTGCTCTGCGTGACCCGGCTGGGAAC TGTGTCCATTTCGTGGCTGAAGAACAAGATTGAGTTGAGATGACACTGTGAT CTAAAAAGAGCGACTTCGGTCGCTCTTTTTTTTACCTGATAAAATGAAGTTA AAGGACTGCGTCATGATTAAGAAAATTTTTGCCCTTCCGGTCATCGAACAAA TCTCCCCTGTCCTCTCCCGTCGTAAACTGGATGAACTGGACCTCATTGTGGTC GATCATCCGCAGGTAAAAGCCTCT	61
gltA-DAS+4-ampR	
GTATTCCGTCTTCCATGTTCACCGTCATTTTCGCAATGGCACGTACCGTTGGC TGGATCGCCCACTGGAGCGAAATGCACAGTGACGGTATGAAGATTGCCCGT CCGCGTCAGCTGTATACAGGATATGAAAAACGCGACTTTAAAAGCGATATC AAGCGTGCGGCCAACGATGAAAACTATTCTGAAAACTATGCGGATGCGTCT TAATAGTCCTGACGGATGGCCTTTTTGCGTTTCTACAAACTCTTTTTGTTTAT TTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATA AATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGT GTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCA GAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTG GGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCC CCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGC GGTATTATCCCGTGTTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACA CTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTT ACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGT GATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAG CTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTT GGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACG ATGCCTACAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTA CTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAA GTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTG ATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGG GGCCAGATGGTAAGCCCTCCCGTATCGTACTTTATCTACACGACGGGGAGTC AGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCAC TGATTAAGCATTGGTAACTGTCAGACTAATGGTTGATTGCTAAGTTGTAAAT ATTTTAACCCGCCGTTCATATGGCGGGTTGATTTTTATATGCCTAAACACAA AAAATTGTAAAAATAAAATCCATTAACAGACCTATATAGATATTTAAAAAG AATAGAACAGCTCAAATTATCAGCAACCCAATACTTTCAATTAAAAACTTCA TGGTAGTCGCATTTATAACCCTATGAAA	62
gltA-DAS+4-purR	
ACCGTCATTTTCGCAATGGCACGTACCGTTGGCTGGATCGCCCACTGGAGCG AAATGCACAGTGACGGTATGAAGATTGCCCGTCCGCGTCAGCTGTATACAG GATATGAAAAACGCGACTTTAAAAGCGATATCAAGCGTGCGGCCAACGATG AAAACTATTCTGAAAACTATGCGGATGCGTCTTAATCCTGACGGATGGCCTT TTTGCGTTTCTACAAACTCTTTTTGTTTATTTTTCTAAATACATTCAAATATGT ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAA GGAAGAGTATGACTGAATACAAGCCCACGGTACGCTTGGCGACGCGCGACG ATGTTCCCCGCGCTGTTCGTACATTAGCTGCGGCCTTTGCAGATTACCCAGC GACGCGCCATACGGTCGATCCGGACCGCCATATCGAGCGTGTCACAGAATT GCAGGAACTTTTCTTAACTCGCGTGGGCCTTGACATCGGAAAGGTCTGGGTG GCTGACGATGGCGCTGCACTGGCTGTTTGGACCACTCCGGAGAGTGTAGAG GCTGGTGCAGTGTTCGCCGAAATTGGTCCTCGTATGGCCGAATTAAGTGGAA GTCGTCTGGCAGCCCAACAACAAATGGAAGGGTTGCTTGCGCCCCACCGTC CGAAAGAACCCGCGTGGTTCCTTGCCACCGTTGGAGTAAGCCCAGATCACC AGGGGAAGGGTTTAGGATCTGCCGTAGTTTACCAGGTGTGGAGGCAGCAG AACGTGCGGGAGTTCCGGCCTTCCTTGAGACGTCGGCGCCGCGCAATTTACC	63

TABLE 7-continued

Synthetic DNA utilized for strain construction.	SEQ ID NO
GTTTTACGAACGTCTTGGATTCACCGTTACGGCGGACGTGGAGGTGCCGGAG GGACCCCGTACTTGGTGTATGACTCGTAAACCGGGAGCCTGATAATGGTTGA TTGCTAAGTTGTAAATATTTTAACCCGCCGTTCATATGGCGGGTTGATTTTTA TATGCCTAAACACAAAAAATTGTAAAAATAAAATCCATTAACAGACCTATA TAGATATTTAAAAAGAATAGAACAGCTCAAATTATCAGCAACCCA	
gltA-DAS+4-zeoR	
GTATTCCGTCTTCCATGTTCACCGTCATTTTCGCAATGGCACGTACCGTTGGC TGGATCGCCCACTGGAGCGAAATGCACAGTGACGGTATGAAGATTGCCCGT CCGCGTCAGCTGTATACAGGATATGAAAAACGCGACTTTAAAAGCGATATC AAGCGTGCGGCCAACGATGAAAACTATTCTGAAAACTATGCGGATGCGTCT TAATAGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGA CTCACTATAGGAGGGCCATCATGGCCAAGTTGACCAGTGCCGTTCCGGTGCT CACCGCGCGCGACGTCGCCGGAGCGGTCGAGTTCTGGACCGACCGGCTCGG GTTCTCCCGGGACTTCGTGGAGGACGACTTCGCCGGTGTGGTCCGGGACGAC GTGACCCTGTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACC CTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCG GAGGTCGTGTCCACGAACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAG ATCGGCGAGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGC AACTGCGTGCACTTTGTGGCAGAGGAGCAGGACTGAGGATAAGTAATGGTT GATTGCTAAGTTGTAAATATTTTAACCCGCCGTTCATATGGCGGGTTGATTTT TATATGCCTAAACACAAAAAATTGTAAAAATAAAATCCATTAACAGACCTA TATAGATATTTAAAAAGAATAGAACAGCTCAAATTATCAGCAACCCAATAC TTTCAATTAAAAACTTCATGGTAGTCGCATTTATAACCCTATGAAA	64
lpd-DAS+4-gentR	
GCGGCGAGCTGCTGGGTGAAATCGGCCTGGCAATCGAAATGGGTTGTGATG CTGAAGACATCGCACTGACCATCCACGCGCACCCGACTCTGCACGAGTCTGT GGGCCTGGCGGCAGAAGTGTTCGAAGGTAGCATTACCGACCTGCCGAACCC GAAAGCGAAGAAGAAGGCGGCCAACGATGAAAACTATTCTGAAAACTATG CGGATGCGTCTTAATAGCGAATCCATGTGGGAGTTTATTCTTGACACAGATA TTTATGATATAATAACTGAGTAAGCTTAACATAAGGAGGAAAAACATATGT TACGCAGCAGCAACGATGTTACGCAGCAGGGCAGTCGCCCTAAAACAAAGT TAGGTGGCTCAAGTATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCA AGTCAAATCCATGCGGGCTGCTCTTGATCTTTTCGGTCGTGAGTTCGGAGAC GTAGCCACCTACTCCCAACATCAGCCGGACTCCGATTACCTCGGGAACTTGC TCCGTAGTAAGACATTCATCGCGCTTGCTGCCTTCGACCAAGAAGCGGTTGT TGGCGCTCTCGCGGCTTACGTTCTGCCCAAGTTTGAGCAGCCGCGTAGTGAG ATCTATATCTATGATCTCGCAGTCTCCGGCGAGCACCGGAGGCAGGGCATTG CCACCGCGCTCATCAATCTCCTCAAGCATGAGGCCAACGCGCTTGGTGCTTA TGTGATCTACGTGCAAGCAGATTACGGTGACGATCCCGCAGTGGCTCTCTAT ACAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATCGACCCAAGT ACCGCCACCTAATTTTTCGTTTGCCGGAACATCCGGCAATTAAAAAAGCGGC TAACCACGCCGCTTTTTTTACGTCTGCAATTTACCTTTCCAGTCTTCTTGCTC CACGTTCAGAGAGACGTTCGCATACTGCTGACCGTTGCTCGTTATTCAGCCT GACAGTATGGTTACTGTC	65
udhA-DAS+4-bsdR	
TCTGGGTATTCACTGCTTTGGCGAGCGCGCTGCCGAAATTATTCATATCGGT CAGGCGATTATGGAACAGAAAGGTGGCGGCAACACTATTGAGTACTTCGTC AACACCACCTTTAACTACCCGACGATGGCGGAAGCCTATCGGGTAGCTGCG TTAAACGGTTTAAACCGCCTGTTTGCGGCCAACGATGAAAACTATTCTGAAA ACTATGCGGATGCGTCTTAATAGTTGACAATTAATCATCGGCATAGTATATC GGCATAGTATAATACGACTCACTATAGGAGGGCCATCATGAAGACCTTCAA CATCTCTCAGCAGGATCTGGAGCTGGTGGAGGTCGCCACTGAGAAGATCAC CATGCTCTATGAGGACAACAAGCACCATGTCGGGGCGGCCATCAGGACCAA GACTGGGGAGATCATCTCTGCTGTCCACATTGAGGCCTACATTGGCAGGGTC ACTGTCTGTGCTGAAGCCATTGCCATTGGGTCTGCTGTGAGCAACGGGCAGA AGGACTTTGACACCATTCTGGCTGTCAGCCACCCCTACTCTGATGAGGTGGA CAGATCCATCAGGGTGGTCAGCCCCTGTGGCATGTGCAGAGAGCTCATCTCT GACTATGCTCCTGACTGCTTTGTGCTCATTGAGATGAATGGCAAGCTGGTCA AAACCACCATTGAGGAACTCATCCCCCTCAAGTACACCAGGAACTAAAGTA AAACTTTATCGAAATGGCCATCCATTCTTGCGCGGATGGCCTCTGCCAGCTG CTCATAGCGGCTGCGCAGCGGTGAGCCAGGACGATAAACCAGGCCAATAGT GCGGCGTGGTTCCGGCTTAATGCACGG	66
zwf-DAS+4-bsdR	
GAAGTGGAAGAAGCCTGGAAATGGGTAGACTCCATTACTGAGGCGTGGGCG ATGGACAATGATGCGCCGAAACCGTATCAGGCCGGAACCTGGGGACCCGTT GCCTCGGTGGCGATGATTACCCGTGATGGTCGTTCCTGGAATGAGTTTGAGG CGGCCAACGATGAAAACTATTCTGAAAACTATGCGGATGCGTCTTAATAGTT	67

TABLE 7-continued

Synthetic DNA utilized for strain construction.	SEQ ID NO
GACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACTCACTAT AGGAGGGCCATCATGAAGACCTTCAACATCTCTCAGCAGGATCTGGAGCTG GTGGAGGTCGCCACTGAGAACATCACCATGCTCTATGAGGACAACAAGCAC CATGTCGGGGCGGCCATCAGGACCAAGACTGGGGAGATCATCTCTGCTGTC CACATTGAGGCCTACATTGGCAGGGTCACTGTCTGTGCTGAAGCCATTGCCA TTGGGTCTGCTGTGAGCAACGGGCAGAAGGACTTTGACACCATTGTGGCTGT CAGCCACCCCTACTCTGATGAGGTGGACAGATCCATCAGGGTGGTCAGCCC CTGTGGCATCTGCAGAGAGCTCATCTCTGACTATGCTCCTGACTGCTTTGTG CTCATTGAGATGAATGGCAAGCTGGTCAAAACCACCATTGAGGAACTCATC CCCCTCAAGTACACCAGGAACTAAAGTAATATCTGCGCTTATCCTTTATGGT TATTTTACCGGTAACATGATCTTGCGCAGATTGTAGAACAATTTTTACACTTT CAGGCCTCGTGCGGATTCACCCACGAGGCTTTTTTTATTACACTGACTGAAA CGTTTTTGCCCTATGAGCTCCGGTTACAGGCGTTTCAGTCATAAATCCTCTGA ATGAAACGCGTTGTGAATC	
dadX-DAS+4-purR	
GCGTGCGCACCATGACGGTGGGGACCGTCTCGATGGATATGCTAGCGGTCG ATTTAACGCCTTGCCCGCAGGCGGGTATTGGTACGCCGGTTGAGCTGTGGGG CAAGGAGATCAAAATTGATGATGTCGCCGCCGCTGCCGGAACGGTGGGCTA TGAGTTGATGTGCGCGCTGGCGCTACGCGTCCCGGTTGTGACGGTGGCGGCC AACGATGAAAACTATTCTGAAAACTATGCGGATGCGTCTTAATCCTGACGG ATGGCCTTTTTGCGTTTCTACAAACTCTTTTTGTTTATTTTTCTAAATACATTC AAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT TGAAAAAGGAAGAGTATGACTGAATACAAGCCCACGGTACGCTTGGCGACG CGCGACGATGTTCCCCGCGCTGTTCGTACATTAGCTGCGGCCTTTGCAGATT ACCCAGCGACGCGCCATACGGTCGATCCGGACCGCCATATCGACCGTCTCA CAGAATTGCAGGAACTTTTCTTAACTCGCGTGGGCCTTGACATCGGAAAGGT CTGGGTGGCTGACGATGGCGCTGCAGTGGCTGTTTGGACCACTCCGGAGAG TGTAGAGGCTGGTGCAGTGTTCGCCGAAATTGGTCCTCGTATGGCCGAATTA AGTGGAAGTCGTCTGGCAGCCCAACAACAAATGGAAGGGTTGCTTGCGCCC CACCGTCCGAAAGAACCCGCGTGGTTCCTTGCCACCGTTGGAGTAAGCCCA GATCACCAGGGGAAGGGTTTAGGATCTGCCGTAGTTTTACCAGGTGTGGAG GCAGCAGAACGTGCGGGAGTTCCGGCCTTCCTTGAGACGTCGGCGCCGCGC AATTTACCGTTTTACGAACGTCTTGGATTCACCGTTACGGCGGACGTGGAGG TGCCGGAGGGACCCCGTACTTGGTGTATGACTCGTAAACCGGGAGCCTGAT AACTTGTTGTAAGCCGGATCGGAGGCAACGTCTTCTGGGTGCAAAAAAATC ATCCATCCGGGTGGTCAGCAACTGTAGTTGTTAATGTGACAGAGCCATTGCC CATGATAGTGTCCATTAAAAGGATGGACACTATTTCCCCGGAACCTGAACTC ACCGCACAGGCGTTCTACATAAAACGCTTACGCTTCATTGTTGACTC	68

Section 4: Dynamic Control Over Protein Levels.

Plasmids expressing fluorescent proteins and silencing guides were transformed into the corresponding hosts strain listed in Table 8. Strains were evaluated in triplicate in an m2p-labs Biolector™, which simultaneously measures fluorescence including GFPuv and mCherry levels, as well as biomass levels.

TABLE 8

Strains used for Dynamic Control over protein levels

Microbe	Synthetic Metabolic Valves	Plasmid	Host Strain
E. coli	RFP-control	pCDF-mcherry1 + PSMART-IN:yibDp-GFPuv	DLF_0002
	Proteolysis	pCDF-mcherry2 + PSMART-IN:yibDp-GFPuv	DLF_0025
	Silencing	pCDF-mcherry1 + pCASCADE-proD + pSMART-IN:yibDp-GFPuv	DLF_01517

TABLE 8-continued

Strains used for Dynamic Control over protein levels

Microbe	Synthetic Metabolic Valves	Plasmid	Host Strain
	Proteolysis + Silencing	pCDF-mcherry2 + pCASCADE-proD + pSMART-IN:yibDp-GFPuv	DLF_0025

OD600 readings were corrected using the formula below, where OD600 refers to an offline measurement, OD600* refers to Biolector biomass reading, t0 indicates the start point, and tf indicates the final point.

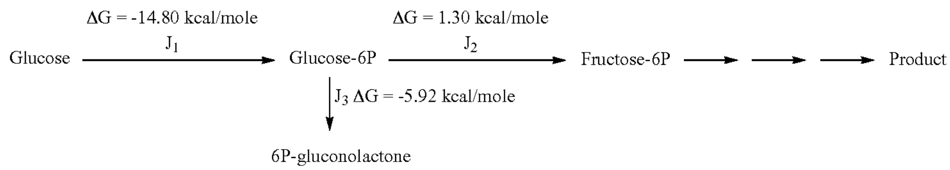
$$OD600_t = (OD600_t^* - OD600_{t0}^*) * \frac{(OD600_{tf} - OD600_{t0})}{(OD600_{tf}^* - OD600_{t0}^*)} + 0.25 \quad \text{Equation S1}$$

Section 5: Metabolic Control

Near Equilibrium Reactions

The impact of Valves on metabolite pools for near equilibrium reactions is illustrated using the G6P node as an example. Abbreviations: Gluc, glucose; G6P, glucose-6-phosphate; F6P, fructose-6-phosphate; 6PGl, 6-phosphate-gluconolactone.

G6P Node without Valves



$$\text{Net Flux} = J_i = e^{\frac{-dG}{RT}} - 1 \quad \text{Equation S3}$$

$$e^{\frac{-dG1}{RT}} - 1 = e^{\frac{-dG2}{RT}} - 1 + e^{\frac{-dG3}{RT}} - 1 \quad \text{Equation S4}$$

$$e^{\frac{-dG1}{RT}} = e^{\frac{-dG2}{RT}} + e^{\frac{-dG3}{RT}} - 1 \quad \text{Equation S5}$$

$$Keq1 = Keq2 + Keq3 - 1 \quad \text{Equation S6}$$

$$Keq1 + 1 = Keq2 + Keq3 \quad \text{Equation S7}$$

$$\frac{[G6P]}{[Gluc]} + 1 = \frac{[F6P]}{[G6P]} + \frac{[6PGl]}{[G6P]} \quad \text{Equation S8}$$

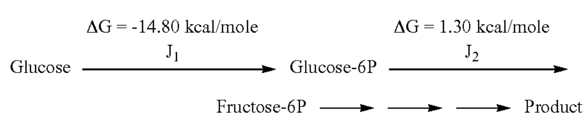
$$\frac{[G6P]}{[Gluc]} + 1 = \frac{[F6P] + [6PGl]}{[G6P]} \quad \text{Equation S9}$$

$$\frac{[G6P]^2}{[Gluc]} + [G6P] = [F6P] + [6PGl] \quad \text{Equation S10}$$

$$[F6P] = \frac{[G6P]^2}{[Gluc]} + [G6P] - [6PGl] \quad \text{Equation S11}$$

G6P Node with Valves

When zwf valve is in effect, $J_3 \approx 0$.



$$\text{Net Flux} = J_i = e^{\frac{-dG}{RT}} - 1 \quad \text{Equation S13}$$

$$e^{\frac{-dG1}{RT}} - 1 = e^{\frac{-dG2}{RT}} - 1 \quad \text{Equation S14}$$

$$Keq1 = Keq2 \quad \text{Equation S15}$$

$$\frac{[G6P]}{[Gluc]} = \frac{[F6P]}{[G6P]} \quad \text{Equation S16}$$

$$[F6P] = \frac{[G6P]^2}{[Gluc]} \quad \text{Equation S17}$$

Impact of Valves

$$[F6P]\text{ network} = \frac{[G6P]^2}{[Gluc]} + [G6P] - [6PGl] \quad \text{Equation S11}$$

$$[F6P]\text{ value} = \frac{[G6P]^2}{[Gluc]} \quad \text{Equation S17}$$

Since close to equilibrium [6PGl]>[G6P]

[F6P]valve>=[F6P]network

The removal of thermodynamically favored reactions near equilibrium from the network will result in increased metabolite pools.

Section 6: Gene Silencing Arrays & Pathway Expression Constructs

The design and construction of CASCADE guides and guide arrays is illustrated below in FIG. **14** and FIG. **15**A-B. The pCASCADE-control plasmid was prepared by swapping the pTet promoter in pcrRNA.Tet[88] with an insulated low phosphate induced ugpB promoter[82]. Two promoters were responsible for regulating gltA gene, and sgRNA was designed for both promoters, resulting in guide gltA1 (G1) and gltA2 (G2).[89] Four promoters were responsible for regulating gapA gene, and sgRNA was designed for the first promoter, since during exponential phase of growth, gapA mRNAs were mainly initiated at the highly efficient gapA P1 promoter and remained high during stationary phase compared to the other three gapA promoters.[90] Multiple promoters upstream of lpd gene were involved in lpd regulation (https://ecocyc.org/gene?orgid=ECOLI&id=EG10543#tab=showAll), thus design of unique and effective sgRNA for lpd only was not possible. Promoter sequences for fabI, udhA and zwf were obtained from EcoCyc database (https://ecocyc.org/). To design CASCADE guide array, CASCADE PAM sites near the −35 or −10 box of the promoter of interest were identified, 30 bp at the 3' end of PAM site was selected as the guide sequence and cloned into pCASCADE plasmid using Q5 site-directed mutagenesis (NEB, MA) following manufacturer's protocol, with the modification that 5% v/v DMSO was added to the Q5 PCR reaction. The pCASCADE-control vector was used as template. pCASCADE plasmids with arrays of two or more guides were prepared as illustrated in FIG. **15**A-B. The pCASCADE guide array plasmid was prepared by sequentially amplifying complementary halves of each smaller guide plasmid by PCR, followed by subsequent DNA assembly. Table 9 lists sgRNA guide sequences and primers used to construct them. All pCASCADE silencing plasmids are listed in Table 10 below and are available at Addgene.

TABLE 9

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
fabI	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	69	
fabI-FOR	GTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAACCCC	70	pCASCADE control
fabI-REV	GGTTATTATAATCACGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGAT	71	
gapAP1	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	72	
gapAP1-FOR	CAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAACCCC	73	pCASCADE control
gapAP1-REV	TAAAATTACAAAAACCGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATC	74	
gltA1	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGTT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	75	
gltA1-FOR	GCGTAAAAGTTATGAAGTT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAAACCCCC	76	pCASACADE control
gltA1-REV	ATTATATGCTTTTCGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATCT	77	
gltA2	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGTT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	78	
gltA2-FOR	GGGACAGTTATTAGTT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAACCCC	79	pCASCADE control
gltA2-REV	GAATGAATTGGTCAATACGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATCT	80	
proD	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AGTGGTTCGCTGGATAACTTTACGGGCATGC*TCGAGTTCCCCGCGCCGCGGGGATAAACCG*	81	
proD-FOR	AACTTTACGGGCATGC*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAAACCCC	82	pCASCADE control
proD-REV	ATCCAGCAACCACTCGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATCT	83	
udhA	*TCGAGTTCCCCGCGCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	84	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
udhA-FOR	TTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAACCCC	85	pCASCADE control
udhA-REV	GCAACAGAATGGTAACGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATC	86	
zwf	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGAT*CGAGTTCCCCGCGCCAGCGGGGATAAACCG*	87	
zwf-FOR	CAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAAAAAACCCC	88	control
zwf-REV	TACTGCTTTTACGAGCGGTTTATCCCCGCTGGCGCGGGGAACTCGAGGTGGTACCAGATC	89	
FG1	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	90	
gltA-FOR	GCGCCAGCGGGGATAAACCGA*AAAGCATATAAT*GCG	91	pCASCADE-gltA1
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	92	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	93	pCASCADE-fabI
fabI-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATACGAACAGATAAACGGTTATTATAATC	94	
FG2	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	95	
gltA2-FOR	GCGCCAGCGGGGATAAACCGT*ATTGACCAATTCATTC*	96	pCASCADE-gltA2
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	97	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	98	pCASCADE-fabI
fabI-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATACGAACAGATAAACGGTTATTATAATC	99	
FU	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	100	
udhA-FOR	GCGCCAGCGGGGATAAACCGTTACCATTCTGTTG	101	pCASCADE-udhA
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	102	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	103	pCASCADE-fabI

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
fabI-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATACGAACAGATAAACGGTTATTATAATC	104	
FZ	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	105	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	106	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	107	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	108	pCASCADE-fabI
fabI-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATACGAACAGATAAACGGTTATTATAATC	109	
G1G2	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	110	
gltA2-FOR	GCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTC*	111	pCASCADE-gltA2
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	112	
	CCGGATGAGCATTCATCAGGCGGGCAAG	113	pCASCADE-gltA1
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	114	
G1U	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCGAAAAGCATATAAT*GCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	115	
udhA-FOR	GCGCCAGCGGGGATAAACCGTTACCATTCTGTTG	116	pCASCADE-udhA
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	117	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	118	pCASCADE-gltA1
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	119	
G1Z	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	120	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	121	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	122	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	123	pCASCADE-gltA1
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	124	
G2U	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCGTATTGACCAATTCATTC*GGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	125	
udhA-FOR	GCGCCAGCGGGGATAAACCGTTACCATTCTGTTG	126	pCASCADE-udhA
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	127	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	128	pCASCADE-gltA2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	129	
G2Z	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCGTATTGACCAATTCATTC*GGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	130	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	131	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	132	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	133	pCASCADE-gltA2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	134	
UZ	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGAT*CGAGTTCCCCGCGCCAGCGGGGATAAACCG*	135	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	136	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	137	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	138	pCASCADE-udhA
udhA-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATTCTTATACATAAAAGC	139	
FG1G2	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	140	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
gltA2-FOR	GCGCCAGCGGGGATAAACCGT*ATTGACCAATTCATTC*	141	pCASCADE-gltA2
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	142	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	143	pCASCADE-FG1
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	144	
G1G2A	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	145	
gapAP1-FOR	GCGCCAGCGGGGATAAACCGGTTTTTGTAATTTTACAGGC	146	pCASCADE-gpaAP1
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	147	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	148	pCASCADE-G1G2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	149	
G1G2U	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	150	
udhA-FOR	GCGCCAGCGGGGATAAACCGTTACCATTCTGTTG	151	pCASCADE-udhA
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	152	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	153	pCASCADE-G1G2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	154	
G1G2Z	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	155	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	156	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	157	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	158	pCASCADE-G1G2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	159	
FG1G2A	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	160	
gapAP1-FOR	GCGCCAGCGGGGATAAACCGGTTTTTGTAATTTTACAGGC	161	pCASCADE-gapAP1
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	162	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	163	pCASCADE-FG1G2
gltA2-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTAATAACTGTC	164	
FG1G2U	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTAT*CGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGTT*CGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	165	
gltA2-FOR	GCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTC*	166	pCASCADE-udhA
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	167	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	168	pCASCADE-FG1G2
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	169	
FG1G2Z	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	170	
gltA2-FOR	GCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTC*	171	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	172	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	173	pCASCADE-FG1G2
gltA1-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGAACTTCATAACTTTTAC	174	
G1G2UA	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	175	
gapA1-FOR	GCGCCAGCGGGGATAAACCGGTTTTTGTAATTTTACAGGC	176	pCASCADE-AP1
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	177	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	178	pCASCADE-G1G2U
udhA-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATTCTTATACATAAAAGC	179	
G1G2UZ	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CT*CGTAAAAGCAGTACAGTGCAC*CGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	180	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	181	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	182	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	183	pCASCADE-G1G2U
udhA-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATTCTTATACATAAAAGC	184	
FG1G2UA	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTA*TCGAGTTCCCCGCGCCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	185	
gapAP1-FOR	GCGCCAGCGGGGATAAACCGGTTTTTGTAATTTTACAGGC	186	pCASCADE-gpaAP1

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.

sgRNA/Primer Name	Sequence	SEQ ID NO	Template
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	187	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	188	pCASCADE-FG1G2U
udhA-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATTCTTATACATAAAAGC	189	
FG1G2UZ	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTAT*CGAGTTCCCCGCGCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	190	
zwf-FOR	GCGCCAGCGGGGATAAACCGCTCGTAAAAG	191	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	192	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	193	pCASCADE-FG1G2U
udhA-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATTCTTATACATAAAAGC	194	
FG1G2UZA	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTGATTATAATAACCGTTTATCTGTTCGTAT*CGAGTTCCCCGCGCCCAGCGGGGATAAACCG*AAAAGCATATAATGCGTAAAAGTTATGAAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TATTGACCAATTCATTCGGGACAGTTATTAGT*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*GTTTTTGTAATTTTACAGGCAACCTTTTAT*TCGAGTTCCCCGCGCCCAGCGGGGATAAACCG*	195	
gapAP1-FOR	GCGCCAGCGGGGATAAACCGGTTTTTGTAATTTTACAGGC	196	pCASCADE-gapA1
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTCATCCGG	197	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGCGGGCAAG	198	pCASCADE-FG1G2UZ
zwf-REV	CGGTTTATCCCCGCTGGCGCGGGGAACTCGATCTTACGGTGCACTGTC	199	
UZ	*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*TTACCATTCTGTTGCTTTTATGTATAAGAA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*CTCGTAAAAGCAGTACAGTGCACCGTAAGA*TCGAGTTCCCCGCGCCAGCGGGGATAAACCG*	200	

TABLE 9-continued

List of sgRNA guide sequences and primers used to construct them. Spacers are italicized.			
sgRNA/Primer Name	Sequence	SEQ ID NO	Template
zwf-FOR	GCGCCAGCGGGGATAAACCGC TCGTAAAAG	201	pCASCADE-zwf
pCASCADE-REV	CTTGCCCGCCTGATGAATGCTC ATCCGG	202	
pCASCADE-FOR	CCGGATGAGCATTCATCAGGC GGGCAAG	203	pCASCADE-udhA
udhA-REV	CGGTTTATCCCCGCTGGCGCG GGGAACTCGATTCTTATACAT AAAAGC	204	

TABLE 10

List of plasmids used in this study.		
Plasmid Utilized in this Study		
Plasmid	Purpose	Source
pSIM5	Recombineering and Strain Construction	Court Lab[54]
pCP20	FRT kanamycin cassette curing	Court Lab[54]
pSMART-HC-Kan	Backbone Vector	Lucigen
pcrRNA.Tet	pCASCADE-control backbone	Beisel Lab[34]
Plasmid Constructed in this Study		
Piasmid	Plasmid Name	Addgene ID
pSMART-Ala2	pSMART-HCKanIN:yibDp-ald*	71326
pSMART-Ala3	pSMART-HCKan-IN:phoBp-ald*	71327
pSMART-Ala4	pSMART-HCKan-IN:phoBp-ald*	71328
pSMART-Ala5	pSMART-HCKan-IN:mipAp-ald*	71329
pSMART-Ala11	pSMART-HCKan-proA-ald*	87172
pSMART-Ala12	pSMART-HCKan-proC-ald*	87173
pSMART-Ala13	pSMART-HCKan-proD-ald*	87174
pSMART-Ala14	pSMART-HCKan-proB-ald*	101079
pSMART-Ala15	pSMART-HCKan-HCEp-ald*	101080
pSMART-Mev2	pSMART-IN:yibDp1-mvaE-IN:phoBp2-mvaS(A110G)	66642
pSMART-Mev3	pSMART-IN:yibDp1-mvaE-IN:mipAp2-mvaS(A110G)	102761
pSMART-Mev4	pSMART-IN:yibDp1-mvaE-IN:phoHp2-mvaS(A110G)	102762
pSMART-Mev5	pSMART-IN:mipAp1-mvaE-IN:yibDp2-mvaS(A110G)	102763
pSMART-3HP	pSMART-3HP-NADPH-rhtA	87143
pCDF-mcherry1	pCDF-proD-mcherry	87144
pCDF-mcherry2	pCDF-proD-mcherry-DAS4	87145
pSMART-GFPuv	pSMART-IN:yibDp-GFPuv	65822
pSMART-GFPuv2	pSMART-IN:phoBp-GFPuv	71517
pSMART-GFPuv3	pSMART-IN:phoUp-GFPuv	71518
pSMART-GFPuv4	pSMART-IN:phoHp-GFPuv	71519
pSMART-GFPuv5	pSMART-IN:mipAp-GFPuv	71520
pCASCADE-control	pCASCADE	65821
pCASCADE-proD	pCASCADE-proD	65820
pCASCADE-gapAP1	pCASCADE-gapAP1	87146
pCASCADE-fabI	pCASCADE-fabI	66635
pCASCADE-FG1	pCASCADE-fabI-gltA1	71340
pCASCADE-FG1G2	pCASCADE-fabI-gltA1-gltA2	71342
pCASCADE-FG1G2A	pCASCADE-fabI-gltA1-gltA2-gapA	87147
pCASCADE-FG1G2U	pCASCADE-fabI-gltA1-gltA2-udhA	66637
pCASCADE-FG1G2UA	pCASCADE-fabI-gltA1-gltA2-udhA-gapA	87154
pCASCADE-FG1G2UZ	pCASCADE-fabI-gltA1-gltA2-udhA-zwf	87148
pCASCADE-FG1G2UZA	pCASCADE-fabI-gltA1-gltA2-udhA-zwf-gapA	87149
pCASCADE-FG1G2Z	pCASCADE-fabI-gltA1-gltA2-zwf	66638
pCASCADE-FG2	pCASCADE-fabI-gltA2	71341
pCASCADE-FU	pCASCADE-fabI-udhA	66636
pCASCADE-FZ	pCASCADE-fabI-zwf	71335
pCASCADE-G1G2	pCASCADE-gltA1-gltA2	71348
pCASCADE-G1G2A	pCASCADE-gltA1-gltA2-gapA	87150
pCASCADE-G1G2U	pCASCADE-gltA1-gltA2-udhA	71343
pCASCADE-G1G2UA	pCASCADE-gltA1-gltA2-udhA-gapA	87151
pCASCADE-G1G2UZ	pCASCADE-gltA1-gltA2-udhA-zwf	87152
pCASCADE-G1G2Z	pCASCADE-gltA1-gltA2-zwf	71347
pCASCADE-G1U	pCASCADE-gltA1-udhA	71339
pCASCADE-G1Z	pCASCADE-gltA1-zwf	71337

TABLE 10-continued

List of plasmids used in this study.		
pCASCADE-G2U	pCASCADE-gltA2-udhA	65819
pCASCADE-G2Z	pCASCADE-gltA2-zwf	71338
pCASCADE-gltA1	pCASCADE-gltA1	71334
pCASCADE-gltA2	pCASCADE-gltA2	65817
pCASCADE-udhA	pCASCADE-udhA	65818
pCASCADE-UZ	pCASCADE-udhA-zwf	87153
pCASCADE-zwf	pCASCADE-zwf	65825

Section 7: 2-Stage Micro-fermentations

E. coli Media Stock Solutions

10× concentrated Ammonium-Citrate 30 salts (1 L), mix 30 g of $(NH_4)_2SO_4$ and 1.5 g citric acid in water with stirring, adjust pH to 7.5 with 10 M NaOH. Autoclave and store at room temperature (RT).

10× concentrated Ammonium-Citrate 90 salts (1 L), mix 90 g of $(NH_4)_2SO_4$ and 2.5 g citric acid in water with stirring, adjust pH to 7.5 with 10 M NaOH. Autoclave and store at RT.

1 M Potassium 3-(N-morpholino) propanesulfonic Acid (MOPS), adjust to pH 7.4 with 50% KOH. Filter sterilize (0.2 μm) and store at RT.

0.5 M potassium phosphate buffer, pH 6.8, mix 248.5 mL of 1.0 M K_2HPO_4 and 251.5 mL of 1.0 M KH_2PO_4 and adjust to a final volume of 1000 mL with ultrapure water. Filter sterilize (0.2 μm) and store at RT.

2 M $MgSO_4$ and 10 mM $CaSO_4$ solutions. Filter sterilize (0.2 μm) and store at RT.

50 g/L solution of thiamine-HCl. Filter sterilize (0.2 μm) and store at 4° C.

500 g/L solution of glucose, dissolve by stirring with heat. Cool, filter sterilize (0.2 μm), and store at RT.

100 g/L yeast extract, autoclave, and store at RT.

100 g/L casamino acid, autoclave, and store at RT.

500× Trace Metal Stock: Prepare a solution of micronutrients in 1000 mL of water containing 10 mL of concentrated H_2SO_4. 0.6 g $CoSO_4{\cdot}7H_2O$, 5.0 g $CuSO_4{\cdot}5H_2O$, 0.6 g $ZnSO_4{\cdot}7H_2O$, 0.2 g $Na_2MoO_4{\cdot}2H_2O$, 0.1 g H_3BO_3, and 0.3 g $MnSO_4{\cdot}H_2O$. Filter sterilize (0.2 μm) and store at RT in the dark.

Prepare a fresh solution of 40 mM ferric sulfate heptahydrate in water, filter sterilize (0.2 μm) before preparing media each time.

Media Components

Prepare the final working medium by aseptically mixing stock solutions based on the following tables in the order written to minimize precipitation, then filter sterilize (with a 0.2 μm filter).

TABLE 11

Seed Media, pH 6.8:

Ingredient	Unit	SM10	SM10++
$(NH_4)_2SO_4$	g/L	9	9
Citric Acid	g/L	0.25	0.25
Potassium Phosphate	mM	5	5
$CoSO_4 \cdot 7H_2O$	g/L	0.0048	0.0048
$CuSO_4 \cdot 5H_2O$	g/L	0.04	0.04
$ZnSO_4 \cdot 7H_2O$	g/L	0.0048	0.0048
$Na_2MoO_4 \cdot 2H_2O$	g/L	0.0016	0.0016
H_3BO_3	g/L	0.0008	0.0008
$MnSO_4 \cdot 7H_2O$	g/L	0.0024	0.0024
$FeSO_4 \cdot 7H_2O$	g/L	0.044	0.044
$MgSO_4$	mM	2.5	2.5
$CaSO_4$	mM	0.06	0.06
Glucose	g/L	45	45
MOPS	niM	200	200
Thiamine-HCl	g/L	001	0.01
Yeast Extract	g/L	1	2.5
Casarnino Acids	g/L	0	2.5

TABLE 12

Production/Wash Media, pH 6.8:

Ingredient	Unit	FGM3	FGM3 No Phosphate	FGM3 Wash	FGM3 + 40 mM phosphate	FGM10
$(NH_4)_2SO_4$	g/L	3	3	3	3	9
Citric Acid	g/L	0.15	0.15	0.15	0.15	0.25
Potassium Phosphate	mM	1.8	0	0	40	5
$CoSO_4{\bullet}7H_2O$	g/L	0.0024	0.0024	0	0.0024	0.0048
$CuSO_4{\bullet}5H_2O$	g/L	0.02	0.02	0.00	0.02	0.04
$ZnSO_4{\bullet}7H_2O$	g/L	0.0024	0.0024	0	0.0024	0.0048
$Na_2MoO_4{\bullet}2H_2O$	g/L	0.0008	0.0008	0	0.0008	0.0016
H_3BO_3	g/L	0.0004	0.0004	0	0.0004	0.0008
$MnSO_4{\bullet}H_2O$	g/L	0.0012	0.0012	0	0.0012	0.0024
$FeSO_4{\bullet}7H_2O$	g/L	0.022	0.022	0	0.022	0.044
$MgSO_4$	mM	2	2	0	2	2.5
$CaSO_4$	mM	0.05	0.05	0	0.05	0.06
Glucose	g/L	45	25	0	45	25
MOPS	mM	200	200	0	200	0
Thiamine-HCl	g/L	0.01	0.01	0	0.01	0.01

Micro-Fermentations

An overview of the micro-fermentation protocol is illustrated in FIG. **16**A-C. Strains were evaluated for production in 96 well plate micro-fermentations, wherein cells were initially grown to mid-log phase, harvested, washed, resuspended and normalized in a phosphate free production medium to an OD600=1, for a 24 hour production stage. The success of the micro-fermentations required: (1) syncing strains up by harvesting all strains in exponential phase; (2) the use of low biomass levels, so that batch sugar could be kept low while enabling significant potential product accumulation; and (3) a method to supply adequate mixing and aeration, while minimizing evaporative losses. To address the final requirement, commercially available microplate sandwich covers and clamps from EnzyScreen™ was used, which greatly reduce evaporative losses while enabling high levels of mixing and aeration in standard 25 mm orbit shakers operating at 400 rpm[92-93]. Micro-fermentation results for alanine production with different insulated phosphate promoters are shown in FIG. **17**. Micro-fermentation results for strains evaluated with gapA and gapN gene alterations are given in FIG. **18**.

Section 8: Micro-Fermentations Robustness Evaluation

During micro-fermentation oxygen robustness studies, production culture volume was varied to achieve desired oxygen transfer rate (OTR) values as previously reported (http://www.enzyscreen.comloxygen_transfer_rates.htm)[92-93], and as listed below in Table 14. Batch glucose levels during the production stage were altered to assess robustness to glucose. Strains utilized in the robustness experiments at the micro-fermentation scale are listed in Table 15. Results from the micro-fermentation robustness studies are given in FIGS. **19**A-D, FIGS. **20**A-D, FIGS. **21**A-D, FIGS. **22**A-D, FIGS. **23**A-D, FIGS. **24**A-D, FIGS. **25**A-D, FIGS. **26**A-D, FIGS. **27**A-D, FIGS. **28**A-D, FIGS. **29**A-D, FIGS. **30**A-D, FIGS. **31**A-D, and FIG. **32**.

TABLE 14

Culture conditions for different OTR values.
25 mm orbit shaker

Max OTR (mmol/L-hr)	Shaking Speed (rpm)	Fill Volume (µL)
25	400	100
20	400	150
15	400	200

TABLE 15

List of strains used for micro-fermentation robustness evaluations and their RS scores.

Strain #	Silencing	Proteolysis	Plasmid	RS
1	gltA1	FU	pSMART-Ala2	89.6
2	gltA1	F	pSMART-Ala2	89.5
3	gltA1	GU	pSMART-Ala2	89.4
4	FG1G2	None	pSMART-Ala2	89.3
5	G1G2	GU	pSMART-Ala2	88.8
6	FG1G2	G	pSMART-Ala2	88.2
7	G1G2	F	pSMART-Ala2	83.4
8	gltA2	FGU	pSMART-Ala2	83.4
9	gltA1	FGU	pSMART-Ala2	83.1
10	G1G2	FGU	pSMART-Ala2	82.3
11	gltA2	U	pSMART-Ala2	82.2
12	gltA2	F	pSMART-Ala2	80.6
13	FG1G2	FG	pSMART-Ala2	80.5
14	None	G	pSMART-Ala2	79.9
15	gltA2	GU	pSMART-Ala2	77.9
16	fabI	FGU	pSMART-Ala2	75.7
17	None	FG	pSMART-Ala2	75.4
18	G1G2	FU	pSMART-Ala2	75.3
19	None	FGU	pSMART-Ala2	73.4
20	None	FU	pSMART-Ala2	73.3
21	gltA1	U	pSMART-Ala2	72.9
22	fabI	FG	pSMART-Ala2	69.1
23	FG1G2	FU	pSMART-Ala2	67.6
24	gltA2	FU	pSMART-Ala2	67.5
25	None	F	pSMART-Ala2	65.6
26	gltA2	FG	pSMART-Ala2	67.1
27	FG1G2	F	pSMART-Ala2	61.1
28	fabI	GU	pSMART-Ala2	59.9
29	fabI	F	pSMART-Ala2	59.6
30	gltA1	FG	pSMART-Ala2	58.1
31	gltA1	None	pSMART-Ala2	57.1
32	None	None	pSMART-Ala2	55.5
33	G1G2	None	pSMART-Ala2	54.1
34	fabI	U	pSMART-Ala2	53.9
35	gltA2	G	pSMART-Ala2	52.8
36	fabI	None	pSMART-Ala2	50.3
37	fabI	FU	pSMART-Ala2	48.4
38	gltA2	None	pSMART-Ala2	47.8
39	FG1G2	FGU	pSMART-Ala2	44.6
40	None	GU	pSMART-Ala2	42.9
41	None	U	pSMART-Ala2	39.3
42	fabI	G	pSMART-Ala2	39.2
43	gltA1	G	pSMART-Ala2	34.7
44	G1G2	FG	pSMART-Ala2	32.8
45	FG1G2	U	pSMART-Ala2	29.4
46	FG1G2	GU	pSMART-Ala2	24.3
47	G1G2	G	pSMART-Ala2	24.1
48	G1G2	U	pSMART-Ala2	−25.3
49	None	None	pSMART-Ala13	55.7
50	None	None	pSMART-Ala12	−31.5
51	None	None	pSMART-Ala15	−103.2
52	None	None	pSMART-Ala11	−114.1
53	None	None	pSMART-Ala14	−441.5

Section 9: Standardized 2-Stage Fermentations

A standardized phosphate limited 2-stage fermentation protocol was utilized for evaluation of all valve strains. This protocol yields highly reproducible growth stage results, with minimal strain to strain variability even with strains making different products. More significant variability was observed during the production stage as a result of differing feed rates and base utilization by different strains. FIG. **33**A gives the growth curves for all valve strains with a 10 g·cdw/L biomass level in 1 L fermentations performed in this study. This consistency is contrasted to the more variable growth of growth associated production strains, given in FIG. **33**B.

TABLE 16

Strains used for mevalonic acid scalability.

Strain #	Silencing	Proteolysis	Plasmid
1	FG1G2	FU	pSMART-Mev2
2	G2Z	FGUA	pSMART-Mev2
3	FG1G2A	FUN	pSMART-Mev2
4	UZ	FGUA	pSMART-Mev2

Section 10: Analytical Methods

TABLE 17

UPLC-MS/MS parameters					
Analyte	Retention Time (min)	ESI Mode	MRM Transition(s)	Cone Voltage	Collision Energy
Alanine	0.5	+	89.95 → 44.08	15	9
C13-Alanine	0.5	+	91.95 → 46.06	15	9

Detailed Description of Figures

FIG. **1**A: An Overview of Dynamic Metabolic Control in 2-Stage Fermentations. Metabolic engineering involves optimizing a metabolic pathway to a desired product to the existing metabolic network of a host, converting feedstocks to a desired product. Filled circles indicate metabolites and lines indicate enzymatic reactions. Traditional optimization in metabolic engineering, often involves three key steps (a) the deletion of competing non-essential metabolic pathways including those leading to undesired byproducts and the overexpression of enzymes in the pathway converting feedstock molecules to the product (indicated by thicker lines) and potentially (b) attenuating enzymes in essential metabolism (indicated by orange lines) to further increase production. This process is iterated to optimize the yield to the desired product (pie charts). By contrast, dynamic metabolic network minimization can be used to fully unlock the potential of commonly used 2-stage fermentation processes (c-d). In the first stage of these processes (c) biomass growth and yield are optimized, while in the second stage (d) product formation is optimized, which is well suited for a 2-stage process (e) in which biomass levels accumulate and consume a limiting nutrient (in this case inorganic phosphate), which when depleted triggers entry into a productive stationary phase. Synthetic metabolic valves utilizing CRISPRi based gene silencing and/or controlled proteolysis can be used (f and g) to greatly reduce the pertinent metabolic network upon the transition to the production stage, (f) and array of silencing guides can be induced, processed by the CASCADE complex into individual guides and used to silencing target multiple genes of interest (GOI). (g) If C-terminal DAD+4 lags are added to enzymes of interest (EOI) through chromosomal modification, they can be inducibly degraded by the clpXP protease in the present of and inducible sspB chaperone. (h) Dynamic control over protein levels in *E. coli* using 2 stage dynamic control with inducible proteolysis and CRISPRi silencing. As cells grow phosphate is depleted, and cells "turn off mCherry and "turn on" GFPuv. Shaded areas represent one standard deviation from the mean, n=3. (i) Relative impact of proteolysis and gene silencing alone and in combination on mCherry degradation, with (j) decays rates.

FIG. **1**B: Strain and Bioprocess Optimization. (a) Conventional approaches for strain and process optimization in metabolic engineering often involves deletion of competing non-essential metabolic pathways and overexpression of pathway enzymes (Filled circles: metabolites; lines: enzymatic reactions. green indicated a production pathway). (a-i) Strain variants are evaluated at screening scale (microtiter plates, shake flasks, etc), (a-ii) the best strains are assessed in larger scale instrumented bioreactors. Numerous design-build-test cycles (a-vi-vii) are used to iteratively optimize both the production strain and process, including the often-critical optimization of environmental (process) variables (a-vii). (a-iii) The best performing strains and associated optimized process conditions are scaled to industrially relevant levels. (b) Rapid strain and bioprocess optimization using 2-stage dynamic metabolic control. The metabolic network in the cell is dynamically minimized to only the steps essential for product formation. This is accomplished in a standardized 2-stage bioprocess (c), where a biomass accumulating growth stage is followed by a production stage, with only a minimal metabolic network. The limitation of a macronutrient can be used to "switch" cellular metabolism from growth to production. The approach results in a smaller subset of potential strain variants for screening (b-i). Metabolic network minimization helps increase relevant metabolite levels (d) and thus production levels, it also enhances process robustness (e), and as a result process and strain scalability (f). The best producers identified from screening are predictably and rapidly scaled to (b-ii) larger instrumented bioreactors, and (b-iii) subsequently to industrially relevant levels. If needed, limited design-build-test cycles (b-iv) are incorporated to guide improvements. Product independent, standardized protocols are followed for strain evaluation at all scales, eliminating the need for intensive process optimization.

FIGS. **2**A-D: Implementation of 2-stage Synthetic Metabolic Valves (SMVs) in *E. coli*. FIG. **2**A depicts SMVs utilizing CRISPRi based gene silencing and/or controlled proteolysis were constructed. (Top) Silencing: An array of inducible silencing guide RNAs (i) can be used to silence expression of multiple genes of interest (GOI) when the native *E. coli* CRISPR/Cascade machinery is expressed, which can process guide arrays into individual guides (ii). (Bottom) Proteolysis: When C-terminal DAS+4 tags are added to enzymes of interest (EOI) (through chromosomal modification), they can be degraded by the clpXP protease (iv) upon the controlled induction of the sspB chaperone (iii). FIG. **2**B depicts dynamic control over protein levels in *E. coli* using inducible proteolysis and CRISPRi silencing. As cells grow phosphate is depleted, cells "turn OFF" mCherry and "turn ON" GFPuv. Shaded areas represent one standard deviation from the mean, r.f.u, relative fluorescence units. FIG. **2**C depicts relative impact of proteolysis and gene silencing alone and in combination on mCherry degradation, n.f.u. normalized fluorescence units (normalized to maximal fluorescence). FIG. **2**D depicts relative impact of proteolysis and gene silencing alone and in combination on observed mCherry fluorescence decays rates (per hour).

FIGS. **3**A-K: Alanine Production in *E. coli* utilizing 2-stage Dynamic Control. FIG. **3**A depicts strain variant design. Primary pathways in central metabolism are shown including: Glycolysis, the Pentose Phosphate Pathway, the Citric Acid Cycle (TCA), Fatty Acid Biosynthesis, and the Soluble Transhydrogenase. Key valve candidate enzymes/genes that are "turned OFF" to reduce flux through central metabolism can include: glucose-6-phosphate dehydrogenase (zwf—"Z"), lipoamide dehydrogenase (lpd—"L"), citrate synthase (gltA—"G"), enoyl-ACP reductase (fabI—"F"), and the soluble transhydrogenase (udhA—"U"). Importantly, dynamic elimination of fabI has been previously demonstrated to increase intracellular malonyl-CoA pools as well as malonyl-CoA flux[55]. Enzymes that are dynamically "turned ON" can include the metabolic pathways to produce the products of interest, in this case alanine. Specific pathway enzymes include an NADPH-dependent alanine dehydrogenase (ald*) and an alanine exporter (alaE). Additionally, as the alanine production pathway utilizes NADPH as a cofactor, the NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase encoded by the gapN gene[56] from *S. mutans* was turned on alone and in combination with turning off the native gapA—"A" gene (NADH dependent glyceraldehyde dehydrogenase). Abbreviation: PTS—glucose phosphotransferase transport system, P—phosphate, BP—bisphosphate, OAA—oxaloacetate, DHAP—dihydroxyacetone phosphate, GA3P—glyceraldehyde-3-phosphate, 1,3-BPG—1,3 bisphosphoglycerate, 3-PG—3-phosphoglycerate, 2-PG—2-phosphoglycerate, PEP—phosphoenolpyruvate, MSA—malonate semialdehyde, ACP—acyl carrier protein, Ru—ribulose, Xu—xylulose, E—erthryose, Ri—ribose, S—sedoheptulose. Strains were engineered with SMVs for the dynamic control of all combinations of valve genes/enzymes, either through gene silencing alone, proteolysis alone, or the combination of both. These strains were evaluated for alanine production in standardized micro-fermentations. FIG. **3**B depicts rank order plot for average alanine titer (black) of all valve strains examined in 2-stage micro-fermentation, grey area represents standard deviation. Alanine production in the control strain was colored in red. FIG. **3**C depicts average alanine titer in 2-stage production in response to different proteolysis and silencing combinations, from 0 g/L (purple) to 5 g/L (red). FIG. **3**D depicts average alanine titer in response to different oxygen transfer rates (OTR) and glucose concentrations evaluated for a single "Valve" alanine strain (Silencing of gltA1 ("G1"), Proteolysis of fabI and udhA ("FU")). The results of this surface were used to calculate a strain-specific robustness score (RS) (refer to text), this strain has the highest RS score. FIG. **3**E depicts a heat map of the robustness score for a subset of 48 "Valve" strains evaluated across multiple process conditions. FIG. **3**F depicts scale up of one of the best producing strain from micro-fermentations (Silencing of fabI-gltA1-gltA2 ("FG1G2"), Proteolysis of fabI, gltA and udhA ("FGU")) to 1 L bioreactors results in a titer of 80 g/L after 48 hrs of production, with a yield of 0.8 g/g. FIG. **3**G depicts overexpression of the alaE alanine exporter in this strain (Panel f) results in significantly improved production, reaching 147 g/L in 27 hrs of production, with a yield of ~1 g/g. (Refer to Supplemental Materials, Section 3 for additional details). FIG. **3**H depicts strains selected for robustness evaluation in micro-fermentations. FIG. **3**I depicts robustness and titer for the most robust "Valve" alanine strain (Silencing_gltA1, Proteolysis_FU). Bottom surface shows heat map for the alanine titer normalized to the median of all process conditions assessed, upper surface shows alanine tiler under all process conditions, the same color scale (alanine titer in g/L) was used for both panels. FIG. **3**J depicts RS3 scores for the selected strains. FIG. **3**K depicts process reproducibility heat map for all conditions evaluated, the same grayscale was used for FIG. **3**J and FIG. **3**K.

FIGS. **4**A-F: Robustness Comparison Between 2-Stage and Growth Associated Approaches. FIG. **4**A depicts rank order of the RS3 scores for all alanine strains evaluated, red bars indicate valve alanine strains, and blue bars indicate growth associated (GA) alanine strains. FIG. **4**B depicts average RS3 score for "Valve" alanine strains with proteolysis "F" valve, and growth associated alanine strains. FIG. **4**C depicts max titer plot for a representative "Valve" alanine (Proteolysis_FGU, Silencing_gltA1), and growth associated alanine strains in micro-fermentation of all conditions evaluated. FIG. **4**D depicts process reproducibility for growth associated alanine strains under all conditions evaluated. FIG. **4**E depicts robustness and titer for a representative robust "Valve" alanine (Proteolysis_FGU, Silencing_gltA1). FIG. **4**F depicts robustness and titer for the GA2 strain. Bottom surface, heat map for the alanine titer normalized to the median of all process conditions assessed, upper surface, alanine titer under all process conditions, the same color scale (alanine titer in g/L) was used for both panels.

FIGS. **5**A-J: Comparisons of "Valve" and growth associated alanine production in micro-fermentations (FIGS. **5**A-D) and 1 L fermentation (FIGS. **5**E-J). Average alanine titer (FIG. **5**A) and robustness score (FIG. **5**B) for all strains used for robustness analysis. Average alanine titer in response to different OTR and glucose concentrations for selected "Valve" (FIG. **5**C) and growth associated (FIG. **5**D) alanine strains. Strains marked by asterisk in (FIG. **5**B) were used for this analysis. These two strains were selected for 1 L performance comparison. FIG. **5**E and FIG. **5**F depicts 1 L performance metrics evaluated, including average specific productivity (SP, g/gdcw-h), average glucose uptake rate (GUR, g/gcdw-h), max titer (g/L), and max yield (g/g). FIG. **5**G and FIG. **5**H depicts μL to 1 L scalability. 1 L data was standardized to the maximal titer within 50 hours of production. Adequate feed was used for growth associated strains to avoid glucose depletion. FIG. **5**I and FIG. **5**J depicts 1 L production profiles for all strains used in scalability plot FIG. **5**G and FIG. **5**H respectively, darker symbols represent growth curves, lighter symbols represent production curves, shape of symbols encode the same strains in FIG. **5**G or FIG. **5**H.

FIG. **6**A-E: Mevalonate Production in *E. coli* utilizing 2-stage Dynamic Control. FIG. **6**A depicts Metabolic Pathways and SMVs for mevalonate production. FIG. **6**B depicts mevalonate production using several production pathway plasmid variants with varied promoter combinations in the control strain. FIG. **6**C depicts micro-fermentation results for a subset of "Valve" strains producing mevalonate, using the best production pathway from FIG. **6**B, along with combinations of proteolytic and silencing SMVs. FIG. **6**D depicts μL to 1 L scalability for a subset of mevalonate strains evaluated at the 1 L scale. n=3 for μL data and n=1 for 1 L data. The maximal titer within 50 hours of production time was used for the correlation. FIG. **6**E depicts production of the best mevalonate strain from FIG. **6**D (Silencing of fabI-gltA1-gltA2 ("FG1G2"), Proteolysis of fabI and udhA ("FU")) in 1 L bioreactors. A titer of 97 g/L was observed in 78 hrs of production. Yields during the production stage reached 0.46 g/g (84% of theoretical yield). (Refer to Supplemental Materials, Section 9 for additional details). FIG. **6**F depicts micro-fermentation results for a subset of strains producing 3-HP. FIG. **6**G depicts μL to 1 L scalability for a subset of 3-HP strains evaluated at the 1 L scale (Supplemental Materials Tables S21 and S22). FIG. **6**H depicts production performance for the best 3-HP strains in the 1 L systems, squares, 3-HP/mevalonic acid titer; circles, OD600. Yields during the production stage reached for the 0.46 g/g for mevalonic acid and 0.63 g/g for 3-HP in the highest producers.

FIG. **7**: Phosphate depletion promoter characterization. A set of GFP reporter vectors were constructed to assess the expression level of 12 previously identified phosphate regulated promoters. Strains were evaluated continuously for GFP expression in the Biolector™ using a standardized protocol wherein in minimal medium limited for phosphate is used. After Biomass levels reach a peak (not shown for clarity), GFP expression begins. Importantly the current set of promoters enables a large range of expression levels.

FIG. **8**: Insulated phosphate depletion promoter characterization. A set of GFP reporter vectors were constructed to assess the expression level of five insulated phosphate regulated promoters in FGM3 media. Strains were evaluated continuously for GFP expression in the Biolector™ using a standardized protocol wherein in minimal medium limited for phosphate is used. After Biomass levels reach a peak (not shown for clarity), GFP expression begins. Importantly the current set of promoters enables a large range of expression levels.

FIG. **9**: Insulated constitutive promoter characterization. A set of GFP reporter vectors were constructed to assess the expression level of five insulated constitutive promoters in FGM3 with 40 mM phosphate media. Shaded area represents standard deviations, n=3. Strains were evaluated continuously for GFP expression in the Biolector™. GFP expression was observed only for promoters proA, proB and proD.

FIG. **10**: Metabolic modeling results for optimal 3-HP flux in two stage fermentations. LEFT: Optimized fluxes during the growth stage where biomass production was used as the objective function. RIGHT: Optimized fluxes during the 3-HP production stage where 3-HP production was used as the objective function (biomass production was set to 0). Fluxes are listed as relative ratios or moles of flux through a given reaction per 100 moles of glucose utilized.

FIG. **11**: Chromosomal modifications.

FIG. **12**: Average maximal growth rates of starting host strains in 1 L FGM10 minimal medium fermentations, n=2.

FIG. **13**A-E: Distribution of glucose utilized during the growth phase of starting host strains in 1 L standard minimal medium fermentations. Mid exponential and final growth period results are given for DLF_0025 as "production" begins in mid-late exponential phase. Results are averages of duplicate fermentations. FIG. **13**A, BW25113; FIG. **13**B, BWapldf; FIG. **13**C, DLF_0001; FIG. **13**D, DLF_0025 at mid-exponential; FIG. **13**E, DLF_0025 at end of growth phase. Unit was gram glucose.

FIG. **14**: pCASCADE-control plasmid construction scheme.

FIG. **15**A-B: pCASCADE construction scheme. FIG. **15**A, single sgRNA cloning;

FIG. **15**B, double sgRNA.

FIG. **16**A-C: Micro-fermentation process overview. (A) An overview of the high throughput micro-fermentation protocol. Freezer stocks (alternatively colonies may be used) are used to inoculate into SM10++ in 96 well plates. Cultures are grown overnight for 16 hours, harvested by centrifugation, washed with no-phosphate medium and resuspended in no-phosphate medium at target biomass levels. (OD600 nm=1.0). EnzyScreen™ covers and clamps are used to reduce evaporation and enable high oxygen transfer rates. The protocol is implemented with a Tecan Evo liquid handler. (B) Representative overnight growth in a 96 well plates culture, distribution of OD600 for overnight culture was plotted. (C) Representative OD600 distribution after normalization using Tecan Evo liquid handler.

FIG. **17**: Micro-fermentation for L-alanine production using different insulated phosphate promoters in DLF_0025 strain.

FIG. **18**: Heatmap for L-alanine production by gapN/gapA strains.

FIGS. **19**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **20**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **21**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **22**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **23**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **24**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **25**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **26**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **27**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **28**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **29**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **30**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIGS. **31**A-D: Alanine production in response to different OTR and glucose concentration in micro-fermentation for 4 strains evaluated for robustness.

FIG. **32**: Alanine production in response to different OTR and glucose concentration in micro-fermentation for one strain evaluated for robustness.

FIGS. **33**A-B: Growth profile for all (FIG. **33**A) valve and (FIG. **33**B) growth associated strains at 1 L scale evaluated in this paper. Growth curves were synced to account for any variations in lag time. Valve strains growth curves were synced to the same mid-exponential point. Growth associated strains growth curves were synced to the same take-off point.

FIG. **34**: Specific Productivity (SP) comparison for strain with highest mevalonate titer from literature and mevalonate strain 1 evaluated in this work.

FIG. **35**: Alanine standard curve from MS measurement. Average and standard deviation for mass spec response from triplicate standard measurement were plotted.

FIGS. **36**A-B: Glucose (FIG. **36**A) and ethanol (FIG. **36**B) standard curves from RI measurement. Average and standard deviation for peak area from triplicate standard measurement were plotted.

FIG. **37**: 3-Hydroxypropionic acid standard curve from TUV measurement. Average and standard deviation for peak area from duplicate standard measurement were plotted.

FIGS. **38**A-D: TUV standard curves for (FIG. **38**A) L-alanine, (FIG. **38**B) D-alanine, (FIG. **38**C) mevalonic acid, and (FIG. **38**D) mevalonolactone. Average and standard deviation for peak area from triplicate standard measurement were plotted.

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While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

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gaagcacagc taacaccacg tcgtccctat ctgctgccct aggtctatga gtggttgctg 120

gataacttta cgggcatgca taaggctcgt ataatatatt cagggagacc acaacggttt 180

ccctctacaa ataattttgt ttaacttt 208

<210> SEQ ID NO 22
<211> LENGTH: 429
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 22

ccaggcatca aataaaacga aaggctcagt cgaaagactg ggcctttcgt tttatctgtt 60

gtttgtcggt gaacgctctc tactagagtc acactggctc accttcgggt gggcctttct 120

gcgtttatac acagctaaca ccacgtcgtc cctatctgct gccctaggtc tatgagtggt 180

tgctggataa cctccttcac agattcccaa tctcttgtta aataacgaaa aagcatcaat 240

taaaacccat gtctttctat attccagcaa tgttttatag ggacatatt gatgaagatg 300

ggtatcacct tagtgaattg ctataagctg ctcttttttg ttcgtgatat actgataaat 360

tgaattttca cacttcatat tcagggagac cacaacggtt tccctctaca aataattttg 420

tttaacttt 429

<210> SEQ ID NO 23
<211> LENGTH: 76
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 23

taacaataaa aatgaaaatg atttccacga tacagaaaaa agagactgtc atcctaattt 60

ttgttgacac tctatc 76

<210> SEQ ID NO 24
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 24

tgccactcag gtatgatggg cagaatattg cctctgcccg ccagaaaaag atcaaaggga 60

aaactgtcca tatgc 75

<210> SEQ ID NO 25
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 25

ccgacaggga ttccatctg 19

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

<400> SEQUENCE: 26

tatgacgacc attttgtcta cagttc 26

<210> SEQ ID NO 27
<211> LENGTH: 75
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 27

ggacttttgt acttcctgtt tcgatttagt tggcaattta ggtagcaaac tcctaatttt 60

tgttgacact ctatc 75

<210> SEQ ID NO 28
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 28

ataaaaacgg cgctaaaaag cgccgttttt tttgacggtg gtaaagccga atcaaaggga 60

aaactgtcca tatgc 75

<210> SEQ ID NO 29
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 29

cctgactgta ctaacggttg ag 22

<210> SEQ ID NO 30
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 30

tgacttttat ggcgttcttt gtttttg 27

<210> SEQ ID NO 31
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 31

ctggtacacg ctgatgaaca cc 22

<210> SEQ ID NO 32
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 32

ctggtcattg ccatttgtgc c 21

<210> SEQ ID NO 33
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 33

gaatcagagc gttccgaccc 20

<210> SEQ ID NO 34
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 34

gtacgcagtt tgccaacgtg 20

<210> SEQ ID NO 35
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 35

aatagcccgc tgatatcatc gataatacta aaaaaacagg gaggctatta tcctaatttt 60

tgttgacact ctatc 75

<210> SEQ ID NO 36
<211> LENGTH: 75
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 36

tacagggatc cagttatcaa taagcaaatt catttgttct ccttcatatg atcaaaggga 60

aaactgtcca tatgc 75

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

<400> SEQUENCE: 37

caagacatgt gtatatcact gtaattc 27

<210> SEQ ID NO 38
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 38

gcgattgcag atttatgatt tgg 23

<210> SEQ ID NO 39
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 39

gcaaaatgct ggctcattg 19

<210> SEQ ID NO 40
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 40

gaactgaatg gcaaactgac tg 22

<210> SEQ ID NO 41
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 41

tggggatgat cgaccaca 18

<210> SEQ ID NO 42
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 42

tatcatcctg aaagcgatgg 20

<210> SEQ ID NO 43
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 43

atctcaccgt gtgatcgg 18

<210> SEQ ID NO 44
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 44

caaaagagat tctgggtatt cact 24

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<210> SEQ ID NO 45
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 45

ctgctggaaa ccatgcg                                                    17


<210> SEQ ID NO 46
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> SEQUENCE: 46

agagcatgtc gttataggag gtgat                                           25


<210> SEQ ID NO 47
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 47

agtactcaac caagtcattc tg                                              22


<210> SEQ ID NO 48
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 48

gagcatggtg atcttctcag t                                               21


<210> SEQ ID NO 49
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 49

gcgatgaatg tcttactacg ga                                              22


<210> SEQ ID NO 50
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 50

gtcgctgggt aatctgcaa                                                  19
```

<210> SEQ ID NO 51
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 51

atcaacgcat atagcgctag cag 23

<210> SEQ ID NO 52
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 52

actgaagccc agacgatc 18

<210> SEQ ID NO 53
<211> LENGTH: 3527
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 53

tcctaatttt tgttgacact ctatcattga tagagttatt ttaccactcc ctatcagtga 60

tagagaaaag tgaaatgaat agttcgacaa agatcgcatt ggtaattacg ttactcgatg 120

ccatggggat tggccttatc atgccagtct tgccaacgtt attacgtgaa tttattgctt 180

cggaagatat cgctaaccac tttggcgtat tgcttgcact ttatgcgtta atgcaggtta 240

tctttgctcc ttggcttgga aaaatgtctg accgatttgg tcggcgccca gtgctgttgt 300

tgtcattaat aggcgcatcg ctggattact tattgctggc tttttcaagt gcgctttgga 360

tgctgtattt aggccgtttg ctttcaggga tcacaggagc tactggggct gtcgcggcat 420

cggtcattgc cgataccacc tcagcttctc aacgcgtgaa gtggttcggt tggttagggg 480

caagttttgg gcttggttta atagcggggc ctattattgg tggttttgca ggagagattt 540

caccgcatag tccctttttt atcgctgcgt tgctaaatat tgtcactttc cttgtggtta 600

tgttttggtt ccgtgaaacc aaaaatacac gtgataatac agataccgaa gtaggggttg 660

agacgcaatc gaattcggta tacatcactt tatttaaaac gatgcccatt ttgttgatta 720

tttatttttc agcgcaattg ataggccaaa ttcccgcaac ggtgtgggtg ctatttaccg 780

aaaatcgttt tggatggaat agcatgatgg ttggcttttc attagcgggt cttggtcttt 840

tacactcagt attccaagcc tttgtggcag gaagaatagc cactaaatgg ggcgaaaaaa 900

cggcagtact gctcggattt attgcagata gtagtgcatt tgccttttta gcgtttatat 960

ctgaaggttg gttagttttc cctgttttaa ttttattggc tggtggtggg atcgctttac 1020

ctgcattaca gggagtgatg tctatccaaa caaagagtca tcagcaaggt gctttacagg 1080

gattattggt gagccttacc aatgcaaccg gtgttattgg cccattactg tttgctgtta 1140

tttataatca ttcactacca atttgggatg gctggatttg gattattggt ttagcgtttt 1200

actgtattat tatcctgcta tcgatgacct tcatgttaac ccctcaagct caggggagta 1260

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aacaggagac aagtgcttag ttatttcgtc accaaatgat gttattccgc gaaatataat   1320
gaccctcttg ataacccaag agcatcacat atacctgccg ttcactatta tttagtgaaa   1380
tgagatatta tgatattttc tgaattgtga ttaaaaaggc aactttatgc ccatgcaaca   1440
gaaactataa aaaatacaga gaatgaaaag aaacagatag attttttagt tctttaggcc   1500
cgtagtctgc aaatcctttt atgattttct atcaaacaaa agaggaaaat agaccagttg   1560
caatccaaac gagagtctaa tagaatgagg tcgaaaagta aatcgcgcgg gtttgttact   1620
gataaagcag gcaagaccta aaatgtgtaa agggcaaagt gtatactttg gcgtcacccc   1680
ttacatattt taggtctttt tttattgtgc gtaactaact tgccatcttc aaacaggagg   1740
gctggaagaa gcagaccgct aacacagtac ataaaaaagg agacatgaac gatgaacatc   1800
aaaaagtttg caaaacaagc aacagtatta acctttacta ccgcactgct ggcaggaggc   1860
gcaactcaag cgtttgcgaa agaaacgaac caaaagccat ataaggaaac atacggcatt   1920
tcccatatta cacgccatga tatgctgcaa atccctgaac agcaaaaaaa tgaaaaatat   1980
caagttcctg agttcgattc gtccacaatt aaaaatatct cttctgcaaa ggcctggac    2040
gtttgggaca gctggccatt acaaaacgct gacggcactg tcgcaaacta tcacggctac   2100
cacatcgtct ttgcattagc cggagatcct aaaaatgcgg atgacacatc gatttacatg   2160
ttctatcaaa aagtcggcga aacttctatt gacagctgga aaaacgctgg ccgcgtcttt   2220
aaagacagcg acaaattcga tgcaaatgat tctatcctaa aagaccaaac acaagaatgg   2280
tcaggttcag ccacatttac atctgacgga aaaatccgtt tattctacac tgatttctcc   2340
ggtaaacatt acggcaaaca aacactgaca actgcacaag ttaacgtatc agcatcagac   2400
agctctttga acatcaacgg tgtagaggat tataaatcaa tctttgacgg tgacggaaaa   2460
acgtatcaaa atgtacagca gttcatcgat gaaggcaact acagctcagg cgacaaccat   2520
acgctgagag atcctcacta cgtagaagat aaaggccaca aatacttagt atttgaagca   2580
aacactggaa ctgaagatgg ctaccaaggc gaagaatctt tatttaacaa agcatactat   2640
ggcaaaagca catcattctt ccgtcaagaa agtcaaaaac ttctgcaaag cgataaaaaa   2700
cgcacggctg agttagcaaa cggcgctctc ggtatgattg agctaaacga tgattacaca   2760
ctgaaaaaag tgatgaaacc gctgattgca tctaacacag taacagatga aattgaacgc   2820
gcgaacgtct ttaaaatgaa cggcaaatgg tacctgttca ctgactcccg cggatcaaaa   2880
atgacgattg acggcattac gtctaacgat atttacatgc ttggttatgt ttctaattct   2940
ttaactggcc catacaagcc gctgaacaaa actggccttg tgttaaaaat ggatcttgat   3000
cctaacgatg taacctttac ttactcacac ttcgctgtac ctcaagcgaa aggaaacaat   3060
gtcgtgatta caagctatat gacaaacaga ggattctacg cagacaaaca atcaacgttt   3120
gcgccaagct tcctgctgaa catcaaaggc aagaaaacat ctgttgtcaa agacagcatc   3180
cttgaacaag gacaattaac agttaacaaa taaaaacgca aaagaaaatg ccgatattga   3240
ctaccggaag cagtgtgacc gtgtgcttct caaatgcctg attcaggctg tctatgtgtg   3300
actgttgagc tgtaacaagt tgtctcaggt gttcaatttc atgttctagt tgctttgttt   3360
tactggtttc acctgttcta ttaggtgtta catgctgttc atctgttaca ttgtcgatct   3420
gttcatggtg aacagcttta aatgcaccaa aaactcgtaa aagctctgat gtatctatct   3480
tttttacacc gttttcatct gtgcatatgg acagttttcc ctttgat                 3527
```

<210> SEQ ID NO 54
<211> LENGTH: 70

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 54

aaatgatttc cacgatacag aaaaaagaga ctgtcatggg cagaatattg cctctgcccg 60

ccagaaaaag 70

<210> SEQ ID NO 55
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 55

ctgtttcgat ttagttggca atttaggtag caaactcggc tttaccaccg tcaaaaaaaa 60

cggcgctttt 70

<210> SEQ ID NO 56
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 56

caagacatgt gtatatcact gtaattcgat atttatgagc agcatcgaaa aatagcccgc 60

tgatatcatc gataatacta aaaaaacagg gaggctatta ccaggcatca aataaaacga 120

aaggctcagt cgaaagactg ggcctttcgt tttatctgtt gtttgtcggt gaacgctctc 180

tactagagtc acactggctc accttcgggt gggcctttct gcgtttatat ctttctgaca 240

ccttactatc ttacaaatgt aacaaaaaag ttattttct gtaattcgag catgtcatgt 300

taccccgcga gcataaaacg cgtgtgtagg aggataatct ttgacggcta gctcagtcct 360

aggtacagtg ctagccatat gaaggagaac aaatgaattt gcttattgat aactggatcc 420

ctgtacgccc gcgaaacggg gggaaagtcc aaatcataaa tctgcaatcg ctatac 476

<210> SEQ ID NO 57
<211> LENGTH: 974
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 57

caagacatgt gtatatcact gtaattcgat atttatgagc agcatcgaaa aatagcccgc 60

tgatatcatc gataatacta aaaaaacagg gaggctatta ccaggcatca aataaaacga 120

aaggctcagt cgaaagactg ggcctttcgt tttatctgtt gtttgtcggt gaacgctctc 180

tactagagtc acactggctc accttcgggt gggcctttct gcgtttatat ctttctgaca 240

ccttactatc ttacaaatgt aacaaaaaag ttattttct gtaattcgag catgtcatgt 300

taccccgcga gcataaaacg cgtgtgtagg aggataatct atggatttgt cacagctaac 360

accacgtcgt ccctatctgc tgcgtgcatt ctatgagtgg ttgctggata accagctcac 420

```
gccgcacctg gtggtggatg tgacgctccc tggcgtgcag gttcctatgg aatatgcgcg    480

tgacgggcaa atcgtactca acattgcgcc gcgtgctgtc ggcaatctgg aactggcgaa    540

tgatgaggtg cgctttaacg cgcgctttgg tggcattccg cgtcaggttt ctgtgccgct    600

ggctgccgtg ctggctatct acgcccgtga aaatggcgca ggcacgatgt ttgagcctga    660

agctgcctac gatgaagata ccagcatcat gaatgatgaa gaggcatcgg cagacaacga    720

aaccgttatg tcggttattg atggcgacaa gccagatcac gatgatgaca ctcatcctga    780

cgatgaacct ccgcagccac cacgcggtgg tcgaccggca ttacgcgttg tgaagtaatt    840

gacggctagc tcagtcctag gtacagtgct agccatatga aggagaacaa atgaatttgc    900

ttattgataa ctggatccct gtacgcccgc gaaacggggg gaaagtccaa atcataaatc    960

tgcaatcgct atac                                                      974
```

<210> SEQ ID NO 58
<211> LENGTH: 970
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 58

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ctattgaaga tgtgggtaac tctgcggcat tcctgtgctc cgatctctct gccggtatct     60

ccggtgaagt ggtccacgtt gacggcggtt tcagcattgc tgcaatgaac gaactcgaac    120

tgaaagcggc caacgatgaa aactattctg aaaactatgc ggatgcgtct taataggaag    180

ttcctattct ctagaaagta taggaacttc cgaatccatg tgggagttta ttcttgacac    240

agatatttat gatataataa ctgagtaagc ttaacataag gaggaaaaac atatgttacg    300

cagcagcaac gatgttacgc agcagggcag tcgccctaaa acaaagttag gtggctcaag    360

tatgggcatc attcgcacat gtaggctcgg ccctgaccaa gtcaaatcca tgcgggctgc    420

tcttgatctt ttcggtcgtg agttcggaga cgtagccacc tactcccaac atcagccgga    480

ctccgattac ctcgggaact tgctccgtag taagacattc atcgcgcttg ctgccttcga    540

ccaagaagcg gttgttggcg ctctcgcggc ttacgttctg cccaagtttg agcagccgcg    600

tagtgagatc tatatctatg atctcgcagt ctccggcgag caccggaggc agggcattgc    660

caccgcgctc atcaatctcc tcaagcatga ggccaacgcg cttggtgctt atgtgatcta    720

cgtgcaagca gattacggtg acgatcccgc agtggctctc tatacaaagt tgggcatacg    780

ggaagaagtg atgcactttg atatcgaccc aagtaccgcc acctaagaag ttcctattct    840

ctagaaagta taggaacttc cgttctgttg gtaaagatgg gcggcgttct gccgcccgtt    900

atctctgtta tacctttctg atatttgtta tcgccgatcc gtctttctcc ccttcccgcc    960

ttgcgtcagg                                                           970
```

<210> SEQ ID NO 59
<211> LENGTH: 2000
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 59

```
tctccaaagc ggccaacgat gaaaactatt ctgaaaacta tgcggatgcg tcttgattga     60

cagctagctc agtcctaggt ataatgctag caactttaaa attaaagagg tatatattaa    120
```

```
tgactaagca atataagaat tacgtaaatg ggagtggaa gctttcggag aatgaaatta    180
agatctatga accagccagt ggggcggaat tggggtcagt cccggcaatg tccactgaag    240
aagttgacta tgtctacgcc tcggccaaaa aagcgcagcc agcatggcgc tcgctttcct    300
atattgagcg tgcggcttat ttgcacaaag tcgcagacat cctgatgcgt gacaaggaga    360
aaattggagc ggtattgtcc aaggaagtag cgaaaggcta caaatccgca gtatcggagg    420
tcgtccgcac cgccgagatt attaattatg cggccgaaga agggcttcgc atggagggtg    480
aggtcttgga gggcggcagt tttgaggcgg catccaagaa aaaaatcgct gtcgtccgtc    540
gcgagccggt gggacttgtg cttgctatta gtccgttcaa ttaccccgtg aatctggccg    600
gctccaagat tgcccctgca ctgatcgcgg gcaatgtaat cgcttttaaa ccaccgaccc    660
aaggatcgat tagtggactt cttttagcgg aggcgtttgc ggaggcaggt cttccagccg    720
gcgtattcaa taccatcacg gggcgtggaa gtgaaatcgg ggattacatc gtggagcacc    780
aggcagtaaa tttcatcaac ttcacgggtt ccacggggat cggggagcgt atcggtaaga    840
tggctgggat gcgtccgatc atgttggaac ttggcggcaa ggatagtgcg attgtgctgg    900
aagacgcaga cttggaattg acagctaaaa acattatcgc tggagccttc gggtatagtg    960
gtcaacgttg cacggcagtt aagcgcgttc ttgttatgga aagtgtcgcg gatgaattgg   1020
tcgagaagat tcgcgagaaa gtgttagctc ttacgattgg aaatccagag gacgatgctg   1080
acatcactcc attgatcgac acgaaatccg cggattacgt cgaggggctg atcaacgacg   1140
cgaacgataa gggagcagcg gctttgaccg agatcaaacg cgaggggaac ctgatctgcc   1200
cgattctttt tgacaaagtc acaactgaca tgcgcttggc atgggaagaa cccttcggcc   1260
cagtcttgcc tattatccgc gttactagcg tagaggaagc aattgaaatt tccaataaat   1320
ccgaatatgg gttgcaagcg agtatcttta ctaacgattt tccacgtgcc tttggtattg   1380
cggaacagtt agaagtcggg acagttcaca tcaacaacaa gacgcagcgc gggacagata   1440
acttcccctt tttgggagca aagaagtctg ggctggaat ccaaggggtg aaatactcca    1500
tcgaagccat gacgacggtg aagagcgttg tttttgacat caagtaaaac ataaggagga   1560
aaaacagatg gcgaaactga cctcggcggt tccggttctg acggcacgtg atgtggcggg   1620
cgcggttgaa ttttggacgg atcgtctggg cttcagtcgt gattttgtgg aagatgactt   1680
cgcaggcgtg gttcgcgatg acgtcaccct gtttatttcc gcagttcagg atcaagtcgt   1740
gccggacaac acgctggctt gggtgtgggt tcgtggcctg gatgaactgt atgcggaatg   1800
gagcgaagtt gtctctacca atttccgtga cgcgagcggt ccggccatga cggaaatcgg   1860
cgaacagccg tggggtcgcg aatttgctct gcgtgacccg gctggcaact gtgtccattt   1920
cgtggctgaa gaacaagatt gagttgagat gacactgtga tctaaaaaga gcgacttcgg   1980
tcgctctttt ttttacctga                                              2000
```

```
<210> SEQ ID NO 60
<211> LENGTH: 2000
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 60
```

```
acgaaaccgg ttactccaac aaagttctgg acctgatcgc tcacatctcc aaatgattga     60
cagctagctc agtcctaggt ataatgctag caactttaaa attaaagagg tatatattaa    120
```

```
tgactaagca atataagaat tacgtaaatg gggagtggaa gctttcggag aatgaaatta    180
agatctatga accagccagt ggggcggaat tggggtcagt cccggcaatg tccactgaag    240
aagttgacta tgtctacgcc tcggccaaaa aagcgcagcc agcatggcgc tcgctttcct    300
atattgagcg tgcggcttat ttgcacaaag tcgcagacat cctgatgcgt gacaaggaga    360
aaattggagc ggtattgtcc aaggaagtag cgaaaggcta caaatccgca gtatcggagg    420
tcgtccgcac cgccgagatt attaattatg cggccgaaga agggcttcgc atggagggtg    480
aggtcttgga gggcggcagt tttgaggcgg catccaagaa aaaaatcgct gtcgtccgtc    540
gcgagccggt gggacttgtg cttgctatta gtccgttcaa ttaccccgtg aatctggccg    600
gctccaagat tgcccctgca ctgatcgcgg gcaatgtaat cgcttttaaa ccaccgaccc    660
aaggatcgat tagtggactt cttttagcgg aggcgtttgc ggaggcaggt cttccagccg    720
gcgtattcaa taccatcacg gggcgtggaa gtgaaatcgg ggattacatc gtggagcacc    780
aggcagtaaa tttcatcaac ttcacgggtt ccacggggat cggggagcgt atcggtaaga    840
tggctgggat gcgtccgatc atgttggaac ttggcggcaa ggatagtgcg attgtgctgg    900
aagacgcaga cttggaattg acagctaaaa acattatcgc tggagccttc gggtatagtg    960
gtcaacgttg cacggcagtt aagcgcgttc ttgttatgga aagtgtcgcg gatgaattgg   1020
tcgagaagat tcgcgagaaa gtgttagctc ttacgattgg aaatccagag gacgatgctg   1080
acatcactcc attgatcgac acgaaatccg cggattacgt cgaggggctg atcaacgacg   1140
cgaacgataa gggagcagcg gctttgaccg agatcaaacg cgaggggaac ctgatctgcc   1200
cgattctttt tgacaaagtc acaactgaca tgcgcttggc atgggaagaa cccttcggcc   1260
cagtcttgcc tattatccgc gttactagcg tagaggaagc aattgaaatt tccaataaat   1320
ccgaatatgg gttgcaagcg agtatcttta ctaacgattt tccacgtgcc tttggtattg   1380
cggaacagtt agaagtcggg acagttcaca tcaacaacaa gacgcagcgc gggacagata   1440
acttcccctt tttgggagca aagaagtctg gggctggaat ccaaggggtg aaatactcca   1500
tcgaagccat gacgacggtg aagagcgttg tttttgacat caagtaaaac ataaggagga   1560
aaaacagatg gcgaaactga cctcggcggt tccggttctg acggcacgtg atgtggcggg   1620
cgcggttgaa ttttggacgg atcgtctggg cttcagtcgt gattttgtgg aagatgactt   1680
cgcaggcgtg gttcgcgatg acgtcaccct gtttatttcc gcagttcagg atcaagtcgt   1740
gccggacaac acgctggctt gggtgtgggt tcgtggcctg gatgaactgt atgcggaatg   1800
gagcgaagtt gtctctacca atttccgtga cgcgagcggt ccggccatga cggaaatcgg   1860
cgaacagccg tggggtcgcg aatttgctct gcgtgacccg gctggcaact gtgtccattt   1920
cgtggctgaa gaacaagatt gagttgagat gacactgtga tctaaaaaga gcgacttcgg   1980
tcgctctttt ttttacctga                                               2000
```

<210> SEQ ID NO 61
<211> LENGTH: 907
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 61

```
tctaccgatt tcaacggcga agtttgcact tccgtgttcg atgctaaagc tggtatcgct     60
ctgaacgaca acttcgtgaa actggtatcc tggtacgaca acgaaaccgg ttactccaac    120
```

```
aaagttctgg acctgatcgc tcacatctcc aaagcggcca acgatgaaaa ctattctgaa    180

aactatgcgg atgcgtcttg atcctgacgg atggcctttt tgcgtttcta caaactcttt    240

ttgtttattt ttctaaatac attcaaatat gtatccgctc atgagacaat aaccctgata    300

aatgcttcaa taatattgaa aaaggaagag taatggcgaa actgacctcg gcggttccgg    360

ttctgacggc acgtgatgtg gcgggcgcgg ttgaattttg gacggatcgt ctgggcttca    420

gtcgtgattt tgtggaagat gacttcgcag gcgtggttcg cgatgacgtc accctgttta    480

tttccgcagt tcaggatcaa gtcgtgccgg acaacacgct ggcttgggtg tgggttcgtg    540

gcctggatga actgtatgcg gaatggagcg aagttgtctc taccaatttc cgtgacgcga    600

gcggtccggc catgacggaa atcggcgaac agccgtgggg tcgcgaattt gctctgcgtg    660

acccggctgg caactgtgtc catttcgtgg ctgaagaaca agattgagtt gagatgacac    720

tgtgatctaa aaagagcgac ttcggtcgct cttttttta cctgataaaa tgaagttaaa    780

ggactgcgtc atgattaaga aaatttttgc ccttccggtc atcgaacaaa tctcccctgt    840

cctctcccgt cgtaaactgg atgaactgga cctcattgtg gtcgatcatc cccaggtaaa    900

agcctct                                                               907
```

<210> SEQ ID NO 62
<211> LENGTH: 1421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 62

```
gtattccgtc ttccatgttc accgtcattt tcgcaatggc acgtaccgtt ggctggatcg     60

cccactggag cgaaatgcac agtgacggta tgaagattgc ccgtccgcgt cagctgtata    120

caggatatga aaaacgcgac tttaaaagcg atatcaagcg tgcggccaac gatgaaaact    180

attctgaaaa ctatgcggat gcgtcttaat agtcctgacg gatggccttt ttgcgtttct    240

acaaactctt tttgtttatt tttctaaata cattcaaata tgtatccgct catgagacaa    300

taaccctgat aaatgcttca ataatattga aaaaggaaga gtatgagtat tcaacatttc    360

cgtgtcgccc ttattccctt ttttgcggca ttttgccttc ctgtttttgc tcacccagaa    420

acgctggtga aagtaaaaga tgctgaagat cagttgggtg cacgagtggg ttacatcgaa    480

ctggatctca acagcggtaa gatccttgag agttttcgcc ccgaagaacg ttttccaatg    540

atgagcactt ttaaagttct gctatgtggc gcggtattat cccgtgttga cgccgggcaa    600

gagcaactcg gtcgccgcat acactattct cagaatgact tggttgagta ctcaccagtc    660

acagaaaagc atcttacgga tggcatgaca gtaagagaat tatgcagtgc tgccataacc    720

atgagtgata acactgcggc caacttactt ctgacaacga tcggaggacc gaaggagcta    780

accgcttttt tgcacaacat gggggatcat gtaactcgcc ttgatcgttg ggaaccggag    840

ctgaatgaag ccataccaaa cgacgagcgt gacaccacga tgcctacagc aatggcaaca    900

acgttgcgca aactattaac tggcgaacta cttactctag cttcccggca acaattaata    960

gactggatgg aggcggataa agttgcagga ccacttctgc gctcggccct tccggctggc   1020

tggtttattg ctgataaatc tggagccggt gagcgtgggt ctcgcggtat cattgcagca   1080

ctggggccag atggtaagcc ctcccgtatc gtagttatct acacgacggg gagtcaggca   1140

actatggatg aacgaaatag acagatcgct gagataggtg cctcactgat taagcattgg   1200
```

taactgtcag actaatggtt gattgctaag ttgtaaatat tttaacccgc cgttcatatg 1260

gcgggttgat ttttatatgc ctaaacacaa aaaattgtaa aaataaaatc cattaacaga 1320

cctatataga tatttaaaaa gaatagaaca gctcaaatta tcagcaaccc aatactttca 1380

attaaaaact tcatggtagt cgcatttata accctatgaa a 1421

<210> SEQ ID NO 63
<211> LENGTH: 1078
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 63

accgtcattt tcgcaatggc acgtaccgtt ggctggatcg cccactggag cgaaatgcac 60

agtgacggta tgaagattgc ccgtccgcgt cagctgtata caggatatga aaaacgcgac 120

tttaaaagcg atatcaagcg tgcggccaac gatgaaaact attctgaaaa ctatgcggat 180

gcgtcttaat cctgacggat ggcctttttg cgtttctaca aactcttttt gtttattttt 240

ctaaatacat tcaaatatgt atccgctcat gagacaataa ccctgataaa tgcttcaata 300

atattgaaaa aggaagagta tgactgaata caagcccacg gtacgcttgg cgacgcgcga 360

cgatgttccc cgcgctgttc gtacattagc tgcggccttt gcagattacc cagcgacgcg 420

ccatacggtc gatccggacc gccatatcga gcgtgtcaca gaattgcagg aacttttctt 480

aactcgcgtg ggccttgaca tcggaaaggt ctgggtggct gacgatggcg ctgcagtggc 540

tgtttggacc actccggaga gtgtagaggc tggtgcagtg ttcgccgaaa ttggtcctcg 600

tatggccgaa ttaagtggaa gtcgtctggc agcccaacaa caaatggaag ggttgcttgc 660

gccccaccgt ccgaaagaac ccgcgtggtt ccttgccacc gttggagtaa gcccagatca 720

ccaggggaag ggtttaggat ctgccgtagt tttaccaggt gtggaggcag cagaacgtgc 780

gggagttccg gccttccttg agacgtcggc gccgcgcaat ttaccgtttt acgaacgtct 840

tggattcacc gttacggcgg acgtggaggt gccggaggga ccccgtactt ggtgtatgac 900

tcgtaaaccg ggagcctgat aatggttgat tgctaagttg taaatatttt aacccgccgt 960

tcatatggcg ggttgatttt tatatgccta aacacaaaaa attgtaaaaa taaaatccat 1020

taacagacct atatagatat ttaaaaagaa tagaacagct caaattatca gcaaccca 1078

<210> SEQ ID NO 64
<211> LENGTH: 869
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 64

gtattccgtc ttccatgttc accgtcattt tcgcaatggc acgtaccgtt ggctggatcg 60

cccactggag cgaaatgcac agtgacggta tgaagattgc ccgtccgcgt cagctgtata 120

caggatatga aaaacgcgac tttaaaagcg atatcaagcg tgcggccaac gatgaaaact 180

attctgaaaa ctatgcggat gcgtcttaat agttgacaat taatcatcgg catagtatat 240

cggcatagta taatacgact cactatagga gggccatcat ggccaagttg accagtgccg 300

ttccggtgct caccgcgcgc gacgtcgccg gagcggtcga gttctggacc gaccggctcg 360 ggttctcccg ggacttcgtg gaggacgact tcgccggtgt ggtccgggac gacgtgaccc 420

tgttcatcag cgcggtccag gaccaggtgg tgccggacaa caccctggcc tgggtgtggg 480

tgcgcggcct ggacgagctg tacgccgagt ggtcggaggt cgtgtccacg aacttccggg 540

acgcctccgg gccggccatg accgagatcg gcgagcagcc gtgggggcgg gagttcgccc 600

tgcgcgaccc ggccggcaac tgcgtgcact ttgtggcaga ggagcaggac tgaggataag 660

taatggttga ttgctaagtt gtaaatattt taacccgccg ttcatatggc gggttgattt 720

ttatatgcct aaacacaaaa aattgtaaaa ataaaatcca ttaacagacc tatatagata 780

tttaaaaaga atagaacagc tcaaattatc agcaacccaa tactttcaat taaaaacttc 840

atggtagtcg catttataac cctatgaaa 869

<210> SEQ ID NO 65
<211> LENGTH: 1000
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 65

gcggcgagct gctgggtgaa atcggcctgg caatcgaaat gggttgtgat gctgaagaca 60

tcgcactgac catccacgcg cacccgactc tgcacgagtc tgtgggcctg gcggcagaag 120

tgttcgaagg tagcattacc gacctgccga acccgaaagc gaagaagaag gcggccaacg 180

atgaaaacta ttctgaaaac tatgcggatg cgtcttaata gcgaatccat gtgggagttt 240

attcttgaca cagatattta tgatataata actgagtaag cttaacataa ggaggaaaaa 300

catatgttac gcagcagcaa cgatgttacg cagcagggca gtcgccctaa aacaaagtta 360

ggtggctcaa gtatgggcat cattcgcaca tgtaggctcg gccctgacca agtcaaatcc 420

atgcgggctg ctcttgatct tttcggtcgt gagttcggag acgtagccac ctactcccaa 480

catcagccgg actccgatta cctcgggaac ttgctccgta gtaagacatt catcgcgctt 540

gctgccttcg accaagaagc ggttgttggc gctctcgcgg cttacgttct gcccaagttt 600

gagcagccgc gtagtgagat ctatatctat gatctcgcag tctccggcga gcaccggagg 660

cagggcattg ccaccgcgct catcaatctc ctcaagcatg aggccaacgc gcttggtgct 720

tatgtgatct acgtgcaagc agattacggt gacgatcccg cagtggctct ctatacaaag 780

ttgggcatac gggaagaagt gatgcacttt gatatcgacc caagtaccgc cacctaattt 840

ttcgtttgcc ggaacatccg gcaattaaaa aagcggctaa ccacgccgct ttttttacgt 900

ctgcaattta cctttccagt cttcttgctc cacgttcaga gagacgttcg catactgctg 960

accgttgctc gttattcagc ctgacagtat ggttactgtc 1000

<210> SEQ ID NO 66
<211> LENGTH: 852
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 66

tctgggtatt cactgctttg gcgagcgcgc tgccgaaatt attcatatcg gtcaggcgat 60

tatggaacag aaaggtggcg gcaacactat tgagtacttc gtcaacacca cctttaacta 120

cccgacgatg gcggaagcct atcgggtagc tgcgttaaac ggtttaaacc gcctgtttgc 180

```
ggccaacgat gaaaactatt ctgaaaacta tgcggatgcg tcttaatagt tgacaattaa    240

tcatcggcat agtatatcgg catagtataa tacgactcac tataggaggg ccatcatgaa    300

gaccttcaac atctctcagc aggatctgga gctggtggag gtcgccactg agaagatcac    360

catgctctat gaggacaaca agcaccatgt cggggcggcc atcaggacca agactgggga    420

gatcatctct gctgtccaca ttgaggccta cattggcagg gtcactgtct gtgctgaagc    480

cattgccatt gggtctgctg tgagcaacgg gcagaaggac tttgacacca ttgtggctgt    540

caggcacccc tactctgatg aggtggacag atccatcagg gtggtcagcc cctgtggcat    600

gtgcagagag ctcatctctg actatgctcc tgactgcttt gtgctcattg agatgaatgg    660

caagctggtc aaaaccacca ttgaggaact catccccctc aagtacacca ggaactaaag    720

taaaacttta tcgaaatggc catccattct tgcgcggatg gcctctgcca gctgctcata    780

gcggctgcgc agcggtgagc caggacgata aaccaggcca atagtgcggc gtggttccgg    840

cttaatgcac gg                                                        852
```

<210> SEQ ID NO 67
<211> LENGTH: 898
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 67

```
gaagtggaag aagcctggaa atgggtagac tccattactg aggcgtgggc gatggacaat     60

gatgcgccga aaccgtatca ggccggaacc tggggacccg ttgcctcggt ggcgatgatt    120

acccgtgatg gtcgttcctg gaatgagttt gaggcggcca acgatgaaaa ctattctgaa    180

aactatgcgg atgcgtctta atagttgaca attaatcatc ggcatagtat atcggcatag    240

tataatacga ctcactatag gagggccatc atgaagacct tcaacatctc tcagcaggat    300

ctggagctgg tggaggtcgc cactgagaag atcaccatgc tctatgagga caacaagcac    360

catgtcgggg cggccatcag gaccaagact ggggagatca tctctgctgt ccacattgag    420

gcctacattg gcagggtcac tgtctgtgct gaagccattg ccattgggtc tgctgtgagc    480

aacgggcaga aggactttga caccattgtg gctgtcaggc acccctactc tgatgaggtg    540

gacagatcca tcagggtggt cagcccctgt ggcatgtgca gagagctcat ctctgactat    600

gctcctgact gctttgtgct cattgagatg aatggcaagc tggtcaaaac caccattgag    660

gaactcatcc ccctcaagta caccaggaac taaagtaata tctgcgctta tcctttatgg    720

ttattttacc ggtaacatga tcttgcgcag attgtagaac aatttttaca ctttcaggcc    780

tcgtgcggat tcacccacga ggcttttttt attacactga ctgaaacgtt tttgccctat    840

gagctccggt tacaggcgtt tcagtcataa atcctctgaa tgaaacgcgt tgtgaatc      898
```

<210> SEQ ID NO 68
<211> LENGTH: 1181
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 68

```
gcgtgcgcac catgacggtg gggaccgtct cgatggatat gctagcggtc gatttaacgc     60
```

```
cttgcccgca ggcgggtatt ggtacgccgg ttgagctgtg gggcaaggag atcaaaattg    120

atgatgtcgc cgccgctgcc ggaacggtgg gctatgagtt gatgtgcgcg ctggcgctac    180

gcgtcccggt tgtgacggtg gcggccaacg atgaaaacta ttctgaaaac tatgcggatg    240

cgtcttaatc ctgacggatg gcctttttgc gtttctacaa actcttttg tttattttc    300

taaatacatt caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa    360

tattgaaaaa ggaagagtat gactgaatac aagcccacgg tacgcttggc gacgcgcgac    420

gatgttcccc gcgctgttcg tacattagct gcggcctttg cagattaccc agcgacgcgc    480

catacggtcg atccggaccg ccatatcgag cgtgtcacag aattgcagga acttttctta    540

actcgcgtgg gccttgacat cggaaaggtc tgggtggctg acgatggcgc tgcagtggct    600

gtttggacca ctccggagag tgtagaggct ggtgcagtgt tcgccgaaat tggtcctcgt    660

atggccgaat taagtggaag tcgtctggca gcccaacaac aaatggaagg gttgcttgcg    720

ccccaccgtc cgaaagaacc cgcgtggttc cttgccaccg ttggagtaag cccagatcac    780

caggggaagg gtttaggatc tgccgtagtt ttaccaggtg tggaggcagc agaacgtgcg    840

ggagttccgg ccttccttga gacgtcggcg ccgcgcaatt taccgtttta cgaacgtctt    900

ggattcaccg ttacggcgga cgtggaggtg ccggagggac cccgtacttg gtgtatgact    960

cgtaaaccgg gagcctgata acttgttgta agccggatcg gaggcaacgt cttctgggtg   1020

caaaaaaatc atccatccgg ctggtcagca actgtagttg ttaatgtgac agagccattg   1080

cccatgatag tgtccattaa aaggatggac actatttccc cggaacctga actcaccgca   1140

caggcgttct acataaaacg cttacgcttc attgttgact c                       1181
```

<210> SEQ ID NO 69
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 69

```
tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt     60

atcgagttcc ccgcgccagc ggggataaac cg                                   92
```

<210> SEQ ID NO 70
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 70

```
gtttatctgt tcgtatcgag ttccccgcgc cagcggggat aaaccgaaaa aaaaaacccc     59
```

<210> SEQ ID NO 71
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 71

```
ggttattata atcaacggtt tatccccgct ggcgcgggga actcgaggtg gtaccagatc     60
```

<210> SEQ ID NO 72
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 72

tcgagttccc cgcgccagcg gggataaacc ggtttttgta attttacagg caacctttta 60

ttcgagttcc ccgcgccagc ggggataaac cg 92

<210> SEQ ID NO 73
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 73

caggcaacct tttattcgag ttccccgcgc cagcggggat aaaccgaaaa aaaaaacccc 59

<210> SEQ ID NO 74
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 74

taaaattaca aaaaccggtt tatccccgct ggcgcgggga actcgaggtg gtaccagatc 60

<210> SEQ ID NO 75
<211> LENGTH: 93
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 75

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccg 93

<210> SEQ ID NO 76
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 76

gcgtaaaagt tatgaagttc gagttccccg cgccagcggg gataaaccga aaaaaaaacc 60

cc 62

<210> SEQ ID NO 77
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 77

attatatgct tttcggttta tccccgctgg cgcggggaac tcgaggtggt accagatct 59

<210> SEQ ID NO 78
<211> LENGTH: 94
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 78

tcgagttccc cgcgccagcg gggataaacc gtattgacca attcattcgg gacagttatt 60

agttcgagtt ccccgcgcca gcggggataa accg 94

<210> SEQ ID NO 79
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 79

gggacagtta ttagttcgag ttccccgcgc cagcggggat aaaccgaaaa aaaaaacccc 59

<210> SEQ ID NO 80
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 80

gaatgaattg gtcaatacgg tttatccccg ctggcgcggg gaactcgagg tggtaccaga 60

tct 63

<210> SEQ ID NO 81
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide

<400> SEQUENCE: 81

tcgagttccc cgcgccagcg gggataaacc gagtggttgc tggataactt tacgggcatg 60

ctcgagttcc ccgcgccagc ggggataaac cg 92

<210> SEQ ID NO 82
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 82

aactttacgg gcatgctcga gttccccgcg ccagcgggga taaaccgaaa aaaaaacccc 60

<210> SEQ ID NO 83
<211> LENGTH: 60

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 83

atccagcaac cactcggttt atccccgctg gcgcggggaa ctcgaggtgg taccagatct 60

<210> SEQ ID NO 84
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 84

tcgagttccc cgcgccagcg gggataaacc gttaccattc tgttgctttt atgtataaga 60

atcgagttcc ccgcgccagc ggggataaac cg 92

<210> SEQ ID NO 85
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 85

ttttatgtat aagaatcgag ttccccgcgc cagcggggat aaaccgaaaa aaaaacccc 59

<210> SEQ ID NO 86
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 86

gcaacagaat ggtaacggtt tatccccgct ggcgcgggga actcgaggtg gtaccagatc 60

<210> SEQ ID NO 87
<211> LENGTH: 92
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

<400> SEQUENCE: 87

tcgagttccc cgcgccagcg gggataaacc gctcgtaaaa gcagtacagt gcaccgtaag 60

atcgagttcc ccgcgccagc ggggataaac cg 92

<210> SEQ ID NO 88
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 88

cagtgcaccg taagatcgag ttccccgcgc cagcggggat aaaccgaaaa aaaaacccc 59

<210> SEQ ID NO 89
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 89

tactgctttt acgagcggtt tatccccgct ggcgcgggga actcgaggtg gtaccagatc 60

<210> SEQ ID NO 90
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 90

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accg 154

<210> SEQ ID NO 91
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 91

gcgccagcgg ggataaaccg aaaagcatat aatgcg 36

<210> SEQ ID NO 92
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 92

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 93
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 93

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 94
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 94

cggtttatcc ccgctggcgc ggggaactcg atacgaacag ataaacggtt attataatc 59

<210> SEQ ID NO 95
<211> LENGTH: 155
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 95

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgtattgacc aattcattcg ggacagttat 120

tagttcgagt tccccgcgcc agcggggata aaccg 155

<210> SEQ ID NO 96
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 96

gcgccagcgg ggataaaccg tattgaccaa ttcattc 37

<210> SEQ ID NO 97
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 97

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 98
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 98

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 99
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 99

cggtttatcc ccgctggcgc ggggaactcg atacgaacag ataaacggtt attataatc 59

<210> SEQ ID NO 100
<211> LENGTH: 153
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

polynucleotide

<400> SEQUENCE: 100

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgttaccatt ctgttgcttt tatgtataag 120

aatcgagttc cccgcgccag cggggataaa ccg 153

<210> SEQ ID NO 101
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 101

gcgccagcgg ggataaaccg ttaccattct gttg 34

<210> SEQ ID NO 102
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 102

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 103
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 103

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 104
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 104

cggtttatcc ccgctggcgc ggggaactcg atacgaacag ataaacggtt attataatc 59

<210> SEQ ID NO 105
<211> LENGTH: 153
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 105

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgctcgtaaa agcagtacag tgcaccgtaa 120

gatcgagttc cccgcgccag cggggataaa ccg 153

<210> SEQ ID NO 106
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 106

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 107
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 107

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 108
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 108

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 109
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 109

cggtttatcc ccgctggcgc ggggaactcg atacgaacag ataaacggtt attataatc 59

<210> SEQ ID NO 110
<211> LENGTH: 156
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 110

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccg 156

<210> SEQ ID NO 111
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 111

gcgccagcgg ggataaaccg tattgaccaa ttcattc 37

<210> SEQ ID NO 112
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 112

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 113
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 113

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 114
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 114

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac 47

<210> SEQ ID NO 115
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 115

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgttaccat tctgttgctt ttatgtataa 120

gaatcgagtt ccccgcgcca gcggggataa accg 154

<210> SEQ ID NO 116
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 116

gcgccagcgg ggataaaccg ttaccattct gttg 34

<210> SEQ ID NO 117
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

primer

<400> SEQUENCE: 117

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 118
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 118

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 119
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 119

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac 47

<210> SEQ ID NO 120
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 120

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgctcgtaa aagcagtaca gtgcaccgta 120

agatcgagtt ccccgcgcca gcggggataa accg 154

<210> SEQ ID NO 121
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 121

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 122
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 122

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 123
<211> LENGTH: 28
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 123

ccggatgagc attcatcagg cgggcaag                                          28


<210> SEQ ID NO 124
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 124

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac                     47


<210> SEQ ID NO 125
<211> LENGTH: 155
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 125

tcgagttccc cgcgccagcg gggataaacc gtattgacca attcattcgg gacagttatt      60

agttcgagtt ccccgcgcca gcggggataa accgttacca ttctgttgct tttatgtata     120

agaatcgagt tccccgcgcc agcggggata aaccg                                 155


<210> SEQ ID NO 126
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 126

gcgccagcgg ggataaaccg ttaccattct gttg                                   34


<210> SEQ ID NO 127
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 127

cttgcccgcc tgatgaatgc tcatccgg                                          28


<210> SEQ ID NO 128
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      primer

<400> SEQUENCE: 128

ccggatgagc attcatcagg cgggcaag                                          28
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<210> SEQ ID NO 129
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 129

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 130
<211> LENGTH: 155
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 130

tcgagttccc cgcgccagcg gggataaacc gtattgacca attcattcgg gacagttatt 60

agttcgagtt ccccgcgcca gcggggataa accgctcgta aaagcagtac agtgcaccgt 120

aagatcgagt tccccgcgcc agcggggata aaccg 155

<210> SEQ ID NO 131
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 131

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 132
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 132

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 133
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 133

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 134
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 134

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 135
<211> LENGTH: 153
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 135

tcgagttccc cgcgccagcg gggataaacc gttaccattc tgttgctttt atgtataaga 60

atcgagttcc ccgcgccagc ggggataaac cgctcgtaaa agcagtacag tgcaccgtaa 120

gatcgagttc cccgcgccag cggggataaa ccg 153

<210> SEQ ID NO 136
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 136

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 137
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 137

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 138
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 138

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 139
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 139

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

<210> SEQ ID NO 140
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 140

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccg 217

<210> SEQ ID NO 141
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 141

gcgccagcgg ggataaaccg tattgaccaa ttcattc 37

<210> SEQ ID NO 142
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 142

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 143
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 143

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 144
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 144

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac 47

<210> SEQ ID NO 145
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 145

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccggttt ttgtaatttt acaggcaacc 180 ttttattcga gttccccgcg ccagcgggga taaaccg 217

<210> SEQ ID NO 146
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 146

gcgccagcgg ggataaaccg gtttttgtaa ttttacaggc 40

<210> SEQ ID NO 147
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 147

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 148
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 148

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 149
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 149

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 150
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 150

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccgttac cattctgttg cttttatgta 180

taagaatcga gttccccgcg ccagcgggga taaaccg 217

<210> SEQ ID NO 151
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 151

gcgccagcgg ggataaaccg ttaccattct gttg 34

<210> SEQ ID NO 152
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 152

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 153
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 153

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 154
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 154

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 155
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 155

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccgctcg taaaagcagt acagtgcacc 180

gtaagatcga gttccccgcg ccagcgggga taaaccg 217

<210> SEQ ID NO 156
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 156

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 157
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 157

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 158
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 158

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 159
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 159

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 160
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 160

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccggtt tttgtaattt tacaggcaac 240

cttttattcg agttccccgc gccagcgggg ataaaccg 278

<210> SEQ ID NO 161
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 161

gcgccagcgg ggataaaccg gtttttgtaa ttttacaggc 40

<210> SEQ ID NO 162
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 162

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 163
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 163

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 164
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 164

cggtttatcc ccgctggcgc ggggaactcg aactaataac tgtc 44

<210> SEQ ID NO 165
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 165

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccgtta ccattctgtt gcttttatgt 240

ataagaatcg agttccccgc gccagcgggg ataaaccg 278

<210> SEQ ID NO 166
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 166

gcgccagcgg ggataaaccg tattgaccaa ttcattc 37

<210> SEQ ID NO 167
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 167

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 168
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 168

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 169
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 169

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac 47

<210> SEQ ID NO 170
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 170

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccgctc gtaaaagcag tacagtgcac 240

cgtaagatcg agttccccgc gccagcgggg ataaaccg 278

<210> SEQ ID NO 171
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 171

gcgccagcgg ggataaaccg tattgaccaa ttcattc 37

<210> SEQ ID NO 172
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 172

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 173
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 173

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 174
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 174

cggtttatcc ccgctggcgc ggggaactcg aacttcataa cttttac 47

<210> SEQ ID NO 175
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 175

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccgttac cattctgttg cttttatgta 180

taagaatcga gttccccgcg ccagcgggga taaaccggtt tttgtaattt tacaggcaac 240

cttttattcg agttccccgc gccagcgggg ataaaccg 278

<210> SEQ ID NO 176
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 176

gcgccagcgg ggataaaccg gtttttgtaa ttttacaggc 40

<210> SEQ ID NO 177
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 177

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 178
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 178

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 179
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 179

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

<210> SEQ ID NO 180
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 180

tcgagttccc cgcgccagcg gggataaacc gaaaagcata taatgcgtaa aagttatgaa 60

gttcgagttc cccgcgccag cggggataaa ccgtattgac caattcattc gggacagtta 120

ttagttcgag ttccccgcgc cagcggggat aaaccgttac cattctgttg cttttatgta 180

taagaatcga gttccccgcg ccagcgggga taaaccgctc gtaaaagcag tacagtgcac 240

cgtaagatcg agttccccgc gccagcgggg ataaaccg 278

<210> SEQ ID NO 181
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 181

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 182
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 182

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 183
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 183

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 184
<211> LENGTH: 48
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 184

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

<210> SEQ ID NO 185
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 185

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccgtta ccattctgtt gcttttatgt 240

ataagaatcg agttccccgc gccagcgggg ataaaccggt ttttgtaatt ttacaggcaa 300

ccttttattc gagttccccg cgccagcggg gataaaccg 339

<210> SEQ ID NO 186
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 186

gcgccagcgg ggataaaccg gtttttgtaa ttttacaggc 40

<210> SEQ ID NO 187
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 187

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 188
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 188

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 189
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 189

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

<210> SEQ ID NO 190
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 190

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccgtta ccattctgtt gcttttatgt 240

ataagaatcg agttccccgc gccagcgggg ataaaccgct cgtaaaagca gtacagtgca 300

ccgtaagatc gagttccccg cgccagcggg gataaaccg 339

<210> SEQ ID NO 191
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 191

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 192
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 192

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 193
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 193

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 194
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 194

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

<210> SEQ ID NO 195
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 195

tcgagttccc cgcgccagcg gggataaacc gttgattata ataaccgttt atctgttcgt 60

atcgagttcc ccgcgccagc ggggataaac cgaaaagcat ataatgcgta aaagttatga 120

agttcgagtt ccccgcgcca gcggggataa accgtattga ccaattcatt cgggacagtt 180

attagttcga gttccccgcg ccagcgggga taaaccgtta ccattctgtt gcttttatgt 240

ataagaatcg agttccccgc gccagcgggg ataaaccgct cgtaaaagca gtacagtgca 300

ccgtaagatc gagttccccg cgccagcggg gataaaccgg tttttgtaat tttacaggca 360

accttttatt cgagttcccc gcgccagcgg ggataaaccg 400

<210> SEQ ID NO 196
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 196

gcgccagcgg ggataaaccg gtttttgtaa ttttacaggc 40

<210> SEQ ID NO 197
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 197

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 198
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 198

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 199
<211> LENGTH: 49
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 199

cggtttatcc ccgctggcgc ggggaactcg atcttacggt gcactgtac 49

<210> SEQ ID NO 200
<211> LENGTH: 153
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 200

tcgagttccc cgcgccagcg gggataaacc gttaccattc tgttgctttt atgtataaga 60

atcgagttcc ccgcgccagc ggggataaac cgctcgtaaa agcagtacag tgcaccgtaa 120

gatcgagttc cccgcgccag cggggataaa ccg 153

<210> SEQ ID NO 201
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 201

gcgccagcgg ggataaaccg ctcgtaaaag 30

<210> SEQ ID NO 202
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 202

cttgcccgcc tgatgaatgc tcatccgg 28

<210> SEQ ID NO 203
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 203

ccggatgagc attcatcagg cgggcaag 28

<210> SEQ ID NO 204
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
primer

<400> SEQUENCE: 204

cggtttatcc ccgctggcgc ggggaactcg attcttatac ataaaagc 48

What is claimed is:

1. A multi-stage fermentation bioprocess for producing a product from a genetically modified microorganism, comprising:

providing a genetically modified microorganism having a production pathway for producing a product that is: an amino acid, acetate, acetoin, acetone, acrylic, malate, fatty acid ethyl esters, isoprenoids, glycerol, ethylene glycol, ethylene, propylene, butylene, isobutylene, ethyl acetate, vinyl acetate, 1,4-butanediol, 2,3-butanediol, butanol, isobutanol, sec-butanol, butyrate, isobutyrate, 2-OH-isobutyrate, 3-OH-butyrate, ethanol, isopropanol, D-lactate, L-lactate, pyruvate, itaconate, levulinate, glucarate, glutarate, caprolactam, adipic acid, propanol, isopropanol, fused alcohols, 1,2-propanediol, 1,3-propanediol, formate, fumaric acid, propionic acid, succinic acid, valeric acid, maleic acid, or poly-hydroxybutyrate;

growing the identified genetically modified microorganism in a media in a growth phase, the genetically modified microorganism comprising:

i. a production pathway comprising at least one production enzyme for biosynthesis of the product; and

ii. one or more synthetic metabolic valves for reducing or eliminating flux through multiple metabolic pathways within the genetically modified microorganism when the synthetic metabolic valves are induced, the one or more synthetic metabolic valves comprising:

a) at least one silencing synthetic metabolic valve that silences gene expression of a gene selected from: fabI, gltA, lpd, zwf, and udhA, or

b) at least one proteolytic synthetic metabolic valve that controls proteolysis of a proteolyzable enzyme selected from: fabI, gltA, lpd, zwf, and udhA;

transitioning to a productive stationary phase, the transition comprising:

depletion of a limiting nutrient;

inducing the one or more synthetic metabolic valves;

activation of the production pathway; and

producing the product.

2. The multi-stage fermentation bioprocess of claim **1**, wherein the microorganism comprises a silencing synthetic metabolic valve and a proteolytic synthetic metabolic valve, and wherein the activation of the silencing synthetic metabolic valve produces a product that enhances the function of the proteolytic synthetic metabolic valve.

3. The multi-stage fermentation bioprocess of claim **1**, wherein the microorganism comprises a chromosomal a deletion or disruption of a cas3 or sspB gene.

4. The multi-stage fermentation bioprocess of claim **1**, wherein the rate of production of said product during the productive stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the synthetic metabolic valves.

5. The multi-stage fermentation bioprocess of claim **1**, wherein the silencing synthetic metabolic valve silences gene expression of a gene selected from: fabI, gltA, lpd, zwf, and udhA and an additional gene.

6. The multi-stage fermentation bioprocess of claim **1**, wherein the proteolytic synthetic metabolic valve that controls proteolysis of a proteolyzable enzyme selected from: fabI, gltA, lpd, zwf, and udhA and an additional enzyme.

7. The multi-stage fermentation bioprocess of claim **1**, wherein at least one silencing synthetic metabolic valve is characterized by CRISPR interference of gene expression of a gene that is a fabI, gltA, lpd, zwf, or udhA gene and expression of a CASCADE plasmid comprising an array of guide RNA genes.

8. The multi-stage fermentation bioprocess of claim **1**, wherein at least one proteolytic synthetic metabolic valve is characterized by expression of the proteolytic enzyme operably linked to a C-terminal DAS4 peptide tag and controlled proteolysis of a fabI, gltA, ldp, zwf, or udhA enzyme by the synthetic metabolic valve is selective for the tag by clpXP protease upon induction of sspB chaperone protein.

9. The multi-stage fermentation bioprocess of claim **1**, wherein the microorganism has reduced level or activity of at least one metabolic enzyme prior to synthetic metabolic valve induction.

10. A multi-stage fermentation bioprocess for producing a product from a genetically modified *E. coli*, comprising:

providing a genetically modified *E. coli* having a production pathway for producing a product that is: an amino acid, acetate, acetoin, acetone, acrylic, malate, fatty acid ethyl esters, isoprenoids, glycerol, ethylene glycol, ethylene, propylene, butylene, isobutylene, ethyl acetate, vinyl acetate, 1,4-butanediol, 2,3-butanediol, butanol, isobutanol, sec-butanol, butyrate, isobutyrate, 2-OH-isobutyrate, 3-OH-butyrate, ethanol, isopropanol, D-lactate, L-lactate, pyruvate, itaconate, levulinate, glucarate, glutarate, caprolactam, adipic acid, propanol, isopropanol, fused alcohols, 1,2-propanediol, 1,3-propanediol, formate, fumaric acid, propionic acid, succinic acid, valeric acid, maleic acid, or poly-hydroxybutyrate;

growing the identified genetically modified *E. coli* in a media in a growth phase, the genetically modified *E. coli* comprising:

i. a production pathway comprising at least one production enzyme for biosynthesis of the product; and

ii. one or more synthetic metabolic valves for reducing or eliminating flux through multiple metabolic pathways within the genetically modified *E. coli* when the synthetic metabolic valves are induced, the one or more synthetic metabolic valves comprising:

a) at least one silencing synthetic metabolic valve that silences gene expression of a gene, or

b) at least one proteolytic synthetic metabolic valve that controls proteolysis of a proteolyzable enzyme;

transitioning to a productive stationary phase, the transition comprising:

depletion of a limiting nutrient;

inducing the one or more synthetic metabolic valves; and

activation of the production pathway; and

producing the product.

11. The multi-stage fermentation bioprocess of claim **10**, wherein the silencing synthetic metabolic valve that silences gene expression of a gene is a gene selected from the group: fabI, gltA, ldp, zwf, or udhA.

12. The multi-stage fermentation bioprocess of claim **10**, wherein the silencing synthetic metabolic valve silences gene expression of a gene selected from: fabI, gltA, lpd, zwf, and udhA and an additional gene.

13. The multi-stage fermentation bioprocess of claim **10**, wherein the proteolytic synthetic metabolic valve that controls proteolysis of a proteolyzable enzyme is an enzyme selected from the group: fabI, gltA, ldp, zwf, or udhA.

14. The multi-stage fermentation bioprocess of claim **10**, wherein the proteolytic synthetic metabolic valve that controls proteolysis of a proteolyzable enzyme selected from: fabI, gltA, lpd, zwf, and udhA and an additional enzyme.

15. The multi-stage fermentation bioprocess of claim **10**, wherein at least one silencing synthetic metabolic valve is characterized by CRISPR interference of gene expression of a gene that is a fabI, gltA, lpd, zwf, or udhA gene and expression of a CASCADE plasmid comprising an array of guide RNA genes.

16. The multi-stage fermentation bioprocess of claim **10**, wherein at least one proteolytic synthetic metabolic valve is characterized by expression of the proteolytic enzyme operably linked to a C-terminal DAS4 peptide tag and controlled proteolysis of a fabI, gltA, ldp, zwf, or udhA enzyme by the synthetic metabolic valve is selective for the tag by clpXP protease upon induction of sspB chaperone protein.

17. The multi-stage fermentation bioprocess of claim **10**, wherein the rate of production of said product during the productive stationary phase is reduced less in response to a change of an environmental condition as compared to a cell lacking the synthetic metabolic valves.

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