

SEQUENCE LISTING

<110> National University of Singapore

<120> PRODUCING BUTYL BUTYRATE FROM LIGNOCELLULOSIC BIOMASS THROUGH
ESCHERICHIA COLI-CLOSTRIDIUM CO-CULTURE

<130> SP103986W0

<150> SG02106918X

<151> 2021-06-24

<160> 45

<170> PatentIn version 3.5

<210> 1

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> SAAT (strawberry) amino acid sequence

<400> 1

Met	Glu	Lys	Ile	Glu	Val	Ser	Ile	Asn	Ser	Lys	His	Thr	Ile	Lys	Pro
1				5					10					15	

Ser	Thr	Ser	Ser	Thr	Pro	Leu	Gln	Pro	Tyr	Lys	Leu	Thr	Leu	Leu	Asp
			20					25					30		

Gln	Leu	Thr	Pro	Pro	Ala	Tyr	Val	Pro	Ile	Val	Phe	Phe	Tyr	Pro	Ile
		35					40					45			

Thr	Asp	His	Asp	Phe	Asn	Leu	Pro	Gln	Thr	Leu	Ala	Asp	Leu	Arg	Gln
	50					55					60				

Ala	Leu	Ser	Glu	Thr	Leu	Thr	Leu	Tyr	Tyr	Pro	Leu	Ser	Gly	Arg	Val
65					70					75					80

Lys	Asn	Asn	Leu	Tyr	Ile	Asp	Asp	Phe	Glu	Glu	Gly	Val	Pro	Tyr	Leu
				85					90					95	

Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys
100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val
130 135 140

Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
145 150 155 160

Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe
165 170 175

Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala
180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln
195 200 205

Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe
210 215 220

Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu
245 250 255

Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg
275 280 285

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
290 295 300

Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
340 345 350

Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
355 360 365

Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
370 375 380

Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
385 390 395 400

Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
405 410 415

Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
420 425 430

Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro
435 440 445

Lys Thr Leu Ile
450

<210> 2

<211> 1356

<212> DNA

<213> Artificial Sequence

<220>

<223> saat (strawberry) nucleotide sequence

<400> 2

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acgccattgc aaccgtacaa acttacgtta cttgatcagt taacaccgcc tgcctacgta	120
cctatcgtat ttttctatcc gatcactgac catgacttca acctgcctca aacattagct	180
gatcttcgtc aggctttatc ggagacactg actttgtact atccactttc tggtcgcgta	240
aagaataact tgtacattga cgactttgag gagggagtgc catacttaga ggctcgcgtt	300
aattgtgaca tgaccgactt cttgcgttta cgtaaaatcg aatgcttgaa tgagtttgta	360
cccatcaagc ctttttagcat ggaagcaatt tccgacgaac gttacccgct gttgggagtt	420
caggtaaagtg tcttcgactc cggaattgcg atcggcgtat cagtctcgca taaactgatt	480
gacggaggga cagccgactg ttttttaaaa tcatgggggtg cagtcttccg tgggtgccgt	540
gaaaatatca tccatccctc gcttagcgag gcggcattgt tatttcctcc ccgtgatgat	600
ttgcccgaag aatacgtaga ccagatggag gccctgtggt ttgctggcaa gaaagtcgcc	660
acgcgtcgtt tcgtgttcgg tgtaaaagcg attagctcaa ttcaggatga ggctaaatcg	720
gaaagcgtgc caaaaccctc tcgcgtccat gcagttaccg gcttcctttg gaaacacctt	780
attgctgcta gtcgcgccct tacttccggt acgacatcga cgcgcttatc tattgcagcc	840
caggcgggta atttgcgtac acgcatgaac atggaaacag ttcttgataa cgcaaccggg	900
aacctgtttt ggtgggcaca ggctatctta gagttatctc aactacgcc agaaatttct	960
gatttaaaat tgtgcgatct tgtaaactct ctgaacgggt ctgtgaaaca atgcaatggg	1020
gattattttg aaacgtttta gggtaaggaa gggatatggac gcatgtgtga gtacctggac	1080
ttccagcgca ccatgtctag catggaacca gcacctgata tttatctggt cagcagctgg	1140
actaatTTTT ttaatccctt ggatttttgt tgggggcgca ccagctggat tgggtgtagct	1200
gggaagatcg agagtgaag ctgcaaattt atcatccttg tgcctacca atgtggttcg	1260
gggattgagg cttgggtaaa cctggaagaa gaaaagatgg ccatgcttga gcaggaccct	1320
cactttcttg ctttggcctc cccaagacc ttaatt	1356

<210> 3

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> VAAT (strawberry) amino acid sequence

<400> 3

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

Ser	Thr	Ser	Ser	Ser	Pro	Leu	Gln	Pro	Tyr	Lys	Leu	Thr	Leu	Leu	Asp
			20					25					30		

Gln	Leu	Thr	Pro	Pro	Ser	Tyr	Val	Pro	Met	Val	Phe	Phe	Tyr	Pro	Ile
		35					40					45			

Thr	Gly	Pro	Ala	Val	Phe	Asn	Leu	Gln	Thr	Leu	Ala	Asp	Leu	Arg	His
	50					55					60				

Ala	Leu	Ser	Glu	Thr	Leu	Thr	Leu	Tyr	Tyr	Pro	Leu	Ser	Gly	Arg	Val
65					70				75						80

Lys	Asn	Asn	Leu	Tyr	Ile	Asp	Asp	Phe	Glu	Glu	Gly	Val	Pro	Tyr	Leu
			85						90					95	

Glu	Ala	Arg	Val	Asn	Cys	Asp	Met	Asn	Asp	Phe	Leu	Arg	Leu	Pro	Lys
			100					105					110		

Ile	Glu	Cys	Leu	Asn	Glu	Phe	Val	Pro	Ile	Lys	Pro	Phe	Ser	Met	Glu
		115					120					125			

Ala	Ile	Ser	Asp	Glu	Arg	Tyr	Pro	Leu	Leu	Gly	Val	Gln	Val	Asn	Ile
	130					135					140				

Phe	Asn	Ser	Gly	Ile	Ala	Ile	Gly	Val	Ser	Val	Ser	His	Lys	Leu	Ile
145					150				155						160

Asp	Gly	Arg	Thr	Ser	Asp	Cys	Phe	Leu	Lys	Ser	Trp	Cys	Ala	Val	Phe
				165					170					175	

Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
195 200 205

Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
210 215 220

Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
245 250 255

Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
275 280 285

Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
290 295 300

Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
305 310 315 320

Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
325 330 335

Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
340 345 350

Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
355 360 365

Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
370 375 380

Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
385 390 395 400

Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
405 410 415

Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
420 425 430

Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
435 440 445

Lys Thr Leu Ile Ser Arg Tyr
450 455

<210> 4

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

<223> vaat (strawberry) nucleotide sequence

<400> 4

atggagaaaa ttgaggtttc tatcatctct aagcacacta ttaagcccag cacatcgtct 60

tcccctcttc agccatacaa gttgaccttg ttggaccaat tgacgccgcc ttcttacgta 120

ccgatggtat ttttctaccc catcacagga ccggccgtgt tcaacttaca aacattggcg 180

gaccttcgtc atgcgcttag cgagacattg acgttatatt atccactgtc aggacgtgta 240

aagaataatt tgtacattga cgactttgag gaagggtgtgc cctatctgga agctcgcgtc 300

aattgcgaca tgaacgactt tcttcgcctg cccaaaattg agtgcttgaa cgaatttgctc 360

ccgattaaac cgttttccat ggaagcgatt tccgacgaac gttatcccct gttgggtgta 420

caggtaaata ttttcaacag cggtatcgca attgggggtta gtgtcagtca caagctgatt 480

gacggccgta caagcgattg ctttcttaaa agttgggtgtg cagtctttcg tggcagccgc 540

gacaagatta tccatcccaa cttgtcacag gccgcgttgc tttttccccc gcgtgatgac	600
ctgcccga aa agtacgctcg ccaaatggaa ggcttgtggt ttgtcggaaa gaaagttgcg	660
acccgccgtt ttgtatattg agctaaggct attagtgtaa ttcaagacga ggcaaagagt	720
gagagtgtac ctaaaccctc acgtgtgcaa gctgtaacga gctttctttg gaagcactta	780
attgccacca gccgtgcatt gacgagcggg accacgtcaa cacgcttgag tatcgccacc	840
caggttggtca atatccgctc gcgtcgtaac atggagactg tgtgggacaa cgcaattgga	900
aaccttatct ggttcgcccc agcaatcctt gaactgagtc acacgacctt ggaaattagt	960
gatcttaagc tgtgtgattt gggttaacct ctgaatggta gtgtaaaaca gtgcaacggt	1020
gactactttg aaacatttat ggggaaggaa ggggtatgggt ccatgtgcga atatcttgat	1080
ttccagcgca ctatgtcgtc tatggagcct gcacctgaga tctacttggt cacgtcgtgg	1140
actaatttct tcaatcaatt agattttggg tggggccgca cgtcttggtat tggagttgca	1200
ggtaagatcg aatccgcatt ttgtaacttg actacattag ttcctacacc ctgtgacact	1260
gggattgagg cgtgggtcaa tttggaagaa gagaagatgg caatgttgga acaggaccct	1320
caattcttag cactggcttc tccgaagaca cttatctccc gttac	1365

<210> 5
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LIAAT (lavender) amino acid sequence

<400> 5

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

Pro	Gln	Ala	Phe	Lys	Asn	His	Lys	Leu	Ser	Tyr	Leu	Asp	Gln	Ile	Gln
		20					25						30		

Ala	Pro	Ile	Tyr	Ile	Pro	Leu	Leu	Phe	Phe	Tyr	Lys	Asn	Glu	Glu	Ser
		35				40						45			

Lys Tyr Pro Asp Gln Ile Ser Gln Arg Phe Lys Gln Ser Leu Ser Glu
50 55 60

Ile Leu Thr Ile Phe Tyr Pro Leu Ala Gly Thr Met Arg His Asn Ser
65 70 75 80

Phe Val Asp Cys Asn Asp Arg Gly Val Glu Phe Val Glu Val Arg Val
85 90 95

His Ala Arg Leu Ala Gln Phe Ile Gln Asp Pro Lys Met Glu Glu Leu
100 105 110

Lys Gln Leu Ile Pro Val Asp Cys Ile Ser His Thr Asp Asp Asp Phe
115 120 125

Leu Leu Leu Val Lys Ile Ser Tyr Phe Asp Cys Gly Glu Val Val Val
130 135 140

Gly Val Cys Met Ser His Lys Ile Gly Asp Gly Ile Ser Leu Ala Ala
145 150 155 160

Phe Met Asn Ala Trp Ala Ala Thr Cys Arg Gly Glu Ser Ser Ser Glu
165 170 175

Ile Ile His Pro Ser Phe Asp Leu Ala Leu His Phe Pro Pro Lys Asp
180 185 190

His Leu Ser Ser Ala Ser Ser Phe Arg Val Ala Ile Ala Gln Glu Asn
195 200 205

Ile Met Thr Lys Arg Leu Val Phe Asp Arg Glu Lys Leu Glu Lys Leu
210 215 220

Arg Lys Arg Ile Ala Ala Ser Ser Asp Gly Val Arg Asp Pro Ser Arg
225 230 235 240

Val Glu Ala Val Ser Val Phe Ile Trp Lys Ser Leu Ile Glu Ala His
245 250 255

Lys Ala Glu Ser His Met Thr Glu Thr Pro Ala Val Ser Ile Ala Ser
260 265 270

His Ala Val Asn Leu Arg Pro Arg Thr Val Pro Gln Met Asp Gln Thr
275 280 285

Phe Gly Asn Cys Tyr Ala Pro Ala Ser Ala Val Val Ser Trp Asp Glu
290 295 300

Asp Tyr Val His His Ser Arg Leu Arg Ala Ala Leu Arg Glu Ile Asp
305 310 315 320

Asp Asp Tyr Ile Asn Lys Val Leu Lys Ala Asp Asn Asn Tyr Leu Thr
325 330 335

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

Ser Trp Trp Arg Phe Pro Val Tyr Lys Val Asp Phe Gly Trp Gly Lys
355 360 365

Pro Val Trp Val Ser Thr Thr Thr Ile Gln Tyr Met Asn Leu Ile Ile
370 375 380

Phe Thr Ser Thr Pro Ser Glu Asp Gly Ile Glu Ala Trp Val Thr Thr
385 390 395 400

Thr His Asn Phe Phe Gln Val Leu Gln Ala Asn Tyr Asn Lys Leu Asp
405 410 415

Thr

<210> 6
<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> liaat (lavender) nucleotide sequence

<400> 6

atggctatga tcatcacaaa acagattcctt cgtccttcgt cgccaacgcc ccaagccttc	60
aagaatcata aattatctta tcttgaccag atccaggctc ccatctatat ccccttgctg	120
tttttttaca aaaacgaaga gagcaagtac cctgaccaaa ttagccaacg tttcaaacia	180
tctctgtccg aaattttgac tatcttctat ccacttgagg gtaccatgag tcacaacagc	240
ttcgtggatt gtaatgaccg tggagtcgaa tttgtggagg tacgctgca cgctcgcttg	300
gctcagttta ttcaggaccc caaaatggag gagctgaagc agcttatccc cgtggattgc	360
atctcccaca cggacgacga ttttctgctt cttgtgaaaa tttcatactt cgattgagg	420
gaagtgggtg taggtgtttg catgtccac aaaattgggt atggaatcag tcttgagg	480
tttatgaacg cgtgggcagc aacgtgtgc ggggagctta gcagcgagat tattcatcca	540
tcattcgatt tagcattaca ctttccacct aaggaccact tgcctcagc atcgtcttc	600
cgtgtagcta tcgctcagga gaacattatg acgaaacgtt tggttttcga tcgcgagaag	660
cttgaaaagt tacgcaagcg tattgcggca agctcggatg gtgtacgtga cccatcacgc	720
gtagaagcgg taagcgtctt tatttggaag agcttgatcg aggctcataa agcagaatcc	780
cacatgaccg aaacaccggc ggtcagtatc gcgtctcacg cagtaaattt acgtccgcgt	840
acagtccttc aaatggatca aacgtttggg aactgctatg cacctgccag cgagtggtta	900
tcattgggacg aagattatgt gcaccattca cgtttacgag ccgctctgag cgaaattgat	960
gacgactata tcaacaaggt tctgaaagca gacaataatt atttaactca agatcaaatt	1020
ggcgacttat tcaaaccgga gaatagtgtt ttatctagtt ggtggcggtt tccggtctat	1080
aaagtggact ttgggtgggg aaaaccggtt tgggtatcaa caaccactat tcagtacatg	1140
aacttaatta tctttactag caccctgtct gaagacggta ttgaagcgtg ggtaaccacc	1200
actcacaact tttttcaggt tttgcaggca aactataaca aactggacac t	1251

<210> 7
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> AAAT amino acid sequence

<400> 7

Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
1 5 10 15

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
20 25 30

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
35 40 45

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
50 55 60

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
65 70 75 80

Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
85 90 95

Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
100 105 110

Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu
115 120 125

Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu
130 135 140

Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg
145 150 155 160

Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr
165 170 175

Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro
180 185 190

Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr
195 200 205

Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser
210 215 220

Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe
225 230 235 240

Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu
245 250 255

Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys
260 265 270

Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val
275 280 285

Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro
290 295 300

Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys
305 310 315 320

Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val
325 330 335

Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala
340 345 350

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

Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn
370 375 380

Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp
385 390 395 400

Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile
405 410 415

Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln
420 425 430

Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn
435 440 445

Leu Arg Ser Thr Ser Gln
450

<210> 8
<211> 1362
<212> DNA
<213> Artificial Sequence

<220>
<223> aaat nucleotide sequence

<400> 8
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caaatcccca ttattatgtg ctacaaggat aatccctcct tgaataaaaa tcgcaaccgc 180
gtaaaagcca ttcgcgaagc cttttcgcg gcacttgtgt attattatcc gttggctgga 240
cgtttgcgtg aggggtccaaa tcgcaaacctt gtcgtagatt gtaatggaga agggattctt 300
ttcgtggaag ccagtgtga cgtaaccttg gaacagttag gagataaaat tttgccccct 360
tgtccgcttt tagaggagtt tctgtataat tttccgggaa gcgacgggtat tattgattgt 420
ccacttctgt tgattcaagt tacttgcttg acgtgtgggg gatttatctt agctttgcgt 480

ttaaatacaca cgatgtgcga cgccgctggc cttttgttat ttcttactgc gattgctgaa	540
atggctcgtg gagcccacgc cccctccatt cttcctgtct gggaacgcga attgctgttt	600
gcgcgcgacc ctccacgtat tacttgtgcc cgtcatgagt acgaagacgt aattgggcac	660
tctgacgggtt cctatgcatc cagcaaccaa agtaacatgg tccaacgcag cttctatttc	720
ggtgcaaagg aaatgcgtgt cctgcgcaag cagattcccc cgacttaat ctctacctgc	780
tccaccttcg atcttattac cgctgtctg tggaaatgcc gcactctggc acttaacatt	840
aatcccaagg aagccgttcg tgtatcctgt attgttaatg ctcgtggcaa acacaacaac	900
gtccgcttac cgctgggcta ttatggaaac gcattcgcct tcccggcggc catttccaag	960
gctgaacctc tgtgtaaaaa tccgcttggg tatgcgttag aacttgtcaa aaaggccaaa	1020
gcgaccatga atgaggagta tcttcgtagt gtagcggacc ttttagtcct tcgcggtcgc	1080
cctcagtatt catcaactgg ttcctactta atcgtttctg acaacactcg tgtcggtttt	1140
ggcgacgtta actttggctg gggacagccg gtatttgccg gccccgtgaa ggctctggat	1200
ctgattagct tttacgttca gcataaaaat aataccgagg atggcatctt ggtgccgatg	1260
tgtctttcaa gtagtgccat ggagcgtttt caacaggaac tggagcgtat caccagagag	1320
cccaaggaag acatttgtaa caacctgcgt agtactagtc aa	1362

<210> 9
 <211> 525
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ATF1 (yeast) amino acid sequence

<400> 9

Met	Asn	Glu	Ile	Asp	Glu	Lys	Asn	Gln	Ala	Pro	Val	Gln	Gln	Glu	Cys
1				5				10						15	

Leu	Lys	Glu	Met	Ile	Gln	Asn	Gly	His	Ala	Arg	Arg	Met	Gly	Ser	Val
			20					25					30		

Glu Asp Leu Tyr Val Ala Leu Asn Arg Gln Asn Leu Tyr Arg Asn Phe
35 40 45

Cys Thr Tyr Gly Glu Leu Ser Asp Tyr Cys Thr Arg Asp Gln Leu Thr
50 55 60

Leu Ala Leu Arg Glu Ile Cys Leu Lys Asn Pro Thr Leu Leu His Ile
65 70 75 80

Val Leu Pro Thr Arg Trp Pro Asn His Glu Asn Tyr Tyr Arg Ser Ser
85 90 95

Glu Tyr Tyr Ser Arg Pro His Pro Val His Asp Tyr Ile Ser Val Leu
100 105 110

Gln Glu Leu Lys Leu Ser Gly Val Val Leu Asn Glu Gln Pro Glu Tyr
115 120 125

Ser Ala Val Met Lys Gln Ile Leu Glu Glu Phe Lys Asn Ser Lys Gly
130 135 140

Ser Tyr Thr Ala Lys Ile Phe Lys Leu Thr Thr Thr Leu Thr Ile Pro
145 150 155 160

Tyr Phe Gly Pro Thr Gly Pro Ser Trp Arg Leu Ile Cys Leu Pro Glu
165 170 175

Glu His Thr Glu Lys Trp Lys Lys Phe Ile Phe Val Ser Asn His Cys
180 185 190

Met Ser Asp Gly Arg Ser Ser Ile His Phe Phe His Asp Leu Arg Asp
195 200 205

Glu Leu Asn Asn Ile Lys Thr Pro Pro Lys Lys Leu Asp Tyr Ile Phe
210 215 220

Lys Tyr Glu Glu Asp Tyr Gln Leu Leu Arg Lys Leu Pro Glu Pro Ile
225 230 235 240

Glu Lys Val Ile Asp Phe Arg Pro Pro Tyr Leu Phe Ile Pro Lys Ser
245 250 255

Leu Leu Ser Gly Phe Ile Tyr Asn His Leu Arg Phe Ser Ser Lys Gly
260 265 270

Val Cys Met Arg Met Asp Asp Val Glu Lys Thr Asp Asp Val Val Thr
275 280 285

Glu Ile Ile Asn Ile Ser Pro Thr Glu Phe Gln Ala Ile Lys Ala Asn
290 295 300

Ile Lys Ser Asn Ile Gln Gly Lys Cys Thr Ile Thr Pro Phe Leu His
305 310 315 320

Val Cys Trp Phe Val Ser Leu His Lys Trp Gly Lys Phe Phe Lys Pro
325 330 335

Leu Asn Phe Glu Trp Leu Thr Asp Ile Phe Ile Pro Ala Asp Cys Arg
340 345 350

Ser Gln Leu Pro Asp Asp Asp Glu Met Arg Gln Met Tyr Arg Tyr Gly
355 360 365

Ala Asn Val Gly Phe Ile Asp Phe Thr Pro Trp Ile Ser Glu Phe Asp
370 375 380

Met Asn Asp Asn Lys Glu Asn Phe Trp Pro Leu Ile Glu His Tyr His
385 390 395 400

Glu Val Ile Ser Glu Ala Leu Arg Asn Lys Lys His Leu His Gly Leu
405 410 415

Gly Phe Asn Ile Gln Gly Phe Val Gln Lys Tyr Val Asn Ile Asp Lys
420 425 430

Val Met Cys Asp Arg Ala Ile Gly Lys Arg Arg Gly Gly Thr Leu Leu
435 440 445

Ser Asn Val Gly Leu Phe Asn Gln Leu Glu Glu Pro Asp Ala Lys Tyr
450 455 460

Ser Ile Cys Asp Leu Ala Phe Gly Gln Phe Gln Gly Ser Trp His Gln
465 470 475 480

Ala Phe Ser Leu Gly Val Cys Ser Thr Asn Val Lys Gly Met Asn Ile
485 490 495

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

Glu Leu Cys Ser Ile Tyr Lys Ala Leu Leu Leu Gly Pro
515 520 525

<210> 10
<211> 1575
<212> DNA
<213> Artificial Sequence

<220>
<223> Aft1 (yeast) nucleotide sequence

<400> 10
atgaatgaaa tcgatgagaa aaatcaggcc cccgtgcaac aagaatgcct gaaagagatg 60
attcagaatg ggcatgctcg gcgtatggga tctgttgaag atctgtatgt tgctctcaac 120
agacaaaact tatatcgaaa cttctgcaca tatggagaat tgagtgatta ctgtactagg 180
gatcagctca cattagcttt gagggaaatc tgcctgaaaa atccaactct ttacatatt 240
gttctaccaa caagatggcc aaatcatgaa aattattatc gcagttccga atactattca 300
cggccacatc cagtgcata ttatatattca gtattacaag aattgaaact gagtggtgtg 360
gttctcaatg aacaacctga gtacagtgc gtaatgaagc aaatattaga agaattcaaa 420
aatagtaagg gttcctatac tgcaaaaatt tttaaactta ctaccacttt gactattcct 480
tactttggac caacaggacc gagttggcgg ctaatttgtc ttccagaaga gcacacagaa 540

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aagtggaaaa aatttatctt tgtatctaata cattgcatgt ctgatggtcg gtcttcgatc      600
cacttttttc atgatttaag agacgaatta aataatatta aaactccacc aaaaaaatta      660
gattacattt tcaagtacga ggaggattac caattattga ggaaacttcc agaaccgatc      720
gaaaagggtga tagacttttag accaccgtac ttgtttattc cgaagtcact tctttcgggt      780
ttcatctaca atcatttgag attttcttca aaagggtgtct gtatgagaat ggatgatgtg      840
gaaaaaacgg atgatgttgt caccgagatc atcaatattt caccaacaga atttcaagcg      900
attaaagcaa atattaaatc aaatatccaa ggtaagtgtg ctatcactcc gtttttacat      960
gtttgttgggt ttgtatctct tcataaatgg ggtaaatttt tcaaaccatt gaacttcgaa     1020
tggcttacgg atatttttat ccccgcatat tgccgctcac aactaccaga tgatgatgaa     1080
atgagacaga tgtacagata tggcgctaac gttggattta ttgacttcac cccctggata     1140
agcgaatttg acatgaatga taacaaagaa aatttttggc cacttattga gcactaccat     1200
gaagtaattt cggaagcttt aagaaataaa aagcatctcc atggcttagg gttcaatata     1260
caaggcttcg ttcaaaaata tgtgaacatt gacaaggtaa tgtgcatcg tgccatcggg      1320
aaaagacgag gaggtacatt gttaagcaat gtaggtctgt ttaatcagtt agaggagccc      1380
gatgccaaat attctatatg cgatttggca tttggccaat ttcaaggatc ctggcaccaa      1440
gcattttcct tgggtgtttg ttcgactaat gtaaagggga tgaatattgt tgttgcttca      1500
acaaagaatg ttgttggtag tcaagaatct ctcgaagagc tttgctccat ttacaaagct      1560
ctccttttag gccct                                     1575

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<210> 11
<211> 220
<212> PRT
<213> Artificial Sequence

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<220>
<223> ATOD (E coli) amino acid sequence

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<400> 11

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Met Lys Thr Lys Leu Met Thr Leu Gln Asp Ala Thr Gly Phe Phe Arg
1           5           10          15

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Asp Gly Met Thr Ile Met Val Gly Gly Phe Met Gly Ile Gly Thr Pro
20 25 30

Ser Arg Leu Val Glu Ala Leu Leu Glu Ser Gly Val Arg Asp Leu Thr
35 40 45

Leu Ile Ala Asn Asp Thr Ala Phe Val Asp Thr Gly Ile Gly Pro Leu
50 55 60

Ile Val Asn Gly Arg Val Arg Lys Val Ile Ala Ser His Ile Gly Thr
65 70 75 80

Asn Pro Glu Thr Gly Arg Arg Met Ile Ser Gly Glu Met Asp Val Val
85 90 95

Leu Val Pro Gln Gly Thr Leu Ile Glu Gln Ile Arg Cys Gly Gly Ala
100 105 110

Gly Leu Gly Gly Phe Leu Thr Pro Thr Gly Val Gly Thr Val Val Glu
115 120 125

Glu Gly Lys Gln Thr Leu Thr Leu Asp Gly Lys Thr Trp Leu Leu Glu
130 135 140

Arg Pro Leu Arg Ala Asp Leu Ala Leu Ile Arg Ala His Arg Cys Asp
145 150 155 160

Thr Leu Gly Asn Leu Thr Tyr Gln Leu Ser Ala Arg Asn Phe Asn Pro
165 170 175

Leu Ile Ala Leu Ala Ala Asp Ile Thr Leu Val Glu Pro Asp Glu Leu
180 185 190

Val Glu Thr Gly Glu Leu Gln Pro Asp His Ile Val Thr Pro Gly Ala
195 200 205

Val Ile Asp His Ile Ile Val Ser Gln Glu Ser Lys
 210 215 220

<210> 12
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> atoD (E. coli) nucleotide sequence

<400> 12
 atgaaaacaa aattgatgac attacaagac gccaccggct tctttcgtga cggcatgacc 60
 atcatgggtgg gcggatttat ggggattggc actccatccc gcctggttga agcattactg 120
 gaatctgggtg ttcgcgacct gacattgata gccaatgata ccgcgtttgt tgataccggc 180
 atcgggtccgc tcatcgtcaa tggtcgagtc cgcaaagtga ttgcttcaca tatcggcacc 240
 aacccggaaa caggtcggcg catgatatct ggtgagatgg acgtcgttct ggtgccgcaa 300
 ggtacgctaa tcgagcaa at tcgctgtggg ggagctggac ttggtggttt tctcacccca 360
 acgggtgtcg gcaccgtcgt agaggaaggc aaacagacac tgacactcga cggtaaaacc 420
 tggctgctcg aacgcccact gcgcgccgac ctggcgctaa ttcgcgctca tcgttgcgac 480
 acacttggca acctgacct tcaacttagc gcccgcaact ttaaccccct gatagccctt 540
 gcggctgata tcacgtgggt agagccagat gaactggctg aaaccggcga gctgcaacct 600
 gaccatattg tcacccttgg tgccgttatc gaccacatca tcgtttcaca ggagagcaaa 660

<210> 13
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ATOA (E. coli) amino acid sequence

<400> 13

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

Asp Gly Asp Ile Val Asn Leu Gly Ile Gly Leu Pro Thr Met Val Ala
20 25 30

Asn Tyr Leu Pro Glu Gly Ile His Ile Thr Leu Gln Ser Glu Asn Gly
35 40 45

Phe Leu Gly Leu Gly Pro Val Thr Thr Ala His Pro Asp Leu Val Asn
50 55 60

Ala Gly Gly Gln Pro Cys Gly Val Leu Pro Gly Ala Ala Met Phe Asp
65 70 75 80

Ser Ala Met Ser Phe Ala Leu Ile Arg Gly Gly His Ile Asp Ala Cys
85 90 95

Val Leu Gly Gly Leu Gln Val Asp Glu Glu Ala Asn Leu Ala Asn Trp
100 105 110

Val Val Pro Gly Lys Met Val Pro Gly Met Gly Gly Ala Met Asp Leu
115 120 125

Val Thr Gly Ser Arg Lys Val Ile Ile Ala Met Glu His Cys Ala Lys
130 135 140

Asp Gly Ser Ala Lys Ile Leu Arg Arg Cys Thr Met Pro Leu Thr Ala
145 150 155 160

Gln His Ala Val His Met Leu Val Thr Glu Leu Ala Val Phe Arg Phe
165 170 175

Ile Asp Gly Lys Met Trp Leu Thr Glu Ile Ala Asp Gly Cys Asp Leu
180 185 190

Ala Thr Val Arg Ala Lys Thr Glu Ala Arg Phe Glu Val Ala Ala Asp
195 200 205

Leu Asn Thr Gln Arg Gly Asp Leu
210 215

<210> 14
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> atoA (E. coli) nucleotide sequence

<400> 14
atggatgcga aacaacgtat tgcgcgccgt gtggcgcaag agcttcgtga tggtgacatc 60
gttaacttag ggatcggttt acccacaatg gtcgccaatt atttaccgga gggattcat 120
atcactctgc aatcggaaaa cggcttcctc ggtttaggcc cggtcacgac agcgcaccca 180
gatctggtga acgctggcgg gcaaccgtgc ggtgttttac ccggtgcagc catgtttgat 240
agcgccatgt catttgcgct aatccgtggc ggtcatattg atgcctgcgt gctcggcggg 300
ttgcaagtag acgaagaagc aaacctcgcg aactgggtag tgcctgggaa aatggtgccc 360
ggatatgggtg gcgcgatgga tctggtgacc gggtcgcgca aagtgatcat cgccatggaa 420
cattgcgcca aagatggttc agcaaaaatt ttgcgccgct gcaccatgcc actcactgcg 480
caacatgcgg tgcatatgct ggttactgaa ctggctgtct ttcgttttat tgacggcaaa 540
atgtggctca ccgaaattgc cgacgggtgt gatttagcca ccgtgcgtgc caaacagaa 600
gctcggtttg aagtcgccgc cgatctgaat acgcaacggg gtgattta 648

<210> 15
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> ctfa (Clostridium acetobutylicum DSM 1731) amino acid sequence

<400> 15

Met Asn Ser Lys Ile Ile Arg Phe Glu Asn Leu Arg Ser Phe Phe Lys
1 5 10 15

Asp Gly Met Thr Ile Met Ile Gly Gly Phe Leu Asn Cys Gly Thr Pro
20 25 30

Thr Lys Leu Ile Asp Phe Leu Val Asn Leu Asn Ile Lys Asn Leu Thr
35 40 45

Ile Ile Ser Asn Asp Thr Cys Tyr Pro Asn Thr Gly Ile Gly Lys Leu
50 55 60

Ile Ser Asn Asn Gln Val Lys Lys Leu Ile Ala Ser Tyr Ile Gly Ser
65 70 75 80

Asn Pro Asp Thr Gly Lys Lys Leu Phe Asn Asn Glu Leu Glu Val Glu
85 90 95

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

Gly Leu Gly Gly Val Leu Thr Lys Thr Gly Leu Gly Thr Leu Ile Glu
115 120 125

Lys Gly Lys Lys Lys Ile Ser Ile Asn Gly Thr Glu Tyr Leu Leu Glu
130 135 140

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

Glu Ala Gly Asn Thr Phe Tyr Lys Gly Thr Thr Lys Asn Phe Asn Pro
165 170 175

Tyr Met Ala Met Ala Ala Lys Thr Val Ile Val Glu Ala Glu Asn Leu
180 185 190

Val Ser Cys Glu Lys Leu Glu Lys Glu Lys Ala Met Thr Pro Gly Val
195 200 205

Leu Ile Asn Tyr Ile Val Lys Glu Pro Ala
210 215

<210> 16
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> ctfA (Clostridium acetobutylicum DSM 1731) nucleotide sequence

<400> 16
atgaactcta aaataattag atttgaaaat ttaaggtcat tcttttaaaga tgggatgaca 60
attatgattg gaggtttttt aaactgtggc actccaacca aattaattga ttttttagtt 120
aatttaaata taaagaattt aacgattata agtaatgata catgttatcc taatacaggt 180
attggtaagt taatatcaaa taatcaagta aaaaagctta ttgcttcata tataggcagc 240
aaccagata ctggcaaaaa actttttaat aatgaacttg aagtagagct ctctcccaa 300
ggaactctag tggaagaat acgtgcaggc ggatctggct taggtgggtg actaactaaa 360
acaggtttag gaactttgat tgaaaaagga aagaaaaaaa tatctataaa tggaacggaa 420
tatttgttag agctacctt tacagccgat gtagcattaa ttaaaggtag tattgtagat 480
gaggccggaa acaccttcta taaaggtact actaaaaact ttaatcccta tatggcaatg 540
gcagctaaaa ccgtaatagt tgaagctgaa aatttagtta gctgtgaaaa actagaaaag 600
gaaaaagcaa tgacccccgg agttcttata aattatatag taaaggagcc tgca 654

<210> 17
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> CTFB (Clostridium acetobutylicum DSM 1731) amino acid sequence

<400> 17

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

Ala Arg Glu Leu Lys Asn Gly Gln Leu Val Asn Leu Gly Val Gly Leu
20 25 30

Pro Thr Met Val Ala Asp Tyr Ile Pro Lys Asn Phe Lys Ile Thr Phe
35 40 45

Gln Ser Glu Asn Gly Ile Val Gly Met Gly Ala Ser Pro Lys Ile Asn
50 55 60

Glu Ala Asp Lys Asp Val Val Asn Ala Gly Gly Asp Tyr Thr Thr Val
65 70 75 80

Leu Pro Asp Gly Thr Phe Phe Asp Ser Ser Val Ser Phe Ser Leu Ile
85 90 95

Arg Gly Gly His Val Asp Val Thr Val Leu Gly Ala Leu Gln Val Asp
100 105 110

Glu Lys Gly Asn Ile Ala Asn Trp Ile Val Pro Gly Lys Met Leu Ser
115 120 125

Gly Met Gly Gly Ala Met Asp Leu Val Asn Gly Ala Lys Lys Val Ile
130 135 140

Ile Ala Met Arg His Thr Asn Lys Gly Gln Pro Lys Ile Leu Lys Lys
145 150 155 160

Cys Thr Leu Pro Leu Thr Ala Lys Ser Gln Ala Asn Leu Ile Val Thr
165 170 175

Glu Leu Gly Val Ile Glu Val Ile Asn Asp Gly Leu Leu Leu Thr Glu
180 185 190

Ile Asn Lys Asn Thr Thr Ile Asp Glu Ile Arg Ser Leu Thr Ala Ala
195 200 205

Asp Leu Leu Ile Ser Asn Glu Leu Arg Pro Met Ala Val
210 215 220

<210> 18

<211> 663

<212> DNA
<213> Artificial Sequence

<220>
<223> ctFB (Clostridium acetobutylicum DSM 1731) nucleotide sequence

<400> 18
atgattaatg ataaaaacct agcgaaagaa ataatagcca aaagagttgc aagagaatta 60
aaaaatggtc aacttgtaaa cttaggtgta ggtcttccta ccatggttgc agattatata 120
ccaaaaaatt tcaaaattac tttccaatca gaaaacggaa tagttggaat gggcgctagt 180
cctaaaataa atgaggcaga taaagatgta gtaaatgcag gaggagacta tacaacagta 240
cttcctgacg gcacatTTTT cgatagctca gtttcgtttt cactaatccg tgggtggtcac 300
gtagatgtta ctgttttagg ggctctccag gtagatgaaa agggtaatat agccaattgg 360
attgttcctg gaaaaatgct ctctgggatg ggtggagcta tggatttagt aaatggagct 420
aagaaagtaa taattgcaat gagacataca aataaaggtc aacctaataat tttaaaaaaa 480
tgtacacttc ccctcacggc aaagtctcaa gcaaatctaa ttgtaacaga acttggagta 540
attgagggtta ttaatgatgg tttacttctc actgaaatta ataaaaacac aaccattgat 600
gaaataaggt cttaaactgc tgcagattta ctcatatcca atgaacttag acccatggct 660
gtt 663

<210> 19
<211> 301
<212> PRT
<213> Artificial Sequence

<220>
<223> PTB (Clostridium acetobutylicum ATCC 824) amino acid sequence

<400> 19

Met Ile Lys Ser Phe Asn Glu Ile Ile Met Lys Val Lys Ser Lys Glu
1 5 10 15

Met Lys Lys Val Ala Val Ala Val Ala Gln Asp Glu Pro Val Leu Glu
20 25 30

Ala Val Arg Asp Ala Lys Lys Asn Gly Ile Ala Asp Ala Ile Leu Val
35 40 45

Gly Asp His Asp Glu Ile Val Ser Ile Ala Leu Lys Ile Gly Met Asp
50 55 60

Val Asn Asp Phe Glu Ile Val Asn Glu Pro Asn Val Lys Lys Ala Ala
65 70 75 80

Leu Lys Ala Val Glu Leu Val Ser Thr Gly Lys Ala Asp Met Val Met
85 90 95

Lys Gly Leu Val Asn Thr Ala Thr Phe Leu Arg Ser Val Leu Asn Lys
100 105 110

Glu Val Gly Leu Arg Thr Gly Lys Thr Met Ser His Val Ala Val Phe
115 120 125

Glu Thr Glu Lys Phe Asp Arg Leu Leu Phe Leu Thr Asp Val Ala Phe
130 135 140

Asn Thr Tyr Pro Glu Leu Lys Glu Lys Ile Asp Ile Val Asn Asn Ser
145 150 155 160

Val Lys Val Ala His Ala Ile Gly Ile Glu Asn Pro Lys Val Ala Pro
165 170 175

Ile Cys Ala Val Glu Val Ile Asn Pro Lys Met Pro Ser Thr Leu Asp
180 185 190

Ala Ala Met Leu Ser Lys Met Ser Asp Arg Gly Gln Ile Lys Gly Cys
195 200 205

Val Val Asp Gly Pro Leu Ala Leu Asp Ile Ala Leu Ser Glu Glu Ala
210 215 220

Ala His His Lys Gly Val Thr Gly Glu Val Ala Gly Lys Ala Asp Ile
225 230 235 240

Phe Leu Met Pro Asn Ile Glu Thr Gly Asn Val Met Tyr Lys Thr Leu
245 250 255

Thr Tyr Thr Thr Asp Ser Lys Asn Gly Gly Ile Leu Val Gly Thr Ser
260 265 270

Ala Pro Val Val Leu Thr Ser Arg Ala Asp Ser His Glu Thr Lys Met
275 280 285

Asn Ser Ile Ala Leu Ala Ala Leu Val Ala Gly Asn Lys
290 295 300

<210> 20

<211> 903

<212> DNA

<213> Artificial Sequence

<220>

<223> ptb (Clostridium acetobutylicum ATCC 824) nucleotide sequence

<400> 20

atgattaaga gttttaatga aattatcatg aaggtaaaga gcaaagaaat gaaaaaagtt 60

gctgttgctg tagcacaaga cgagccagta cttgaagcag taagagatgc taagaaaaat 120

ggtattgcag atgctattct tgttggagac catgacgaaa tcgtgtcaat cgcgcttaaa 180

ataggaatgg atgtaaatga ttttgaaata gtaaacgagc ctaacgttaa gaaagctgct 240

ttaaaggcag tagagcttgt atcaactgga aaagctgata tggtaatgaa gggacttgta 300

aatacagcaa ctttcttaag atctgtatta aacaaagaag ttggacttag aacaggaaaa 360

actatgtctc acgttgcagt atttgaaact gagaaatttg atagactatt atttttaaca 420

gatgttgctt tcaatactta tcctgaatta aaggaaaaaa ttgatatagt aaacaattca 480

gttaagggttg cacatgcaat aggaattgaa aatccaaagg ttgctccaat ttgtgcagtt 540

gaggttataa accctaaaat gccatcaaca cttgatgcag caatgctttc aaaaatgagt 600

gacagaggac aaattaaagg ttgtgtagtt gacggacctt tagcacttga tatagcttta 660

tcagaagaag cagcacatca taaggaggta acaggagaag ttgctggaaa agctgatatc 720

ttcttaatgc caaacataga aacaggaaat gtaatgtata agactttaac atatacaact	780
gattcaaaaa atggaggaat cttagttgga acttctgcac cagttgtttt aacttcaaga	840
gctgacagcc atgaaacaaa aatgaactct atagcacttg cagctttagt tgcaggcaat	900
aaa	903

<210> 21
 <211> 355
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BUK (Clostridium acetobutylicum ATCC 824) amino acid sequence

<400> 21

Met	Tyr	Arg	Leu	Leu	Ile	Ile	Asn	Pro	Gly	Ser	Thr	Ser	Thr	Lys	Ile
1				5					10					15	

Gly	Ile	Tyr	Asp	Asp	Glu	Lys	Glu	Ile	Phe	Glu	Lys	Thr	Leu	Arg	His
			20					25						30	

Ser	Ala	Glu	Glu	Ile	Glu	Lys	Tyr	Asn	Thr	Ile	Phe	Asp	Gln	Phe	Gln
		35						40					45		

Phe	Arg	Lys	Asn	Val	Ile	Leu	Asp	Ala	Leu	Lys	Glu	Ala	Asn	Ile	Glu
	50					55					60				

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

Ile	Val	Ser	Gly	Thr	Tyr	Ala	Val	Asn	Gln	Lys	Met	Leu	Glu	Asp	Leu
				85					90					95	

Lys	Val	Gly	Val	Gln	Gly	Gln	His	Ala	Ser	Asn	Leu	Gly	Gly	Ile	Ile
			100					105						110	

Ala	Asn	Glu	Ile	Ala	Lys	Glu	Ile	Asn	Val	Pro	Ala	Tyr	Ile	Val	Asp
		115						120				125			

Pro Val Val Val Asp Glu Leu Asp Glu Val Ser Arg Ile Ser Gly Met
130 135 140

Ala Asp Ile Pro Arg Lys Ser Ile Phe His Ala Leu Asn Gln Lys Ala
145 150 155 160

Val Ala Arg Arg Tyr Ala Lys Glu Val Gly Lys Lys Tyr Glu Asp Leu
165 170 175

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

Lys Asp Gly Arg Val Ile Glu Val Asn Asn Thr Leu Asp Gly Glu Gly
195 200 205

Pro Phe Ser Pro Glu Arg Ser Gly Gly Val Pro Ile Gly Asp Leu Val
210 215 220

Arg Leu Cys Phe Ser Asn Lys Tyr Thr Tyr Glu Glu Val Met Lys Lys
225 230 235 240

Ile Asn Gly Lys Gly Gly Val Val Ser Tyr Leu Asn Thr Ile Asp Phe
245 250 255

Lys Ala Val Val Asp Lys Ala Leu Glu Gly Asp Lys Lys Cys Ala Leu
260 265 270

Ile Tyr Glu Ala Phe Thr Phe Gln Val Ala Lys Glu Ile Gly Lys Cys
275 280 285

Ser Thr Val Leu Lys Gly Asn Val Asp Ala Ile Ile Leu Thr Gly Gly
290 295 300

Ile Ala Tyr Asn Glu His Val Cys Asn Ala Ile Glu Asp Arg Val Lys
305 310 315 320

Phe Ile Ala Pro Val Val Arg Tyr Gly Gly Glu Asp Glu Leu Leu Ala
325 330 335

Leu Ala Glu Gly Gly Leu Arg Val Leu Arg Gly Glu Glu Lys Ala Lys
340 345 350

Glu Tyr Lys
355

<210> 22
<211> 1065
<212> DNA
<213> Artificial Sequence

<220>
<223> buk (Clostridium acetobutylicum ATCC 824) nucleotide sequence

<400> 22
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aacactatat ttgatcaatt tcaattcaga aagaatgtaa ttttagatgc gttaaaagaa 180
gcaaacatag aagtaagttc tttaaagtct gtagttggaa gaggcggact cttaaagcca 240
atagtaagtg gaacttatgc agtaaataca aaaatgcttg aagaccttaa agtaggagtt 300
caaggtcagc atgctgcaaa tcttggtgga attattgcaa atgaaatagc aaaagaaata 360
aatgttccag catacatagt tgatccagtt gttgtggatg agcttgatga agtttcaaga 420
atatcaggaa tggctgacat tccaagaaaa agtatattcc atgcattaaa tcaaaaagca 480
gttgctagaa gatatgcaaa agaagttgga aaaaaatacg aagatcttaa tttaatcgta 540
gtccacatgg gtggaggtag tttagtaggt actcataaag atggtagagt aatagaagtt 600
aataatacac ttgatggaga aggtccattc tcaccagaaa gaagtggtagg agttccaata 660
ggagatcttg taagattgtg cttcagcaac aaatatactt atgaagaagt aatgaaaaag 720
ataaacggca aaggcggagt tgtagtttac ttaaatacta tcgattttta ggctgtagtt 780
gataaagctc ttgaaggaga taagaaatgt gcacttatat atgaagcttt cacattccag 840
gtagcaaaag agataggaaa atgttcaacc gttttaaaag gaaatgtaga tgcaataatc 900

ttaacaggcg gaattgcgta caacgagcat gtatgtaatg ccatagagga tagagtaaaa	960
ttcatagcac ctgtagttag atatggtgga gaagatgaac ttcttgact tgcagaaggt	1020
ggacttagag ttttaagagg agaagaaaaa gctaaggaat acaaa	1065

<210> 23
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ilov pTKEI-tLOV (Addgene)

<400> 23	
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tttgccctcag atggttttct cgagctaacc gaatacagcc gtgaagaagt tctgggtcgt	120
aatgctcgtt tcctgcaggg ccggaacc gaccaagcta cggttcagaa aattcgcgat	180
gcaattcgcg atcagcgtga gactaccgtt caattgatca actacaccaa aagcggtaaa	240
aaattttggga acctgttgca tcttcaaccg gtatttgacc aaaaaggcga gcttcagtac	300
tttatcggcg tgcagctgga tgttagtac catgtgagcg gtcaccatca ccatcaccat	360

<210> 24
 <211> 476
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> P_adhE

<400> 24	
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tgacaatacg ctttttgaca gcatttttca cctcctaact acttaaaatt gctatcattc	120
gttattgtta tctagttgtg caaaacatgc taatgtagcc accaaatcat actacaattt	180
attaactggt agctataatg gcgaaaagcg atgctgaaag gtgtcagctt tgcaaaaatt	240
tgatttggat cacgtaatca gtaccagaa gtgagtaatc ttgcttacgc cacctggaag	300
tgacgcatta gagataataa ctctaattgt taaactcttt tagtaaatca cagtgagtgt	360

gagcgcgagt aagcttttga ttttcatagg ttaagcaaat catcaccgca ctgactatac 420

tctcgtattc gagcagatga tttactaaaa aagttaaaca ttatcaggag agcatt 476

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Psaat-f

<400> 25

ggaaaagatt gaggtcagta t 21

<210> 26

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<212> DNA

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