

SEQUENCE LISTING

<110> DSM IP Assets BV
 Verwaal, René
 Damveld, Robbertus Antonius
 Sagt, Cornelis, Maria, Jacobus
 Wu, Liang

<120> Dicarboxylic acid production in eukaryotes

<130> 26347WO

<140> 26347WO
 <141> 2008-11-14

<160> 29

<170> PatentIn version 3.2

<210> 1
 <211> 538
 <212> PRT
 <213> Actinobacillus succinogenes

<400> 1

Met Thr Asp Leu Asn Lys Leu Val Lys Glu Leu Asn Asp Leu Gly Leu
 1 5 10 15

Thr Asp Val Lys Glu Ile Val Tyr Asn Pro Ser Tyr Glu Gln Leu Phe
 20 25 30

Glu Glu Glu Thr Lys Pro Gly Leu Glu Gly Phe Asp Lys Gly Thr Leu
 35 40 45

Thr Thr Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly Arg
 50 55 60

Ser Pro Lys Asp Lys Tyr Ile Val Cys Asp Glu Thr Thr Lys Asp Thr
 65 70 75 80

Val Trp Trp Asn Ser Glu Ala Ala Lys Asn Asp Asn Lys Pro Met Thr
 85 90 95

Gln Glu Thr Trp Lys Ser Leu Arg Glu Leu Val Ala Lys Gln Leu Ser
 100 105 110

Gly Lys Arg Leu Phe Val Val Glu Gly Tyr Cys Gly Ala Ser Glu Lys
 115 120 125

His Arg Ile Gly Val Arg Met Val Thr Glu Val Ala Trp Gln Ala His
 130 135 140

Phe Val Lys Asn Met Phe Ile Arg Pro Thr Asp Glu Glu Leu Lys Asn
 145 150 155 160

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

Asn Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala Phe Asn
 180 185 190

Ile Thr Glu Gly Ile Gln Leu Ile Gly Gly Thr Trp Tyr Gly Gly Glu
 195 200 205

Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Phe Leu Pro Leu Lys
 210 215 220

Gly Val Ala Ser Met His Cys Ser Ala Asn Val Gly Lys Asp Gly Asp
 225 230 235 240

Val Ala Ile Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr Leu Ser
 245 250 255

Thr Asp Pro Lys Arg Gln Leu Ile Gly Asp Asp Glu His Gly Trp Asp
 260 265 270

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

Asn Leu Ser Gln Glu Asn Glu Pro Asp Ile Tyr Gly Ala Ile Arg Arg
 290 295 300

Asp Ala Leu Leu Glu Asn Val Val Val Arg Ala Asp Gly Ser Val Asp
 305 310 315 320

Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr Pro Ile
 325 330 335

Tyr His Ile Asp Asn Ile Val Arg Pro Val Ser Lys Ala Gly His Ala
 340 345 350

Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu Pro Pro
 355 360 365

Val Ser Lys Leu Thr Pro Glu Gln Thr Glu Tyr Tyr Phe Leu Ser Gly
 370 375 380

Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Val Thr Glu Pro Thr
 385 390 395 400

Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu His Pro
 405 410 415

Ile Gln Tyr Ala Asp Val Leu Val Glu Arg Met Lys Ala Ser Gly Ala
 420 425 430

Glu Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys Arg Ile
 435 440 445

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

Ile Glu Lys Ala Glu Met Gly Glu Leu Pro Ile Phe Asn Leu Ala Ile
 465 470 475 480

Pro Lys Ala Leu Pro Gly Val Asp Pro Ala Ile Leu Asp Pro Arg Asp
 485 490 495

Thr Tyr Ala Asp Lys Ala Gln Trp Gln Val Lys Ala Glu Asp Leu Ala
 500 505 510

Asn Arg Phe Val Lys Asn Phe Val Lys Tyr Thr Ala Asn Pro Glu Ala
 515 520 525

Ala Lys Leu Val Gly Ala Gly Pro Lys Ala
 530 535

<210> 2
 <211> 1617
 <212> DNA
 <213> Actinobacillus succinogenes

<400> 2
 atgactgact taaacaaact cgtaaagaa cttaatgact tagggcttac cgatgttaag 60
 gaaattgtgt ataacccgag ttatgaacaa cttttcgagg aagaaaccaa accggggttg 120

```

gaggggtttcg ataaagggac gttaaccacg cttggcgcgg ttgccgtcga tacggggatt 180
tttaccggtc gttcaccgaa agataaatat atcgtttgcg atgaaactac gaaagacacc 240
gtttggtgga acagcgaagc ggcgaaaaac gataacaaac cgatgacgca agaaacttgg 300
aaaagtttga gagaattagt ggcgaaacaa ctttccggta aacgtttatt cgtggtagaa 360
ggttactgcg gcgccagtga aaaacaccgt atcgggtgtgc gtatggttac tgaagtggca 420
tggcaggcgc attttgtgaa aaacatgttt atccgaccga ccgatgaaga gttgaaaaat 480
ttcaaagcgg attttaccgt gttaaacggg gctaaatgta ctaatccgaa ctggaaagaa 540
caaggtttga acagtgaaaa ctttgtcgct ttcaatatta ccgaaggat tcaagcttatc 600
ggcggacttt ggtacggcgg tgaaatgaaa aaaggatatgt tctcaatgat gaactacttc 660
ctgccgttaa aagggtgtggc ttccatgcac tgttccgcca acgtaggtaa agacgggtgac 720
gtggctattt tcttcggttt atccggtacg ggtaaaacaa cgctttcgac cgatcctaaa 780
cgccaattaa tcggtgatga cgaacacggg tgggatgaat ccggcgtatt taactttgaa 840
ggcggttggt acgcgaaaaac cattaactta tctcaagaaa acgaaccgga tatttacggc 900
gcaatccgtc gtgacgcatt attagaaaac gtcgtggttc gtgcagacgg ttccgttgac 960
tttgacgacg gttcaaaaac agaaaatacc cgtgtttcat atccgattta ccacatcgac 1020
aacatcgttc gtccggtatc gaaagccggg catgcaacca aagtgatttt cttaccgcg 1080
gacgcattcg gcgtattgcc gccggtttca aaactgactc cggaacaaac cgaatactac 1140
ttcttatccg gctttactgc aaaattagcg ggtacggaac gcggcgtaac cgaaccgact 1200
ccgacattct cggcctgttt cgggtgcggc ttcttaagcc tgcattccgat tcaatatgcg 1260
gacgtgttgg tcgaacgcat gaaagcctcc ggtgcggaag cttatttggg gaacaccggg 1320
tggaacggca cgggtaaacg tatttcaatc aaagataccc gcggtattat cgatgcgatt 1380
ttggacgggt caatcgaaaa agcggaaatg ggcgaattgc caatctttaa tttagcgatt 1440
cctaaagcat taccgggtgt tgatcctgct attttggatc cgcgcgatac ttacgcagac 1500
aaagcgcaat ggcaagttaa agcgggaagat ttggcaaacc gtttcgtgaa aaactttgtg 1560
aaatatacgg cgaatccgga agcgggtaaa ttagttggcg ccggtccaaa agcataa 1617

```

```

<210> 3
<211> 538
<212> PRT
<213> Artificial sequence

```

<220>

<223> PEPCK A.s. wherein EGY is replaced with DAF

<400> 3

Met	Thr	Asp	Leu	Asn	Lys	Leu	Val	Lys	Glu	Leu	Asn	Asp	Leu	Gly	Leu
1				5					10					15	

Thr	Asp	Val	Lys	Glu	Ile	Val	Tyr	Asn	Pro	Ser	Tyr	Glu	Gln	Leu	Phe
			20					25					30		

Glu	Glu	Glu	Thr	Lys	Pro	Gly	Leu	Glu	Gly	Phe	Asp	Lys	Gly	Thr	Leu
		35					40					45			

Thr	Thr	Leu	Gly	Ala	Val	Ala	Val	Asp	Thr	Gly	Ile	Phe	Thr	Gly	Arg
	50					55					60				

Ser	Pro	Lys	Asp	Lys	Tyr	Ile	Val	Cys	Asp	Glu	Thr	Thr	Lys	Asp	Thr
65					70					75					80

Val	Trp	Trp	Asn	Ser	Glu	Ala	Ala	Lys	Asn	Asp	Asn	Lys	Pro	Met	Thr
			85						90					95	

Gln	Glu	Thr	Trp	Lys	Ser	Leu	Arg	Glu	Leu	Val	Ala	Lys	Gln	Leu	Ser
			100					105					110		

Gly	Lys	Arg	Leu	Phe	Val	Val	Asp	Ala	Phe	Cys	Gly	Ala	Ser	Glu	Lys
		115					120					125			

His	Arg	Ile	Gly	Val	Arg	Met	Val	Thr	Glu	Val	Ala	Trp	Gln	Ala	His
	130					135					140				

Phe	Val	Lys	Asn	Met	Phe	Ile	Arg	Pro	Thr	Asp	Glu	Glu	Leu	Lys	Asn
145					150					155					160

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

Asn	Trp	Lys	Glu	Gln	Gly	Leu	Asn	Ser	Glu	Asn	Phe	Val	Ala	Phe	Asn
			180					185					190		

Ile	Thr	Glu	Gly	Ile	Gln	Leu	Ile	Gly	Gly	Thr	Trp	Tyr	Gly	Gly	Glu
		195					200					205			

Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Phe Leu Pro Leu Lys
 210 215 220

Gly Val Ala Ser Met His Cys Ser Ala Asn Val Gly Lys Asp Gly Asp
 225 230 235 240

Val Ala Ile Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr Leu Ser
 245 250 255

Thr Asp Pro Lys Arg Gln Leu Ile Gly Asp Asp Glu His Gly Trp Asp
 260 265 270

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

Asn Leu Ser Gln Glu Asn Glu Pro Asp Ile Tyr Gly Ala Ile Arg Arg
 290 295 300

Asp Ala Leu Leu Glu Asn Val Val Val Arg Ala Asp Gly Ser Val Asp
 305 310 315 320

Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr Pro Ile
 325 330 335

Tyr His Ile Asp Asn Ile Val Arg Pro Val Ser Lys Ala Gly His Ala
 340 345 350

Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu Pro Pro
 355 360 365

Val Ser Lys Leu Thr Pro Glu Gln Thr Glu Tyr Tyr Phe Leu Ser Gly
 370 375 380

Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Val Thr Glu Pro Thr
 385 390 395 400

Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu His Pro
 405 410 415

Ile Gln Tyr Ala Asp Val Leu Val Glu Arg Met Lys Ala Ser Gly Ala
 420 425 430

Glu Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys Arg Ile

435 440 445
 Ser Ile Lys Asp Thr Arg Gly Ile Ile Asp Ala Ile Leu Asp Gly Ser
 450 455 460

 Ile Glu Lys Ala Glu Met Gly Glu Leu Pro Ile Phe Asn Leu Ala Ile
 465 470 475 480

 Pro Lys Ala Leu Pro Gly Val Asp Pro Ala Ile Leu Asp Pro Arg Asp
 485 490 495

 Thr Tyr Ala Asp Lys Ala Gln Trp Gln Val Lys Ala Glu Asp Leu Ala
 500 505 510

 Asn Arg Phe Val Lys Asn Phe Val Lys Tyr Thr Ala Asn Pro Glu Ala
 515 520 525

 Ala Lys Leu Val Gly Ala Gly Pro Lys Ala
 530 535

<210> 4
 <211> 1617
 <212> DNA
 <213> Artificial sequence

<220>
 <223> nt PEPCK A.s. EGY replaced with DAF

<400> 4
 atgactgact taaacaaact cgttaaagaa cttaatgact tagggcttac cgatgttaag 60
 gaaattgtgt ataacccgag ttatgaacaa cttttcgagg aagaaaccaa accggggttg 120
 gagggtttcg ataaagggac gttaaccacg cttggcgcgg ttgccgtcga tacggggatt 180
 tttaccggtc gttcaccgaa agataaatat atcgtttgcg atgaaactac gaaagacacc 240
 gtttggtgga acagcgaagc ggcgaaaaac gataacaaac cgatgacgca agaaacttgg 300
 aaaagtttga gagaattagt ggcgaaacaa ctttccggta aacgtttatt cgtggttagac 360
 gcattctgcg gcgccagtga aaaacacCGT atcgggtgtgc gtatggttac tgaagtggca 420
 tggcaggcgc attttgtgaa aaacatgttt atccgaccga ccgatgaaga gttgaaaaat 480
 ttcaaagcgg attttaccgt gttaaaccgt gctaaatgta ctaatccgaa ctggaaagaa 540
 caaggtttga acagtgaaaa ctttgtcgct ttcaatatta ccgaaggat tcaagcttatc 600
 ggcggtactt ggtacggcgg tgaaatgaaa aaaggatatgt tctcaatgat gaactacttc 660

```

ctgccgttaa aaggtgtggc ttccatgcac tgttccgcca acgtaggtaa agacggtgac 720
gtggctatatt tcttcggttt atccggtaac ggtaaaacaa cgctttcgac cgatcctaaa 780
cgccaattaa tcggtgatga cgaacacggt tgggatgaat ccggcgtatt taactttgaa 840
ggcggttggt acgcgaaaac cattaactta tctcaagaaa acgaaccgga tatttacggc 900
gcaatccgctc gtgacgcatt attagaaaac gtcgtggttc gtgcagacgg ttccgttgac 960
tttgacgacg gttcaaaaac agaaaatacc cgtgtttcat atccgattta ccacatcgac 1020
aacatcgttc gtccggtatc gaaagccggt catgcaacca aagtgatttt cttaaccgcg 1080
gacgcattcg gcgtattgcc gccggtttca aaactgactc cggaacaaac cgaatactac 1140
ttcttatccg gctttactgc aaaattagcg ggtacggaac gcggcgtaac cgaaccgact 1200
ccgacattct cggcctgttt cgggtcggca ttcttaagcc tgcacccgat tcaatatgcg 1260
gacgtgttgg tcgaacgcat gaaagcctcc ggtgcggaag cttatttggt gaacaccggt 1320
tggaacggca cgggtaaacy tatttcaatc aaagataccc gcggtattat cgatgcgatt 1380
ttggacgggt caatcgaaaa agcggaaatg gggaattgc caatctttaa tttagcgatt 1440
cctaaagcat taccgggtgt tgatcctgct attttggatc cgcgcgatac ttacgcagac 1500
aaagcgcaat ggcaagttaa agcgggaagat ttggcaaacc gtttcgtgaa aaactttgtg 1560
aaatatacgg cgaatccgga agcggctaaa ttagttggcg ccggtccaaa agcataa 1617

```

```

<210> 5
<211> 538
<212> PRT
<213> Mannheimia succiniciproducens

```

```

<400> 5

```

```

Met Thr Asp Leu Asn Gln Leu Thr Gln Glu Leu Gly Ala Leu Gly Ile
1           5           10          15

```

```

His Asp Val Gln Glu Val Val Tyr Asn Pro Ser Tyr Glu Leu Leu Phe
20           25           30

```

```

Ala Glu Glu Thr Lys Pro Gly Leu Glu Gly Tyr Glu Lys Gly Thr Val
35           40           45

```

```

Thr Asn Gln Gly Ala Val Ala Val Asn Thr Gly Ile Phe Thr Gly Arg
50           55           60

```


Ser Pro Lys Asp Lys Tyr Ile Val Leu Asp Asp Lys Thr Lys Asp Thr
65 70 75 80

Val Trp Trp Thr Ser Glu Lys Val Lys Asn Asp Asn Lys Pro Met Ser
85 90 95

Gln Asp Thr Trp Asn Ser Leu Lys Gly Leu Val Ala Asp Gln Leu Ser
100 105 110

Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn Lys Asp
115 120 125

Thr Arg Leu Ala Val Arg Val Val Thr Glu Val Ala Trp Gln Ala His
130 135 140

Phe Val Thr Asn Met Phe Ile Arg Pro Ser Ala Glu Glu Leu Lys Gly
145 150 155 160

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

Asn Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala Phe Asn
180 185 190

Ile Thr Glu Gly Val Gln Leu Ile Gly Gly Thr Trp Tyr Gly Gly Glu
195 200 205

Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Phe Leu Pro Leu Arg
210 215 220

Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Lys Asp Gly Asp
225 230 235 240

Thr Ala Ile Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr Leu Ser
245 250 255

Thr Asp Pro Lys Arg Gln Leu Ile Gly Asp Asp Glu His Gly Trp Asp
260 265 270

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

Asn Leu Ser Ala Glu Asn Glu Pro Asp Ile Tyr Gly Ala Ile Lys Arg

290		295		300											
Asp 305	Ala	Leu	Leu	Glu	Asn 310	Val	Val	Val	Leu	Asp 315	Asn	Gly	Asp	Val	Asp 320
Tyr	Ala	Asp	Gly	Ser 325	Lys	Thr	Glu	Asn 330	Thr	Arg	Val	Ser	Tyr	Pro 335	Ile
Tyr	His	Ile	Gln	Asn 340	Ile	Val	Lys	Pro 345	Val	Ser	Lys	Ala	Gly 350	Pro	Ala
Thr	Lys	Val 355	Ile	Phe	Leu	Ser	Ala 360	Asp	Ala	Phe	Gly	Val 365	Leu	Pro	Pro
Val	Ser 370	Lys	Leu	Thr	Pro	Glu 375	Gln	Thr	Lys	Tyr	Tyr 380	Phe	Leu	Ser	Gly
Phe 385	Thr	Ala	Lys	Leu	Ala 390	Gly	Thr	Glu	Arg	Gly 395	Ile	Thr	Glu	Pro	Thr 400
Pro	Thr	Phe	Ser 405	Ala	Cys	Phe	Gly	Ala 410	Ala	Phe	Leu	Ser	Leu	His 415	Pro
Thr	Gln	Tyr	Ala 420	Glu	Val	Leu	Val	Lys 425	Arg	Met	Gln	Glu	Ser 430	Gly	Ala
Glu	Ala	Tyr 435	Leu	Val	Asn	Thr	Gly 440	Trp	Asn	Gly	Thr	Gly 445	Lys	Arg	Ile
Ser 450	Ile	Lys	Asp	Thr	Arg	Gly 455	Ile	Ile	Asp	Ala	Ile 460	Leu	Asp	Gly	Ser
Ile 465	Asp	Lys	Ala	Glu	Met 470	Gly	Ser	Leu	Pro	Ile 475	Phe	Asp	Phe	Ser	Ile 480
Pro	Lys	Ala	Leu	Pro 485	Gly	Val	Asn	Pro	Ala 490	Ile	Leu	Asp	Pro	Arg 495	Asp
Thr	Tyr	Ala	Asp 500	Lys	Ala	Gln	Trp	Glu 505	Glu	Lys	Ala	Gln	Asp 510	Leu	Ala
Gly	Arg	Phe 515	Val	Lys	Asn	Phe	Glu 520	Lys	Tyr	Thr	Gly	Thr 525	Ala	Glu	Gly

Gln Ala Leu Val Ala Ala Gly Pro Lys Ala
 530 535

<210> 6
 <211> 1617
 <212> DNA
 <213> Mannheimia succiniciproduces

<400> 6
 atgacagatc ttaatcaatt aactcaagaa cttggtgctt taggtattca tgatgtacaa 60
 gaagtttgtgt ataacccgag ctatgaactt ctttttgctg aagaaaccaa accaggttta 120
 gaaggttatg aaaaaggtag tgtgactaat caaggagcgg ttgctgtaaa taccggtatt 180
 ttcaccggtc gttctccgaa agataaatat atcgtttttag acgacaaaac taaagatacc 240
 gtatggtgga ccagcgaaaa agttaaaaaac gataacaaac caatgagcca agatacctgg 300
 aacagtttga aaggtttagt tgccgatcaa ctttccggta aacgtttatt tgttgttgac 360
 gcattctgcg gcgcgaataa agatacgcgt ttagctgttc gtgtggttac tgaagttgca 420
 tggcaggcgc attttgtaac aaatatgttt atccgccctt cagcggaaga attaaaaggt 480
 ttcaaacctg atttcgtggt aatgaacggt gcaaaatgta caaatcctaa ctggaaagaa 540
 caaggggttaa attccgaaaa cttcggttgcg ttcaacatta cagaaggcgt tcaattaatc 600
 ggcggtactt ggtacggtgg tgaaatgaaa aaaggatatgt tctcaatgat gaactacttc 660
 ttaccgcttc gtggtattgc atcaatgcac tgttccgcaa acgttggtaa agacggcgat 720
 accgcaatth tcttcggttt gtcaggcaca ggtaaaacga cattatcaac agatcctaaa 780
 cgtcaactaa tcggtgatga cgaacacggt tgggacgatg aaggcgtatt taacttcgaa 840
 ggtggttgct acgcgaaaac cattaactta tccgctgaaa acgagccgga tatctatggc 900
 gctatcaaac gtgacgcatt attggaaaaac gtggttggtt tagataacgg tgacgttgac 960
 tatgcagacg gttccaaaaac agaaaataca cgtgttttctt atccgattta tcacattcaa 1020
 aatatcgta aacctgtttc taaagctggt ccggcaacta aagttatctt cttgtctgcc 1080
 gatgcattcg gtgtattacc gccggtgtct aaattaactc cggaacaaac caaatactat 1140
 ttcttatccg gtttcaactgc gaaattagcg ggtacggaac gcggtattac agagcctaca 1200
 ccaacattct ctgcatgttt tgggtcggct tttttaagct tgcacccgac acaatatgcc 1260
 gaagtgttag taaaacgtat gcaagaatca ggtgcggaag cgtatcttgt taatacaggt 1320
 tggaacggta ccggcaaacg tatctcaatt aaagataccc gtggtattat tgatgcaatt 1380

```

ttagacggct caattgataa agcggaaatg ggctcattac caatcttcga tttctcaatt 1440
cctaaagcat tacctgggtgt taaccctgca atcttagatc cgcgcgatac ttatgcggat 1500
aaagcgcaat ggaagaaaa agctcaagat cttgcaggtc gctttgtgaa aaactttgaa 1560
aaatataccg gtacggcgga aggtcaggca ttagttgctg ccggtcctaa agcataa 1617

```

```

<210> 7
<211> 1617
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> PEPCK A.s. optimised for A. niger

```

```

<400> 7
atgaccgacc tcaacaagct cgtcaaggaa ttgaacgacc ttggattgac tgatgtcaag 60
gagatcgtct acaaccccag ctacgagcag ctgttcgaag aagaaaccaa gcccggtctg 120
gaaggattcg acaagggcac cctcaccact ctgggtgctg ttgctgttga cactggtatc 180
ttcacgggcc gctctcccaa ggacaagtac attgtctgct atgagactac caaggacacc 240
gtctggtgga actccgaggc tgccaagaac gacaacaagc ccatgactca ggaaacctgg 300
aagtccctcc gtgagcttgt tgccaagcag ctctccggca agcgtctgtt cgttgttgat 360
gctttctgct gtgcctccga gaagcacctg atcgggtgtc gcatgggtcac cgagggtgcc 420
tggcaggctc acttcgtcaa gaacatgttc atccgcccc cgcacgagga gctcaagaac 480
ttcaaggccg acttcaccgt cctcaacggg gccaaagtga ccaaccccaa ctggaaggag 540
cagggctctga actccgagaa cttcgtcgtt ttcaacatca ccgaggggat ccagctgctc 600
ggtggtacct ggtacggtgg tgagatgaag aagggcatgt tctccatgat gaactacttc 660
cttcctctca aggggtgttg ctccatgcac tgctctgcca acgtcggcaa ggacggtgat 720
gttgccatct tcttcggtct gtctggcaact ggcaagacca ccctctccac cgaccccaag 780
cgccagttga ttggtgatga cgaacacggc tgggatgaga gcggtgtttt caacttcgag 840
ggtggctgct acgccaagac catcaacctg agccaggaga acgagcctga catctacggt 900
gccatccgcc gtgatgctct cctcgagaac gttgttgtcc gcgccgatgg cagcgttgac 960
ttcgatgacg gcagcaagac cgagaacact cgtgtctcct acccatcta ccacattgac 1020
aacattgtcc gccctgtctc caaggccggg cagccacca aggtcatctt cttgactgcc 1080
gatgctttcg gtgtccttcc tcctgtctcc aagctcacc cgcagcagac cgaatactac 1140

```

```

ttcctgtctg gcttcaactgc caagcttgct ggcaccgagc gtggtgtgac cgagcctact 1200
cctaccttct ctgcttgctt cgggtgctgt ttcctctccc tgcaccccat ccagtacgcc 1260
gatgtccttg ttgagcgcac gaaggcctcc ggtgctgagg cctacctggt caacactggc 1320
tggaacggca ctggcaagcg tatctccatc aaggacaccc gtggtatcat tgatgccatt 1380
ttggatggca gcattgagaa ggctgagatg ggtgagctcc ccatcttcaa cctggccatc 1440
cccaaggctc tccccggtgt tgaccccgcc atcctggacc ctctgacac ctacgccgac 1500
aaggcccagt ggcaggtcaa ggctgaggac cttgccaaacc gcttcgtcaa gaacttcgtc 1560
aagtacactg ccaaccccgga ggctgccaaag ctctcggtg ctggtcccaa ggcgtaa 1617

```

<210> 8

<211> 1617

<212> DNA

<213> Artificial sequence 2

<220>

<223> PEPCK M.s. optimised for A. niger

<400> 8

```

atgaccgacc tcaaccagct caccaggag cttggtgctc ttggtatcca cgatgtgcag 60
gaggttgtct acaaccccag ctacgagctt ctgttcgctg aggaaaccaa gcccggtctg 120
gaaggatacg agaagggtag cgtcaccaac caggggtgctg ttgctgtcaa cactggtatc 180
ttcactggcc gtccccccaa ggacaagtag attgtcctcg atgacaagac caaggacacc 240
gtctggtgga cctccgagaa ggtcaagaac gacaacaagc ccatgagcca ggacacctgg 300
aactcgctga agggctcttg tgccgaccag ctctccggca agcgtctgtt cgtcgtcgat 360
gctttctgcg gtgccaacaa ggacacccgc ctggccgtcc gcgttgctac cgaggttgcc 420
tggcaggctc acttcgtcac caacatgttc atccgcccct ctgctgagga gctcaagggt 480
ttcaagcccg acttcgtcgt catgaacggt gccaaagtga ccaaccccaa ctggaaggag 540
cagggctctga actccgagaa cttcgttgct ttcaacatca ccgaggggtg gcagctgac 600
ggtggtacct ggtacggtgg tgagatgaag aagggcatgt tctccatgat gaactacttc 660
cttcctctcc gtggcattgc ctccatgcac tgctctgcca acgtcggcaa ggacggtgac 720
actgccatct tcttcggtct gtctggcaact ggcaagacca ccctcagcac tgacccaag 780
cgccagttga ttggtgatga cgaacacggc tgggatgatg aggggtgttt caacttcgag 840
ggtggctgct acgccaagac catcaacctg tctgctgaga acgagcctga catctacggt 900
gccatcaagc gtgatgccct cctcgagaac gttgttgtcc tcgacaacgg cgatgttgac 960

```

```

tacgccgatg gcagcaagac tgagaacacc cgtgtcagct accccatcta ccacatccag 1020
aacattgtca agcctgtctc caaggccggt cctgccacca aggtcatctt cctgtctgcc 1080
gatgctttcg gtgtccttcc tcctgtctcc aagctcacc ccgagcagac caagtactac 1140
ttcctgtctg gcttcaactgc caagctgggt ggtactgagc gtggtatcac cgagcctact 1200
cccaccttct ccgctgtctt cgggtgtgct ttctgtgagc tgcacccac ccagtacgct 1260
gaggttctcg tcaagcgcac gcaggagtcc ggtgtgagc cctacctcgt caacactggc 1320
tggaacggca ccggcaagcg tatctccatc aaggacaccc gtggtatcat tgatgccatt 1380
ttggatggct ccattgacaa ggctgagatg ggctccctcc ccattctcga cttctccatc 1440
cccaaggccc tccccggtgt caaccccgcc atcctcgacc ctctgtgacac ctacgccgac 1500
aaggcccagt gggaggagaa ggcccaggat cttgtctggc gcttcgtcaa gaacttcgag 1560
aagtacactg gtactgcgga aggccaggcc ttggttgctg ctggtcctaa agcgtaa 1617

```

```

<210> 9
<211> 1617
<212> DNA
<213> Artificial sequence

<220>
<223> PEPCK A.s. optimised for S.cerevisiae

```

```

<400> 9
atgactgatt tgaacaaatt ggtcaaggaa ttgaatgatt tgggtttgac tgacgtcaag 60
gaaattgtct acaacccatc ttacgaacaa ttattcgaag aagaaaccaa gccaggtttg 120
gaaggtttcg acaagggtag tttgaccact ttaggtgctg ttgctgttga caccggtatt 180
ttcaccggtc gttctccaaa ggacaaatac attgtttgtg atgaaaccac caaggacacc 240
gtctgggtga actctgaagc tgccaagaac gataacaagc caatgactca agaaacctgg 300
aaatctttga gagaattggg tgccaagcaa ttgtctggta agagattatt cgttggtgac 360
gctttctgtg gtgcttctga aaagcacaga attggtgtca gaatggcac tgaagttgct 420
tggcaagctc atttcgtcaa gaacatgttc atcagaccaa ctgacgaaga attgaagaac 480
ttcaaggctg acttcaccgt tttgaatggg gccaaagtga ccaacccaaa ctggaaggaa 540
caaggtttga actctgaaaa ctttgttgct ttcaacatca ctgaaggat ccaattgatt 600
gggtgtacct ggtacggtag tgaaatgaag aagggtatgt tctccatgat gaactatttc 660
ttgccattga aaggtgttgc ttccatgcac tgttctgcc aatgtcggtaa ggatgggtgac 720

```

```

gttgccatct tcttcggtct atccggtact ggtaagacca ctctatccac tgacccaaag 780
agacaattga ttggtgatga cgaacacggt tgggacgaat ctggtgtctt taactttgaa 840
ggtggttggt acgccaagac catcaactta tctcaagaaa acgaaccaga tatctacggt 900
gccatccgtc gtgatgcttt gttggaaaac gttggtgtca gagctgacgg ttctgttgac 960
ttcgacgacg gttccaagac tgaaaacacc agagtttctt acccaatcta ccacattgac 1020
aacattgtca gacctgtttc caaggctggt cagctacca aggttatctt cttgactgct 1080
gatgctttcg gtgtcttgcc acctgtttcc aaattgactc cagaacaaac cgaatactac 1140
ttcttgctcg gtttcaactgc caaattggct ggtactgaaa gaggtgtcac tgaaccaact 1200
ccaactttct ctgcttgttt cgggtgctgct ttcttatctt tgcaccaat ccaatacgtc 1260
gatgtcttgg ttgaaagaat gaaggcttct ggtgctgaag cttacttggc caacaccggt 1320
tggaacggta ccggttaagag aatctccatc aaggatacca gaggtatcat tgatgctatc 1380
ttggacgggt ccattgaaaa ggctgaaatg ggtgaattgc caatcttcaa cttggccatt 1440
ccaaaggctt tgccagggtg tgacccagcc atcttagatc caagagacac ctacgctgac 1500
aaggctcaat ggcaagtcaa ggctgaagat ttggctaaca gattcgtcaa gaactttgtc 1560
aaatacactg ctaaccaga agctgccaaa ttggttggtg ctggtccaaa ggcttaa 1617

```

```

<210> 10
<211> 1617
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> PEPCK M.s. optimised for S. cerevisiae

```

```

<400> 10
atgaccgatt tgaaccaatt gactcaagaa ttgggtgctt tgggtattca cgatgtccaa 60
gaagttgtct acaacccatc ttacgaattg ttgtttgctg aagaaaccaa gccaggtttg 120
gaagggttac aaaagggtag tgttaccaac caagggtgctg ttgctgtcaa caccgggtatc 180
ttcaccggtc gttctccaaa ggacaaatac attgtcttgg atgacaagac caaggacact 240
gtctgggtga cttctgaaaa ggtcaagaac gacaacaaac caatgtccca agacacttgg 300
aactctttaa agggtttagt cgctgaccaa ttgtctggta agagattatt cgttgtcgat 360
gctttctgtg gtgccaacaa ggacaccaga ttagctgtca gagttgtcac tgaagttgct 420
tggcaagctc acttcgttac caacatgttc atcagaccat ctgctgaaga attgaaaggc 480
ttcaagccag atttcgttgt catgaacggt gccaaatgta ccaacccaaa ctggaaggaa 540

```

caagggtttga actctgaaaa ctttgttgct ttcaacatca ctgaagggtgt tcaattgatt 600
 ggtggtacct ggtacggtgg tgaaatgaag aagggtatgt tctccatgat gaactacttc 660
 ttgccattga gaggtattgc ttccatgcac tgttctgccca atgtcggtaa ggacggtgac 720
 actgccatct tcttcggtct atccggtacc ggtaagacca ctttgtccac tgacccaaag 780
 agacaattga ttggtgatga cgaacacggt tgggatgacg aagggtgtttt caactttgaa 840
 ggtggttggt acgccaagac catcaactta tctgctgaaa atgaaccaga tatctacggt 900
 gccatcaagc gtgacgctct attggaaaac gttggtgttt tggacaatgg tgacgtcgat 960
 tatgctgacg gttccaagac tgaaaacacc agagtttctt acccaatcta ccatattcaa 1020
 aacattgtca agccagtttc caaggctggt ccagctacca aagttatctt cttgtctgct 1080
 gatgctttcg gtgttttgcc tctgtttcc aagttgactc cagaacaaac caagtactac 1140
 ttcttgtctg gtttcaccgc caagttggct ggtactgaaa gaggtatcac tgaaccaact 1200
 ccaactttct ctgcttgttt cggctgctgcc ttttctctt tgcacccaac tcaatacgtc 1260
 gaagttttgg tcaagagaat gcaagaatct ggtgctgaag cttacttggc caacactggt 1320
 tggaacggta ccggtgaagag aatctccatc aaagatacca gaggtatcat cgatgccatc 1380
 ttggatggtt ccattgacaa ggctgaaatg ggttctttgc caattttcga tttctccatt 1440
 ccaaaggctt tgccaggtgt caaccagcc atcttagacc caagagacac ctacgctgac 1500
 aaagctcaat gggaagaaaa ggctcaagac ttggctggta gattcgtcaa gaacttcgaa 1560
 aaatacactg gtactgctga aggtcaagct ttgggtgctg ctggtccaaa ggcctaa 1617

<210> 11
 <211> 898
 <212> DNA
 <213> Artificial sequence

<220>
 <223> GPDA promotor

<400> 11
 tcagcgtcca attcgagctc tgtacagtga ccggtgactc tttctggcat gcggagacac 60
 ggacggtcgc agagaggagg gctgagtaat aagcgcactc atgtcagctc tggcgtctg 120
 aggtgcagtg gatgattatt aatccgggac cggccgcccc tccgccccga agtggaaagg 180
 ctggtgtgcc cctcgttgac caagaatcta ttgcatcatc ggagaatatg gagcttcac 240
 gaatcaccgg cagtaagcga aggagaatgt gaagccaggg gtgtatagcc gtcggcgaaa 300


```

tagcatgcca ttaacctagg tacagaagtc caattgcttc cgatctggta aaagattcac 360
gagatagtag cttctccgaa gtaggtagag cgagtacccg gcgcgtaagc tccctaattg 420
gcccacccgg catctgtagg gcgtccaaat atcgtgcctc tcctgctttg cccggtgtat 480
gaaaccggaa aggccgctca ggagctggcc agcggcgag accgggaaca caagctggca 540
gtcgacccat ccggtgctct gcactcgacc tgctgaggtc cctcagtccc tggtaggcag 600
ctttgccccg tctgtccgcc cgggtgtgtc gcgggggtga caaggtcgtt gcgtcagtcc 660
aacatttggt gccatatttt cctgctctcc ccaccagctg ctcttttctt ttctctttct 720
tttcccatct tcagtatatt catcttccca tccaagaacc tttatttccc ctaagtaagt 780
actttgctac atccatactc catccttccc atcccttatt cctttgaacc tttcagttcg 840
agctttccca cttcatcgca gcttgactaa cagctacccc gcttgagcca ccgtcaaa 898

```

```

<210> 12
<211> 1000
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> TDH1 promotor

```

```

<400> 12
cttccctttt acagtgttc ggaaaagcac agcgttgtcc aagggaacaa tttttcttca 60
agttaatgca taagaaatat ctttttttat gtttagctaa gtaaaagcag cttggagtaa 120
aaaaaaaaat gagtaaattt ctcgatggat tagtttctca caggtaacat acaaaaaacc 180
aagaaaagcc cgcttctgaa aactacagtt gacttgatg ctaaagggcc agactaatgg 240
gaggagaaaa agaaacgaat gtatatgtc atttactc tatatcacca tatggaggat 300
aagttgggct gagcttctga tccaatttat tctatccatt agttgctgat atgtcccacc 360
agccaacact tgatagtatc tactcgccat tcacttccag cagcgccagt aggggtgttg 420
agcttagtaa aaatgtgcgc accacaagcc tacatgactc cacgtcacat gaaaccacac 480
cgtggggcct tgttgcgcta ggaataggat atgcgacgaa gacgcttctg cttagtaacc 540
acaccacatt ttcagggggg cgatctgctt gcttccttta ctgtcacgag cggcccataa 600
tcgcgctttt tttttaaaaag gcgcgagaca gcaaacagga agctcgggtt tcaaccttcg 660
gagtggctgc agatctggag actggatctt tacaatacag taaggcaagc caccatctgc 720
ttcttaggtg catgcgacgg tatccacgtg cagaacaaca tagtctgaag aaggggggga 780
ggagcatggt cattctctgt agcagtaaga gcttggtgat aatgaccaa actggagtct 840

```

cgaaatcata taaatagaca atatattttc acacaatgag atttgtagta cagttctatt 900
 ctctctcttg cataaataag aaattcatca agaacttggg ttgatatttc accaacacac 960
 acaaaaaaca gtacttcact aaatttacac acaaaaacaaa 1000

<210> 13
 <211> 500
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TDH1 terminator

<400> 13
 ataaagcaat cttgatgagg ataatgattt ttttttgaat atacataaat actaccgttt 60
 ttctgctaga ttttgtgaag acgtaaataa gtacatatta ctttttaagc caagacaaga 120
 ttaagcatta actttaccct tttctcttct aagtttcaat actagttatc actgtttaaa 180
 agttatggcg agaacgtcgg cggttaaaat atattaccct gaacgtgggtg aattgaagtt 240
 ctaggatggg ttaaagattt ttcctttttg ggaaataagt aaacaatata ttgctgcctt 300
 tgcaaaacgc acataccac aatatgtgac tattggcaaa gaacgcatta tcctttgaag 360
 aggtggatac tgatactaag agagtctcta ttccggctcc acttttagtc cagagattac 420
 ttgtcttctt acgtatcaga acaagaaagc atttccaaag taattgcatt tgcccttgag 480
 cagtatatat atactaagaa 500

<210> 14
 <211> 340
 <212> PRT
 <213> Artificial sequence

<220>
 <223> MDH3 *S. cerevisiae* lacking SKL targeting signal

<400> 14

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

Leu Ser Leu Leu Leu Lys Leu Ser Pro Tyr Val Ser Glu Leu Ala Leu
 20 25 30

Tyr Asp Ile Arg Ala Ala Glu Gly Ile Gly Lys Asp Leu Ser His Ile
 35 40 45

Asn Thr Asn Ser Ser Cys Val Gly Tyr Asp Lys Asp Ser Ile Glu Asn
50 55 60

Thr Leu Ser Asn Ala Gln Val Val Leu Ile Pro Ala Gly Val Pro Arg
65 70 75 80

Lys Pro Gly Leu Thr Arg Asp Asp Leu Phe Lys Met Asn Ala Gly Ile
85 90 95

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

Ile Leu Val Ile Ser Asn Pro Val Asn Ser Leu Val Pro Ile Ala Val
115 120 125

Glu Thr Leu Lys Lys Met Gly Lys Phe Lys Pro Gly Asn Val Met Gly
130 135 140

Val Thr Asn Leu Asp Leu Val Arg Ala Glu Thr Phe Leu Val Asp Tyr
145 150 155 160

Leu Met Leu Lys Asn Pro Lys Ile Gly Gln Glu Gln Asp Lys Thr Thr
165 170 175

Met His Arg Lys Val Thr Val Ile Gly Gly His Ser Gly Glu Thr Ile
180 185 190

Ile Pro Ile Ile Thr Asp Lys Ser Leu Val Phe Gln Leu Asp Lys Gln
195 200 205

Tyr Glu His Phe Ile His Arg Val Gln Phe Gly Gly Asp Glu Ile Val
210 215 220

Lys Ala Lys Gln Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Phe Ala
225 230 235 240

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

Pro Glu Thr Glu Ser Leu Ser Ala Phe Val Tyr Leu Pro Gly Leu Lys
260 265 270

Asn Gly Lys Lys Ala Gln Gln Leu Val Gly Asp Asn Ser Ile Glu Tyr
 275 280 285

Phe Ser Leu Pro Ile Val Leu Arg Asn Gly Ser Val Val Ser Ile Asp
 290 295 300

Thr Ser Val Leu Glu Lys Leu Ser Pro Arg Glu Glu Gln Leu Val Asn
 305 310 315 320

Thr Ala Val Lys Glu Leu Arg Lys Asn Ile Glu Lys Gly Lys Ser Phe
 325 330 335

Ile Leu Asp Ser
 340

<210> 15
 <211> 1023
 <212> DNA
 <213> Artificial sequence

<220>
 <223> MDH3 nt *S. cerevisiae* lacking nt encoding SKL targeting signal

<400> 15
 atggttaagg ttgccatctt aggtgcttct ggtggtgtcg gtcaaccatt atctctatta 60
 ttgaaattgt ctccatacgt ttctgaattg gctttgtacg atatcagagc tgctgaagggt 120
 attggttaagg atttgtccca catcaacacc aactcctctt gtgttggtta cgacaaggat 180
 tccatcgaaa aacttttgtc caatgctcaa gttgtcttga ttccagctgg tgttccaaga 240
 aagccagggt tgaccagaga tgatttgttc aagatgaacg ctggtatcgt taagtctttg 300
 gttactgctg tcggtaaatt tgcccaaac gctcgtatct tagtcatctc caaccctgtt 360
 aactcttttg ttccaattgc cgttgaaact ttgaagaaga tgggtaagtt caagccagggt 420
 aacgttatgg gtgtcaccaa cttggatttg gtcagagctg aaactttctt ggttgactac 480
 ttgatgttga agaaccctaaa gatcgggtcaa gaacaagaca agaccacat gcacagaaag 540
 gtcaccgtca tcggtggtca ctctggtgaa accatcatct caatcatcac tgacaaatcc 600
 ttggttttcc aattggacaa gcaatacgaa catttcatcc acagagtcca attcgggtgt 660
 gacgaaattg tcaaggccaa gcaagggtgcc ggttctgcta ccttgtccat ggctttcgct 720
 ggtgccaaat ttgctgaaga agtcttacgt tctttccaca acgaaaagcc agaaactgaa 780
 tctttgtctg ctttcgtcta cttgccagggt ttgaagaacg gtaagaaggc tcaacaatta 840

```

gtcggtgaca actccattga atactttctct ttgccaattg ttttgagaaa cggttccgtt      900
gtttccattg acactttctgt tttggaaaaa ttgtctccaa gagaagaaca attgggtcaac      960
actgctgtca aggaattgag aaagaacatt gaaaagggtg agtctttcat cttggacagt    1020
taa                                                                    1023

```

```

<210> 16
<211> 472
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> Fumarase R. oryzae lacking first 23 aa + M

```

```

<400> 16

```

```

Met Ser Ser Ala Ser Ala Ala Leu Gln Lys Phe Arg Ala Glu Arg Asp
1           5           10           15

```

```

Thr Phe Gly Asp Leu Gln Val Pro Ala Asp Arg Tyr Trp Gly Ala Gln
          20           25           30

```

```

Thr Gln Arg Ser Leu Gln Asn Phe Asp Ile Gly Gly Pro Thr Glu Arg
          35           40           45

```

```

Met Pro Glu Pro Leu Ile Arg Ala Phe Gly Val Leu Lys Lys Ala Ala
          50           55           60

```

```

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

```

```

Ile Gln Lys Ala Ala Asp Glu Val Ile Asp Gly Ser Leu Ile Asp His
          85           90           95

```

```

Phe Pro Leu Val Val Trp Gln Thr Gly Ser Gly Thr Gln Thr Lys Met
          100          105          110

```

```

Asn Val Asn Glu Val Ile Ser Asn Arg Ala Ile Glu Leu Leu Gly Gly
          115          120          125

```

```

Glu Leu Gly Ser Lys Ala Pro Val His Pro Asn Asp His Val Asn Met
          130          135          140

```

```

Ser Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Met His Val Ala Ala
145           150          155          160

```

Val Val Glu Ile His Gly Arg Leu Ile Pro Ala Leu Thr Thr Leu Arg
 165 170 175

Asp Ala Leu Gln Ala Lys Ser Ala Glu Phe Glu His Ile Ile Lys Ile
 180 185 190

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

Phe Ser Gly Tyr Thr Gln Gln Leu Thr Tyr Gly Ile Ala Arg Val Gln
 210 215 220

Gly Thr Leu Glu Arg Leu Tyr Asn Leu Ala Gln Gly Gly Thr Ala Val
 225 230 235 240

Gly Thr Gly Leu Asn Thr Arg Lys Gly Phe Asp Ala Lys Val Ala Glu
 245 250 255

Ala Ile Ala Ser Ile Thr Gly Leu Pro Phe Lys Thr Ala Pro Asn Lys
 260 265 270

Phe Glu Ala Leu Ala Ala His Asp Ala Leu Val Glu Ala His Gly Ala
 275 280 285

Leu Asn Thr Val Ala Cys Ser Leu Met Lys Ile Ala Asn Asp Ile Arg
 290 295 300

Tyr Leu Gly Ser Gly Pro Arg Cys Gly Leu Gly Glu Leu Ser Leu Pro
 305 310 315 320

Glu Asn Glu Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr
 325 330 335

Gln Cys Glu Ala Met Thr Met Val Cys Ala Gln Val Met Gly Asn Asn
 340 345 350

Thr Ala Ile Ser Val Ala Gly Ser Asn Gly Gln Phe Glu Leu Asn Val
 355 360 365

Phe Lys Pro Val Met Ile Lys Asn Leu Ile Gln Ser Ile Arg Leu Ile
 370 375 380

Ser Asp Ala Ser Ile Ser Phe Thr Lys Asn Cys Val Val Gly Ile Glu
385 390 395 400

Ala Asn Glu Lys Lys Ile Ser Ser Ile Met Asn Glu Ser Leu Met Leu
405 410 415

Val Thr Ala Leu Asn Pro His Ile Gly Tyr Asp Lys Ala Ala Lys Cys
420 425 430

Ala Lys Lys Ala His Lys Glu Gly Thr Thr Leu Lys Glu Ala Ala Leu
435 440 445

Ser Leu Gly Tyr Leu Thr Ser Glu Glu Phe Asp Gln Trp Val Arg Pro
450 455 460

Glu Asp Met Ile Ser Ala Lys Asp
465 470

<210> 17

<211> 1419

<212> DNA

<213> Artificial sequence

<220>

<223> FumR nt cpo for *S. cerevisiae* lacking nt encoding first 23 aa + M

<400> 17

```
atgtcctctg cttctgctgc ttgcaaaaa ttcagagctg aaagagatac cttcggtgac      60
ttgcaagttc cagctgaccg ttactggggg gctcaaaactc aaagatcttt gcaaaaacttt      120
gacattgggtg gtccaactga aagaatgcc aaccattaa tcagagcttt cgggtgttttg      180
aagaaggctg ctgccaccgt caacatgacc tacggtttgg acccaaagg tggatgaagcc      240
atccaaaagg ctgctgacga agttatogat gggtctttga ttgaccattt cccattgggt      300
gtctggcaaa ccggttctgg tactcaaac aagatgaacg tcaatgaagt catctccaac      360
agagccattg aattgttggg tggatgaatta gggtccaagg ctccagtcca cccaaacgat      420
catgtcaaca tgtctcaatc ttccaacgac actttcccaa ctgccatgca cgttgctgcc      480
gttggtgaaa ttcacggtag attgattcca gctttgacca ctttgagaga tgctttgcaa      540
gccaaatctg ctgaattcga acacatcatc aagattggta gaaccactt gcaagatgct      600
acccattga ctttaggtca agaattctcc gggttacttc aacaattgac ctacgggtatt      660
gctcgtgttc aagggtacttt ggaaagatta tacaacttgg ctcaagggtg tactgctgtc      720
```

```

ggctactgggtt tgaacaccag aaaggggtttc gatgccaaagg ttgctgaagc cattgcttcc 780
atcactgggtt taccattcaa gaccgctcca aacaaattcg aagctttggc tgctcacgac 840
gctttgggtt aagctcacgg tgctttgaac accggttgctt gttctttgat gaagattgcc 900
aacgatatcc gttacttggg ttctgggtcca agatgtgggt taggtgaatt gtctctacca 960
gaaaacgaac caggttcttc catcatgccg ggtaagggtca acccaactca atgtgaagct 1020
atgaccatgg tttgtgctca agtcatgggt aacaacactg ccatctctgt tgctgggtcc 1080
aacgggtcaat tcgaattgaa tgtctttaaa ccagtcatga tcaagaactt gatccaatcc 1140
atcagattaa tctctgacgc ttccatctct ttcaccaaga actgtgttgt cggtattgaa 1200
gctaacgaaa agaagatctc ctccatcatg aacgaatctt tgatgttggt cactgctttg 1260
aaccctcaca ttggttacga caaggctgcc aagtgtgcca agaaggctca caaggaagggt 1320
accactttga aagaagctgc totatctttg gggttacttga cctctgaaga attcgaccaa 1380
tggggttagac ctgaggacat gatttctgcc aaggattaa 1419

```

```

<210> 18
<211> 600
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> TDH3 promotor

```

```

<400> 18
ttagtcaaaa aattagcctt ttaattctgc tgtaaccctg acatgcccaa aatagggggc 60
gggttacaca gaatatataa catcgtaggt gtctgggtga acagtttatt cctggcatcc 120
actaaatata atggagcccg ctttttaagc tggcatccag aaaaaaaaaa aatcccagca 180
ccaaaatatt gttttcttca ccaaccatca gttcataggt ccattctctt agcgcaacta 240
cagagaacag gggcacaaac aggcaaaaaa cgggcacaaac ctcaatggag tgatgcaacc 300
tgcttgaggt aaatgatgac acaaggcaat tgaccacgc atgtatctat ctcatcttct 360
tacaccttct attaccttct gctctctctg atttggaaaa agctgaaaaa aaaggttgaa 420
accagttccc tgaaattatt cccctacttg actaataagt atataaagac ggtaggtatt 480
gattgtaatt ctgtaaatct atttcttaaa cttcttaaat tctactttta tagttagtct 540
tttttttagt tttaaaacac caagaactta gtttcgaata aacacacata aacaaacaaa 600

```

```

<210> 19

```


<211> 300
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TDH3 terminator

<400> 19
 gtgaatttac tttaaattctt gcattttaaat aaatttttctt tttatagctt tatgacttag 60
 tttcaattta tatactatatt taatgacatt ttcgattcat tgattgaaag ctttgtgttt 120
 tttcttgatg cgctattgca ttgttcttgt ctttttcgcc acatgtaata tctgtagtag 180
 atacctgata cattgtggat gctgagtgaa attttagtta ataatggagg cgctcttaat 240
 aattttgggg atattggctt ttttttttaa agtttacaaa tgaatttttt ccgccaggat 300

<210> 20
 <211> 1966
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TDH3p-MDH3-TDH3t synthetic construct

<400> 20
 ggatccggcg cgccacgcgt ggccggcctt agtcaaaaaa ttagcctttt aattctgctg 60
 taaccctgtac atgccccaaa tagggggcgg gttacacaga atatataaca tcgtagggtg 120
 ctgggtgaac agtttattcc tggcatccac taaatataat ggagcccgct ttttaagctg 180
 gcatccagaa aaaaaaagaa tcccagcacc aaaatattgt tttcttcacc aaccatcagt 240
 tcatagggtcc attctcttag cgcaactaca gagaacaggg gcacaaacag gcaaaaaacg 300
 ggcacaacct caatggagtg atgcaacctg cctggagtaa atgatgacac aaggcaattg 360
 acccagcat gtatctatct cattttctta caccttctat taccttctgc tctctctgat 420
 ttggaaaaag ctgaaaaaaa aggttgaaac cagttccctg aaattattcc cctacttgac 480
 taataagtat ataaagacgg taggtattga ttgtaattct gtaaattctat ttcttaaact 540
 tcttaaattc tacttttata gttagtcttt tttttagttt taaaacacca agaacttagt 600
 ttcgaataaa cacacataaa caaacaaaat ggttaagggt gccatcttag gtgcttctgg 660
 tgggtgcggc caaccattat ctctattatt gaaattgtct ccatacgttt ctgaattggc 720
 tttgtacgat atcagagctg ctgaaggat tggttaaggat ttgtcccaca tcaacaccaa 780
 ctctcttctg gttggttacg acaaggattc catcgaaaac actttgtcca atgctcaagt 840
 tgtcttgatt ccagctgggtg ttccaagaaa gccagggttg accagagatg atttgttcaa 900

```

gatgaacgct ggtatcgtta agtctttggt tactgctgtc ggtaaatttg ccccaaacgc 960
tcgtatctta gtcacatcca accctgttaa ctctttgggt ccaattgccg ttgaaacttt 1020
gaagaagatg ggtaagttca agccaggtaa cgttatgggt gtcaccaact tggatttggt 1080
cagagctgaa actttcttgg ttgactactt gatggtgaag aacccaaaga tcggtcaaga 1140
acaagacaag accaccatgc acagaaaggt caccgtcatc ggtggtcact ctggtgaaac 1200
catcattcca atcatcactg acaaatcctt gggtttccaa ttggacaagc aatacgaaca 1260
tttcatccac agagtccaat tcggtgggtga cgaaattgtc aaggccaagc aaggtgccgg 1320
ttctgctacc ttgtccatgg ctttcgctgg tgccaaattt gctgaagaag tcttacgttc 1380
tttccacaac gaaaagccag aaactgaatc tttgtctgct ttcgtctact tgccaggttt 1440
gaagaacggt aagaaggctc aacaattagt cggtgacaac tccattgaat acttctcttt 1500
gccaatgtt ttgagaaaacg gttccgttgt ttccattgac acttctgttt tggaaaaatt 1560
gtctccaaga gaagaacaat tggtaaacac tgctgtcaag gaattgagaa agaacattga 1620
aaagggtaag tctttcatct tggacagtta aggtgaattt actttaaatc ttgcatttaa 1680
ataaattttc tttttatagc tttatgactt agtttcaatt tatatactat tttaatgaca 1740
ttttcgattc attgattgaa agctttgtgt tttttcttga tgcgctattg cattgttctt 1800
gtctttttcg ccacatgtaa tatctgtagt agatacctga tacattgtgg atgctgagtg 1860
aaattttagt taataatgga ggcgctctta ataattttgg ggatattggc tttttttttt 1920
aaagtttaca aatgaatttt ttccgccagg atgggcccgc ggccgc 1966

```

<210> 21

<211> 2950

<212> DNA

<213> Artificial sequence

<220>

<223> TDH1p-FUMR-TDH1t synthetic construct

<400> 21

```

ggatcccttc ccttttacag tgcttcggaa aagcacagcg ttgtccaagg gaacaatttt 60
tcttcaagtt aatgcataag aaatatcttt ttttatgttt agctaagtaa aagcagcttg 120
gagtaaaaaa aaaaatgagt aaatttctcg atggattagt ttctcacagg taacataaca 180
aaaaccaaga aaagcccgtc tctgaaaact acagttgact tgtatgctaa agggccagac 240
taatgggagg agaaaaagaa acgaatgtat atgctcattt acactctata tcaccatagt 300

```

gaggataagt	tgggctgagc	ttctgatcca	at ttatttcta	tccattagtt	gctgatatgt	360
cccaccagcc	aacacttgat	agtatcta	cgccattcac	ttccagcagc	gccagtaggg	420
ttgttgagct	tagtaaaaat	gtgcgcacca	caagcctaca	tgactccacg	tcacatgaaa	480
ccacaccgtg	gggccttggt	gcgctaggaa	taggatatgc	gacgaagacg	cttctgctta	540
gtaaccacac	cacat tttca	gggggtcgat	ctgcttgctt	cctttactgt	cacgagcggc	600
ccataatcgc	gct ttt tttt	taaaaggcgc	gagacagcaa	acaggaagct	cggttttcaa	660
ccttcggagt	ggtcgcagat	ctggagactg	gatc tttaca	atacagtaag	gcaagccacc	720
atctgcttct	taggtgcatg	cgacggtatc	cacgtgcaga	acaacatagt	ctgaagaagg	780
gggggaggag	catgttcatt	ctctgtagca	gtaagagctt	ggtgataatg	acaaaaactg	840
gagtctcgaa	atcatataaa	tagacaatat	at tttcacac	aatgagattt	gtagtacagt	900
tctatttctct	ctcttgcata	aataagaaat	tcatcaagaa	cttggtttga	tatttcacca	960
acacacacaa	aaaacagtac	ttcactaaat	ttacacacaa	aacaaaatgt	cctctgcttc	1020
tgctgctttg	caaaaattca	gagctgaaag	agataccttc	ggtgacttgc	aagttccagc	1080
tgaccgttac	tggggtgctc	aaactcaaag	atctttgcaa	aactttgaca	ttggtggtcc	1140
aactgaaaga	atgccagaac	cattaatcag	agctttcggg	gttttgaaga	aggctgctgc	1200
caccgtcaac	atgacctacg	gtttggaccc	aaagggtggg	gaagccatcc	aaaaggctgc	1260
tgacgaagtt	atcgatgggt	ctttgattga	ccatttccca	ttggttgctc	ggcaaaccgg	1320
ttctgggtact	caaaccaaga	tgaacgtcaa	tgaagtcatc	tccaacagag	ccattgaatt	1380
gttgggtggg	gaattagggt	ccaaggctcc	agtccaccca	aacgatcatg	tcaacatgtc	1440
tcaatcttcc	aacgacactt	tcccaactgc	catgcacggt	gctgccgttg	ttgaaattca	1500
cggtagattg	attccagctt	tgaccacttt	gagagatgct	ttgcaagcca	aatctgctga	1560
attcgaacac	atcatcaaga	ttggtagaac	ccacttgcaa	gatgctaccc	cattgacttt	1620
agggtcaagaa	ttctccgggt	acaactcaaca	attgacctac	ggtattgctc	gtgttcaagg	1680
tactttggaa	agattataca	acttggtcca	agggtgtact	gctgtcggta	ctggtttgaa	1740
caccagaaag	ggtttcgatg	ccaagggtgc	tgaagccatt	gcttccatca	ctggtttacc	1800
attcaagacc	gctccaaaca	aattcgaagc	tttggctgct	cacgacgctt	tggttgaagc	1860
tcacgggtgct	ttgaacaccg	ttgcttggtc	tttgatgaag	attgccaacg	atatccgtta	1920
cttgggttct	ggtccaagat	gtggtttagg	tgaattgtct	ctaccagaaa	acgaaccagg	1980
ttcttccatc	atgccaggta	agggtcaacc	aactcaatgt	gaagctatga	ccatggtttg	2040

```

tgctcaagtc atgggtaaca acactgccat ctctgttgct ggttccaacg gtcaattcga 2100
attgaatgtc tttaaaccag tcatgatcaa gaacttgatc caatccatca gattaatctc 2160
tgacgcttcc atctctttca ccaagaactg tggtgtcggt attgaagcta acgaaaagaa 2220
gatctcctcc atcatgaacg aatctttgat gttggtcact gctttgaacc ctcacattgg 2280
ttacgacaag gctgccaaagt gtgccaaaga ggctcacaag gaaggtacca ctttgaaaga 2340
agctgctcta tctttgggtt acttgacctc tgaagaattc gaccaatggg ttagacctga 2400
ggacatgatt tctgccaaagg attaaggccc gggcataaag caatcttgat gaggataatg 2460
atTTTTTTTT gaatatacat aaatactacc gtttttctgc tagattttgt gaagacgtaa 2520
ataagtacat attacttttt aagccaagac aagattaagc attaacttta cccttttctc 2580
ttctaagttt caatactagt tatcactggt taaaagttat ggcgagaacg tcggcggtta 2640
aaatatatta ccctgaacgt ggtgaattga agttctagga tggtttaaag atttttcctt 2700
tttgggaaat aagtaaacia tatattgctg cctttgcaaa acgcacatac ccacaatatg 2760
tgactattgg caaagaacgc attatccttt gaagaggtgg atactgatac taagagagtc 2820
tctattccgg ctccactttt agtccagaga ttacttgtct tcttacgtat cagaacaaga 2880
aagcatttcc aaagtaattg catttgccct tgagcagtat atatatacta agaaggcgcg 2940
ccgcggccgc 2950

```

```

<210> 22
<211> 1139
<212> PRT
<213> Artificial sequence

<220>
<223> FRDg Trypanosoma brucei lacking C-terminal targeting sequence SKI

<400> 22

```

```

Met Val Asp Gly Arg Ser Ser Ala Ser Ile Val Ala Val Asp Pro Glu
1          5          10          15

```

```

Arg Ala Ala Arg Glu Arg Asp Ala Ala Ala Arg Ala Leu Leu Gln Asp
20          25          30

```

```

Ser Pro Leu His Thr Thr Met Gln Tyr Ala Thr Ser Gly Leu Glu Leu
35          40          45

```

```

Thr Val Pro Tyr Ala Leu Lys Val Val Ala Ser Ala Asp Thr Phe Asp

```

50		55		60											
Arg	Ala	Lys	Glu	Val	Ala	Asp	Glu	Val	Leu	Arg	Cys	Ala	Trp	Gln	Leu
65					70					75					80
Ala	Asp	Thr	Val	Leu	Asn	Ser	Phe	Asn	Pro	Asn	Ser	Glu	Val	Ser	Leu
				85					90					95	
Val	Gly	Arg	Leu	Pro	Val	Gly	Gln	Lys	His	Gln	Met	Ser	Ala	Pro	Leu
			100					105					110		
Lys	Arg	Val	Met	Ala	Cys	Cys	Gln	Arg	Val	Tyr	Asn	Ser	Ser	Ala	Gly
		115					120					125			
Cys	Phe	Asp	Pro	Ser	Thr	Ala	Pro	Val	Ala	Lys	Ala	Leu	Arg	Glu	Ile
	130					135					140				
Ala	Leu	Gly	Lys	Glu	Arg	Asn	Asn	Ala	Cys	Leu	Glu	Ala	Leu	Thr	Gln
145					150					155					160
Ala	Cys	Thr	Leu	Pro	Asn	Ser	Phe	Val	Ile	Asp	Phe	Glu	Ala	Gly	Thr
				165					170					175	
Ile	Ser	Arg	Lys	His	Glu	His	Ala	Ser	Leu	Asp	Leu	Gly	Gly	Val	Ser
			180					185					190		
Lys	Gly	Tyr	Ile	Val	Asp	Tyr	Val	Ile	Asp	Asn	Ile	Asn	Ala	Ala	Gly
		195					200					205			
Phe	Gln	Asn	Val	Phe	Phe	Asp	Trp	Gly	Gly	Asp	Cys	Arg	Ala	Ser	Gly
	210					215					220				
Met	Asn	Ala	Arg	Asn	Thr	Pro	Trp	Val	Val	Gly	Ile	Thr	Arg	Pro	Pro
225					230					235					240
Ser	Leu	Asp	Met	Leu	Pro	Asn	Pro	Pro	Lys	Glu	Ala	Ser	Tyr	Ile	Ser
				245					250					255	
Val	Ile	Ser	Leu	Asp	Asn	Glu	Ala	Leu	Ala	Thr	Ser	Gly	Asp	Tyr	Glu
			260					265					270		
Asn	Leu	Ile	Tyr	Thr	Ala	Asp	Asp	Lys	Pro	Leu	Thr	Cys	Thr	Tyr	Asp
		275					280					285			

Trp Lys Gly Lys Glu Leu Met Lys Pro Ser Gln Ser Asn Ile Ala Gln
 290 295 300

Val Ser Val Lys Cys Tyr Ser Ala Met Tyr Ala Asp Ala Leu Ala Thr
 305 310 315 320

Ala Cys Phe Ile Lys Arg Asp Pro Ala Lys Val Arg Gln Leu Leu Asp
 325 330 335

Gly Trp Arg Tyr Val Arg Asp Thr Val Arg Asp Tyr Arg Val Tyr Val
 340 345 350

Arg Glu Asn Glu Arg Val Ala Lys Met Phe Glu Ile Ala Thr Glu Asp
 355 360 365

Ala Glu Met Arg Lys Arg Arg Ile Ser Asn Thr Leu Pro Ala Arg Val
 370 375 380

Ile Val Val Gly Gly Gly Leu Ala Gly Leu Ser Ala Ala Ile Glu Ala
 385 390 395 400

Ala Gly Cys Gly Ala Gln Val Val Leu Met Glu Lys Glu Ala Lys Leu
 405 410 415

Gly Gly Asn Ser Ala Lys Ala Thr Ser Gly Ile Asn Gly Trp Gly Thr
 420 425 430

Arg Ala Gln Ala Lys Ala Ser Ile Val Asp Gly Gly Lys Tyr Phe Glu
 435 440 445

Arg Asp Thr Tyr Lys Ser Gly Ile Gly Gly Asn Thr Asp Pro Ala Leu
 450 455 460

Val Lys Thr Leu Ser Met Lys Ser Ala Asp Ala Ile Gly Trp Leu Thr
 465 470 475 480

Ser Leu Gly Val Pro Leu Thr Val Leu Ser Gln Leu Gly Gly His Ser
 485 490 495

Arg Lys Arg Thr His Arg Ala Pro Asp Lys Lys Asp Gly Thr Pro Leu
 500 505 510

Pro Ile Gly Phe Thr Ile Met Lys Thr Leu Glu Asp His Val Arg Gly
 515 520 525

Asn Leu Ser Gly Arg Ile Thr Ile Met Glu Asn Cys Ser Val Thr Ser
 530 535 540

Leu Leu Ser Glu Thr Lys Glu Arg Pro Asp Gly Thr Lys Gln Ile Arg
 545 550 555 560

Val Thr Gly Val Glu Phe Thr Gln Ala Gly Ser Gly Lys Thr Thr Ile
 565 570 575

Leu Ala Asp Ala Val Ile Leu Ala Thr Gly Gly Phe Ser Asn Asp Lys
 580 585 590

Thr Ala Asp Ser Leu Leu Arg Glu His Ala Pro His Leu Val Asn Phe
 595 600 605

Pro Thr Thr Asn Gly Pro Trp Ala Thr Gly Asp Gly Val Lys Leu Ala
 610 615 620

Gln Arg Leu Gly Ala Gln Leu Val Asp Met Asp Lys Val Gln Leu His
 625 630 635 640

Pro Thr Gly Leu Ile Asn Pro Lys Asp Pro Ala Asn Pro Thr Lys Phe
 645 650 655

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

Gln Gly Lys Arg Phe Val Asn Glu Leu Asp Leu Arg Ser Val Val Ser
 675 680 685

Lys Ala Ile Met Glu Gln Gly Ala Glu Tyr Pro Gly Ser Gly Gly Ser
 690 695 700

Met Phe Ala Tyr Cys Val Leu Asn Ala Ala Gln Lys Leu Phe Gly
 705 710 715 720

Val Ser Ser His Glu Phe Tyr Trp Lys Lys Met Gly Leu Phe Val Lys
 725 730 735

Ala Asp Thr Met Arg Asp Leu Ala Ala Leu Ile Gly Cys Pro Val Glu
740 745 750

Ser Val Gln Gln Thr Leu Glu Glu Tyr Glu Arg Leu Ser Ile Ser Gln
755 760 765

Arg Ser Cys Pro Ile Thr Arg Lys Ser Val Tyr Pro Cys Val Leu Gly
770 775 780

Thr Lys Gly Pro Tyr Tyr Val Ala Phe Val Thr Pro Ser Ile His Tyr
785 790 795 800

Thr Met Gly Gly Cys Leu Ile Ser Pro Ser Ala Glu Ile Gln Met Lys
805 810 815

Asn Thr Ser Ser Arg Ala Pro Leu Ser His Ser Asn Pro Ile Leu Gly
820 825 830

Leu Phe Gly Ala Gly Glu Val Thr Gly Gly Val His Gly Gly Asn Arg
835 840 845

Leu Gly Gly Asn Ser Leu Leu Glu Cys Val Val Phe Gly Arg Ile Ala
850 855 860

Gly Asp Arg Ala Ser Thr Ile Leu Gln Arg Lys Ser Ser Ala Leu Ser
865 870 875 880

Phe Lys Val Trp Thr Thr Val Val Leu Arg Glu Val Arg Glu Gly Gly
885 890 895

Val Tyr Gly Ala Gly Ser Arg Val Leu Arg Phe Asn Leu Pro Gly Ala
900 905 910

Leu Gln Arg Ser Gly Leu Ser Leu Gly Gln Phe Ile Ala Ile Arg Gly
915 920 925

Asp Trp Asp Gly Gln Gln Leu Ile Gly Tyr Tyr Ser Pro Ile Thr Leu
930 935 940

Pro Asp Asp Leu Gly Met Ile Asp Ile Leu Ala Arg Ser Asp Lys Gly
945 950 955 960

Thr Leu Arg Glu Trp Ile Ser Ala Leu Glu Pro Gly Asp Ala Val Glu

		965						970						975	
Met	Lys	Ala	Cys	Gly	Gly	Leu	Val	Ile	Glu	Arg	Arg	Leu	Ser	Asp	Lys
			980					985					990		
His	Phe	Val	Phe	Met	Gly	His	Ile	Ile	Asn	Lys	Leu	Cys	Leu	Ile	Ala
		995					1000					1005			
Gly	Gly	Thr	Gly	Val	Ala	Pro	Met	Leu	Gln	Ile	Ile	Lys	Ala	Ala	
	1010					1015					1020				
Phe	Met	Lys	Pro	Phe	Ile	Asp	Thr	Leu	Glu	Ser	Val	His	Leu	Ile	
	1025					1030					1035				
Tyr	Ala	Ala	Glu	Asp	Val	Thr	Glu	Leu	Thr	Tyr	Arg	Glu	Val	Leu	
	1040					1045					1050				
Glu	Glu	Arg	Arg	Arg	Glu	Ser	Arg	Gly	Lys	Phe	Lys	Lys	Thr	Phe	
	1055					1060					1065				
Val	Leu	Asn	Arg	Pro	Pro	Pro	Leu	Trp	Thr	Asp	Gly	Val	Gly	Phe	
	1070					1075					1080				
Ile	Asp	Arg	Gly	Ile	Leu	Thr	Asn	His	Val	Gln	Pro	Pro	Ser	Asp	
	1085					1090					1095				
Asn	Leu	Leu	Val	Ala	Ile	Cys	Gly	Pro	Pro	Val	Met	Gln	Arg	Ile	
	1100					1105					1110				
Val	Lys	Ala	Thr	Leu	Lys	Thr	Leu	Gly	Tyr	Asn	Met	Asn	Leu	Val	
	1115					1120					1125				
Arg	Thr	Val	Asp	Glu	Thr	Glu	Pro	Ser	Gly	Ser					
	1130					1135									

<210> 23

<211> 3421

<212> DNA

<213> Artificial sequence

<220>

<223> cpo nt FRDg T. brucei lacking nt coding for C-terminal SKI

<400> 23

atgggttgatg gtagatcttc tgcttcatt gttgccgttg acccagaaag agctgccaga

gaaagagatg	ctgctgccag	agctttgttg	caagactctc	cattgcacac	caccatgcaa	120
tacgctacct	ctggtttgga	attgactggt	ccatacgctt	tgaagggtgt	tgcttctgct	180
gacactttcg	acagagccaa	ggaagttgct	gatgaagtct	tgagatgtgc	ctggcaattg	240
gctgacaccg	ttttgaactc	tttcaaccca	aactctgaag	tctctttagt	cggtagatta	300
ccagtcggtc	aaaagcatca	aatgtctgct	ccattgaaac	gtgtcatggc	ttgttgtcaa	360
agagtctaca	actcctctgc	tggttgtttc	gacccatcca	ctgctccagt	tgccaaggct	420
ttgagagaaa	ttgctttggg	taaggaaaga	aacaatgctt	gtttggaagc	tttgactcaa	480
gcttgctacct	tgccaaaactc	tttcgtcatt	gatttcgaag	ctggtactat	ctccagaaaag	540
cacgaacacg	cttctttgga	tttgggtggg	gtttccaagg	gttacatcgt	cgattacgtc	600
attgacaaca	tcaatgctgc	tggtttccaa	aacgttttct	ttgactgggg	tggtgactgt	660
cgtgcctccg	gtatgaacgc	cagaaacact	ccatgggttg	tcggtatcac	tagacctcct	720
tccttggaaca	tggtgccaaa	ccctccaaaag	gaagcttctt	acatctccgt	catctctttg	780
gacaatgaag	ctttggctac	ctctgggtgat	tacgaaaact	tgatctacac	tgctgacgat	840
aaaccattga	cctgtaccta	cgattggaaa	ggtaaggaat	tgatgaagcc	atctcaatcc	900
aatatcgctc	aagtttccgt	caagtgttac	tctgccatgt	acgctgacgc	tttggctacc	960
gcttgtttca	tcaagcgtga	cccagccaag	gtcagacaat	tgttggatgg	ttggagatac	1020
gttagagaca	ccgtcagaga	ttaccgtgtc	tacgtcagag	aaaacgaaaag	agttgccaaag	1080
atgttcgaaa	ttgccactga	agatgctgaa	atgagaaaaga	gaagaatttc	caacacttta	1140
ccagctcgtg	tcattgttgt	tggtgggtgg	ttggctgggt	tgtccgctgc	cattgaagct	1200
gctggttgtg	gtgctcaagt	tgttttgatg	gaaaaggaag	ccaagttggg	tggttaactct	1260
gccaaaggcta	cctctggtat	caacgggttg	ggtactagag	ctcaagctaa	ggcttccatt	1320
gtcgatgggtg	gtaagtactt	cgaaagagat	acctacaagt	ctgggtatcgg	tggtaacacc	1380
gatccagctt	tggttaagac	tttgtccatg	aaatctgctg	acgctatcgg	ttggttgact	1440
tctctaggtg	ttccattgac	tgttttgtcc	caattaggtg	gtcactccag	aaagagaact	1500
cacagagctc	cagacaagaa	ggatggtaact	ccattgccaa	ttggtttcac	catcatgaaa	1560
actttagaag	atcatgttag	aggtaacttg	tccggtagaa	tcaccatcat	ggaaaactgt	1620
tccgttacct	ctttgttgtc	tgaaaccaag	gaaagaccag	acggtaccaa	gcaaatcaga	1680
gttaccgggtg	tcgaattcac	tcaagctggg	tctggtaaga	ccaccatttt	ggctgatgct	1740

gttatcttgg ccaccggtgg tttctccaac gacaagactg ctgattcttt gttgagagaa 1800
 catgccccac acttggttaa cttcccaacc accaacggtc catgggctac tggatgatgt 1860
 gtcaagttgg ctcaaagatt aggtgctcaa ttgggtcgata tggacaaggt tcaattgcac 1920
 ccaactgggt tgatcaaccc aaaggaccca gccaacccaa ccaaattctt ggggccagaa 1980
 gctctaagag gttctggtgg tgttttgttg aacaaacaag gtaagagatt tgtcaacgaa 2040
 ttggatttga gatctgttgt ttccaaggcc atcatggaac aagggtgctga ataccaggt 2100
 tctgggtggt ccatgtttgc ttactgtgtc ttgaacgctg ctgctcaaaa attgtttggt 2160
 gtttcctctc acgaattcta ctggaagaag atgggtttgt tcgtcaaggc tgacaccatg 2220
 agagacttgg ctgctttgat tggttgtcca gttgaatccg ttcaacaaac tttagaagaa 2280
 tacgaaagat tatccatctc tcaaagatct tgtccaatta ccagaaaatc tgtttaccca 2340
 tgtgttttgg gtaccaaagg tcatactat gtgcctttg tctactccatc tatccactac 2400
 accatgggtg gttgtttgat ttctccatct gctgaaatcc aatgaagaa cacttcttcc 2460
 agagctccat tgtccactc caaccctaac ttgggtttat tcgggtgctgg tgaagtcacc 2520
 ggtggtgtcc acggtggtaa cagattaggt ggtaactctt tgttggaatg tgtgttttc 2580
 ggtagaattg ccggtgacag agcttctacc attttgcaaa gaaagtcctc tgctttgtct 2640
 ttcaagggtc ggaccactgt tgttttgaga gaagtcagag aagggtggtgt ctacggtgct 2700
 ggttcccggt tcttgagatt caacttacca ggtgctctac aaagatctgg tctatccttg 2760
 ggtcaattca ttgccatcag aggtgactgg gacggtcaac aattgattgg ttactactct 2820
 ccaatcactt tgccagacga tttgggtatg attgacattt tggccagatc tgacaagggt 2880
 actttacgtg aatggatctc tgctttggaa ccagggtgacg ctgtcgaaat gaaggcttgt 2940
 ggtggtttgg tcatcgaaag aagattatct gacaagcact tcgttttcat gggtcacatt 3000
 atcaacaagc tatgtttgat tgctggtggt accggtgttg ctccaatgtt gcaaatcatc 3060
 aaggccgctt tcatgaagcc attcatcgac actttggaat ccgtccactt gatctacgtc 3120
 gctgaagatg tctactgaatt gacttacaga gaagtttttg aagaacgtcg tcgtgaatcc 3180
 agaggtaaat tcaagaaaac tttcgttttg aacagacctc ctccattatg gactgacggt 3240
 gtcggtttca tcgaccgtgg tatcttgacc aaccacgttc aaccaccatc tgacaactta 3300
 ttggttgcca tctgtggtcc accagttatg caaagaattg tcaaggccac tttaaagact 3360
 ttaggttaca acatgaactt ggtcagaacc gttgacgaaa ctgaaccatc tggaagttaa 3420
 g 3421

<210> 24
 <211> 1000
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TDH3Sc promotor

<400> 24
 ctatttttcga ggaccttggtc accttgagcc caagagagcc aagatttaaa ttttcctatg 60
 acttgatgca aattcccaaa gctaataaca tgcaagacac gtacgggtcaa gaagacatat 120
 ttgacctctt aacagggttca gacgcgactg cctcatcagt aagaccctgt gaaaagaact 180
 tacctgaaaa aaacgaatat atactagcgt tgaatgttag cgtcaacaac aagaagtta 240
 atgacgcgga ggccaaggca aaaagattcc ttgattacgt aagggagtta gaatcatttt 300
 gaataaaaaa cacgctttttt cagttcgagt ttatcattat caatactgcc atttcaaaga 360
 atacgtaaat aattaatagt agtgattttc ctaactttat ttagtcaaaa aattagcctt 420
 ttaattctgc tgtaaccctgt acatgcccac aatagggggc ggggttacaca gaatatataa 480
 catcgtaggt gtctgggtga acagtttatt cctggcatcc actaaatata atggagccccg 540
 ctttttaagc tggcatccag aaaaaaaaaa aatcccagca ccaaaatatt gttttcttca 600
 ccaaccatca gttcataggt ccattctctt agcgcaacta cagagaacag gggcacaaac 660
 aggcaaaaaa cgggcacaaac ctcaatggag tgatgcaacc tgcttgaggt aaatgatgac 720
 acaaggcaat tgaccacgc atgtatctat ctcatcttct tacaccttct attaccttct 780
 gctctctctg atttgaaaaa agctgaaaaa aaagggtgaa accagttccc tgaaattatt 840
 ccctacttg actaataagt atataaagac ggtaggtatt gattgtaatt ctgtaaatct 900
 atttcttaaa cttcttaaat tctactttta tagttagtct ttttttagt tttaaaacac 960
 caagaactta gtttcgaata aacacacata aacaaacaaa 1000

<210> 25
 <211> 500
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TDH3Sc terminator

<400> 25
 gtgaatttac tttaaactct gcatttaaat aaattttctt tttatagctt tatgacttag 60

```

tttcaattta tataactatatt taatgacatt ttcgattcat tgattgaaag ctttgtgttt      120
tttcttgatg cgctattgca ttgttcttgt ctttttcgcc acatgtaata tctgtagtag      180
atacctgata cattgtggat gctgagtga attttagtta ataatggagg cgctcttaat      240
aattttgggg atattggctt ttttttttaa agtttacaaa tgaatttttt ccgccaggat      300
aacgattctg aagttactct tagcgttcct atcggtacag ccatcaaatc atgcctataa      360
atcatgccta tatttgctg cagtcagtat catctacatg aaaaaaactc ccgcaatttc      420
ttatagaata cgttgaaaat taaatgtacg cgccaagata agataacata tatctagatg      480
cagtaatata cacagattcc                                                    500

```

```

<210> 26
<211> 1180
<212> PRT
<213> Saccharomyces cerevisiae

```

```

<400> 26

```

```

Met Ser Ser Ser Lys Lys Leu Ala Gly Leu Arg Asp Asn Phe Ser Leu
1           5           10           15

```

```

Leu Gly Glu Lys Asn Lys Ile Leu Val Ala Asn Arg Gly Glu Ile Pro
          20           25           30

```

```

Ile Arg Ile Phe Arg Ser Ala His Glu Leu Ser Met Arg Thr Ile Ala
          35           40           45

```

```

Ile Tyr Ser His Glu Asp Arg Leu Ser Met His Arg Leu Lys Ala Asp
50           55           60

```

```

Glu Ala Tyr Val Ile Gly Glu Glu Gly Gln Tyr Thr Pro Val Gly Ala
65           70           75           80

```

```

Tyr Leu Ala Met Asp Glu Ile Ile Glu Ile Ala Lys Lys His Lys Val
          85           90           95

```

```

Asp Phe Ile His Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ser Glu Phe
          100          105          110

```

```

Ala Asp Lys Val Val Lys Ala Gly Ile Thr Trp Ile Gly Pro Pro Ala
115           120           125

```

```

Glu Val Ile Asp Ser Val Gly Asp Lys Val Ser Ala Arg His Leu Ala

```

130		135		140
Ala Arg Ala Asn Val Pro Thr Val Pro Gly Thr Pro Gly Pro Ile Glu				
145		150		155 160
Thr Val Gln Glu Ala Leu Asp Phe Val Asn Glu Tyr Gly Tyr Pro Val				
	165		170	175
Ile Ile Lys Ala Ala Phe Gly Gly Gly Gly Arg Gly Met Arg Val Val				
	180		185	190
Arg Glu Gly Asp Asp Val Ala Asp Ala Phe Gln Arg Ala Thr Ser Glu				
	195		200	205
Ala Arg Thr Ala Phe Gly Asn Gly Thr Cys Phe Val Glu Arg Phe Leu				
	210		215	220
Asp Lys Pro Lys His Ile Glu Val Gln Leu Leu Ala Asp Asn His Gly				
225		230		235 240
Asn Val Val His Leu Phe Glu Arg Asp Cys Ser Val Gln Arg Arg His				
	245		250	255
Gln Lys Val Val Glu Val Ala Pro Ala Lys Thr Leu Pro Arg Glu Val				
	260		265	270
Arg Asp Ala Ile Leu Thr Asp Ala Val Lys Leu Ala Lys Val Cys Gly				
	275		280	285
Tyr Arg Asn Ala Gly Thr Ala Glu Phe Leu Val Asp Asn Gln Asn Arg				
	290		295	300
His Tyr Phe Ile Glu Ile Asn Pro Arg Ile Gln Val Glu His Thr Ile				
305		310		315 320
Thr Glu Glu Ile Thr Gly Ile Asp Ile Val Ser Ala Gln Ile Gln Ile				
	325		330	335
Ala Ala Gly Ala Thr Leu Thr Gln Leu Gly Leu Leu Gln Asp Lys Ile				
	340		345	350
Thr Thr Arg Gly Phe Ser Ile Gln Cys Arg Ile Thr Thr Glu Asp Pro				
	355		360	365

Ser Lys Asn Phe Gln Pro Asp Thr Gly Arg Leu Glu Val Tyr Arg Ser
 370 375 380

Ala Gly Gly Asn Gly Val Arg Leu Asp Gly Gly Asn Ala Tyr Ala Gly
 385 390 395 400

Ala Thr Ile Ser Pro His Tyr Asp Ser Met Leu Val Lys Cys Ser Cys
 405 410 415

Ser Gly Ser Thr Tyr Glu Ile Val Arg Arg Lys Met Ile Arg Ala Leu
 420 425 430

Ile Glu Phe Arg Ile Arg Gly Val Lys Thr Asn Ile Pro Phe Leu Leu
 435 440 445

Thr Leu Leu Thr Asn Pro Val Phe Ile Glu Gly Thr Tyr Trp Thr Thr
 450 455 460

Phe Ile Asp Asp Thr Pro Gln Leu Phe Gln Met Val Ser Ser Gln Asn
 465 470 475 480

Arg Ala Gln Lys Leu Leu His Tyr Leu Ala Asp Leu Ala Val Asn Gly
 485 490 495

Ser Ser Ile Lys Gly Gln Ile Gly Leu Pro Lys Leu Lys Ser Asn Pro
 500 505 510

Ser Val Pro His Leu His Asp Ala Gln Gly Asn Val Ile Asn Val Thr
 515 520 525

Lys Ser Ala Pro Pro Ser Gly Trp Arg Gln Val Leu Leu Glu Lys Gly
 530 535 540

Pro Ser Glu Phe Ala Lys Gln Val Arg Gln Phe Asn Gly Thr Leu Leu
 545 550 555 560

Met Asp Thr Thr Trp Arg Asp Ala His Gln Ser Leu Leu Ala Thr Arg
 565 570 575

Val Arg Thr His Asp Leu Ala Thr Ile Ala Pro Thr Thr Ala His Ala
 580 585 590

Leu Ala Gly Ala Phe Ala Leu Glu Cys Trp Gly Gly Ala Thr Phe Asp
 595 600 605

Val Ala Met Arg Phe Leu His Glu Asp Pro Trp Glu Arg Leu Arg Lys
 610 615 620

Leu Arg Ser Leu Val Pro Asn Ile Pro Phe Gln Met Leu Leu Arg Gly
 625 630 635 640

Ala Asn Gly Val Ala Tyr Ser Ser Leu Pro Asp Asn Ala Ile Asp His
 645 650 655

Phe Val Lys Gln Ala Lys Asp Asn Gly Val Asp Ile Phe Arg Val Phe
 660 665 670

Asp Ala Leu Asn Asp Leu Glu Gln Leu Lys Val Gly Val Asn Ala Val
 675 680 685

Lys Lys Ala Gly Gly Val Val Glu Ala Thr Val Cys Tyr Ser Gly Asp
 690 695 700

Met Leu Gln Pro Gly Lys Lys Tyr Asn Leu Asp Tyr Tyr Leu Glu Val
 705 710 715 720

Val Glu Lys Ile Val Gln Met Gly Thr His Ile Leu Gly Ile Lys Asp
 725 730 735

Met Ala Gly Thr Met Lys Pro Ala Ala Ala Lys Leu Leu Ile Gly Ser
 740 745 750

Leu Arg Thr Arg Tyr Pro Asp Leu Pro Ile His Val His Ser His Asp
 755 760 765

Ser Ala Gly Thr Ala Val Ala Ser Met Thr Ala Cys Ala Leu Ala Gly
 770 775 780

Ala Asp Val Val Asp Val Ala Ile Asn Ser Met Ser Gly Leu Thr Ser
 785 790 795 800

Gln Pro Ser Ile Asn Ala Leu Leu Ala Ser Leu Glu Gly Asn Ile Asp
 805 810 815

Thr Gly Ile Asn Val Glu His Val Arg Glu Leu Asp Ala Tyr Trp Ala
 820 825 830

Glu Met Arg Leu Leu Tyr Ser Cys Phe Glu Ala Asp Leu Lys Gly Pro
 835 840 845

Asp Pro Glu Val Tyr Gln His Glu Ile Pro Gly Gly Gln Leu Thr Asn
 850 855 860

Leu Leu Phe Gln Ala Gln Gln Leu Gly Leu Gly Glu Gln Trp Ala Glu
 865 870 875 880

Thr Lys Arg Ala Tyr Arg Glu Ala Asn Tyr Leu Leu Gly Asp Ile Val
 885 890 895

Lys Val Thr Pro Thr Ser Lys Val Val Gly Asp Leu Ala Gln Phe Met
 900 905 910

Val Ser Asn Lys Leu Thr Ser Asp Asp Ile Arg Arg Leu Ala Asn Ser
 915 920 925

Leu Asp Phe Pro Asp Ser Val Met Asp Phe Phe Glu Gly Leu Ile Gly
 930 935 940

Gln Pro Tyr Gly Gly Phe Pro Glu Pro Leu Arg Ser Asp Val Leu Arg
 945 950 955 960

Asn Lys Arg Arg Lys Leu Thr Cys Arg Pro Gly Leu Glu Leu Glu Pro
 965 970 975

Phe Asp Leu Glu Lys Ile Arg Glu Asp Leu Gln Asn Arg Phe Gly Asp
 980 985 990

Ile Asp Glu Cys Asp Val Ala Ser Tyr Asn Met Tyr Pro Arg Val Tyr
 995 1000 1005

Glu Asp Phe Gln Lys Ile Arg Glu Thr Tyr Gly Asp Leu Ser Val
 1010 1015 1020

Leu Pro Thr Lys Asn Phe Leu Ala Pro Ala Glu Pro Asp Glu Glu
 1025 1030 1035

Ile Glu Val Thr Ile Glu Gln Gly Lys Thr Leu Ile Ile Lys Leu

1040		1045		1050
Gln Ala Val Gly Asp Leu Asn Lys Lys Thr Gly Gln Arg Glu Val				
1055		1060		1065
Tyr Phe Glu Leu Asn Gly Glu Leu Arg Lys Ile Arg Val Ala Asp				
1070		1075		1080
Lys Ser Gln Asn Ile Gln Ser Val Ala Lys Pro Lys Ala Asp Val				
1085		1090		1095
His Asp Thr His Gln Ile Gly Ala Pro Met Ala Gly Val Ile Ile				
1100		1105		1110
Glu Val Lys Val His Lys Gly Ser Leu Val Lys Lys Gly Glu Ser				
1115		1120		1125
Ile Ala Val Leu Ser Ala Met Lys Met Glu Met Val Val Ser Ser				
1130		1135		1140
Pro Ala Asp Gly Gln Val Lys Asp Val Phe Ile Lys Asp Gly Glu				
1145		1150		1155
Ser Val Asp Ala Ser Asp Leu Leu Val Val Leu Glu Glu Glu Thr				
1160		1165		1170
Leu Pro Pro Ser Gln Lys Lys				
1175		1180		

<210> 27
 <211> 3543
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 27	
atgagcagta gcaagaaatt ggccggtctt agggacaatt tcagtttgct cggcgaaaag	60
aataagatct tggtcgccaa tagaggtgaa attccgatta gaatttttag atctgctcat	120
gagctgtcta tgagaaccat cgccatatac tcccatgagg accgtctttc aatgcacagg	180
ttgaaggcgg acgaagcgta tgttatcggg gaggagggcc agtatacacc tgtgggtgct	240
tacttggtgaa tggacgagat catcgaaatt gcaaagaagc ataaggtgga tttcatccat	300
ccagggttatg ggttcttgtc tgaaaattcg gaatttgccg acaaagtagt gaaggccggt	360

atcacttggg	tgggccctcc	agctgaagtt	attgactctg	tgggtgacaa	agtctctgcc	420
agacacttgg	cagcaagagc	taacgttcoct	accgttcccg	gtactccagg	acctatcgaa	480
actgtgcaag	aggcacttga	cttcgttaat	gaatacggct	acccggtgat	cattaaggcc	540
gcctttggtg	gtggtggtag	aggtatgaga	gtcgttagag	aagggtgacg	cgtggcagat	600
gcctttcaac	gtgctacctc	cgaagcccgt	actgccttcg	gtaatgggtac	ctgctttgtg	660
gaaagattct	tggacaagcc	aaagcatatt	gaagttcaat	tgttggtctg	taaccacgga	720
aacgtgggtc	atctttttcg	aagagactgt	tctgtgcaaa	gaagacacca	aaaagttgtc	780
gaagtcgctc	cagcaaagac	tttgccccgt	gaagttcgtg	acgctatttt	gacagatgct	840
gttaaattag	ctaagggtatg	tggttacaga	aacgcaggta	ccgccgaatt	cttggttgac	900
aacaaaaaca	gacactattt	cattgaaatt	aatccaagaa	ttcaagtgga	gcataaccatc	960
actgaagaaa	tcaccggtat	tgacattggt	tctgccccaa	tccagattgc	cgcagggtgcc	1020
actttgactc	aactagggtct	attacaggat	aaaatcacca	cccgtgggtt	ttccatccaa	1080
tgctgtatta	ccactgaaga	tccctctaag	aattttccaa	cggataaccg	tcgcctggag	1140
gtctatcggt	ctgccggtgg	taatgggtgtg	agattggacg	gtggtaacgc	ttatgcaggt	1200
gctactatct	cgcctcacta	cgactcaatg	ctgggtcaaat	gttcattgctc	tggttctact	1260
tatgaaatcg	tccgtaggaa	gatgattcgt	gccctgatcg	aattcagaat	cagaggtggt	1320
aagaccaaca	ttcccttcoct	attgactctt	ttgaccaatc	cagtttttat	tgaggggtaca	1380
tactggacga	cttttattga	cgacacccca	caactgttcc	aaatgggtatc	gtcacaaaac	1440
agagcgcaaa	aactgttaca	ctatttggca	gacttggcag	ttaacgggtc	ttctattaag	1500
gggtcaaattg	gcttgccaaa	actaaaatca	aatccaagtg	tccccattt	gcacgatgct	1560
cagggcaatg	tcatcaacgt	tacaaagtct	gcaccacat	ccgatggag	acaagtgcta	1620
ctggaaaagg	gaccatctga	atttgccaag	caagtcagac	agttcaatgg	tactctactg	1680
atggacacca	cctggagaga	cgctcatcaa	tctctacttg	caacaagagt	cagaaccac	1740
gatttggtcta	caatcgctcc	aacaaccgca	catgcccttg	caggtgcttt	cgcttttagaa	1800
tgttgggggtg	gtgctacatt	cgacgttgca	atgagattct	tgcattgagga	tccatgggaa	1860
cgtctgagaa	aattaagatc	tctgggtgct	aatattccat	tccaaatgtt	attacgtgggt	1920
gccaacgggtg	tggcttactc	ttcattacct	gacaatgcta	ttgaccattt	tgtcaagcaa	1980
gccaaaggata	atgggtgttg	tatatattaga	gtttttgatg	ccttgaatga	tttagaacia	2040
ttaaaagttg	gtgtgaatgc	tgtcaagaag	gccgggtgggtg	ttgtcgaagc	tactgtttgt	2100

```

tactctggtg acatgcttca gccaggtaag aaatacaact tagactacta cctagaagtt 2160
gttgaaaaaa tagttcaaat gggtagacat atcttgggta ttaaggatat ggcagggtact 2220
atgaaaccgg ccgctgccaa attattaatt ggctccctaa gaaccagata tccggattta 2280
ccaattcatg ttcacagtca tgactccgca ggtactgctg ttgctgtctat gactgcatgt 2340
gccctagcag gtgctgatgt tgtcgatgta gctatcaatt caatgtcggg cttaacttcc 2400
caaccatcaa ttaatgcact gttggcttca ttagaaggta acattgatac tgggattaac 2460
gttgagcatg ttcgtgaatt agatgcatac tgggccgaaa tgagactggt gtattcttgt 2520
ttcgaggccg acttgaaggg accagatcca gaagtttacc aacatgaaat cccagggtgt 2580
caattgacta acttgttatt ccaagctcaa caactgggtc ttggtgaaca atgggctgaa 2640
actaaaagag cttacagaga agccaattac ctactgggag atattgttaa agttacccca 2700
acttctaagg ttgtcgggtga tttagctcaa ttcattggtt ctaacaaact gacttccgac 2760
gatattagac gtttagctaa ttctttggac tttcctgact ctgttatgga cttttttgaa 2820
ggtttaattg gtcaaccata cgggtgggttc ccagaaccat taagatctga tgtattgaga 2880
aacaagagaa gaaagttgac gtgccgtcca ggtttagaat tagaaccatt tgatctcgaa 2940
aaaattagag aagacttgca gaacagattc ggtgatattg atgaatgcga tgttgcttct 3000
tacaatatgt atccaagggg ctatgaagat ttccaaaaga tcagagaaac atacggtgat 3060
ttatcagttc taccaaccaa aaatttccta gcaccagcag aacctgatga agaaatcgaa 3120
gtcaccatcg aacaaggtaa gactttgatt atcaaattgc aagctggttg tgacttaaat 3180
aagaaaactg ggcaaagaga agtgatattt gaattgaacg gtgaattaag aaagatcaga 3240
gttgagaca agtcacaaaa catacaatct gttgctaaac caaaggctga tgtccacgat 3300
actcacaaa tcggtgcacc aatggctggg gttatcatag aagttaaagt acataaaggg 3360
tctttgggtg aaaagggcga atcgattgct gttttgagtg ccatgaaaat ggaaatgggt 3420
gtctcttcac cagcagatgg tcaagttaaa gacgttttca ttaaggatgg tgaaagtgtt 3480
gacgcatcag atttgttggg tgtcctagaa gaagaaaccc taccctcatc caaaaaaaag 3540
taa 3543

```

```

<210> 28
<211> 30
<212> DNA
<213> Artificial sequence

```

<220>

<223> P1 primer

<400> 28

ggactagtat gagcagtagc aagaaattgg

30

<210> 29

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> P2 primer

<400> 29

ccgctcgagt tactttttttt gggatggggg t

31