

SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research
Organisation
Nourish Ingredients Pty Ltd

<120> Production of short chain fatty acids

<130> 531934PCT

<150> AU 2020900780

<151> 2020-03-13

<160> 30

<170> PatentIn version 3.5

<210> 1

<211> 363

<212> PRT

<213> Euonymus alatus

<400> 1

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20 25 30

Pro Lys Gly Leu Leu Arg Leu Leu Ser Leu Leu Pro Val Leu Tyr Leu
35 40 45

Leu Leu Ile Ala Pro Leu Asn Ile Ser Ser Phe Ile Leu Ser Ser Ile
50 55 60

Thr Gly Phe Phe Leu Ala Trp Leu Thr Thr Phe Lys Val Ile Ser Phe
65 70 75 80

Ala Phe Asp Gln Gly Pro Leu Tyr Pro Leu Pro Gln Asn Leu Leu His
85 90 95

Phe Ile Ser Ile Ala Cys Leu Pro Ile Thr Ile Lys Arg Asn Pro Ser
100 105 110

Pro Lys Leu Lys Ser Thr Thr Asn Pro Ser Pro Ile Ser His Leu Leu
115 120 125

Lys Lys Ala Phe Met Ser Phe Pro Ser Lys Val Leu Phe His Trp Val
130 135 140

Ile Ala His Leu Tyr Gln Tyr Lys Lys Tyr Met Asp Pro Asn Val Val
145 150 155 160

Leu Val Ile Tyr Cys Cys His Val Tyr Val Met Leu Asp Ile Ser Leu
165 170 175

Ser Leu Cys Ala Thr Leu Ala Glu Phe Leu Cys Gly Phe Asp Val Glu
180 185 190

Pro Gln Phe Lys Glu Pro Tyr Leu Ala Thr Ser Leu Gln Asp Phe Trp
195 200 205

Gly Arg Arg Trp Asn Ile Ile Val Ser Ser Val Leu Arg Ser Thr Val
210 215 220

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

Ala Tyr Phe Pro Ala Ile Ile Ala Thr Phe Val Val Ser Gly Val Met
245 250 255

His Asp Val Val Tyr Tyr Val Tyr Met Met His Met Tyr Pro Lys Trp
260 265 270

Asp Met Thr Gly His Phe Val Leu His Gly Ile Cys Glu Ala Leu Glu
275 280 285

Val Glu Met Lys Cys Lys Arg Ser Arg Ser Asp Lys Trp Arg Arg His
290 295 300

Pro Ala Val Asp Trp Val Met Val Met Gly Phe Val Met Gly Thr Ser
305 310 315 320

Val Ser Leu Leu Phe Val Pro Leu Leu Arg Asp Asn Val Asp Gln Ile
325 330 335

Val Ala Glu Glu Tyr Ser Ile Leu Phe Asn Phe Val Arg Glu Lys Ile
340 345 350

Val Met Leu Gly Thr Arg Phe Val Cys Gly Asn
355 360

<210> 2
<211> 1092
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of *Euonymus alatus* 1,2-diacyl-sn-glycerol:acetyl-CoA acetyltransferase (EaDAcT) in pAT001, codon optimised for expression in yeast.

<400> 2
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tgtttgtctt atgcttacta cttcagctct agattgccaa aaggtttggt gaggttggtg 120
tctttgttgc cagtcttgta ctgttggttg attgccccat tgaacatctc gtccttcatt 180
ttgtcatcta tcaccggttt tttcttggct tggttgacta cttcaaggt tatttctttc 240
gcttttgatc aggggtccatt atacccattg ccacaaaatt tgttgcaatt catttccatt 300

4/42

Glu Tyr Leu Val Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe
 420 425 430

Thr Gly Met Met Ala Gln Ile Pro Leu Ala Trp Ile Val Gly Arg Phe
 435 440 445

Phe Arg Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile
 450 455 460

Gly Gln Pro Val Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu
 465 470 475 480

Asn Arg Glu Ala Pro Thr Ala Gly Thr
 485

<210> 4
 <211> 1470
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the protein coding region of *Capra hircus*
 (goat) diacylglycerol O-acyltransferase 1 isoform X1 (ChDGAT1-X1)
 in pAT002, codon optimised for expression in yeast.

<400> 4
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 ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttctggtcat 180
 tgggatttga gatgtcatag attgcaggac agcttggttct cttctgattc tggtttttct 240
 aactacaggg gtattttgaa ctggtgcggt gttatgttga ttttgtctaa cgctaggctg 300
 ttcttgaga acttgattaa gtacggtatc ttggttgatc caatccaggt tgtttctttg 360
 ttctgaagg atccatattc ttggccagct ttgtgttgg ttatcgttgc taacattttt 420
 gctgttgctg ccttccaagt cgaaaaaaga ttggctgttg gtgctttgac tgaacaagca 480
 ggtttggtgt tgcattggtt taacttggct accattttgt gttttccagc tgcagttgct 540
 ttcttggttg aatctattac tccagtcggt tctgttttgg ctttgatggt ttacactatc 600
 ctgttcctaa agctgttctc ctacagagat gttaatttgt ggtgtagaga aagacgtgct 660
 ggtgctaaag ctaaagctgc tttggctggt aaaaaagcta atggtggtgc agctcaaaga 720
 actgtttctt acccagataa cttgacttac agggacttgt actacttttt gttagctcca 780
 actttgtgct acgaattgaa tttccaaga agcccaagga tcagaaagag gtttttgttg 840
 agaaggttgt tggagatgtt gtttttgacc caattgcaag tcggtttgat ccaacaatgg 900
 atggttccag ctattcagaa ttctatgaag ccattcaagg acatggacta ctctagaatc 960
 gtcgaaagat tattgaagtt ggccgttcca aaccatttga tctggttgat ttttttctac 1020
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 aaatgggctg ctagaactgg tgtttttttg gcttctgctt tcttccacga atacttggtt 1260
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 ttggcatgga tagttggttag attcttcaga ggtaattacg gtaatgctgc tgtttggtt 1380
 tccttgatta ttggtcaacc agttgctgtt ttgatgtacg ttcatgatta ctacgtcttg 1440
 aacagagaag ctccaactgc tggacttaaa 1470

<210> 5
 <211> 482
 <212> PRT
 <213> Capra hircus

<400> 5

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Leu Gly Leu Glu Ser Glu Ser Leu Ala Pro Gly Leu Cys Val His Ser
20 25 30

Cys Ala Pro Leu Ala Ser Ala Gly Lys Leu Ser Gly Arg Leu Gly Ala
35 40 45

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

Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn
65 70 75 80

Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu
85 90 95

Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln Val Val Ser
100 105 110

Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Leu Cys Leu Val Ile
115 120 125

Val Ala Asn Ile Phe Ala Val Ala Ala Phe Gln Val Glu Lys Arg Leu
130 135 140

Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu Leu Leu His Gly Val
145 150 155 160

Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala Val Ala Phe Leu Leu
165 170 175

Glu Ser Ile Thr Pro Val Gly Ser Val Leu Ala Leu Met Val Tyr Thr
180 185 190

Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp Val Asn Leu Trp Cys
 195 200 205

Arg Glu Arg Arg Ala Gly Ala Lys Ala Lys Ala Ala Leu Ala Gly Lys
 210 215 220

Lys Ala Asn Gly Gly Ala Ala Gln Arg Thr Val Ser Tyr Pro Asp Asn
 225 230 235 240

Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu Cys
 245 250 255

Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe Leu
 260 265 270

Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val Gly
 275 280 285

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

Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys Leu
 305 310 315 320

Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu Phe
 325 330 335

His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp Arg
 340 345 350

Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe Trp
 355 360 365

Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Leu Arg His Phe Tyr
 370 375 380

Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr Gly
 385 390 395 400

Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile Pro
 405 410 415

Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln Ile
 420 425 430

Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly Asn
 435 440 445

Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val Leu
 450 455 460

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

Gly Thr

<210> 6
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the protein coding region of *Capra hircus* (goat) diacylglycerol O-acyltransferase 1 isoform X2 (ChDGAT1-X2) in pAT003, codon optimised for expression in yeast.

<400> 6
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 aaattgtctg gtagattggg tgctgaaggt ttgttgccag gtactccaag atgtcataga 180
 ttgcaagatt cttgtttctc ctctgattct ggtttctcta actacagagg tattttgaac 240
 tgggtgcgttg tcatgttgat tttgtctaata gctaggctgt tcttgagaa cttgattaag 300
 tacggtatct tggttgatcc aatccagggt gtttcttgt tcttgaagga tccatattct 360
 tggccagctt tgtgtttggt tatcgttgct aacatttttg ctgttgctgc cttccaagtc 420
 gaaaaaagat tggctgttgg tgctttgact gaacaagctg gtttgttgtt gcatgggtgtt 480
 aacttggtta ccattttgtg ttttccagct gctgttgcat ttctgttgga atctattact 540
 ccagttgggt ccgttttggc tttgatgggt tacactatcc tgttcctaaa gctgttctcc 600
 tacagagatg ttaatttgtg gtgtagagaa agacgtgctg gtgctaaagc taaagctgct 660
 ttggctggta aaaaagctaa tgggtggtgct gctcaaagaa ctgtttctta cccagataac 720
 ttgacttaca gggacttgta ctactttttg ttcgctccaa ctttgtgcta cgaattgaat 780
 tttccaagaa gccaagaat ccgtaagagg tttttgttga gaagggtgtt ggagatgttg 840
 tttttgacct aattgcaagt cggtttgatc caacaatgga tggttccagc tattcagaat 900
 tctatgaagc cattcaagga catggactac tctagaatcg tcgaaagatt attgaagttg 960
 gccgttccaa accatttgat ctggttgatt ttttctact ggctgttcca ctcttgcttg 1020
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 agattgtggg cttttactgg tatgatggct caaattccat tggcatggat agttggtaga 1320
 ttcttcagag gtaattacgg taatgctgct gtttggttgt ctttgattat tgggtcaacca 1380
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 ggtacttaa 1449

<210> 7
<211> 489
<212> PRT
<213> Ovis aries

<400> 7

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Glu Val Arg Asp Val Gly Ala Gly Gly Asp Ala Pro Val Arg Asp Thr
35 40 45

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asp Leu Arg
50 55 60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
65 70 75 80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
85 90 95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
100 105 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
210 215 220

Lys Ala Ala Leu Ala Gly Lys Lys Ala Asn Gly Gly Ala Ala Gln Arg
225 230 235 240

Thr Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe

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<210> 8
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
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<223> Nucleotide sequence of the protein coding region of *Ovis aries*
(sheep) diacylglycerol O-acyltransferase 1 isoform X1
(OaDGAT1-X1) in pAT004, codon optimised for expression in yeast.

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<400> 8
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ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttctgggtcat      180
tggtgatttga gatgtcatag attgcaggac agcttgttct cttctgattc tggtttttct      240
aactacaggg gtattttgaa ctggtgcggt gttatgttga ttttgtctaa cgctaggctg      300
ttcttggaga acttgattaa gtacgggtatc ttggttgatc caatccaggt tgtttccttg      360
ttcttgaagg atccatattc ttggccagct ttgtgtttgg ttatcgttgc taacattttt      420
gctgttgctg ctttccaagt cgaaaaaaga ttggctgttg gtgctttgac tgaacaagca      480
ggtttgttgt tgcattggtg taacttggct accattttgt gttttccagc tgcagttgct      540
ttcttgttgg aatctattac tccagtcggt tctgttttgg ctttgatggt ttacactatc      600
ctgttcctaa agctgttctc ctacagagat gttaatttgt ggtgtagaga aagacgtgct      660
ggtgctaaag ctaaagctgc tttggctggt aaaaaagcta atggtggtgc agctcaaaga      720
actgtttctt acccagataa cttgacttac agggacttgt actacttttt gttcgctcca      780
actttgtgct acgaattgaa ttttccaaga agcccaagga tcagaaagag gtttttgttg      840
agaaggttgt tggagatggt gtttttgacc caattgcaag tcggtttgat ccaacaatgg      900
atggttccag ctattcagaa ttctatgaag ccattcaagg acatggacta ctctagaatc      960
gtcgaagatg tattgaagtt ggccgttcca aaccatttga tctggttgat ttttttctac     1020
tggctgttcc actcttgctt gaatgctggt gcagaattga tgcaatttgg tgacagagaa     1080
ttttacagag actggtggaa ctctgaatcc attacttact tttggcagaa ctggaacatc     1140
ccagttcata agtgggtgtt gagacatttc tacaagccaa tgttgcgtag aggttcttct     1200
aaatgggctg ctagaactgg tgtttttttg gcttctgctt tcttccacga atacttggtt     1260
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ttggcatgga tagttggtag attcttcaga ggtaattacg gtaatgctgc tgtttggttg     1380
tccttgatta ttggtcaacc agttgctggt ttgatgtacg ttcattgatta ctacgtcttg     1440
aacagagaag ctccaactgc tgggtacttaa                                     1470
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<210> 9
<211> 467
<212> PRT
<213> *Ovis aries*

<400> 9

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Glu Val Arg Asp Val Gly Ala Gly Gly Asp Ala Pro Val Arg Asp Thr
 35 40 45

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asp Leu Arg
 50 55 60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
 65 70 75 80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
 85 90 95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
 100 105 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
 115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
 130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
 145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
 165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
 180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
 195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
 210 215 220

Lys Ala Ala Leu Ala Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu
 225 230 235 240

Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
 245 250 255

Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val
 260 265 270

Gly Leu Ile Gln Gln Trp Met Val Pro Ala Ile Gln Asn Ser Met Lys
 275 280 285

Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys
 290 295 300

Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu
305 310 315 320

Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp
325 330 335

Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe
340 345 350

Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Leu Arg His Phe
355 360 365

Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr
370 375 380

Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile
385 390 395 400

Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln
405 410 415

Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly
420 425 430

Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val
435 440 445

Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu Ala Pro Thr
450 455 460

Ala Gly Thr
465

<210> 10
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Ovis aries
(sheep) diacylglycerol O-acyltransferase 1 isoform X2
(OaDGAT1-X2) in pAT005, codon optimised for expression in yeast.

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ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttctggtcat 180
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aactacaggg gtattttgaa ctggtgcgtt gttatgttga ttttgtctaa cgctaggctg 300
ttcttgaga acttgattaa gtacgggtatc ttggttgatc caatccaggt tgtttctttg 360
ttctgaagg atccatattc ttggccagct ttgtgtttgg ttatcgttgc taacattttt 420

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
 115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
 130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
 145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
 165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
 180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
 195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
 210 215 220

Lys Ala Ala Leu Ala Gly Lys Ala Ala Asn Gly Gly Ala Ala Gln Arg
 225 230 235 240

Thr Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Gly Glu Asp Pro Ala
 245 250 255

Gly Gly Trp Gly Asp Cys Pro Ala Ala Trp Pro Ala Ser Pro Ala Leu
 260 265 270

Pro Ser Arg Ser Leu Leu Leu Pro Leu Arg Pro His Pro Val Leu Arg
 275 280 285

Ala Gln Leu Pro Pro Leu Pro Pro His Pro Lys Ala Leu Pro Ala Ala
 290 295 300

Ala Thr Pro Gly Asp Ala Val Pro His Pro Ala Pro Gly Gly Ala Asp
 305 310 315 320

Pro Ala Val Asp Gly Pro Gly His Pro Glu Leu His Glu Ala Leu Gln
 325 330 335

Gly His Gly Leu Leu Pro His Arg Gly Ala Pro Pro Glu Ala Gly Gly
 340 345 350

Glu Trp Pro Ala Gly Trp Gly Arg Val Gly Ala Gly Gly Ala Val Leu
 355 360 365

Ala Pro Gly Thr His Ser Pro Gln Val Pro Asn His Leu Ile Trp Leu
 370 375 380

Ile Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu
385 390 395 400

Leu Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Trp Val
405 410 415

Ala Leu Pro Gly Arg Gly Trp Trp Gly Pro Pro Leu Gly Leu Gly Pro
420 425 430

Glu Pro Leu Pro Thr Leu Pro Arg Pro Arg Arg Asn Ser Glu Ser Ile
435 440 445

Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile
450 455 460

Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala
465 470 475 480

Ala Arg Thr Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu
485 490 495

Val Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met
500 505 510

Met Ala Gln Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly
515 520 525

Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro
530 535 540

Val Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu
545 550 555 560

Ala Pro Ala Ala Gly Thr
565

<210> 12
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bos taurus
(cattle) diacylglycerol O-acyltransferase 1 isoform X1
(BtDGAT1-X1) in pAT006, codon optimised for expression in yeast.

<400> 12
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ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttcaggatcat 180
tgggatttga gatgtcatag attgcaggac agcttgttct cttctgattc tgggttttct 240
aactacaggg gtattttgaa ctggtgcgtt gttatgttga ttttgtctaa cgctaggctg 300

ttcttggaga acttgattaa gtacggatc ttggttgatc caatccaggt tgtttctttg	360
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gctgttgctg cttccaagt cgaaaaaaga ttggctgttg gtgctttgac tgaacaagca	480
ggtttgttgt tgcattgtgt taacttggct accatTTTgt gttttccagc tgcagttgct	540
ttcttgttgg aatctattac tccagttggg tccgttttgg ctttgatggg ttacactatc	600
ctgttcctaa agctgttctc ctacagagat gttaatTTgt ggtgtagaga aagacgtgct	660
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gattgtccag cagcttggcc tgcttctcca gctttgccat ctagatcttt gttgttacca	840
ttaagaccac atccagtttt gagagcacia ttgccacat tgcctccaca tccaaaggct	900
ttgcctgctg ctgctactcc aggtgatgct gttccacatc ctgctccagg tgggtccgat	960
ccagctgttg atgggtccagg tcatccagaa ttgcatgaag ctttacaagg tcatggtttg	1020
ttgccacata gaggtgctcc acctgaagct ggtggtgaat ggccagcagg ttggggtaga	1080
gttggtgcag gcggtgctgt tttggctcca ggtactcatt ctccacaagt tccaaacct	1140
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ttgatgcaat ttggtgacag agaattttac agagattggg ggtgggttgc tttgccaggt	1260
agaggatggg ggggtccacc attaggtttg ggtccagaac cattgccaac tttgccaaga	1320
ccaagaagaa actctgaatc cattacctac ttttggcaga actggaacat tcctgttcat	1380
aagtgggtgca tcagacattt ctataagcca atgttgagaa ggggttcttc taaatgggct	1440
gctagaactg ctgttttttt ggcttctgct ttcttccacg aatacttggg ttctatccca	1500
ttgagaatgt tcagattgtg ggcttttact ggtatgatgg ctcaaattcc attggcttgg	1560
atagtggta gattcttcag aggttaattac ggtaatgctg ctgtttgggt gtccttgatt	1620
attggtcaac cagttgcagt tttgatgtac gttcatgatt actacgtctt gaacagagaa	1680
gctccagctg ccggtactta a	1701

<210> 13
 <211> 467
 <212> PRT
 <213> Bos taurus

<400> 13

Met	Gly	Asp	Arg	Gly	Gly	Ala	Gly	Gly	Ser	Arg	Arg	Arg	Arg	Thr	Gly
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Ser	Arg	Pro	Ser	Ile	Gln	Gly	Gly	Ser	Gly	Pro	Ala	Ala	Ala	Glu	Glu
			20					25					30		

Glu	Val	Arg	Asp	Val	Gly	Ala	Gly	Gly	Asp	Ala	Pro	Val	Arg	Asp	Thr
			35				40						45		

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asp Leu Arg
 50 55 60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
 65 70 75 80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
 85 90 95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
 100 105 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
 115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
 130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
 145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
 165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
 180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
 195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
 210 215 220

Lys Ala Ala Leu Ala Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu
 225 230 235 240

Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
 245 250 255

Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val
 260 265 270

Gly Leu Ile Gln Gln Trp Met Val Pro Ala Ile Gln Asn Ser Met Lys
 275 280 285

Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys
 290 295 300

Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu
 305 310 315 320

Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp

325

330

335

Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe
340 345 350

Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
355 360 365

Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr
370 375 380

Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile
385 390 395 400

Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln
405 410 415

Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly
420 425 430

Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val
435 440 445

Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu Ala Pro Ala
450 455 460

Ala Gly Thr
465

<210> 14
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bos taurus
(cattle) diacylglycerol O-acyltransferase 1 isoform X2
(BtDGAT1-X2) in pAT007, codon optimised for expression in yeast.

<400> 14
atgggtgata gagtggtgc tgggtgttct agaagaagaa ggacaggttc tagaccatct 60
attcaagggtg gttctggtcc agctgctgct gaagaagagg ttagagatgt tgggtgccggt 120
ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttcaggtcat 180
tgggatttga gatgtcatag attgcaggac agcttgttct cttctgattc tggtttttct 240
aactacaggg gtattttgaa ctggtgcgtt gttatgttga ttttgtctaa cgctaggctg 300
ttcttgagga acttgattaa gtacggtatc ttggttgatc caatccaggt tgtttctttg 360
ttcttgaagg atccatattc ttggccagct ttgtgtttgg ttatcgttgc taacattttt 420
gctgttgctg cttccaagt cgaaaaaaga ttggctgttg gtgctttgac tgaacaagca 480
ggtttgttgt tgcattggtt taacttggct accattttgt gttttccagc tgcagttgct 540
ttcttgttgg aatctattac tccagttggt tccgttttgg ctttgatggt ttacactatc 600

ctgttcctaa agctgttctc ctacagagat gttaatttgt ggtgtagaga aagacgtgct 660
ggtgctaaag ctaaagctgc tttggctgac ttgtactact ttttgtttgc tccaaccttg 720
tgctacgaat tgaattttcc aagatctccc aggatcagaa agaggttttt gttgagaaga 780
ttgctggaaa tgctgttttt gacccaattg caagtcggtt tgattcaaca atggatgggt 840
ccagctatcc agaattctat gaagccattc aaggatatgg actactccag aatcgtcgaa 900
aggttgttga aattggcagt tccaaaccat ttgatctggc tgattttttt ctactggttg 960
ttccactctt gcttgaatgc tgttgacagaa ttgatgcaat ttggtgacag agaattttac 1020
agagactggt ggaactctga atccattact tacttttggc agaactggaa catcccagtt 1080
cataagtggg gtatcagaca tttctacaag ccaatgttgc gtagaggttc ttctaaatgg 1140
gctgctagaa cagcagtttt tttggcttct gctttcttcc acgaatactt ggtttctatc 1200
ccattgagaa tgttcagatt gtgggctttt actggtatga tggctcaaat tccattagct 1260
tggatcggtg gtagattctt cagaggtaat tatggtaatg ctgccgtttg gttgtccttg 1320
attattgggtc aaccagttgc tgttttgatg tacgttcatg attactacgt cttgaacaga 1380
gaagctcctg ctgctggtac ttaa 1404

<210> 15
<211> 519
<212> PRT
<213> Bubalus bubalis

<400> 15

Met Cys Pro Gln Glu Gly Lys Gly Ser Pro Gly Leu Ser Pro Tyr Lys
1 5 10 15

Thr Gly Gly Leu Ala Gln Cys Pro Gly Trp Pro Pro Gly Gly Arg Val
20 25 30

Val Gly Gly Arg Trp Gly Cys Cys Leu Glu Pro Ala Ser Gly Ala Gly
35 40 45

Pro Gly Leu Ser Cys Ala Pro Pro Pro Leu Pro Pro Ala Glu Gly Trp
50 55 60

Leu Pro Ser Pro Pro Asp Pro Ala Leu Gly Ala Gly Leu Ser Glu Val
65 70 75 80

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

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
100 105 110

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
115 120 125

Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
 130 135 140

Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
 145 150 155 160

Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala Phe Gln
 165 170 175

Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu
 180 185 190

Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala
 195 200 205

Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val Leu Ala
 210 215 220

Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp
 225 230 235 240

Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala Lys Ala
 245 250 255

Ala Leu Ala Gly Lys Lys Ala Asn Gly Gly Ala Ala Gln Arg Thr Val
 260 265 270

Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu Phe
 275 280 285

Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile
 290 295 300

Arg Lys Arg Phe Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr
 305 310 315 320

Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Ala Ile Gln
 325 330 335

Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu
 340 345 350

Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe
 355 360 365

Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Met
 370 375 380

Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser
 385 390 395 400

Ile Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys

405

410

415

Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp
 420 425 430

Ala Ala Arg Thr Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr
 435 440 445

Leu Val Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly
 450 455 460

Met Met Ala Gln Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg
 465 470 475 480

Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln
 485 490 495

Pro Val Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg
 500 505 510

Glu Ala Pro Ala Ala Gly Thr
 515

<210> 16
 <211> 1560
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the protein coding region of Bubulus
 bubulis (water buffalo) diacylglycerol O-acyltransferase 1
 isoform X1 (BbDGAT1-X1) in pAT008, codon optimised for expression
 in yeast.

<400> 16
 atgtgcccac aagaaggtaa aggttctcca ggtttgtctc catacaaac tgggtggttg 60
 gctcaatgtc caggttggcc accaggtggt agagttgttg gtggtagatg gggttgttgt 120
 ttggaaccag cttctggtgc tgggccaggt ttatcttggtg ctccaccacc attgccacca 180
 gctgaagggtt ggttgccatc tccaccagat ccagctttag gtgccggttt gtctgaagtt 240
 ggttctgaag gtcctttgtt ggcttctgct gttgattcta gatgtcacag attgcaggat 300
 tccttgttct cttctgattc tggtttctct aactacaggg gtattttgaa ctggtgcgtt 360
 gttatgttga ttttgtctaa cgctaggctg ttcttgaga acttgattaa gtacggtatc 420
 ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 480
 ttgtgtttgg ttatcggtgc taacatTTTT gctgttgctg cttccaagt cgaaaaaaga 540
 ttggctgttg gtgctttgac tgaacaagct ggtttgttgt tgcattggtg taacttggt 600
 accattttgt gttttccagc tgctgttgca tttctgttgg aatctattac tccagtcggt 660
 tctgttttgg ctttgatggt ttacactatc ctgttcctaa agttgttctc ctacagagat 720
 gttaatttgt ggtgcagaga aagacgtgct ggtgctaaag ctaaagctgc tttggctggt 780

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aaaaaagcta acggtggtgc tgctcaaaga actgtttctt atccagataa cttgacctac      840
agggacttgt actacttttt gtttgctcca accttgtgct acgaattgaa tttccaaga      900
tctcccagga tcagaaagag gttttgttg agaagattgc tggaaatgct gtttttgacc      960
caattgcaag tcggtttgat tcaacaatgg atggttccag ctatccagaa ttctatgaag     1020
ccattcaagg atatggacta ctccagaatc gtcgaaaggt tgttgaaatt ggcagttcca     1080
aaccatttga tctggctgat ttttttctac tggttgttcc actcttgctt gaatgcagtt     1140
gctgaattga tgcaatttgg tgacagagaa ttttacagag actggtggaa ctctgaatcc     1200
attacttact tttggcagaa ctggaacatc ccagttcata agtggtgtat cagacatttc     1260
tacaagccaa tgcttagaag gggttcttct aaatgggctg ctagaacagc agtttttttg     1320
gcctctgctt tttccacga atacttggtt tctatcccat tgagaatgtt cagattgtgg     1380
gcttttactg gtatgatggc tcaaatcca ttagcttgga tcgttggtag attcttcaga     1440
ggtaattatg gtaatgctgc cgtttggtt tccttgatta ttggtcaacc agttgctgtt     1500
ttgatgtacg ttcatgatta ctacgtcttg aacagagaag ctccagctgc aggtacttaa     1560

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<210> 17
<211> 504
<212> PRT
<213> Bubalus bubalis

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<400> 17

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Met Cys Pro Gln Glu Gly Lys Gly Ser Pro Gly Leu Ser Pro Tyr Lys
1           5           10          15

```

```

Thr Gly Gly Leu Ala Gln Cys Pro Gly Trp Pro Pro Gly Gly Arg Val
          20          25          30

```

```

Val Gly Gly Arg Trp Gly Cys Cys Leu Glu Pro Ala Ser Gly Ala Gly
          35          40          45

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```

Pro Gly Leu Ser Cys Ala Pro Pro Pro Leu Pro Pro Ala Glu Gly Trp
          50          55          60

```

```

Leu Pro Ser Pro Pro Asp Pro Ala Leu Gly Ala Gly Leu Ser Glu Val
65          70          75          80

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```

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

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Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
          100          105          110

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Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
          115          120          125

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Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
          130          135          140

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Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
 145 150 155 160

Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala Phe Gln
 165 170 175

Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu
 180 185 190

Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala
 195 200 205

Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val Leu Ala
 210 215 220

Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp
 225 230 235 240

Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala Lys Ala
 245 250 255

Ala Leu Ala Gly Lys Lys Ala Asn Gly Gly Ala Ala Gln Arg Thr Val
 260 265 270

Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu Phe
 275 280 285

Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile
 290 295 300

Arg Lys Arg Phe Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr
 305 310 315 320

Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Ala Ile Gln
 325 330 335

Asn Ser Met Lys Pro Phe Lys Val Pro Asn His Leu Ile Trp Leu Ile
 340 345 350

Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu
 355 360 365

Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu
 370 375 380

Ser Ile Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp
 385 390 395 400

Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys
 405 410 415

Trp Ala Ala Arg Thr Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu
420 425 430

Tyr Leu Val Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr
435 440 445

Gly Met Met Ala Gln Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe
450 455 460

Arg Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly
465 470 475 480

Gln Pro Val Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn
485 490 495

Arg Glu Ala Pro Ala Ala Gly Thr
500

<210> 18
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bubulus
bubulis (water buffalo) diacylglycerol O-acyltransferase 1
isoform X2 (BbDGAT1-X2) in pAT009, codon optimised for expression
in yeast.

<400> 18
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gctcaatgtc caggttggcc accaggtggt agagttgttg gtggtagatg gggttgttgt 120
ttggaaccag cttctggtgc tgggtccaggt ttatcttgtg ctccaccacc attgccacca 180
gctgaaggtt ggttgccatc tccaccagat ccagctttag gtgccggttt gtctgaagtt 240
ggttctgaag gtcctttgtt ggcttctgct gttgattcta gatgtcacag attgcaggat 300
tccttgttct cttctgattc tggtttctct aactacaggg gtattttgaa ctggtgcgtt 360
gttatgttga ttttgtctaa cgctaggctg ttcttggaga acttgattaa gtacggtatc 420
ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 480
ttgtgtttgg ttatcggttc taacattttt gctgttgctg cttccaagt cgaaaaaaga 540
ttggctgttg gtgctttgac tgaacaagct ggtttgttgt tgcattggtt taacttggct 600
accattttgt gttttccagc tgctgttgca tttctgttgg aatctattac tccagtcggt 660
tctgttttgg ctttgatggt ttacactatc ctgttcctaa agttgttctc ctacagagat 720
gttaatttgt ggtgcagaga aagacgtgct ggtgctaaag ctaaagctgc tttggctggt 780
aaaaaagcta acggtggtgc tgctcaaaga actgtttctt atccagataa cttgacctac 840
agggacttgt actacttttt gtttgctcca accttgtgct acgaattgaa tttccaaga 900
tctcccagga tcagaaagag gtttttgttg agaagattgc tggaaatgct gtttttgacc 960
caattgcaag tcggtttgat tcaacaatgg atggttccag ctatccagaa ttctatgaag 1020

ccattcaagg ttcctaacca cttgatctgg ttgattttct tctactgggtt gttccactct	1080
tgcttgaatg cagttgctga attgatgcaa tttggtgaca gagaatttta cagagactgg	1140
tggaactctg aatccattac ttacttttgg cagaactgga acatcccagt tcataagtgg	1200
tgtatcagac atttctacaa gccaatgctt agaaggggtt cttctaaatg ggctgctaga	1260
acagcagttt ttttggcctc tgcttttttc cacgaatact tggtttctat cccattgaga	1320
atgttcagat tgtgggcttt tactgggatg atggctcaaa ttccattagc ttggatcggt	1380
ggtagattct tcagaggtaa ttatggtaat gctgccgttt gggtgtcctt gattattggt	1440
caaccagttg ctgttttgat gtacgttcat gattactacg tcttgaacag agaagctcca	1500
gctgcaggta cttaa	1515

<210> 19
 <211> 499
 <212> PRT
 <213> Bubalus bubalis

<400> 19

Met	Arg	Trp	Leu	Trp	Asp	Gly	Ser	Ser	Asp	Ser	Glu	Trp	Ala	Gly	Tyr
1			5						10					15	

Gly	Gly	Phe	Trp	Ala	Gly	Pro	Ser	Ser	Gly	Tyr	Pro	His	Arg	Leu	Ser
		20					25						30		

Ser	Trp	Asp	Ser	Trp	Ala	Trp	Glu	Pro	Cys	Ser	Pro	Cys	Gln	Lys	Ala
		35					40					45			

Gly	Ala	Glu	Ser	Arg	Arg	Arg	Gly	Pro	Gly	Gly	Ser	Glu	Pro	His	Cys
50						55					60				

Val	Cys	Ser	Pro	Gly	Trp	Thr	Trp	Arg	Arg	Cys	His	Arg	Leu	Gln	Asp
65				70						75				80	

Ser	Leu	Phe	Ser	Ser	Asp	Ser	Gly	Phe	Ser	Asn	Tyr	Arg	Gly	Ile	Leu
			85						90					95	

Asn	Trp	Cys	Val	Val	Met	Leu	Ile	Leu	Ser	Asn	Ala	Arg	Leu	Phe	Leu
			100					105					110		

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

Ser	Leu	Phe	Leu	Lys	Asp	Pro	Tyr	Ser	Trp	Pro	Ala	Leu	Cys	Leu	Val
	130					135					140				

Ile	Val	Ala	Asn	Ile	Phe	Ala	Val	Ala	Ala	Phe	Gln	Val	Glu	Lys	Arg
145				150					155						160

Leu	Ala	Val	Gly	Ala	Leu	Thr	Glu	Gln	Ala	Gly	Leu	Leu	Leu	His	Gly
			165						170					175	

Val Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala Val Ala Phe Leu
180 185 190

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

Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp Val Asn Leu Trp
210 215 220

Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala Lys Ala Ala Leu Ala Gly
225 230 235 240

Lys Lys Ala Asn Gly Gly Ala Ala Gln Arg Thr Val Ser Tyr Pro Asp
245 250 255

Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu
260 265 270

Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
275 280 285

Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val
290 295 300

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

Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys
325 330 335

Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu
340 345 350

Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp
355 360 365

Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe
370 375 380

Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
385 390 395 400

Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr
405 410 415

Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile
420 425 430

Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln
435 440 445

Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly
 450 455 460

Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val
 465 470 475 480

Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu Ala Pro Ala
 485 490 495

Ala Gly Thr

<210> 20
 <211> 1500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the protein coding region of Bubulus
 bubulis (water buffalo) diacylglycerol O-acyltransferase 1
 isoform X3 (BbDGAT1-X3) in pAT010, codon optimised for expression
 in yeast.

<400> 20
 atgaggtggt tgtgggatgg ttcctctgat tctgaatggg ctggttatgg tggtttttgg 60
 gctgggtccat cttctggtta tccacataga ttgtcatctt gggattcttg ggcttgggaa 120
 ccatgttctc catgtcaaaa agctgggtgct gaacttagaa gaagaggtcc aggcggttct 180
 gaaccacatt gtgtttgttc tccaggttgg acttgagaa gatgtcatag attgcaagac 240
 agcttgttct cttccgattc tggtttttct aactacaggg gtattttgaa ctggtgcgtt 300
 gttatgttga ttttgtctaa cgctaggctg ttcttgagaa acttgattaa gtacggtatc 360
 ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 420
 ttgtgtttgg ttatcggttg taacatTTTT gctgttgctg cttccaagt cgaaaaaaga 480
 ttggctgttg gtgctttgac tgaacaagca gggttgttgt tgcattggtt taacttggct 540
 accattttgt gttttccagc tgctgttgca ttcttgttgg aatctattac tccagttggt 600
 tccgttttgg ctttgatggt ttacactatc ctgttcctaa agctgttctc ctacagagat 660
 gttaatttgt ggtgtagaga aagacgtgct ggtgctaaag ctaaagctgc tttggctggt 720
 aaaaaagcta atgggtgtgc tgctcaaaga actgtttctt acccagataa cttgacttac 780
 agggacttgt actacttttt gtctgctcca actttgtgct acgaattgaa tttccaaga 840
 tctcccagga tcagaaagag gtttttgttg agaagattgc tggaaatgct gtttttgacc 900
 caattgcaag tcggtttgat tcaacaatgg atgggtccag ctattcagaa ttctatgaag 960
 ccattcaagg acatggacta ctctagaatc gtcgaaaggt tgttgaaatt ggccgttcca 1020
 aaccatttga tctggctgat ttttttctac tggttgttcc actcttgctt gaatgcagtt 1080
 gctgaattga tgcaatttgg tgacagagaa ttttacagag actggtggaa ctctgaatcc 1140
 attacttact tttggcagaa ctggaacatc ccagttcata agtggtgtat cagacatttc 1200

Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val Leu Ala
210 215 220

Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr Arg Asp
225 230 235 240

Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala Lys Ala
245 250 255

Ala Leu Ala Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu Cys Tyr
260 265 270

Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe Leu Leu
275 280 285

Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val Gly Leu
290 295 300

Ile Gln Gln Trp Met Val Pro Ala Ile Gln Asn Ser Met Lys Pro Phe
305 310 315 320

Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys Leu Ala
325 330 335

Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu Phe His
340 345 350

Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp Arg Glu
355 360 365

Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe Trp Gln
370 375 380

Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe Tyr Lys
385 390 395 400

Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr Ala Val
405 410 415

Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile Pro Leu
420 425 430

Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln Ile Pro
435 440 445

Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly Asn Ala
450 455 460

Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val Leu Met
465 470 475 480

Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu Ala Pro Ala Ala Gly
485 490 495

Thr

<210> 22
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bubulus bubulis (water buffalo) diacylglycerol O-acyltransferase 1 isoform X4 (BbDGAT1-X4) in pAT011, codon optimised for expression in yeast.

<400> 22
atgtgccac aagaaggtaa aggttctcca ggtttgtctc catacaaac tgggtggttg 60
gctcaatgtc caggttggcc accaggtggt agagttgttg gtggtagatg gggttgttgt 120
ttggaaccag cttctggtgc tgggtccaggt ttatcttgtg ctccaccacc attgccacca 180
gctgaaggtt ggttgccatc tccaccagat ccagctttag gtgccggttt gtctgaagtt 240
ggttctgaag gtcctttgtt ggcttctgct gttgattcta gatgtcacag attgcaggat 300
tccttgttct cttctgattc tggtttctct aactacaggg gtattttgaa ctggtgctgt 360
gttatgttga ttttgtctaa cgctaggctg ttcttggaga acttgattaa gtacgggtatc 420
ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 480
ttgtgtttgg ttatcggttc taacattttt gctgttgctg ccttccaagt cgaaaaaaga 540
ttggctgttg gtgctttgac tgaacaagct ggtttgttgt tgcattggtg taacttggct 600
accattttgt gttttccagc tgctgttgca tttctgttgg aatctattac tccagtcggt 660
tctgttttgg ctttgatggt ttacactatc ctgttcctaa agttgttctc ctacagagat 720
gttaatttgt ggtgcagaga aagacgtgct ggtgctaaag ctaaagctgc tttggctgac 780
ttgtactact ttttgtttgc tccaaccttg tgctacgaat tgaattttcc aagatctccc 840
aggatcagaa agaggttttt gttgagaaga ttgctggaaa tgctgttttt gacccaattg 900
caagtcgggt tgattcaaca atggatggtt ccagctatcc agaattctat gaagccattc 960
aaggatatgg actactccag aatcgctcaa aggttgttga aattggcagt tccaaaccat 1020
ttgatctggc tgattttttt ctactggttg ttccactctt gcttgaatgc agttgctgaa 1080
ttgatgcaat ttggtgacag agaattttac agagactggt ggaactctga atccattact 1140
tacttttggc agaactggaa catcccagtt cataagtggg gtatcagaca tttctacaag 1200
ccaatgctta gaaggggttc ttctaaatgg gctgctagaa cagcagtttt tttggcctct 1260
gcttttttcc acgaatactt ggtttctatc ccattgagaa tgttcagatt gtgggctttt 1320
actggtatga tggctcaaat tccattagct tggatcggtg gtagattctt cagaggtaat 1380
tatggtaatg ctgccgtttg gttgtccttg attattgggt aaccagttgc tgttttgatg 1440
tacgttcatg attactacgt cttgaacaga gaagctccag ctgcaggtac ttaa 1494

<210> 23
 <211> 474
 <212> PRT
 <213> Bubalus bubalis

<400> 23

Met Cys Pro Gln Glu Gly Lys Gly Ser Pro Gly Leu Ser Pro Tyr Lys
 1 5 10 15

Thr Gly Gly Leu Ala Gln Cys Pro Gly Trp Pro Pro Gly Gly Arg Val
 20 25 30

Val Gly Gly Arg Trp Gly Cys Cys Leu Glu Pro Ala Ser Gly Ala Gly
 35 40 45

Pro Gly Leu Ser Cys Ala Pro Pro Pro Leu Pro Pro Ala Glu Gly Trp
 50 55 60

Leu Pro Ser Pro Pro Asp Pro Ala Leu Gly Ala Gly Leu Ser Glu Val
 65 70 75 80

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

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
 100 105 110

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
 115 120 125

Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
 130 135 140

Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
 145 150 155 160

Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala Phe Gln
 165 170 175

Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu
 180 185 190

Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala
 195 200 205

Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Ala Val Leu Leu Pro Gly
 210 215 220

Arg Gln Pro Leu Val Pro Arg Ala Gln Gly Trp Gly Gln Gly Gln Gly
 225 230 235 240

Cys Phe Gly Arg Ser Leu Leu Leu Pro Leu Arg Pro Asp Pro Val Leu
245 250 255

Arg Ala Gln Leu Pro Pro Leu Pro Pro His Pro Lys Ala Leu Pro Ala
260 265 270

Ala Ala Thr Pro Gly Asp Ala Val Pro His Pro Ala Pro Gly Gly Ala
275 280 285

Asp Pro Ala Val Asp Gly Pro Gly His Pro Glu Leu His Glu Ala Leu
290 295 300

Gln Gly His Gly Leu Leu Pro His Arg Gly Ala Pro Pro Glu Ala Gly
305 310 315 320

Gly Pro Gln Pro Pro His Leu Ala His Leu Leu Leu Leu Ala Leu Pro
325 330 335

Leu Leu Pro Glu Arg Arg Gly Arg Ala His Ala Val Trp Arg Pro Arg
340 345 350

Val Leu Pro Gly Leu Val Glu Leu Arg Val Tyr His Leu Leu Leu Ala
355 360 365

Glu Leu Glu His Pro Cys Ser Gln Val Val His Gln Thr Leu Leu Gln
370 375 380

Ala His Ala Pro Ala Gly Gln Gln Gln Val Gly Ser Gln Asp Gly Ser
385 390 395 400

Ile Ser Gly Leu Arg Leu Leu Pro Arg Val Pro Gly Glu His Pro Pro
405 410 415

Ala His Val Pro Pro Leu Gly Leu His Gly His Asp Gly Ala Asp Pro
420 425 430

Ala Gly Leu Asp Ser Gly Pro Leu Leu Pro Arg Gln Leu Arg Gln Arg
435 440 445

Ser Arg Val Ala Val Thr His His Trp Ala Ala Gly Gly Arg Pro Asp
450 455 460

Val Arg Pro Arg Leu Leu Arg Ala Gln Pro
465 470

<210> 24
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bubulus
bubulis (water buffalo) diacylglycerol O-acyltransferase 1
isoform X5 (BbDGAT1-X5) in pAT012, codon optimised for expression

in yeast.

<400> 24
atgtgcccac aagaaggtaa aggttctcca ggtttgtctc catacaaac tgggtggttg 60
gctcaatgtc caggttggcc accaggtggt agagttgttg gtggtagatg gggttgttgt 120
ttggaaccag cttctggtgc tgggtccaggt ttatcttgtg ctccaccacc attgccacca 180
gctgaagggtt ggttgccatc tccaccagat ccagcttttag gtgccggttt gtctgaagtt 240
ggttctgaag gtcctttgtt ggcttctgct gttgattcta gatgtcacag attgcaggat 300
tccttgttct cttctgattc tggtttctct aactacaggg gtattttgaa ctggtgcgtt 360
gttatgttga ttttgtctaa cgctaggctg ttcttggaga acttgattaa gtacgggtatc 420
ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 480
ttgtgtttgg ttatcggtgc taacattttt gctgttgctg ccttccaagt cgaaaaaaga 540
ttggctgttg gtgctttgac tgaacaagct ggtttgttgt tgcattggtg taacttggct 600
accattttgt gttttccagc tgctgttgca tttctgttgg aatctattac tccagctgtt 660
ttgttgccag gtagacaacc attggttcca agagcacaag gttgggggtca aggtcaaggt 720
tgttttggta gatctttgtt gttaccattg aggccagatc ctgttttgag agcacaattg 780
ccacctttac caccacatcc aaaggctttg cctgctgctg ctactccagg tgatgctgtt 840
ccacatccag ctccaggtgg tgcagatcct gcagttgatg gtcctgggtca tccagaattg 900
catgaagcct tacaagggtc tggtttggtt ccacatagag gtgccccacc tgaagccggt 960
ggtccacaac cacctcattt ggctcatttg ttattattgg cattgcctct gttgccagag 1020
agaagaggta gagcacatgc tgtttggagg ccaagagttt tgccagggtt ggttgaattg 1080
agagtttacc acttgttgtt ggccgaattg gaacatccat gttctcaagt tgttcaccaa 1140
actttgttgc aagctcatgc tccagctggt caacaacagg ttggttctca agatggttct 1200
atttccggtt tgagattatt gcctagagtt ccaggtgaac atccaccagc tcatgttcca 1260
ccattgggtt tacatggtca tgatggtgct gaccagctg gtttagattc tgggtccatta 1320
ttgccaagac aattgagaca gagatctaga gttgctgtta ctcatcattg ggctgccggt 1380
ggtagaccag atgttagacc aagattattg agagcccaac cataa 1425

<210> 25
<211> 467
<212> PRT
<213> Bubalus bubalis

<400> 25

Met Gly Asp Arg Gly Gly Ala Gly Gly Ser Arg Arg Arg Arg Thr Gly
1 5 10 15

Ser Arg Pro Ser Ile Gln Gly Gly Ser Gly Pro Ala Ala Val Glu Glu
20 25 30

Glu Val Arg Asp Ala Gly Ala Gly Gly Asp Ala Pro Val Arg Asp Thr
35 40 45

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asp Leu Arg
 50 55 60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
 65 70 75 80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
 85 90 95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
 100 105 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
 115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
 130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
 145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
 165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
 180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
 195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
 210 215 220

Lys Ala Ala Leu Ala Asp Leu Tyr Tyr Phe Leu Phe Ala Pro Thr Leu
 225 230 235 240

Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
 245 250 255

Leu Leu Arg Arg Leu Leu Glu Met Leu Phe Leu Thr Gln Leu Gln Val
 260 265 270

Gly Leu Ile Gln Gln Trp Met Val Pro Ala Ile Gln Asn Ser Met Lys
 275 280 285

Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Val Glu Arg Leu Leu Lys
 290 295 300

Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Leu
 305 310 315 320

Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp
325 330 335

Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Ile Thr Tyr Phe
340 345 350

Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
355 360 365

Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Ala Ala Arg Thr
370 375 380

Ala Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Ile
385 390 395 400

Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln
405 410 415

Ile Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Arg Gly Asn Tyr Gly
420 425 430

Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Val Ala Val
435 440 445

Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Arg Glu Ala Pro Ala
450 455 460

Ala Gly Thr
465

<210> 26
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bubulus
bubulis (water buffalo) diacylglycerol O-acyltransferase 1
isoform X6 (BbDGAT1-X6) in pAT013, codon optimised for expression
in yeast.

<400> 26
atgggtgata gaggtggtgc tgggtggttct agaagaagaa ggacaggttc tagaccatct 60
attcaagggtg gttctggtcc agctgctggt gaagaagagg ttagagatgc tgggtgccggt 120
ggtgatgctc cagttagaga tactgataag gatggtgatg ttgatgttgg ttcagggtcat 180
tggtgattga gatgtcatag attgcaggac agcttgttct cttctgattc tggtttttct 240
aactacaggg gtattttgaa ctggtgcgtt gttatgttga ttttgtctaa cgctaggctg 300
ttcttgagga acttgattaa gtacggtatc ttggttgatc caatccaggt tgtttctttg 360
ttcttgaagg atccatattc ttggccagct ttgtgtttgg ttatcgttgc taacattttt 420
gctgttgctg cttccaagt cgaaaaaaga ttggctgttg gtgctttgac tgaacaagca 480

ggtttgttgt tgcatggtgt taacttggct accatthttgt gttttccagc agcagttgct	540
ttcttgttgg aatctattac tccagttggt tccgttttgg ctttgatggt ttacactatc	600
ctgttcctaa agctgttctc ctacagagat gttaatttgt ggtgtagaga aagacgtgct	660
ggtgctaaag ctaaaagtgc tttggctgac ttgtactact ttttgtttgc tccaaccttg	720
tgctacgaat tgaattttcc aagatctccc aggatcagaa agagggttttt gttgagaaga	780
ttgctggaaa tgctgttttt gacccaattg caagtcgggt tgattcaaca atggatgggt	840
ccagctatcc agaattctat gaagccattc aaggatatgg actactccag aatcgtcgaa	900
aggttgttga aattggcagt tccaaacctt ttgatctggc tgattttttt ctactggttg	960
ttccactctt gcttgaatgc tgttgcagaa ttgatgcaat ttggtgacag agaattttac	1020
agagactggt ggaactctga atccattact tacttttggc agaactggaa catcccagtt	1080
cataagtgggt gtatcagaca tttctacaag ccaatgttgc gtagaggttc ttctaaatgg	1140
gctgctagaa cagcagtttt tttggcttct gctttcttcc acgaatactt ggtttctatc	1200
ccattgagaa tgttcagatt gtgggctttt actggtatga tggctcaaat tccattagct	1260
tggatcgttg gtagattctt cagaggtaat tatggtaatg ctgccgtttg gttgtccttg	1320
attattggtc aaccagttgc tgttttgatg tacgttcatg attactacgt cttgaacaga	1380
gaagctccag ctgcaggtac ttaa	1404

<210> 27
 <211> 459
 <212> PRT
 <213> Bubalus bubalis

<400> 27

Met Cys Pro Gln Glu Gly Lys Gly Ser Pro Gly Leu Ser Pro Tyr Lys
1 5 10 15

Thr Gly Gly Leu Ala Gln Cys Pro Gly Trp Pro Pro Gly Gly Arg Val
20 25 30

Val Gly Gly Arg Trp Gly Cys Cys Leu Glu Pro Ala Ser Gly Ala Gly
35 40 45

Pro Gly Leu Ser Cys Ala Pro Pro Pro Leu Pro Pro Ala Glu Gly Trp
50 55 60

Leu Pro Ser Pro Pro Asp Pro Ala Leu Gly Ala Gly Leu Ser Glu Val
65 70 75 80

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

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
100 105 110

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala

115	120	125
Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro 130 135 140		
Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala 145 150 155 160		
Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala Phe Gln 165 170 175		
Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala Gly Leu 180 185 190		
Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro Ala Ala 195 200 205		
Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Ala Val Leu Leu Pro Gly 210 215 220		
Arg Gln Pro Leu Val Pro Arg Ala Gln Gly Trp Gly Gln Gly Gln Gly 225 230 235 240		
Cys Phe Gly Arg Ser Leu Leu Leu Pro Leu Arg Pro Asp Pro Val Leu 245 250 255		
Arg Ala Gln Leu Pro Pro Leu Pro Pro His Pro Lys Ala Leu Pro Ala 260 265 270		
Ala Ala Thr Pro Gly Asp Ala Val Pro His Pro Ala Pro Gly Gly Ala 275 280 285		
Asp Pro Ala Val Asp Gly Pro Gly His Pro Glu Leu His Glu Ala Leu 290 295 300		
Gln Gly Pro Gln Pro Pro His Leu Ala His Leu Leu Leu Ala Leu 305 310 315 320		
Pro Leu Leu Pro Glu Arg Arg Gly Arg Ala His Ala Val Trp Arg Pro 325 330 335		
Arg Val Leu Pro Gly Leu Val Glu Leu Arg Val Tyr His Leu Leu Leu 340 345 350		
Ala Glu Leu Glu His Pro Cys Ser Gln Val Val His Gln Thr Leu Leu 355 360 365		
Gln Ala His Ala Pro Ala Gly Gln Gln Gln Val Gly Ser Gln Asp Gly 370 375 380		
Ser Ile Ser Gly Leu Arg Leu Leu Pro Arg Val Pro Gly Glu His Pro 385 390 395 400		

Pro Ala His Val Pro Pro Leu Gly Leu His Gly His Asp Gly Ala Asp
405 410 415

Pro Ala Gly Leu Asp Ser Gly Pro Leu Leu Pro Arg Gln Leu Arg Gln
420 425 430

Arg Ser Arg Val Ala Val Thr His His Trp Ala Ala Gly Gly Arg Pro
435 440 445

Asp Val Arg Pro Arg Leu Leu Arg Ala Gln Pro
450 455

<210> 28
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of the protein coding region of Bubulus bubulis (water buffalo) diacylglycerol O-acyltransferase 1 isoform X7 (BbDGAT1-X7) in pAT014, codon optimised for expression in yeast.

<400> 28
atgtgcccac aagaaggtaa aggttctcca ggtttgtctc catacaaaac tgggtggttg 60
gctcaatgtc caggttggcc accaggtggt agagttgttg gtggtagatg gggttgttgt 120
ttggaaccag cttctggtgc tgggccaggt ttatcttggt ctccaccacc attgccacca 180
gctgaagggtt ggttgccatc tccaccagat ccagctttag gtgccggttt gtctgaagtt 240
ggttctgaag gtcctttggt ggcttctgct gttgattcta gatgtcacag attgcaggat 300
tccttgttct cttctgattc tggtttctct aactacaggg gtattttgaa ctggtgcgtt 360
gttatgttga ttttgtctaa cgctaggctg ttcttgaga acttgattaa gtacgggtatc 420
ttggttgatc caatccaggt tgtttctttg ttcttgaagg atccatattc ttggccagct 480
ttgtgtttgg ttatcgttgc taacatTTTT gctgttgctg ccttccaagt cgaaaaaaga 540
ttggctgttg gtgctttgac tgaacaagct ggtttgttgt tgcattggtt taacttggct 600
accattttgt gttttccagc tgctgttgca tttctgttgg aatctattac tccagctgtt 660
ttgttgccag gtagacaacc attggttcca agagcacaag gttgggggtca aggtcaaggt 720
tgttttggta gatctttggt gttaccattg aggccagatc ctgttttgag agcacaattg 780
ccacctttac caccacatcc aaaggctttg cctgctgctg ctactccagg tgatgctgtt 840
ccacatccag ctccaggtgg tgcagatcct gcagttgatg gtcctggtca tccagaattg 900
catgaagcct tacaagggtc acaaccacct catttggtc acttggtgtt gttagctttg 960
ccattattgc cagagagaag aggtagagca catgctgttt ggaggccaag agttttgcca 1020
ggtttggttg aattgagagt ttaccatttg ttgctggccg aattggaaca tccatgttct 1080
caagttgttc accaaaacttt gttgcaagct catgctccag ctggtcaaca acaggttggt 1140
tctcaagatg gttctatttc cggtttgaga ttgctacaa gagttccagg tgaacatcca 1200

ccagctcatg ttccaccatt gggtttacat ggatcatgatg gtgctgaccc agctgggtta 1260
gattctggtc cattattacc aagacagttg agacagagat ctagagttgc tggttactcat 1320
cattgggctg ccggtagtag accagatgtt agaccaagat tattgagagc ccaaccataa 1380

<210> 29
<211> 489
<212> PRT
<213> Bos taurus

<400> 29

Met Gly Asp Arg Gly Gly Ala Gly Gly Ser Arg Arg Arg Arg Thr Gly
1 5 10 15

Ser Arg Pro Ser Ile Gln Gly Gly Ser Gly Pro Ala Ala Ala Glu Glu
20 25 30

Glu Val Arg Asp Val Gly Ala Gly Gly Asp Ala Pro Val Arg Asp Thr
35 40 45

Asp Lys Asp Gly Asp Val Asp Val Gly Ser Gly His Trp Asp Leu Arg
50 55 60

Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser
65 70 75 80

Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser
85 90 95

Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val
100 105 110

Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp
115 120 125

Pro Ala Leu Cys Leu Val Ile Val Ala Asn Ile Phe Ala Val Ala Ala
130 135 140

Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Ala
145 150 155 160

Gly Leu Leu Leu His Gly Val Asn Leu Ala Thr Ile Leu Cys Phe Pro
165 170 175

Ala Ala Val Ala Phe Leu Leu Glu Ser Ile Thr Pro Val Gly Ser Val
180 185 190

Leu Ala Leu Met Val Tyr Thr Ile Leu Phe Leu Lys Leu Phe Ser Tyr
195 200 205

Arg Asp Val Asn Leu Trp Cys Arg Glu Arg Arg Ala Gly Ala Lys Ala
210 215 220

Lys Ala Ala Leu Ala Gly Lys Ala Ala Asn Gly Gly Ala Ala Gln Arg
 225 230 235 240

Thr Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe
 245 250 255

Leu Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro
 260 265 270

Arg Ile Arg Lys Arg Phe Leu Leu Arg Arg Leu Leu Glu Met Leu Phe
 275 280 285

Leu Thr Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Ala
 290 295 300

Ile Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile
 305 310 315 320

Val Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu
 325 330 335

Ile Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu
 340 345 350

Leu Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser
 355 360 365

Glu Ser Ile Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys
 370 375 380

Trp Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser
 385 390 395 400

Lys Trp Ala Ala Arg Thr Ala Val Phe Leu Ala Ser Ala Phe Phe His
 405 410 415

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Thr Gly Met Met Ala Gln Ile Pro Leu Ala Trp Ile Val Gly Arg Phe
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Phe Arg Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile
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