

SEQUENCE LISTING

<110> National University Of Singapore
 <120> METHOD OF CONVERTING GREASE CONTAINING HIGH CONTENT OF FREE FATTY ACIDS TO FATTY ACID ESTERS AND CATALYSTS FOR USE IN SAID METHOD
 <130> 1202327
 <160> 6
 <170> PatentIn version 3.5
 <210> 1
 <211> 1029
 <212> DNA
 <213> Candida antarctica
 <300>
 <308> GenBank: Z30645.1
 <309> 2006-06-12
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 ctcgatgcgg gtctgacctg ccagggtgct tcgccatcct cgggtctcaa acccatcctt 180
 ctcgtccccg gaaccggcac cacaggtcca cagtcgttcg actcgaactg gatccccctc 240
 tcaacgcagt tgggttacac accctgctgg atctcacccc cgccgttcac gctcaacgac 300
 acccaggtca acacggagta catggtcaac gccatcaccc cgctctacgc tggttcgggc 360
 aacaacaagc ttcccgtgct tacctggtcc cagggtgggc tggttgcaca gtgggggtctg 420
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 aagggcaccg tcctcgccgg ccctctcgat gcactcgcg ttagtgcacc ctccgtatgg 540
 cagcaaacca ccggttcggc actcaccacc gcactccgaa acgcagggtg tctgacctag 600
 atcgtgcccc ccaccaacct ctactcggcg accgacgaga tcgttcagcc tcagggtgtcc 660
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 tgtggggccgc tgttcgtcat cgaccatgca ggctcgtc cctcgcagtt ctctacgtc 780
 gtcggtcgat ccgccctgcg ctccaccacg ggccaggctc gtagtgcaga ctatggcatt 840
 acggactgca accctcttcc cgccaatgat ctgactcccg agcaaaaggt cgccgcggct 900
 gcgctcctgg cgccggcagc tgcagccatc gtggcggggc caaagcagaa ctgcgagccc 960
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 <213> Candida antarctica
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 <308> GenBank: Z30645.1

<309> 2006-06-12

<313> (1)..(342)

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Met Lys Leu Leu Ser Leu Thr Gly Val Ala Gly Val Leu Ala Thr Cys
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Ala Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln
 35 40 45

Gly Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly
 50 55 60

Thr Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu
 65 70 75 80

Ser Thr Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe
 85 90 95

Met Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile
 100 105 110

Thr Ala Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr
 115 120 125

Trp Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro
 130 135 140

Ser Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr
 145 150 155 160

Lys Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala
 165 170 175

Pro Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu
 180 185 190

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

Ser Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu
 210 215 220

Asp Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val
 225 230 235 240

Cys Gly Pro Leu Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln
 245 250 255

Phe Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln
260 265 270

Ala Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala
275 280 285

Asn Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Leu Ala
290 295 300

Pro Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro
305 310 315 320

Asp Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys
325 330 335

Ser Gly Ile Val Thr Pro
340

<210> 3
<211> 1224
<212> DNA
<213> Thermomyces lanuginosus

<300>
<308> GenBank: EU022703.1
<309> 2007-12-30
<313> (1)..(1224)

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agtcctattc gtcgaggtat gtggccacgc aatactctca tgcattgcct ttcgacctgc 120
tgtactaaga ctgcacatac agaggtctcg caggatctgt ttaaccagtt caatctcttt 180
gcacagtatt ctgcagccgc atactgcgga aaaaacaatg atgccccagc tggtaaaaac 240
attacgtgca cgggaaatgc ctgccccgag gtagagaagg cggatgcaac gtttctctac 300
tcgtttgaag agtaagtgtc gacataagtg caggcactcg ccgtggaaat agcagactga 360
ccgggaagtg cagctctgga gtgggcatg tcaccggctt cttgtctctc gacaacacga 420
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ttaacttcga cttgaaagaa ataaatgaca tttgtctccg ctgcagggga catgacggct 540
tcacttcgtc ctggaggtct gtagccgata cgtaaggca gaaggaggat gatgctgtga 600
gggagcatcc cgactatcgc gtggtgttta ccggacatag cttgggtggg gcattggcaa 660
ctgttgccgg agcagacctg cgtggaaatg ggtatgatat cgacgtggta ttagtaaaac 720
gagatcatgc gggaaagtgc aggaagtctg atacacgcat attagttttc atatggcgcc 780
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gatatcgtga agatagaagg catcgatgcc accggcggca ataaccagcc taacattccg 1020
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 <211> 291
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 <213> Thermomyces lanuginosus

<300>
 <308> GenBank: EU022703.1
 <309> 2007-12-30
 <313> (1)..(291)

<400> 4

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Asn Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Gly Lys Asn Asn
35 40 45

Asp Ala Pro Ala Gly Thr Asn Ile Thr Cys Thr Gly Asn Ala Cys Pro
50 55 60

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

Gly Val Gly Asp Val Thr Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys
85 90 95

Leu Ile Val Leu Ser Phe Arg Gly Ser Arg Ser Ile Glu Asn Trp Ile
100 105 110

Gly Asn Leu Asn Phe Asp Leu Lys Glu Ile Asn Asp Ile Cys Ser Gly
115 120 125

Cys Arg Gly His Asp Gly Phe Thr Ser Ser Trp Arg Ser Val Ala Asp
130 135 140

Thr Leu Arg Gln Lys Val Glu Asp Ala Val Arg Glu His Pro Asp Tyr
145 150 155 160

Arg Val Val Phe Thr Gly His Ser Leu Gly Gly Ala Leu Ala Thr Val
165 170 175

Ala Gly Ala Asp Leu Arg Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser
Page 4

180 185 190
 Tyr Gly Ala Pro Arg Val Gly Asn Arg Ala Phe Ala Glu Phe Leu Thr
 195 200 205
 Val Gln Thr Gly Gly Thr Leu Tyr Arg Ile Thr His Thr Asn Asp Ile
 210 215 220
 Val Pro Arg Leu Pro Pro Arg Glu Phe Gly Tyr Ser His Ser Ser Pro
 225 230 235 240
 Glu Tyr Trp Ile Lys Ser Gly Thr Leu Val Pro Val Thr Arg Asn Asp
 245 250 255
 Ile Val Lys Ile Glu Gly Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro
 260 265 270
 Asn Ile Pro Asp Ile Pro Ala His Leu Trp Tyr Phe Gly Leu Ile Gly
 275 280 285
 Thr Cys Leu
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<210> 5
 <211> 2457
 <212> DNA
 <213> *Serratia marcescens*

<300>
 <308> GenBank: DQ841349.1
 <309> 2006-08-16
 <313> (1)..(2457)

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 tcgcacgcct aatatattagg gctaatacta tttctaccga tgttggtcct ctgaccagct 180
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 gaaaacgcgt cgaaagcgct gttttccgac gccttgcca tctccaccta cgcttaccac 360
 aatatcgata acggcttcga cgaaggctac caccagaccg gtttcggtct tggcctgccg 420
 ctgacgctga tcaccgcgct gatcggcagc acccaatcgc agggcggcct gccccgcatt 480
 ccctggaacc ccgactccga acaggccgag caggagacgg tgaacaatgc cggctggctg 540
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 ggcgagaccg ccggttacac caccgcgag gccgaggtgc tgggcaaata tgacagcgaa 660
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tcactgggcg tacacgatgc gccgcacgcc tccgccacca acaatatcgt caacttcaac	1140
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cgcggaata cctgggtgga agacctgaac cgcaacgcgg aaacgcacag cggaccgacg	1380
tttatcatcg gcagcgacgg caatgatttg atcaagggcg gcaaaggcaa cgactatctc	1440
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agcacctgc gcagcaaaga aacctcctgg ctgattttca gcaaagaggt ggatcatcag	1680
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ggcggcgacg gcgatgacgt cctgcaggct gcgagccacg acgcctggct gttcggcaac	1800
gccggcaacg acacgctgat cggccatgcc ggcggaacc tgacctcgt cggcggcagc	1860
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<210> 6
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 <213> *Serratia marcescens*

 <300>
 <308> GenBank: DQ841349.1
 <309> 2006-08-16
 <313> (1)..(614)

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 35 40 45
 Leu Pro Leu Thr Leu Ile Thr Ala Leu Ile Gly Ser Thr Gln Ser Gln
 50 55 60
 Gly Gly Leu Pro Arg Ile Pro Trp Asn Pro Asp Ser Glu Gln Ala Ala
 65 70 75 80
 Gln Glu Thr Val Asn Asn Ala Gly Trp Ser Val Ile Ser Ala Ala Gln
 85 90 95
 Leu Gly Tyr Ala Gly Lys Thr Asp Ala Arg Gly Thr Tyr Tyr Gly Glu
 100 105 110
 Thr Ala Gly Tyr Thr Thr Ala Gln Ala Glu Val Leu Gly Lys Tyr Asp
 115 120 125
 Ser Glu Gly Asn Leu Thr Ala Ile Gly Ile Ser Phe Arg Gly Thr Ser
 130 135 140
 Gly Pro Arg Glu Ser Leu Ile Gly Asp Thr Ile Gly Asp Val Ile Asn
 145 150 155 160
 Asp Leu Leu Ala Gly Phe Gly Pro Lys Gly Tyr Ala Asp Gly Tyr Thr
 165 170 175
 Leu Asn Ala Phe Gly Asn Leu Leu Gly Asp Val Ala Lys Phe Ala Gln
 180 185 190
 Ala His Gly Leu Ser Gly Glu Asp Val Val Val Ser Gly His Ser Leu
 195 200 205
 Gly Gly Leu Ala Val Asn Ser Met Ala Ala Gln Ser Asp Ala Asn Trp
 210 215 220
 Gly Gly Phe Tyr Ala Gln Ser Asn Tyr Val Ala Phe Ala Ser Pro Thr
 225 230 235 240
 Gln Tyr Glu Ala Gly Gly Lys Val Ile Asn Ile Gly Tyr Glu Asn Asp
 245 250 255
 Pro Val Phe Arg Ala Leu Asp Gly Thr Ser Leu Thr Leu Pro Ser Leu
 260 265 270

Gly Val His Asp Ala Pro His Ala Ser Ala Thr Asn Asn Ile Val Asn
 275 280 285

Phe Asn Asp His Tyr Ala Ser Asp Ala Trp Asn Leu Leu Pro Phe Ser
 290 295 300

Ile Leu Asn Ile Pro Thr Trp Leu Ser His Leu Pro Phe Phe Tyr Gln
 305 310 315 320

Asp Gly Leu Met Arg Val Leu Asn Ser Glu Phe Tyr Ser Leu Thr Asp
 325 330 335

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

Asn Thr Trp Val Glu Asp Leu Asn Arg Asn Ala Glu Thr His Ser Gly
 355 360 365

Pro Thr Phe Ile Ile Gly Ser Asp Gly Asn Asp Leu Ile Lys Gly Gly
 370 375 380

Lys Gly Asn Asp Tyr Leu Glu Gly Arg Asp Gly Asp Asp Ile Phe Arg
 385 390 395 400

Asp Ala Gly Gly Tyr Asn Leu Ile Ala Gly Gly Lys Gly His Asn Ile
 405 410 415

Phe Asp Thr Gln Gln Ala Leu Lys Asn Thr Glu Val Ala Tyr Asp Gly
 420 425 430

Asn Thr Leu Tyr Leu Arg Asp Ala Lys Gly Gly Ile Thr Leu Ala Asp
 435 440 445

Asp Ile Ser Thr Leu Arg Ser Lys Glu Thr Ser Trp Leu Ile Phe Ser
 450 455 460

Lys Glu Val Asp His Gln Val Thr Ala Ala Gly Leu Lys Ser Asp Ser
 465 470 475 480

Gly Leu Lys Ala Tyr Ala Ala Ala Thr Thr Gly Gly Asp Gly Asp Asp
 485 490 495

Val Leu Gln Ala Arg Ser His Asp Ala Trp Leu Phe Gly Asn Ala Gly
 500 505 510

Asn Asp Thr Leu Ile Gly His Ala Gly Gly Asn Leu Thr Phe Val Gly
 515 520 525

Gly Ser Gly Asp Asp Ile Leu Lys Gly Ala Gly Asn Gly Asn Thr Phe
 530 535 540

Leu Phe Ser Gly Asp Phe Gly Arg Asp Gln Leu Tyr Gly Phe Asn Ala
545 550 555 560

Thr Asp Lys Leu Val Phe Ile Gly Thr Glu Gly Ala Ser Gly Asn Ile
565 570 575

Arg Asp Tyr Ala Thr Gln Gln Asn Asp Asp Leu Val Leu Ala Phe Gly
580 585 590

His Gly Gln Val Thr Leu Ile Gly Val Ser Leu Asp His Phe Asn Thr
595 600 605

Asp Arg Val Val Leu Ala
610