

## SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> Modified sterol acyltransferases

<130> 32957-WO-PCT

<160> 15

<170> PatentIn version 3.5

<210> 1

<211> 610

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 1

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Arg Arg Leu Asn Ser Ala Glu Ala Asn Lys Arg His Ser Val Thr Tyr  
20 25 30

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

Ser Thr Thr Ser Leu Val Glu Pro Val Glu Ser Thr Glu Gly Val Glu  
50 55 60

Ser Thr Glu Ala Glu Arg Val Ala Gly Lys Gln Glu Gln Glu Glu Glu  
65 70 75 80

Tyr Pro Val Asp Ala His Met Gln Lys Tyr Leu Ser His Leu Lys Ser  
85 90 95

Lys Ser Arg Ser Arg Phe His Arg Lys Asp Ala Ser Lys Tyr Val Ser  
100 105 110

Phe Phe Gly Asp Val Ser Phe Asp Pro Arg Pro Thr Leu Leu Asp Ser  
115 120 125

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Ala Ile Asn Val Pro Phe Gln Thr Thr Phe Lys Gly Pro Val Leu Glu  
130 135 140

Lys Gln Leu Lys Asn Leu Gln Leu Thr Lys Thr Lys Thr Lys Ala Thr  
145 150 155 160

Val Lys Thr Thr Val Lys Thr Thr Glu Lys Thr Asp Lys Ala Asp Ala  
165 170 175

Pro Pro Gly Glu Lys Leu Glu Ser Asn Phe Ser Gly Ile Tyr Val Phe  
180 185 190

Ala Trp Met Phe Leu Gly Trp Ile Ala Ile Arg Cys Cys Thr Asp Tyr  
195 200 205

Tyr Ala Ser Tyr Gly Ser Ala Trp Asn Lys Leu Glu Ile Val Gln Tyr  
210 215 220

Met Thr Thr Asp Leu Phe Thr Ile Ala Met Leu Asp Leu Ala Met Phe  
225 230 235 240

Leu Cys Thr Phe Phe Val Val Phe Val His Trp Leu Val Lys Lys Arg  
245 250 255

Ile Ile Asn Trp Lys Trp Thr Gly Phe Val Ala Val Ser Ile Phe Glu  
260 265 270

Leu Ala Phe Ile Pro Val Thr Phe Pro Ile Tyr Val Tyr Tyr Phe Asp  
275 280 285

Phe Asn Trp Val Thr Arg Ile Phe Leu Phe Leu His Ser Val Val Phe  
290 295 300

Val Met Lys Ser His Ser Phe Ala Phe Tyr Asn Gly Tyr Leu Trp Asp  
305 310 315 320

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Ile Lys Gln Glu Leu Glu Tyr Ser Ser Lys Gln Leu Gln Lys Tyr Lys  
 325 330 335

Glu Ser Leu Ser Pro Glu Thr Arg Glu Ile Leu Gln Lys Ser Cys Asp  
 340 345 350

Phe Cys Leu Phe Glu Leu Asn Tyr Gln Thr Lys Asp Asn Asp Phe Pro  
 355 360 365

Asn Asn Ile Ser Cys Ser Asn Phe Phe Met Phe Cys Leu Phe Pro Val  
 370 375 380

Leu Val Tyr Gln Ile Asn Tyr Pro Arg Thr Ser Arg Ile Arg Trp Arg  
 385 390 395 400

Tyr Val Leu Glu Lys Val Cys Ala Ile Ile Gly Thr Ile Phe Leu Met  
 405 410 415

Met Val Thr Ala Gln Phe Phe Met His Pro Val Ala Met Arg Cys Ile  
 420 425 430

Gln Phe His Asn Thr Pro Thr Phe Gly Gly Trp Ile Pro Ala Thr Gln  
 435 440 445

Glu Trp Phe His Leu Leu Phe Asp Met Ile Pro Gly Phe Thr Val Leu  
 450 455 460

Tyr Met Leu Thr Phe Tyr Met Ile Trp Asp Ala Leu Leu Asn Cys Val  
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Ala Glu Leu Thr Arg Phe Ala Asp Arg Tyr Phe Tyr Gly Asp Trp Trp  
 485 490 495

Asn Cys Val Ser Phe Glu Glu Phe Ser Arg Ile Trp Asn Val Pro Val  
 500 505 510

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His Lys Phe Leu Leu Arg His Val Tyr His Ser Ser Met Gly Ala Leu  
 515 520 525

His Leu Ser Lys Ser Gln Ala Thr Leu Phe Thr Phe Phe Leu Ser Ala  
 530 535 540

Val Phe His Glu Met Ala Met Phe Ala Ile Phe Arg Arg Val Arg Gly  
 545 550 555 560

Tyr Leu Phe Met Phe Gln Leu Ser Gln Phe Val Trp Thr Ala Leu Ser  
 565 570 575

Asn Thr Lys Phe Leu Arg Ala Arg Pro Gln Leu Ser Asn Val Val Phe  
 580 585 590

Ser Phe Gly Val Cys Ser Gly Pro Ser Ile Ile Met Thr Leu Tyr Leu  
 595 600 605

Thr Leu  
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<210> 2  
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 <212> DNA  
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<211> 642

<212> PRT

<213> *Saccharomyces cerevisiae*

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Gln Lys Leu Asn Ala Ala Asp Ala Gly Lys Arg Gln Ser Ile Thr Val  
20 25 30

Asp Asp Glu Gly Glu Leu Tyr Gly Leu Asp Thr Ser Gly Asn Ser Pro  
35 40 45

Ala Asn Glu His Thr Ala Thr Thr Ile Thr Gln Asn His Ser Val Val  
50 55 60

Ala Ser Asn Gly Asp Val Ala Phe Ile Pro Gly Thr Ala Thr Glu Gly  
65 70 75 80

Asn Thr Glu Ile Val Thr Glu Glu Val Ile Glu Thr Asp Asp Asn Met  
85 90 95

Phe Lys Thr His Val Lys Thr Leu Ser Ser Lys Glu Lys Ala Arg Tyr  
100 105 110

Arg Gln Gly Ser Ser Asn Phe Ile Ser Tyr Phe Asp Asp Met Ser Phe  
115 120 125

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

Thr Lys Phe Val Gly Pro Thr Leu Glu Lys Glu Ile Arg Arg Arg Glu  
145 150 155 160

Lys Glu Leu Met Ala Met Arg Lys Asn Leu His His Arg Lys Ser Ser  
165 170 175

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Pro Asp Ala Val Asp Ser Val Gly Lys Asn Asp Gly Ala Ala Pro Thr  
180 185 190

Thr Val Pro Thr Ala Ala Thr Ser Glu Thr Val Val Thr Val Glu Thr  
195 200 205

Thr Ile Ile Ser Ser Asn Phe Ser Gly Leu Tyr Val Ala Phe Trp Met  
210 215 220

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

His Asn Gly Ser Phe Lys Asp Ser Glu Ile Leu Lys Phe Met Thr Thr  
245 250 255

Asn Leu Phe Thr Val Ala Ser Val Asp Leu Leu Met Tyr Leu Ser Thr  
260 265 270

Tyr Phe Val Val Gly Ile Gln Tyr Leu Cys Lys Trp Gly Val Leu Lys  
275 280 285

Trp Gly Thr Thr Gly Trp Ile Phe Thr Ser Ile Tyr Glu Phe Leu Phe  
290 295 300

Val Ile Phe Tyr Met Tyr Leu Thr Glu Asn Ile Leu Lys Leu His Trp  
305 310 315 320

Leu Ser Lys Ile Phe Leu Phe Leu His Ser Leu Val Leu Leu Met Lys  
325 330 335

Met His Ser Phe Ala Phe Tyr Asn Gly Tyr Leu Trp Gly Ile Lys Glu  
340 345 350

Glu Leu Gln Phe Ser Lys Ser Ala Leu Ala Lys Tyr Lys Asp Ser Ile  
355 360 365

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Asn Asp Pro Lys Val Ile Gly Ala Leu Glu Lys Ser Cys Glu Phe Cys  
370 375 380

Ser Phe Glu Leu Ser Ser Gln Ser Leu Ser Asp Gln Thr Gln Lys Phe  
385 390 395 400

Pro Asn Asn Ile Ser Ala Lys Ser Phe Phe Trp Phe Thr Met Phe Pro  
405 410 415

Thr Leu Ile Tyr Gln Ile Glu Tyr Pro Arg Thr Lys Glu Ile Arg Trp  
420 425 430

Ser Tyr Val Leu Glu Lys Ile Cys Ala Ile Phe Gly Thr Ile Phe Leu  
435 440 445

Met Met Ile Asp Ala Gln Ile Leu Met Tyr Pro Val Ala Met Arg Ala  
450 455 460

Leu Ala Val Arg Asn Ser Glu Trp Thr Gly Ile Leu Asp Arg Leu Leu  
465 470 475 480

Lys Trp Val Gly Leu Leu Val Asp Ile Val Pro Gly Phe Ile Val Met  
485 490 495

Tyr Ile Leu Asp Phe Tyr Leu Ile Trp Asp Ala Ile Leu Asn Cys Val  
500 505 510

Ala Glu Leu Thr Arg Phe Gly Asp Arg Tyr Phe Tyr Gly Asp Trp Trp  
515 520 525

Asn Cys Val Ser Trp Ala Asp Phe Ser Arg Ile Trp Asn Ile Pro Val  
530 535 540

His Lys Phe Leu Leu Arg His Val Tyr His Ser Ser Met Ser Ser Phe  
545 550 555 560

Lys Leu Asn Lys Ser Gln Ala Thr Leu Met Thr Phe Phe Leu Ser Ser



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565

570

575

Val Val His Glu Leu Ala Met Tyr Val Ile Phe Lys Lys Leu Arg Phe  
580 585 590

Tyr Leu Phe Phe Phe Gln Met Leu Gln Met Pro Leu Val Ala Leu Thr  
595 600 605

Asn Thr Lys Phe Met Arg Asn Arg Thr Ile Ile Gly Asn Val Ile Phe  
610 615 620

Trp Leu Gly Ile Cys Met Gly Pro Ser Val Met Cys Thr Leu Tyr Leu  
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Thr Phe

<210> 4

<211> 1929

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 4

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ttagacacct ccggcaactc accagccaat gaacacacag ctaccacaat tacacagaat 180

cacagcgtgg tggcctcaaa cggagacgtc gcattcatcc caggaactgc taccgaaggc 240

aatacagaga ttgtaactga agaagtgatt gagaccgatg ataacatgtt caagacccat 300

gtgaagactt taagctccaa agagaaggca cggatataggc aagggtcctc taactttata 360

tcgtatttcg atgatatgtc atttgaacac aggcccagta tattagatgg gtcagttaac 420

gagcccttca agaccaaatt cgtgggacct actttagaaa aggagatcag aagaaggagg 480

aaagagctaa tggccatgcg caaaaattta caccaccgca agtcctccc agatgctgtc 540

gactcagtag ggaaaaatga tggcgccgcc ccaactactg ttccaactgc cgccacctca 600

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 cataatggta gcttcaagga ttcggagatc ttgaaattta tgactacgaa ttgttcaact 780  
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 gagttttgt ttgttatctt ctacatgtat ttaacagaaa acatcctaaa actacactgg 960  
 ctgtccaaga tcttctttt ttgcattct ttagttttat tgatgaaaat gcattctttc 1020  
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 aacatcccag tgcataagtt ttgttaaga catgtttacc atagttcaat gagttcattc 1680  
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 caaatgccat tagtagcttt aacaaatact aaattcatga ggaacagaac cataatcgga 1860  
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<210> 5

<211> 241

&lt;212&gt; PRT

&lt;213&gt; Ustilago maydis

&lt;400&gt; 5

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Thr Ser Pro Lys Arg Ser Trp Ile Ile Val Ser Ala Ala Leu Val Gly  
 20 25 30

Phe Cys Ala Leu Ile Ala Ala Leu Asp Ser Ile Arg Ser Ser Phe Tyr  
 35 40 45

Ile Phe Asp His Lys Ala Ile Tyr Lys Ile Ala Ser Thr Ala Val Ala  
 50 55 60

Asn His Pro Gly Asn Ala Thr Ala Ile Phe Asp Asp Val Leu Asp Asn  
 65 70 75 80

Leu Arg Ala Asp Pro Lys Leu Ala Pro Tyr Ile Asn Lys Asn His Phe  
 85 90 95

Ser Asp Glu Ser Glu Trp Met Phe Asn Asn Ala Gly Gly Ala Met Gly  
 100 105 110

Ser Met Phe Ile Ile His Ala Ser Val Thr Glu Tyr Leu Ile Phe Phe  
 115 120 125

Gly Thr Pro Val Gly Thr Glu Gly His Thr Gly Arg His Thr Ala Asp  
 130 135 140

Asp Tyr Phe Asn Ile Leu Thr Gly Asn Gln Tyr Ala Phe Pro Ala Gly  
 145 150 155 160

Ala Leu Lys Ala Glu His Tyr Pro Ala Gly Ser Val His His Leu Arg  
 165 170 175

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Arg Gly Thr Val Lys Gln Tyr Met Met Pro Glu Asp Gly Cys Trp Ala  
 180 185 190

Leu Glu Leu Ala Gln Gly Trp Ile Pro Pro Met Leu Pro Phe Gly Leu  
 195 200 205

Ala Asp Val Leu Ser Ser Thr Leu Asp Leu Pro Thr Phe Gly Ile Thr  
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Val Trp Ile Thr Ala Arg Glu Met Val Gly Asn Leu Leu Ile Gly Lys  
 225 230 235 240

Phe

<210> 6

<211> 726

<212> DNA

<213> Ustilago maydis

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actgcggtcg ccaaccatcc aggcaatgcg acggccatct ttgatgatgt cctcgacaac 240

cttcgtgccg accccaagct cgcgccttac atcaacaaga atcattcag cgacgagtca 300

gaatggatgt tcaacaatgc cggtggtgct atgggtagca tgttcatcat tcatgcttcc 360

gtcaccgagt acctgatctt ctttggcact cccgtcggaa ccgagggtca cactggtcgt 420

cacacagccg atgactactt caacatcctt accggtaacc aatacgcttt cccagctggt 480

gcgctcaagg cggagcacta ccctgccgga tcagtgcacc atcttcgccg cggaacggtc 540

aagcagtaca tgatgcctga agacgggtgc tgggcgctcg agcttgctca gggctggatc 600

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<211> 384

<212> PRT

<213> Pichia pastoris

<400> 7

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20 25 30

Tyr Leu Lys Thr Leu Gly His Leu Thr Gly Ala Asn Asn Thr Met Glu  
35 40 45

Ser Leu Phe Gly Ile Ala Pro Asn Val Asp Gln Ala Ser Lys Asn His  
50 55 60

Trp Leu Arg Thr Val Asn Asp Ser Ile Ala Leu Ala Arg Pro Gly Glu  
65 70 75 80

Arg Leu Val Tyr Gly Val Asn Ala Pro Leu His Phe Phe Asp Glu Thr  
85 90 95

Ala Tyr Thr Tyr Ala Ser Ile Leu Gly Arg Ser Asn Ile Ile Arg Gln  
100 105 110

Phe Thr Thr Leu Met Ile Leu Met Ile Leu Phe Gly Trp Gly Leu Tyr  
115 120 125

Leu Ser Val Ala Ser Phe Ser Tyr Tyr Phe Val Phe Asp Lys Ala Ile  
130 135 140

Phe Asn His Pro Arg Tyr Leu Lys Asn Gln Met Ser Leu Glu Ile His  
145 150 155 160

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Gln Ala Leu Thr Ala Ile Pro Thr Met Val Leu Leu Thr Val Pro Trp  
165 170 175

Phe Leu Ile Glu Leu Arg Gly Tyr Ser Lys Leu Tyr Phe Asp Val Asn  
180 185 190

Glu Ser Thr Gly Gly Trp Lys Ala Ile Ile Trp Gln Ile Pro Cys Phe  
195 200 205

Ile Met Phe Thr Asp Cys Cys Ile Tyr Phe Ile His Arg Trp Leu His  
210 215 220

Trp Pro Ser Val Tyr Lys Arg Leu His Lys Pro His His Lys Trp Ile  
225 230 235 240

Val Cys Thr Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr  
245 250 255

Ala Gln Ser Leu Pro Tyr His Leu Tyr Gly Met Leu Phe Pro Leu His  
260 265 270

Lys Val Ser Tyr Leu Ile Leu Phe Gly Leu Val Asn Phe Trp Thr Val  
275 280 285

Met Ile His Asp Gly Glu Tyr Leu Ser Arg Asp Pro Ile Val Asn Gly  
290 295 300

Ala Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly  
305 310 315 320

Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Met Pro  
325 330 335

Asp Lys Glu Leu Phe Asp Lys Asn Lys Lys Lys Asp Val Lys Thr Trp  
340 345 350

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Arg Ser Gln Val Lys Gln Ala Asp Ser Ile Arg Glu Asp Leu Glu Gly  
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Lys Glu Asp Phe Arg Glu Tyr Gly Thr Glu Glu Lys Leu Lys Ser Thr  
 370 375 380

<210> 8

<211> 1155

<212> DNA

<213> Pichia pastoris

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 cgttggttgc actggccatc cgtgtataag cgtttgaca agcctcacca caagtggatt 720  
 gttgtacac ctttgctag tcatgccttc catccagtgt atggttatgc acaatcacta 780  
 ccttaccatt tgtatggaat gttgtttcca ctacacaagg tgagctatct gatcttattt 840  
 gggcttgtga acttttggac tgttatgac catgatggag aatacctgtc cagagaccct 900  
 atagtcaatg gagctgcttg tcatacagtg catcacctat acttcaacta caattacggc 960  
 cagttcacia cactttggga ccgtcttggg ggatcataca gaatgccaga caaggaactc 1020

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tttgataaga acaagaagaa agatgtaaag acatggcgtt cacaagtcaa gcaggccgat 1080

tcgataagag aagacttaga gggaaaagaa gatttccgtg agtatggaac tgaggaaaaa 1140

cttaaaagca catag 1155

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 9

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<210> 10

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 10

cacacggtct cacaagacaa cgttggacaa ctgc 34

<210> 11

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 11

cacacggtct caatcaaacg aaaagacaac gttggac 37

<210> 12

<211> 66

<212> DNA

<213> Artificial Sequence

<220>



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<223> primer

<400> 12

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actgca

66

<210> 13

<211> 58

<212> DNA

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<223> primer

<400> 13

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<210> 14

<211> 57

<212> DNA

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<212> DNA

<213> Artificial Sequence

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<223> primer

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