

SEQUENCE LISTING

<110> DSM IP Assets BV

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<120> Dicarboxylic acid production in a filamentous fungus

<130> 26344

<140> 26344WO

<141> 2008-11-14

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 533

<212> PRT

<213> Aspergillus niger

<400> 1

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Arg	Leu	Leu	Ser	Ser	Asn	Ser	Arg	Pro	Val	Gln	His	Phe	Pro	Arg	Leu
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Gln	Thr	Leu	Thr	Ser	Thr	Ser	Ser	Lys	Arg	Ala	Phe	Gly	Thr	Thr	Val
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Lys	Met	Ser	Ser	Ala	Thr	Arg	Ile	Glu	Thr	Asp	Ala	Phe	Gly	Glu	Ile
65					70					75					80

Glu	Val	Pro	Ala	Asp	Lys	Tyr	Trp	Gly	Ala	Gln	Thr	Gln	Arg	Ser	Leu
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Gly	Asn	Phe	Asp	Ile	Asn	Gln	Pro	Gln	Asp	Arg	Met	Pro	Glu	Pro	Val
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Val	Lys	Ala	Phe	Gly	Ile	Leu	Lys	Gly	Ala	Ala	Ala	Glu	Val	Asn	Met
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Lys Phe Gly Leu Asp Pro Lys Ile Gly Glu Ala Ile Lys Gln Ala Ala
 130 135 140

Ala Glu Val Ala Glu Gly Lys Leu Met Asp His Phe Pro Leu Val Val
 145 150 155 160

Trp Gln Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val
 165 170 175

Ile Ser Asn Arg Ala Ile Glu Ile Leu Gly Gly Glu Lys Gly Ser Lys
 180 185 190

Lys Pro Val His Pro Asn Asp His Val Asn Met Ser Ala Ser Ser Asn
 195 200 205

Asp Ser Phe Pro Thr Ala Met His Ile Ala Ala Val Val Glu Leu Glu
 210 215 220

Asn Thr Leu Leu Pro Ser Leu Arg Ser Leu Arg Asp Ala Leu Gln Val
 225 230 235 240

Lys Val Glu Lys Phe Asp Lys Ile Ile Lys Ile Gly Arg Thr His Leu
 245 250 255

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

Ala Gln Leu Asp Arg Asn Ile Glu Arg Val Glu Thr Ser Ile Pro His
 275 280 285

Leu Arg Tyr Leu Ala Gln Gly Gly Thr Ala Val Gly Thr Gly Leu Asn
 290 295 300

Thr Phe Lys Gly Phe Asp Glu Ala Ile Ala Ala Glu Val Thr Lys Leu
 305 310 315 320

Thr Gly Thr Glu Phe Lys Thr Ala Pro Asn Lys Phe Glu Val Leu Ala
 325 330 335

Ala His Asp Ser Ile Val Glu Ala Ser Gly Ala Leu Asn Thr Leu Ala
 340 345 350

Cys Ser Leu Phe Lys Ile Ala Gln Asp Ile Arg Tyr Leu Gly Ser Gly
 355 360 365

Pro Arg Cys Gly Leu Gly Glu Leu Val Leu Pro Glu Asn Glu Pro Gly
 370 375 380

Ser Ser Ile Met Pro Gly Lys Val Asn Pro Thr Gln Cys Glu Ser Leu
 385 390 395 400

Thr Met Val Cys Ser Gln Val Met Gly Asn His Val Ala Ala Thr Val
 405 410 415

Gly Gly Met Asn Gly Gln Phe Glu Leu Asn Val Phe Lys Pro Leu Met
 420 425 430

Ile Arg Asn Leu Leu His Ser Val Arg Ile Leu Ala Asp Gly Met Ala
 435 440 445

Ser Phe Glu Lys Asn Leu Val His Gly Leu Glu Ala Asn Glu Pro Arg
 450 455 460

Ile Asn Ser Leu Leu His Glu Ser Leu Met Leu Val Thr Cys Leu Asn
 465 470 475 480

Pro Val Ile Gly Tyr Asp Met Ala Ser Lys Val Ala Lys Asn Ala His
 485 490 495

Lys Lys Gly Leu Thr Leu Lys Gln Ser Ala Met Glu Leu Lys Ala Leu
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Ser Glu Glu Asp Phe Asp Lys Tyr Val Arg Pro Glu Leu Met Leu Ser
 515 520 525

Pro Lys Glu Lys Lys
 530

<210> 2
 <211> 1601
 <212> DNA
 <213> *Aspergillus niger*

<400> 2
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 gccgtcgctt tcacccccgc ctggttcagt tgccgtcgctt ttctgagctc caatagccga 120

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cctgttcaac acttcccccg tcttcagacc ttgacttcca cctccagcaa gagagccttt 180
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atcaaccagc cccaggaccg catgcctgag cccgttgtca aggctttcgg tatcctcaag 360
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<210> 3
<211> 467
<212> PRT
<213> Artificial sequence

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<220>

<223> mFUM A. niger minus 67 aa targeting signal

<400> 3

Met Ser Ala Thr Arg Ile Glu Thr Asp Ala Phe Gly Glu Ile Glu Val
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Pro Ala Asp Lys Tyr Trp Gly Ala Gln Thr Gln Arg Ser Leu Gly Asn
 20 25 30

Phe Asp Ile Asn Gln Pro Gln Asp Arg Met Pro Glu Pro Val Val Lys
 35 40 45

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

Gly Leu Asp Pro Lys Ile Gly Glu Ala Ile Lys Gln Ala Ala Ala Glu
 65 70 75 80

Val Ala Glu Gly Lys Leu Met Asp His Phe Pro Leu Val Val Trp Gln
 85 90 95

Thr Gly Ser Gly Thr Gln Ser Asn Met Asn Ser Asn Glu Val Ile Ser
 100 105 110

Asn Arg Ala Ile Glu Ile Leu Gly Gly Glu Lys Gly Ser Lys Lys Pro
 115 120 125

Val His Pro Asn Asp His Val Asn Met Ser Ala Ser Ser Asn Asp Ser
 130 135 140

Phe Pro Thr Ala Met His Ile Ala Ala Val Val Glu Leu Glu Asn Thr
 145 150 155 160

Leu Leu Pro Ser Leu Arg Ser Leu Arg Asp Ala Leu Gln Val Lys Val
 165 170 175

Glu Lys Phe Asp Lys Ile Ile Lys Ile Gly Arg Thr His Leu Gln Asp
 180 185 190

Ala Thr Pro Leu Thr Leu Gly Gln Glu Phe Ser Gly Tyr Val Ala Gln
 195 200 205

Leu Asp Arg Asn Ile Glu Arg Val Glu Thr Ser Ile Pro His Leu Arg
 210 215 220

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

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

Thr Glu Phe Lys Thr Ala Pro Asn Lys Phe Glu Val Leu Ala Ala His
 260 265 270

Asp Ser Ile Val Glu Ala Ser Gly Ala Leu Asn Thr Leu Ala Cys Ser
 275 280 285

Leu Phe Lys Ile Ala Gln Asp Ile Arg Tyr Leu Gly Ser Gly Pro Arg
 290 295 300

Cys Gly Leu Gly Glu Leu Val Leu Pro Glu Asn Glu Pro Gly Ser Ser
 305 310 315 320

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

Val Cys Ser Gln Val Met Gly Asn His Val Ala Ala Thr Val Gly Gly
 340 345 350

Met Asn Gly Gln Phe Glu Leu Asn Val Phe Lys Pro Leu Met Ile Arg
 355 360 365

Asn Leu Leu His Ser Val Arg Ile Leu Ala Asp Gly Met Ala Ser Phe
 370 375 380

Glu Lys Asn Leu Val His Gly Leu Glu Ala Asn Glu Pro Arg Ile Asn
 385 390 395 400

Ser Leu Leu His Glu Ser Leu Met Leu Val Thr Cys Leu Asn Pro Val
 405 410 415

Ile Gly Tyr Asp Met Ala Ser Lys Val Ala Lys Asn Ala His Lys Lys
 420 425 430

Gly Leu Thr Leu Lys Gln Ser Ala Met Glu Leu Lys Ala Leu Ser Glu

435 440 445

Glu Asp Phe Asp Lys Tyr Val Arg Pro Glu Leu Met Leu Ser Pro Lys
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Glu Lys Lys
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<210> 4
<211> 1404
<212> DNA
<213> Artificial sequence

<220>
<223> nt mFUM minus putative targeting signal

<400> 4

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cgcatgcctg agcccgttgt caaggctttc ggtatcctca agggtgctgc tgctgaagtg 180

aacatgaagt tcggccttga cccaagatc ggcgaggcca tcaagcaggc tgccgccgag 240

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ccccacctcc gctacctggc tcagggtggt accgccgtcg gtactggtct gaacaccttc 720

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tccggtcccc gctgcggtct tgggtgaactg gtctctcccg agaacgagcc tggttcttcc 960

atcatgcccg gcaagggttaa cccactcag tgcgagtccc ttaccatggt ctgctcccag 1020

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<210> 5
<211> 898
<212> DNA
<213> Artificial sequence

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<220>
<223> GPDA promotor

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<400> 5
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ctggtgtgcc cctcgttgac caagaatcta ttgcatcatc ggagaatatg gagcttcac 240
gaatcaccgg cagtaagcga aggagaatgt gaagccaggg gtgtatagcc gtcggcgaaa 300
tagcatgcc ttaacctagg tacagaagtc caattgcttc cgatctggta aaagattcac 360
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aacatttgtt gccatatatt cctgctctcc ccaccagctg ctcttttctt ttctctttct 720
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