

N 7764 ST25.txt
SEQUENCE LISTING

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<110> Norddeutsche Pflanzenzucht (NPZ)
        Universität Göttingen

<120> Verfahren zur Herstellung von mehrfach ungesättigten Fettsäuren
        in transgenen Organismen

<130> N 7764

<150> EP 07 103 183.5
<151> 2007-02-27

<160> 43

<170> PatentIn version 3.3

<210> 1
<211> 1350
<212> DNA
<213> Mantoniella squamata

<220>
<221> Nukleinsäure
<222> (1)..(1350)
<223> delta6-Desaturase

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cacatgcgca gcccgaaggc ctggaagatg ctgaaagccc tgcccaatcg ccccgcgtag      300
acccccagga gccaaagacc agacggggccg atgtctggaag atttcgccaa gtggcgcgct      360
cagctcgaaa aagagggggtt tttcaagccc agcatcgctc acgtcgcata ccgcatcgcc      420
gagcttgagg cgatgttcgc cctgggctgc tacatcatgt cgctgggcta ccccgctgct      480
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gggcacaact ccctgacggg gaacatcttg ctggacaagc ggatccaagc ggcgacgtgc      600
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aagacggcgg tggaggacaa ccgaccgagg ggattcagcc gcgcgtgggc ccgtgctcag      780
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tcccacgtgc tgcgcaccgc gaccatcaag tacgcggggg gatactcgtg gcccgtcgcg      960
tacctgtggt tcagcttcgg caactggatc gcatacatgt acctctttgc tcacttctcg      1020
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gcggtagatc acacagtgga catcgacccc tccaaggggt acgtcaactg gctcatggga      1140
tacctcaatt gccaggatcat ccaccacctc ttcccggaac tgccgcagtt ccgccagccc      1200

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gagggtgagca gacggttcgt cgcctttgcc aaaaagtgga acctcaacta caaggtgctc 1260
 acctactacg gcgcgtggaa ggctaccttc actaacctcg acaccgtggg gcaacactac 1320
 tacaagcacg ggaaggcgca cgctcactag 1350

<210> 2
 <211> 449
 <212> PRT
 <213> Mantoniella squamata

<220>
 <221> Aminosäuresequenz
 <222> (1)..(449)
 <223> Mantoniella squamata delta6-Desaturase
 <400> 2

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 Thr Arg Gly Lys Leu Ser Ala Asp Leu Ala Lys Leu Glu Pro His Lys
 20 25 30
 Leu Ala Gln Thr Phe Asp Thr Arg Trp Val Arg Val Gly Asp Val Glu
 35 40 45
 Tyr Asp Val Thr Asn Phe Lys His Pro Gly Gly Ser Val Ile Phe Tyr
 50 55 60
 Met Leu Ser Asn Thr Gly Ala Asp Ala Thr Glu Ala Phe Asn Glu Phe
 65 70 75 80
 His Met Arg Ser Pro Lys Ala Trp Lys Met Leu Lys Ala Leu Pro Asn
 85 90 95
 Arg Pro Ala Glu Thr Pro Arg Ser Gln Asp Pro Asp Gly Pro Met Leu
 100 105 110
 Glu Asp Phe Ala Lys Trp Arg Ala Gln Leu Glu Lys Glu Gly Phe Phe
 115 120 125
 Lys Pro Ser Ile Ala His Val Ala Tyr Arg Ile Ala Glu Leu Ala Ala
 130 135 140
 Met Phe Ala Leu Gly Cys Tyr Ile Met Ser Leu Gly Tyr Pro Val Val
 145 150 155 160
 Ala Ser Ile Val Phe Gly Ala Phe Phe Gly Ala Arg Cys Gly Trp Val
 165 170 175
 Gln His Glu Gly Gly His Asn Ser Leu Thr Gly Asn Ile Trp Leu Asp
 180 185 190

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Lys Arg Ile Gln Ala Ala Thr Cys Gly Phe Gly Leu Ser Thr Ser Gly
 195 200 205
 Asp Met Trp Asn Gln Met His Asn Lys His His Ala Thr Pro Gln Lys
 210 215 220
 Val Arg His Asp Met Asp Leu Asp Thr Thr Pro Ala Val Ala Phe Phe
 225 230 235 240
 Lys Thr Ala Val Glu Asp Asn Arg Pro Arg Gly Phe Ser Arg Ala Trp
 245 250 255
 Ser Arg Ala Gln Ala Trp Thr Phe Val Pro Val Thr Ser Gly Leu Leu
 260 265 270
 Val Gln Met Phe Trp Ile Tyr Val Leu His Pro Arg Gln Val Ala Arg
 275 280 285
 Lys Lys Asn Tyr Glu Glu Ala Ser Trp Met Ile Leu Ser His Val Leu
 290 295 300
 Arg Thr Ala Thr Ile Lys Tyr Ala Gly Gly Tyr Ser Trp Pro Val Ala
 305 310 315 320
 Tyr Leu Trp Phe Ser Phe Gly Asn Trp Ile Ala Tyr Met Tyr Leu Phe
 325 330 335
 Ala His Phe Ser Thr Ser His Thr His Leu Glu Val Val Pro Ser Asp
 340 345 350
 Lys His Ile Ser Trp Val Asn Tyr Ala Val Asp His Thr Val Asp Ile
 355 360 365
 Asp Pro Ser Lys Gly Tyr Val Asn Trp Leu Met Gly Tyr Leu Asn Cys
 370 375 380
 Gln Val Ile His His Leu Phe Pro Asp Met Pro Gln Phe Arg Gln Pro
 385 390 395 400
 Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys Lys Trp Asn Leu Asn
 405 410 415
 Tyr Lys Val Leu Thr Tyr Tyr Gly Ala Trp Lys Ala Thr Phe Thr Asn
 420 425 430
 Leu Asp Thr Val Gly Gln His Tyr Tyr Lys His Gly Lys Ala His Ala
 435 440 445
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N 7764 ST25.txt

<210> 3
 <211> 1449
 <212> DNA
 <213> Mantoniella squamata

<220>
 <221> Nukleinsäure
 <222> (1)..(1449)
 <223> delta5-Desaturase

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aaacactcca ccccgatga ctgttggtc atcgtccacg gcaagggtga cgacgtcacc      180
tccttcgtgc ccagacaccc gggagggaac atgatctggg tcaaagccgg tggggactgc      240
acgcagcttt tcgattcgta ccatccatt aagaccagg ctgtgctgga caagtactac      300
atcggcgagg tacagcgctg gagcggggat gagaaaaaga tcattgagta caacgacgac      360
atgaaaaagg ggaaatttta catggattgt aaagtcgccg tagagaagta cttcaaggac      420
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tacaccaacg tggagggggg agacccggat atccgatgcg cccagagaa ggacatccgc      780
cgcgtaacg aacatcagcc gcacgagagt taccacccc tgcagcacgt ctaccttct      840
ttcgcgtatg gcttgctctc cttcaagagc tgcttcgcgg acgacttcaa cgcgtagggcg      900
agcgggcgca tcggctgggt gaaggttgcg aagttcacgc gggcgaggc ggtttccttc      960
tggggctcca aggtgctgtg ggcgttttat tacctctatt tgcccgccac gtactcccct     1020
cactcgggcc tgaggatcgt ggcgcttgtc accatcaccg aggtgatcac gggctggctc     1080
ctggcgttca tgtttcaagt ggcgcacgtg gtgggcgacg tgaggttctt caaactgtca     1140
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gcgcacgggt caaaattctg gatgcacttc tccggcgggc tcaactacca ggtagctcac     1260
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gtcgcgaagg agtacggcct tgagtacgcc gtgtaccca cgttttggtc cgcgctctcg     1380
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<210> 4
 <211> 482
 <212> PRT
 <213> Mantoniella squamata

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<220>

<221> Aminosäuresequenz

<222> (1)..(482)

<223> Mantoniella squamata delta5-Desaturase

<400> 4

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

Lys Tyr Thr Thr Ala Asp Val Glu Lys His Ser Thr Pro Asp Asp Cys
35 40 45

Trp Leu Ile Val His Gly Lys Val Tyr Asp Val Thr Ser Phe Val Pro
50 55 60

Arg His Pro Gly Gly Asn Met Ile Trp Val Lys Ala Gly Gly Asp Cys
65 70 75 80

Thr Gln Leu Phe Asp Ser Tyr His Pro Ile Lys Thr Gln Ala Val Leu
85 90 95

Asp Lys Tyr Tyr Ile Gly Glu Val Gln Arg Val Ser Gly Asp Glu Lys
100 105 110

Lys Ile Ile Glu Tyr Asn Asp Asp Met Lys Lys Gly Lys Phe Tyr Met
115 120 125

Asp Cys Lys Val Ala Val Glu Lys Tyr Phe Lys Asp Thr Lys Gln Asp
130 135 140

Pro Arg Val His Val Glu Met Tyr Val Lys Thr Phe Val Ile Leu Ala
145 150 155 160

Gly Val Ala Val Cys His Tyr Cys Ser Phe Phe Leu Thr Ser Ser Phe
165 170 175

Leu Val Ser Ala Val Phe Ala Ala Leu His Gly Met Trp Lys Ala Glu
180 185 190

Val Gly Val Ser Ile Gln His Asp Ala Asn His Gly Ala Tyr Gly Lys
195 200 205

Ser Arg Gly Phe Leu His Ala Met Gln Leu Thr Leu Asp Val Val Gly
210 215 220

Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Val Gly His His Ala
225 230 235 240

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Tyr Thr Asn Val Glu Gly Val Asp Pro Asp Ile Arg Cys Ala Pro Glu
245 250 255

Lys Asp Ile Arg Arg Val Asn Glu His Gln Pro His Glu Ser Tyr His
260 265 270

Pro Leu Gln His Val Tyr Leu Phe Phe Ala Tyr Gly Leu Leu Ser Phe
275 280 285

Lys Ser Cys Phe Ala Asp Asp Phe Asn Ala Trp Ala Ser Gly Arg Ile
290 295 300

Gly Trp Val Lys Val Ala Lys Phe Thr Arg Gly Glu Ala Val Ser Phe
305 310 315 320

Trp Gly Ser Lys Val Leu Trp Ala Phe Tyr Tyr Leu Tyr Leu Pro Ala
325 330 335

Thr Tyr Ser Pro His Ser Gly Leu Arg Ile Val Ala Leu Val Thr Ile
340 345 350

Thr Glu Val Ile Thr Gly Trp Leu Leu Ala Phe Met Phe Gln Val Ala
355 360 365

His Val Val Gly Asp Val Arg Phe Phe Lys Leu Ser Glu Glu Gly Lys
370 375 380

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

Ala His Gly Ser Lys Phe Trp Met His Phe Ser Gly Gly Leu Asn Tyr
405 410 415

Gln Val Ala His His Leu Phe Pro Gly Val Cys His Cys His Tyr Pro
420 425 430

Ala Ile Ala Pro Ile Ile Met Lys Val Ala Lys Glu Tyr Gly Leu Glu
435 440 445

Tyr Ala Val Tyr Pro Thr Phe Trp Ser Ala Leu Ser Ala His Phe Thr
450 455 460

His Leu Lys Asn Val Gly Gln Lys Thr Tyr Val Pro Ser Leu Gln Thr
465 470 475 480

Ile Gly

<210> 5
<211> 1476
<212> DNA

<213> *Ostreococcus tauri*

<220>

<221> misc_feature

<222> (1)..(1476)

<223> Nukleinsäure der delta5-Desaturase

<300>

<308> Genbank / CR954212

<309> 2005-04-30

<313> (1)..(1476)

<400> 5

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acggcgggcg aggtggcgac gcacgcgcgg gcggatgatt gctgggtgat cgtgcgcggc      180
ggcgtgtacg acgtgacggc gttcgtgccg agacatccgg gtgggaacat gatttacgtc      240
aaagcggggg gggagtgcac ggcgcttttt gattcgtatc atccggagaa ggcgcggggg      300
gtgctggaga agtacaggat cggtgacttg acgcgagagg aggggtcggc ggcggtggg      360
gacatcgtgg agtacgcgaa ggatgacttg aaggacggtg cgttctttgc cgattgcaa      420
gccggggcg cgaagtattt caaagaaaat aagctcgatc cgcgcgtgca ctgggagatg      480
tacgcgaaga cggcgggcat tttggtgggg atcgtcgtcg ggcaactatta ctcgttcttc      540
gcgccggggc tgagcttcgg cgccgcgctc gcgtttgccc cgttgcacgg cacgtgtaag      600
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taccacacgt tttggtccgc cctgcgcgcg cacttccggc acctcgccaa cgtcggccgc     1440
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<210> 6

<211> 491

<212> PRT

<213> *Ostreococcus tauri*

<220>

<221> Aminosäuresequenz

<222> (1)..(491)

<223> Aminosäuresequenz der delta5-Desaturase

<400> 6

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 20 25 30

Val Asp Ala Asp Ala Arg Thr Tyr Thr Ala Ala Glu Val Ala Thr His
 35 40 45

Ala Arg Ala Asp Asp Cys Trp Val Ile Val Arg Gly Gly Val Tyr Asp
 50 55 60

Val Thr Ala Phe Val Pro Arg His Pro Gly Gly Asn Met Ile Tyr Val
 65 70 75 80

Lys Ala Gly Gly Glu Cys Thr Ala Leu Phe Asp Ser Tyr His Pro Glu
 85 90 95

Lys Ala Arg Gly Val Leu Glu Lys Tyr Arg Ile Gly Asp Leu Thr Arg
 100 105 110

Glu Glu Gly Ser Ala Ala Asp Gly Asp Ile Val Glu Tyr Ala Lys Asp
 115 120 125

Asp Leu Lys Asp Gly Ala Phe Phe Ala Asp Cys Lys Ala Gly Ala Ala
 130 135 140

Lys Tyr Phe Lys Glu Asn Lys Leu Asp Pro Arg Val His Trp Glu Met
 145 150 155 160

Tyr Ala Lys Thr Ala Ala Ile Leu Val Gly Ile Val Val Gly His Tyr
 165 170 175

Tyr Ser Phe Phe Ala Pro Gly Val Ser Phe Gly Ala Ala Leu Ala Phe
 180 185 190

Ala Ala Leu His Gly Thr Cys Lys Ala Glu Val Gly Val Ser Ile Gln
 195 200 205

His Asp Ala Asn His Gly Ala Tyr Gly Asn Ser Arg Thr Trp Leu His
 210 215 220

Ala Met Gln Leu Thr Leu Asp Val Val Gly Ala Ser Ser Phe Met Trp
 225 230 235 240

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Lys Gln Gln His Val Ala Gly His His Ala Tyr Thr Asn Val Glu Gly
245 250 255

Ile Asp Pro Asp Ile Arg Cys Ser Glu Lys Asp Ile Arg Arg Val Asn
260 265 270

Glu His Gln Pro His Glu Pro Tyr His Val Phe Gln His Val Tyr Leu
275 280 285

Ala Phe Met Tyr Gly Leu Leu Ser Leu Lys Ser Cys Phe Val Asp Asp
290 295 300

Phe Asn Ala Tyr Phe Ser Gly Arg Ile Gly Trp Val Lys Val Met Lys
305 310 315 320

Phe Thr Arg Gly Glu Ala Ile Ala Phe Trp Gly Thr Lys Leu Leu Trp
325 330 335

Ala Ala Tyr Tyr Leu Ala Leu Pro Leu Lys Met Ser His Arg Pro Leu
340 345 350

Gly Glu Leu Leu Ala Leu Trp Ala Val Thr Glu Phe Val Thr Gly Trp
355 360 365

Leu Leu Ala Phe Met Phe Gln Val Ala His Val Val Gly Glu Val His
370 375 380

Phe Phe Thr Leu Asp Ala Lys Asn Arg Val Asn Leu Gly Trp Gly Glu
385 390 395 400

Ala Gln Leu Met Ser Ser Ala Asp Phe Ala His Gly Ser Lys Phe Trp
405 410 415

Thr His Phe Ser Gly Gly Leu Asn Tyr Gln Val Val His His Leu Phe
420 425 430

Pro Gly Val Cys His Val His Tyr Pro Ala Leu Ala Pro Ile Ile Lys
435 440 445

Ala Ala Ala Glu Lys His Gly Leu His Tyr Gln Ile Tyr Pro Thr Phe
450 455 460

Trp Ser Ala Leu Arg Ala His Phe Arg His Leu Ala Asn Val Gly Arg
465 470 475 480

Ala Ala Tyr Val Pro Ser Leu Gln Thr Val Gly
485 490

<210> 7
<211> 1371

N 7764 ST25.txt

<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> misc_feature
<222> (1)..(1371)
<223> Nukleinsäuresequenz der delta6-Desaturase

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ctggcgaaga cgttcgcgag gcggtacgtc gtgatcgagg ggggtggagta cgatgtgacg    180
gattttaagc acccgggagg aacggttatt ttctatgcgt tgtcaaacac cggggcggac    240
gcgacggaag cgttcaagga gtttcatcat cggtcgagaa aggcgaggaa agccttggcg    300
gcgctcccgt ctcgaccggc caagacggcc aaggtggacg acgcggagat gctccaagat    360
ttcgccaagt ggcggaaaga attggagaga gatggattct tcaagccctc tccggcgcac    420
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gctcgatacg tcgtctcctc ggtgctcgtg tacgcttgct ttttcggcgc ccgatgcggt    540
tggtgacgac acgagggcgg acacagctcg ctgacgggca acatttggtg ggacaagcgc    600
atccaggcct tcacagccgg gttcgggtct gccggtagcg gcgacatgtg gaactcgatg    660
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cccgcggtgg cgttcttcaa caccgcggtg gaagacaatc gtccccgtgg ctttagcaag    780
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<210> 8
<211> 456
<212> PRT
<213> *Ostreococcus tauri*

<220>
<221> Aminosäuresequenz
<222> (1)..(456)
<223> Aminosäuresequenz der delta6-Desaturase

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20 25 30

Ala Glu Lys Met Glu Pro Ala Ala Leu Ala Lys Thr Phe Ala Arg Arg
35 40 45

Tyr Val Val Ile Glu Gly Val Glu Tyr Asp Val Thr Asp Phe Lys His
50 55 60

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

Ala Thr Glu Ala Phe Lys Glu Phe His His Arg Ser Arg Lys Ala Arg
85 90 95

Lys Ala Leu Ala Ala Leu Pro Ser Arg Pro Ala Lys Thr Ala Lys Val
100 105 110

Asp Asp Ala Glu Met Leu Gln Asp Phe Ala Lys Trp Arg Lys Glu Leu
115 120 125

Glu Arg Asp Gly Phe Phe Lys Pro Ser Pro Ala His Val Ala Tyr Arg
130 135 140

Phe Ala Glu Leu Ala Ala Met Tyr Ala Leu Gly Thr Tyr Leu Met Tyr
145 150 155 160

Ala Arg Tyr Val Val Ser Ser Val Leu Val Tyr Ala Cys Phe Phe Gly
165 170 175

Ala Arg Cys Gly Trp Val Gln His Glu Gly Gly His Ser Ser Leu Thr
180 185 190

Gly Asn Ile Trp Trp Asp Lys Arg Ile Gln Ala Phe Thr Ala Gly Phe
195 200 205

Gly Leu Ala Gly Ser Gly Asp Met Trp Asn Ser Met His Asn Lys His
210 215 220

His Ala Thr Pro Gln Lys Val Arg His Asp Met Asp Leu Asp Thr Thr
225 230 235 240

Pro Ala Val Ala Phe Phe Asn Thr Ala Val Glu Asp Asn Arg Pro Arg
245 250 255

Gly Phe Ser Lys Tyr Trp Leu Arg Leu Gln Ala Trp Thr Phe Ile Pro
260 265 270

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Val Thr Ser Gly Leu Val Leu Leu Phe Trp Met Phe Phe Leu His Pro
275 280 285

Ser Lys Ala Leu Lys Gly Gly Lys Tyr Glu Glu Leu Val Trp Met Leu
290 295 300

Ala Ala His Val Ile Arg Thr Trp Thr Ile Lys Ala Val Thr Gly Phe
305 310 315 320

Thr Ala Met Gln Ser Tyr Gly Leu Phe Leu Ala Thr Ser Trp Val Ser
325 330 335

Gly Cys Tyr Leu Phe Ala His Phe Ser Thr Ser His Thr His Leu Asp
340 345 350

Val Val Pro Ala Asp Glu His Leu Ser Trp Val Arg Tyr Ala Val Asp
355 360 365

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

Gly Tyr Leu Asn Cys Gln Val Ile His His Leu Phe Pro Ser Met Pro
385 390 395 400

Gln Phe Arg Gln Pro Glu Val Ser Arg Arg Phe Val Ala Phe Ala Lys
405 410 415

Lys Trp Asn Leu Asn Tyr Lys Val Met Thr Tyr Ala Gly Ala Trp Lys
420 425 430

Ala Thr Leu Gly Asn Leu Asp Asn Val Gly Lys His Tyr Tyr Val His
435 440 445

Gly Gln His Ser Gly Lys Thr Ala
450 455

<210> 9
<211> 1434
<212> DNA
<213> Phaeodactylum tricornutum

<220>
<221> misc_feature
<222> (1)..(1434)
<223> Nukleinsäure der delta6-Desaturase

<300>
<308> Genbank / AY082393
<309> 2002-04-01
<313> (1)..(1434)

<400> 9
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| gtctacgacg tgtccaactg gcacgaacat cccggaggcg ccgtcatttt cacgcacgcc | 180 |
| ggtgacgaca tgacggacat tttcgtgcc tttcacgcac ccggatcgca gtcgctcatg | 240 |
| aagaagttct acattggcga attgctcccc gaaaccaccg gcaaggagcc gcagcaaadc | 300 |
| gcctttgaaa agggctaccg cgatctgcgc tccaaactca tcatgatggg catgttcaag | 360 |
| tccaacaagt ggttctacgt ctacaagtgc ctacgcaaca tggccatttg ggccgccgcc | 420 |
| tgtgctctcg tcttttactc ggaccgcttc tgggtacacc tggccagcgc cgtcatgctg | 480 |
| ggaacattct ttcagcagtc gggatggttg gcacacgact ttctgcacca ccaggtcttc | 540 |
| accaagcgca agcacgggga tctcggagga ctcttttggg ggaacctcat gcagggttac | 600 |
| tccgtacagt ggtggaaaaa caagcacaac ggacaccacg ccgccccaa cctccactgc | 660 |
| tcctccgacg tcgcgcaaga tggggacccg gacatcgata ccatgcccct tctcgcttg | 720 |
| tccgtccagc aagcccagtc ttaccgggaa ctccaagccg acggaaagga ttcgggtttg | 780 |
| gtcaagttca tgatccgtaa ccaatcctac ttttactttc ccatcttggt gtcgccccgc | 840 |
| ctgtcgtggt tgaacgagtc cttcaagtgc gcctttgggc ttggagctgc gtcggagaac | 900 |
| gctgctctcg aactcaaggc caagggtctt cagtaccccc ttttgaaaaa ggctggcatc | 960 |
| ctgctgcact acgcttgat gcttacagtt tcgtccggct ttggacgctt ctggttcgcg | 1020 |
| tacaccgcat tttactttct aaccgcgacc gcgtcctgtg gattcttgct cgccattgtc | 1080 |
| tttggcctcg gccacaacgg catggccacc tacaatgccg acgcccgtcc ggacttctgg | 1140 |
| aagctccaag tcaccacgac tcgcaacgtc acgggaggac acggtttccc ccaagccttt | 1200 |
| gtcgactggt tctgtggtgg cctccagtac caagtgcacc accacttatt cccagcctg | 1260 |
| ccccgacaca atctggccaa gacacacgca ctggtcgaat cgttctgcaa ggagtggggt | 1320 |
| gtccagtacc acgaagccga ccttgtggac gggaccatgg aagtcttgca ccatttgggc | 1380 |
| agcgtggccg gcgaattcgt cgtggatttt gtacgcgatg gacccgccat gtaa | 1434 |

<210> 10
 <211> 477
 <212> PRT
 <213> Phaeodactylum tricornutum

<220>
 <221> Aminosäuresequenz
 <222> (1)..(477)
 <223> Aminosäuresequenz der delta6-Desaturase

<400> 10

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Gly | Gly | Asp | Ala | Arg | Ala | Ser | Lys | Gly | Ser | Thr | Ala | Ala |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Ile | Ser | Trp | Gln | Glu | Val | Lys | Thr | His | Ala | Ser | Pro | Glu | Asp |
| | | 20 | | | | | | 25 | | | | | 30 | | |

N 7764 ST25.txt

Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His
35 40 45

Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met
50 55 60

Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met
65 70 75 80

Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu
85 90 95

Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys
100 105 110

Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr
115 120 125

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val
130 135 140

Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu
145 150 155 160

Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

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

Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys
195 200 205

His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val
210 215 220

Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp
225 230 235 240

Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys
245 250 255

Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr
260 265 270

Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe
275 280 285

Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu
290 295 300

N 7764 ST25.txt

Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile
 305 310 315 320

Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg
 325 330 335

Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser
 340 345 350

Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met
 355 360 365

Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val
 370 375 380

Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe
 385 390 395 400

Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu
 405 410 415

Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val
 420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu
 435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly
 450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
 465 470 475

<210> 11
 <211> 1410
 <212> DNA
 <213> Phaeodactylum tricornutum

<220>
 <221> misc_feature
 <222> (1)..(1410)
 <223> Nukleinsäure der delta5-Desaturase

<300>
 <308> Genbank / AY082392
 <309> 2002-04-01
 <313> (1)..(1410)

<400> 11
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 gctgctacca tatcgacgca ggaacgcctt tgcagtctgt cttcgctcaa aggcgaagaa 120
 gtctgcatcg acggaatcat ctatgacctc caatcattcg atcatcccgg ggggtgaaacg 180

N 7764 ST25.txt

| | |
|--|------|
| atcaaaatgt ttggtggcaa cgatgtcact gtacagtaca agatgattca cccgtaccat | 240 |
| accgagaagc atttggaaaa gatgaagcgt gtcggcaagg tgacggattt cgtctgcgag | 300 |
| tacaagttcg ataccgaatt tgaacgcgaa atcaaacgag aagtcttcaa gattgtgcga | 360 |
| cgaggcaagg atttcggtac tttgggatgg ttcttccgtg cgttttgcta cattgccatt | 420 |
| ttcttctacc tgcagtacca ttgggtcacc acgggaacct cttggctgct ggccgtggcc | 480 |
| tacggaatct cccaagcgat gattggcatg aatgtccagc acgatgccaa ccacggggcc | 540 |
| acctccaagc gtccctgggt caacgacatg ctaggcctcg gtgcggattt tattggtggt | 600 |
| tccaagtggc tctggcagga acaacactgg acccaccacg cttacaccaa tcacgccgag | 660 |
| atggatcccg atagctttgg tgccgaacca atgctcctat tcaacgacta tcccttgat | 720 |
| catcccgctc gtacctggct acatcgcttt caagcattct ttacatgcc cgtcttggt | 780 |
| ggatactggt tgtccgctgt cttcaatcca caaattcttg acctccagca acgcggcgca | 840 |
| ctttccgtcg gtatccgtct cgacaacgct ttcattcact cgcgacgcaa gtatgcggtt | 900 |
| ttctggcggg ctgtgtacat tgcggtgaac gtgattgctc cgttttacac aaactccggc | 960 |
| ctcgaatggt cctggcgtgt ctttgaaac atcatgctca tgggtgtggc ggaatcgctc | 1020 |
| gcgctggcgg tcctgttttc gttgtcgac aatttcgaat ccgcggatcg cgatccgacc | 1080 |
| gccccactga aaaagacggg agaaccagtc gactggttca agacacaggc cgaaacttcc | 1140 |
| tgcacttacg gtggattcct ttccggttgc ttcacgggag gtctcaactt tcaggttgaa | 1200 |
| caccacttgt tcccacgcat gagcagcgtc tggatatccct acattgcccc caaggtccgc | 1260 |
| gaaatttgcg ccaaacacgg cgtccactac gcctactacc cgtggatcca ccaaaacttt | 1320 |
| ctctccaccg tccgctacat gcacgcggcc gggaccggtg ccaactggcg ccagatggcc | 1380 |
| agagaaaatc ccttgaccgg acgggcgtaa | 1410 |

<210> 12
 <211> 469
 <212> PRT
 <213> Phaeodactylum tricornutum

<220>
 <221> Aminosäuresequenz
 <222> (1)..(469)
 <223> Aminosäuresequenz der delta5-Desaturase

<400> 12

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Asp | Ala | Asp | Lys | Leu | Arg | Gln | Arg | Gln | Thr | Thr | Ala | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | His | Asn | Ala | Ala | Thr | Ile | Ser | Thr | Gln | Glu | Arg | Leu | Cys | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Leu | Lys | Gly | Glu | Glu | Val | Cys | Ile | Asp | Gly | Ile | Ile | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |

N 7764 ST25.txt

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
 50 55 60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
 65 70 75 80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp
 85 90 95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys
 100 105 110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu
 115 120 125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu
 130 135 140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala
 145 150 155 160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala
 165 170 175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly
 180 185 190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln
 195 200 205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp
 210 215 220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp
 225 230 235 240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met
 245 250 255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile
 260 265 270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp
 275 280 285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala
 290 295 300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly
 305 310 315 320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val
325 330 335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe
340 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu
355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly
370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu
385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala
405 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr
420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His
435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro
450 455 460

Leu Thr Gly Arg Ala
465

N 7764 ST25.txt

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gtttatcatc attcttcaat ttccctcatt tgggtgggcta ttgctcatca cgctcctggc 540
ggtgaagcat attggtctgc ggctctgaac tcaggagtgc atgttctcat gtatgcgtat 600
tacttcttgg ctgcctgcct tcgaagtagc ccaaagttaa aaaataagta ccttttttgg 660
ggcagggtact tgacacaatt ccaaagtgtc cagtttatgc tgaacttagt gcaggcttac 720
tacgacatga aaacgaatgc gccatatcca caatggctga tcaagatttt gttctactac 780
atgatctcgt tgctgtttct tttcggcaat ttttacgtac aaaaatacat caaacctct 840
gacggaaagc aaaagggagc taaaactgag tga 873

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<210> 14
 <211> 290
 <212> PRT
 <213> Physcomitrella patens

<220>
 <221> Aminosäuresequenz
 <222> (1)..(290)
 <223> Aminosäuresequenz der delta6-Elongase
 <400> 14

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser
1 5 10 15

Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp
20 25 30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile
35 40 45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu
50 55 60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu
65 70 75 80

Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser
85 90 95

Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr
100 105 110

Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile
115 120 125

Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr
130 135 140

Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His
145 150 155 160

N 7764 ST25.txt

Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His
165 170 175

His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly
180 185 190

Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg
195 200 205

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

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

Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile
245 250 255

Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr
260 265 270

Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys
275 280 285

Thr Glu
290

<210> 15
<211> 903
<212> DNA
<213> *Ostreococcus tauri*

<220>
<221> misc_feature
<222> (1)..(903)
<223> Nukleinsäuresequenz der delta5-Elongase

<400> 15
atgagcgct ccggtgcgt gtcgccgcg atcgcgtccg ccgcgtacgc gtacgcgacg 60
tacgcctacg cttttgagt gtcgcacgcg aatggcatcg acaacgtcga cgcgcgcgag 120
tggatcgggtg cgctgtcgtt gaggctcccg gcgatcgca cgacgatgta cctgttggtc 180
tgcttggtcg gaccgaggtt gatggcgaag cgcgaggcgt tcgacccgaa ggggttcgatg 240
ctggcgatca atgcgtatca gacggcggtt aacgtcgtcg tgctcgggat gttcgcgcga 300
gagatctcgg ggctggggca gcccggtgtg ggggtcaacca tgccgtggag cgatagaaaa 360
tcgtttaaga tcctcctcgg ggtgtggttg cactacaaca acaaataattt ggagctattg 420
gacactgtgt tcatgggttc gcgcaagaag acgaagcagt tgagcttctt gcacgtttat 480
catcacgcc tggtgatctg ggcgtggtgg ttggtgtgtc acttgatggc cacgaacgat 540
tgtatcgatg cctacttcgg cgcggcgtgc aactcgttca ttcacatcgt gatgtactcg 600

N 7764 ST25.txt

| | |
|---|-----|
| tattatctca tgtcggcgct cggcattcga tgcccgtgga agcgatacat caccaggt | 660 |
| caaatgctcc aattcgtcat tgtcttcgcg cagccgtgt tcgtgctgcg tcagaagcac | 720 |
| tgcccggtca cccttccttg ggcgcaaagt ttcgtcatga cgaacatgct cgtgctcttc | 780 |
| gggaacttct acctcaaggc gtactcgaac aagtcgcgcg gcgacggcg gagttccgtg | 840 |
| aaaccagccg agaccacgcg cgcgcccagc gtgcgacgca cgcgatctcg aaaaattgac | 900 |
| taa | 903 |

<210> 16
 <211> 300
 <212> PRT
 <213> *Ostreococcus tauri*

<220>
 <221> Aminosäuresequenz
 <222> (1)..(300)
 <223> Aminosäuresequenz der delta5-Elongase

<400> 16

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Ser | Gly | Ala | Leu | Leu | Pro | Ala | Ile | Ala | Ser | Ala | Ala | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Tyr | Ala | Thr | Tyr | Ala | Tyr | Ala | Phe | Glu | Trp | Ser | His | Ala | Asn | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asp | Asn | Val | Asp | Ala | Arg | Glu | Trp | Ile | Gly | Ala | Leu | Ser | Leu | Arg |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Ala | Ile | Ala | Thr | Thr | Met | Tyr | Leu | Leu | Phe | Cys | Leu | Val | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Leu | Met | Ala | Lys | Arg | Glu | Ala | Phe | Asp | Pro | Lys | Gly | Phe | Met |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Tyr | Asn | Ala | Tyr | Gln | Thr | Ala | Phe | Asn | Val | Val | Val | Leu | Gly |
| | | | 85 | | | | | | 90 | | | | | 95 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ala | Arg | Glu | Ile | Ser | Gly | Leu | Gly | Gln | Pro | Val | Trp | Gly | Ser |
| | | 100 | | | | | | 105 | | | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Pro | Trp | Ser | Asp | Arg | Lys | Ser | Phe | Lys | Ile | Leu | Leu | Gly | Val |
| | | 115 | | | | | 120 | | | | | 125 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Leu | His | Tyr | Asn | Asn | Lys | Tyr | Leu | Glu | Leu | Leu | Asp | Thr | Val | Phe |
| | 130 | | | | | 135 | | | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Arg | Lys | Lys | Thr | Lys | Gln | Leu | Ser | Phe | Leu | His | Val | Tyr |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | His | Ala | Leu | Leu | Ile | Trp | Ala | Trp | Trp | Leu | Val | Cys | His | Leu | Met |
| | | | 165 | | | | | | 170 | | | | | 175 | |

N 7764 ST25.txt

Ala Thr Asn Asp Cys Ile Asp Ala Tyr Phe Gly Ala Ala Cys Asn Ser
180 185 190

Phe Ile His Ile Val Met Tyr Ser Tyr Tyr Leu Met Ser Ala Leu Gly
195 200 205

Ile Arg Cys Pro Trp Lys Arg Tyr Ile Thr Gln Ala Gln Met Leu Gln
210 215 220

Phe Val Ile Val Phe Ala His Ala Val Phe Val Leu Arg Gln Lys His
225 230 235 240

Cys Pro Val Thr Leu Pro Trp Ala Gln Met Phe Val Met Thr Asn Met
245 250 255

Leu Val Leu Phe Gly Asn Phe Tyr Leu Lys Ala Tyr Ser Asn Lys Ser
260 265 270

Arg Gly Asp Gly Ala Ser Ser Val Lys Pro Ala Glu Thr Thr Arg Ala
275 280 285

Pro Ser Val Arg Arg Thr Arg Ser Arg Lys Ile Asp
290 295 300

<210> 17
<211> 27
<212> DNA
<213> Artificial

<220>
<223> DNA Primer

<220>
<221> misc_feature
<222> (1)..(27)
<223> 5'-RACE-Primer

<400> 17
catccgggcg gcagcgatcat cttctac

27

<210> 18
<211> 25
<212> DNA
<213> Artificial

<220>
<223> DNA Primer

<220>
<221> misc_feature
<222> (1)..(25)
<223> 3'-RACE-Primer

<400> 18
ggagaagagg tggtggatga cctgg

25

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> 5'-RACE-Primer

<400> 19
 ccgagtgagg ggagtacgtg gcggg

25

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(24)
 <223> 3'-RACE-Primer

<400> 20
 cactctccgg cgggctcaac tacc

24

<210> 21
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(36)
 <223> Primer MSdelta6 forward

<400> 21
 atgcgcggcc gcacataatg tgcctccca aggaat

36

<210> 22
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(29)

<223> Primer Msdelta6 reverse
 <400> 22
 gcattctaga ctagtgagcg tgcgccttc 29

<210> 23
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(38)
 <223> Primer Msdelta5 forward

<400> 23
 atgcccatgg acataatgcc cccgcgcgag accaccac 38

<210> 24
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(30)
 <223> Primer Msdelta5 reverse

<400> 24
 gcataccggt tcacccgatg gtttgaaggc 30

<210> 25
 <211> 37
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer

<220>
 <221> misc_feature
 <222> (1)..(37)
 <223> Primer Ptdelta6 forward

<400> 25
 atgcgcggcc gcacataatg ggcaaaggag gggacgc 37

<210> 26
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> DNA Primer


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<220>
<221> misc_feature
<222> (1)..(33)
<223> Primer Ptdelta6 reverse

<400> 26
gcattctaga ttacatggcg ggtccatcg c gta 33

<210> 27
<211> 37
<212> DNA
<213> Artificial

<220>
<223> DNA Primer

<220>
<221> misc_feature
<222> (1)..(37)
<223> Primer Ptdelta5 forward

<400> 27
atgcccatgg acataatggc tccggatgcg gataagc 37

<210> 28
<211> 30
<212> DNA
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