

SEQUENCE LISTING

<110> Axxence Holding B.V.

<120> Production of a flavour compound in a host cell

<130> P6070045PCT

<150> 17202546.2

<151> 2017-11-20

<160> 117

<210> 1

<211> 531

<212> PRT

<213> Rhodobacter capsulatus

<220>

<223> Tyrosine ammonia lyase enzyme from Rhodobacter capsulatus (RcTAL)

<400> 1

Met Thr Leu Gln Ser Gln Thr Ala Lys Asp Cys Leu Ala Leu Asp Gly
1 5 10 15

Ala Leu Thr Leu Val Gln Cys Glu Ala Ile Ala Thr His Arg Ser Arg
20 25 30

Ile Ser Val Thr Pro Ala Leu Arg Glu Arg Cys Ala Arg Ala His Ala
35 40 45

Arg Leu Glu His Ala Ile Ala Glu Gln Arg His Ile Tyr Gly Ile Thr
50 55 60

Thr Gly Phe Gly Pro Leu Ala Asn Arg Leu Ile Gly Ala Asp Gln Gly
65 70 75 80

Ala Glu Leu Gln Gln Asn Leu Ile Tyr His Leu Ala Thr Gly Val Gly
85 90 95

Pro Lys Leu Ser Trp Ala Glu Ala Arg Ala Leu Met Leu Ala Arg Leu
100 105 110

Asn Ser Ile Leu Gln Gly Ala Ser Gly Ala Ser Pro Glu Thr Ile Asp
115 120 125

Arg Ile Val Ala Val Leu Asn Ala Gly Phe Ala Pro Glu Val Pro Ala
130 135 140

Gln Gly Thr Val Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala His Met
145 150 155 160

Val Leu Ala Leu Gln Gly Arg Gly Arg Met Ile Asp Pro Ser Gly Arg
165 170 175

Val Gln Glu Ala Gly Ala Val Met Asp Arg Leu Cys Gly Gly Pro Leu
180 185 190

Thr Leu Ala Ala Arg Asp Gly Leu Ala Leu Val Asn Gly Thr Ser Ala
195 200 205

Met Thr Ala Ile Ala Ala Leu Thr Gly Val Glu Ala Ala Arg Ala Ile
210 215 220

Asp Ala Ala Leu Arg His Ser Ala Val Leu Met Glu Val Leu Ser Gly
225 230 235 240

His Ala Glu Ala Trp His Pro Ala Phe Ala Glu Leu Arg Pro His Pro
245 250 255

Gly Gln Leu Arg Ala Thr Glu Arg Leu Ala Gln Ala Leu Asp Gly Ala
260 265 270

Gly Arg Val Cys Arg Thr Leu Thr Ala Ala Arg Arg Leu Thr Ala Ala
275 280 285

Asp Leu Arg Pro Glu Asp His Pro Ala Gln Asp Ala Tyr Ser Leu Arg
290 295 300

Val Val Pro Gln Leu Val Gly Ala Val Trp Asp Thr Leu Asp Trp His
305 310 315 320

Asp Arg Val Val Thr Cys Glu Leu Asn Ser Val Thr Asp Asn Pro Ile

325

330

335

Phe Pro Glu Gly Cys Ala Val Pro Ala Leu His Gly Gly Asn Phe Met
 340 345 350

Gly Val His Val Ala Leu Ala Ser Asp Ala Leu Asn Ala Ala Leu Val
 355 360 365

Thr Leu Ala Gly Leu Val Glu Arg Gln Ile Ala Arg Leu Thr Asp Glu
 370 375 380

Lys Leu Asn Lys Gly Leu Pro Ala Phe Leu His Gly Gly Gln Ala Gly
 385 390 395 400

Leu Gln Ser Gly Phe Met Gly Ala Gln Val Thr Ala Thr Ala Leu Leu
 405 410 415

Ala Glu Met Arg Ala Asn Ala Thr Pro Val Ser Val Gln Ser Leu Ser
 420 425 430

Thr Asn Gly Ala Asn Gln Asp Val Val Ser Met Gly Thr Ile Ala Ala
 435 440 445

Arg Arg Ala Arg Ala Gln Leu Leu Pro Leu Ser Gln Ile Gln Ala Ile
 450 455 460

Leu Ala Leu Ala Leu Ala Gln Ala Met Asp Leu Leu Asp Asp Pro Glu
 465 470 475 480

Gly Gln Ala Gly Trp Ser Leu Thr Ala Arg Asp Leu Arg Asp Arg Ile
 485 490 495

Arg Ala Val Ser Pro Gly Leu Arg Ala Asp Arg Pro Leu Ala Gly His
 500 505 510

Ile Glu Ala Val Ala Gln Gly Leu Arg His Pro Ser Ala Ala Ala Asp
 515 520 525

Pro Pro Ala
 530

<210> 2
 <211> 1596
 <212> DNA
 <213> Rhodobacter capsulatus

<220>
 <223> Tyrosine ammonia lyase enzyme from Rhodobacter capsulatus
 (RcTAL) (codon optimised)

<400> 2
 atgaccctgc aatcccagac tgcaaaggac tgcctggcgc tggatggtgc actgacactg 60
 gttcagtgcg aagcaattgc cactcaccgc tcacggatct ccgtcacacc agcattgcgg 120
 gaacgctgcg cccgcgcgca cgcacgtctg gagcacgcta tcgcagaaca gcgtcacatc 180
 tatggtatca ccaccggctt cggaccactg gctaatcgcc tgatcgggtgc agatcagggc 240
 gccgaactcc agcagaacct catctaccac cttgctactg gcgtgggccc aaaactctcc 300
 tgggctgaag cacgtgcact catgctggct cgtctcaact ccataccttca gggcgcactt 360
 ggtgcatcac cagaaacat cgaccgtatc gttgccgttc tgaacgctgg cttcgcccca 420
 gaagtcccag ctgagggcac cgttggtgca tctggcgatc tgacccact ggctcacatg 480
 gtgctggcgc ttcagggctg aggtcgtatg atcgatccat ccggccgtgt tcaggaagcc 540
 ggcgcagtga tggatcgctt gtgcggtggc cactgacct tggcagcccg tgacgggtctg 600
 gctctggtca acggtacttc cgctatgacc gcaatcgctg ctttgaccgg tgtggaggct 660
 gcgcgcgcaa tcgacgccgc attgcgccac tccgctgtgc tcatggaggt tctctccggc 720
 cacgctgagg cttggcacc tgcatcttgc gaactccgcc cacaccagg ccagctgcgc 780
 gcaaccgaac gtctggcca ggctctcgat ggcgccggtc gcgtttgccg caccttgacc 840
 gcggcccgtc gcctgaccgc agctgatctg cgccctgagg atcaccagc ccaggacgcc 900
 tactccctgc gcgtgggtgc acagctggtt ggcgctgtct gggacaccct cgattggcac 960
 gatcgctgcg tgacctgcga actcaactct gtgaccgaca acccaatctt cccggaaggc 1020
 tgcgctgttc cagcactgca cggcggcaac ttcattggcg tgcacgtcgc actggcgtcg 1080
 gacgccctga acgctgcatt ggttaccctg gcaggtctgg tggagcgcca gatcgcacgc 1140
 cttactgatg agaagctgaa caagggactt ccggcattcc ttcacggtgg tcaggctggc 1200

cttcagtccg gcttcatggg cgcgcaggtc accgcaaccg cgctccttgc tgaaatgcgc 1260
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gtcagcatgg gcaccatcgc tgcacgccgc gctcgcgcac agctgctccc actgtcccag 1380
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ccgggcctgc gcgcagatcg cccactggcc ggccacatcg aggcagtcgc tcagggtctg 1560
cgccaccctt ccgcagcagc tgatccacca gcataa 1596

<210> 3
<211> 510
<212> PRT
<213> Saccharothrix espanaensis

<220>
<223> Tyrosine ammonia lyase enzyme from Saccharothrix espanaensis
(SeSam8)

<400> 3

Met Thr Gln Val Val Glu Arg Gln Ala Asp Arg Leu Ser Ser Arg Glu
1 5 10 15

Tyr Leu Ala Arg Val Val Arg Ser Ala Gly Trp Asp Ala Gly Leu Thr
20 25 30

Ser Cys Thr Asp Glu Glu Ile Val Arg Met Gly Ala Ser Ala Arg Thr
35 40 45

Ile Glu Glu Tyr Leu Lys Ser Asp Lys Pro Ile Tyr Gly Leu Thr Gln
50 55 60

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

Gly Gly Ser Leu Ile Ser His Leu Gly Thr Gly Gln Gly Ala Pro Leu
85 90 95

Ala Pro Glu Val Ser Arg Leu Ile Leu Trp Leu Arg Ile Gln Asn Met
100 105 110

Arg Lys Gly Tyr Ser Ala Val Ser Pro Val Phe Trp Gln Lys Leu Ala
115 120 125

Asp Leu Trp Asn Lys Gly Phe Thr Pro Ala Ile Pro Arg His Gly Thr
130 135 140

Val Ser Ala Ser Gly Asp Leu Gln Pro Leu Ala His Ala Ala Leu Ala
145 150 155 160

Phe Thr Gly Val Gly Glu Ala Trp Thr Arg Asp Ala Asp Gly Arg Trp
165 170 175

Ser Thr Val Pro Ala Val Asp Ala Leu Ala Ala Leu Gly Ala Glu Pro
180 185 190

Phe Asp Trp Pro Val Arg Glu Ala Leu Ala Phe Val Asn Gly Thr Gly
195 200 205

Ala Ser Leu Ala Val Ala Val Leu Asn His Arg Ser Ala Leu Arg Leu
210 215 220

Val Arg Ala Cys Ala Val Leu Ser Ala Arg Leu Ala Thr Leu Leu Gly
225 230 235 240

Ala Asn Pro Glu His Tyr Asp Val Gly His Gly Val Ala Arg Gly Gln
245 250 255

Val Gly Gln Leu Thr Ala Ala Glu Trp Ile Arg Gln Gly Leu Pro Arg
260 265 270

Gly Met Val Arg Asp Gly Ser Arg Pro Leu Gln Glu Pro Tyr Ser Leu
275 280 285

Arg Cys Ala Pro Gln Val Leu Gly Ala Val Leu Asp Gln Leu Asp Gly
290 295 300

Ala Gly Asp Val Leu Ala Arg Glu Val Asp Gly Cys Gln Asp Asn Pro
305 310 315 320

Ile Thr Tyr Glu Gly Glu Leu Leu His Gly Gly Asn Phe His Ala Met
325 330 335

Pro Val Gly Phe Ala Ser Asp Gln Ile Gly Leu Ala Met His Met Ala
340 345 350

Ala Tyr Leu Ala Glu Arg Gln Leu Gly Leu Leu Val Ser Pro Val Thr
355 360 365

Asn Gly Asp Leu Pro Pro Met Leu Thr Pro Arg Ala Gly Arg Gly Ala
370 375 380

Gly Leu Ala Gly Val Gln Ile Ser Ala Thr Ser Phe Val Ser Arg Ile
385 390 395 400

Arg Gln Leu Val Phe Pro Ala Ser Leu Thr Thr Leu Pro Thr Asn Gly
405 410 415

Trp Asn Gln Asp His Val Pro Met Ala Leu Asn Gly Ala Asn Ser Val
420 425 430

Phe Glu Ala Leu Glu Leu Gly Trp Leu Thr Val Gly Ser Leu Ala Val
435 440 445

Gly Val Ala Gln Leu Ala Ala Met Thr Gly His Ala Ala Glu Gly Val
450 455 460

Trp Ala Glu Leu Ala Gly Ile Cys Pro Pro Leu Asp Ala Asp Arg Pro
465 470 475 480

Leu Gly Ala Glu Val Arg Ala Ala Arg Asp Leu Leu Ser Ala His Ala
485 490 495

Asp Gln Leu Leu Val Asp Glu Ala Asp Gly Lys Asp Phe Gly
500 505 510

<210> 4

<211> 1533

<212> DNA

<213> Saccharothrix espanaensis

<220>

<223> Tyrosine ammonia lyase enzyme from *Saccharothrix espanaensis*
(SeSam8) (codon optimised)

<400> 4

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gttgttcgtt ccgcaggctg ggacgcaggc ctcaccagct gcaccgatga agaaatcgtg	120
cgcatgggtg catccgcacg caccattgag gaatacctga agtctgataa gccgatctac	180
ggcctcacc agggttcgg tccactggtc ctgttcgatg cagattccga actggaacag	240
ggcggctctc tcatctccca tctgggcacc ggccagggtg caccgcttgc accggaagtg	300
tcccgcctga ttctgtggct ccgcattcaa aacatgcgca agggctattc ggctgtcagt	360
cctgtgttct ggcaaaaact ggccgacctc tggaacaagg gcttcacccc tgctatccct	420
cgccacggca ccgtgtccgc cagcggcgat ctccagcctc tggcacacgc tgccctggct	480
tttaccggcg tgggcgaggc atggaccgt gatgcagacg gccgttggtc caccgtgcca	540
gccgtggacg cattagcagc actgggtgca gagccgttcg attggccagt gcgcgaggct	600
ttggccttcg tgaacggtac gggcgcatca ctcgcggtgg cagttctcaa ccacagatcc	660
gctctccgtc tcgtacgagc atgtgcagtc ttgtctgccc gtttggttac cttgctagga	720
gctaatacctg aacactacga tgtcggccac ggagtcgcaa ggggacaagt tggccagctg	780
accgcggcgg aatggattcg gcagggacta ccacgcggca tgggtccgaga cggttcgcgc	840
cctcttcaag aaccatacag cttgcgctgt gccccccagg tccttggcgc ggtgctggac	900
cagctggatg gtgcaggcga tgttctggcc cgcgaagtgg atggctgcca ggacaatcct	960
atcacctacg agggcgaact gctgcacggc ggtaacttcc acgctatgcc agtcggcttc	1020
gcatccgacc agatcggctt ggcatgcac atggcagctt atctggctga acgccagctc	1080
ggcctgctgg tgagcccgtt gaccaacggc gacctgccac caatgctgac cccacgcgt	1140
ggacgcggtg ccggcctggc gggcgttcag atctccgcaa cctccttcgt ctctcgcac	1200
cgccagctgg tgttcccagc tagcctcacc accctcccaa ccaacggctg gaaccaggac	1260
catgtcccaa tggctctgaa cggcgcaaac agcgtgttcg aagctcttga actgggttgg	1320
ctgaccgtgg gtagcctggc agtcggcgtg gccagctcg ctgcaatgac cggccacgca	1380

gctgagggcg tgtgggccga gttggcaggc atctgcccac cactggatgc tgaccgcca 1440
 ctgggcgcgg aggtccgcgc tgctcgcgat ctctctccg cacacgtga ccagctgctc 1500
 gttgacgagg ctgatggcaa agacttcggc taa 1533

<210> 5
 <211> 506
 <212> PRT
 <213> Flavobacterium johnsoniae

<220>
 <223> Tyrosine ammonia lyase enzyme from Flavobacterium johnsoniae
 (FjTAL)

<400> 5

Met Asn Thr Ile Asn Glu Tyr Leu Ser Leu Glu Glu Phe Glu Ala Ile
 1 5 10 15

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

Val Asn Glu Ser Phe Asn Phe Leu Lys Glu Phe Ser Gly Asn Lys Val
 35 40 45

Ile Tyr Gly Val Asn Thr Gly Phe Gly Pro Met Ala Gln Tyr Arg Ile
 50 55 60

Lys Glu Ser Asp Gln Ile Gln Leu Gln Tyr Asn Leu Ile Arg Ser His
 65 70 75 80

Ser Ser Gly Thr Gly Lys Pro Leu Ser Pro Val Cys Ala Lys Ala Ala
 85 90 95

Ile Leu Ala Arg Leu Asn Thr Leu Ser Leu Gly Asn Ser Gly Val His
 100 105 110

Pro Ser Val Ile Asn Leu Met Ser Glu Leu Ile Asn Lys Asp Ile Thr
 115 120 125

Pro Leu Ile Phe Glu His Gly Gly Val Gly Ala Ser Gly Asp Leu Val
 130 135 140

Gln Leu Ser His Leu Ala Leu Val Leu Ile Gly Glu Gly Glu Val Phe
 145 150 155 160

Tyr Lys Gly Glu Arg Arg Pro Thr Pro Glu Val Phe Glu Ile Glu Gly
 165 170 175

Leu Lys Pro Ile Gln Val Glu Ile Arg Glu Gly Leu Ala Leu Ile Asn
 180 185 190

Gly Thr Ser Val Met Thr Gly Ile Gly Val Val Asn Val Tyr His Ala
 195 200 205

Lys Lys Leu Leu Asp Trp Ser Leu Lys Ser Ser Cys Ala Ile Asn Glu
 210 215 220

Leu Val Gln Ala Tyr Asp Asp His Phe Ser Ala Glu Leu Asn Gln Thr
 225 230 235 240

Lys Arg His Lys Gly Gln Gln Glu Ile Ala Leu Lys Met Arg Gln Asn
 245 250 255

Leu Ser Asp Ser Thr Leu Ile Arg Lys Arg Glu Asp His Leu Tyr Ser
 260 265 270

Gly Glu Asn Thr Glu Glu Ile Phe Lys Glu Lys Val Gln Glu Tyr Tyr
 275 280 285

Ser Leu Arg Cys Val Pro Gln Ile Leu Gly Pro Val Leu Glu Thr Ile
 290 295 300

Asn Asn Val Ala Ser Ile Leu Glu Asp Glu Phe Asn Ser Ala Asn Asp
 305 310 315 320

Asn Pro Ile Ile Asp Val Lys Asn Gln His Val Tyr His Gly Gly Asn
 325 330 335

Phe His Gly Asp Tyr Ile Ser Leu Glu Met Asp Lys Leu Lys Ile Val
 340 345 350

Ile Thr Lys Leu Thr Met Leu Ala Glu Arg Gln Leu Asn Tyr Leu Leu
 355 360 365

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

Leu Gly Phe Asn Phe Gly Met Gln Gly Val Gln Phe Thr Ala Thr Ser
 385 390 395 400

Thr Thr Ala Glu Ser Gln Met Leu Ser Asn Pro Met Tyr Val His Ser
 405 410 415

Ile Pro Asn Asn Asn Asp Asn Gln Asp Ile Val Ser Met Gly Thr Asn
 420 425 430

Ser Ala Val Ile Thr Ser Lys Val Ile Glu Asn Ala Phe Glu Val Leu
 435 440 445

Ala Ile Glu Met Ile Thr Ile Val Gln Ala Ile Asp Tyr Leu Gly Gln
 450 455 460

Lys Asp Lys Ile Ser Ser Val Ser Lys Lys Trp Tyr Asp Glu Ile Arg
 465 470 475 480

Asn Ile Ile Pro Thr Phe Lys Glu Asp Gln Val Met Tyr Pro Phe Val
 485 490 495

Gln Lys Val Lys Asp His Leu Ile Asn Asn
 500 505

<210> 6
 <211> 1521
 <212> DNA
 <213> Flavobacterium johnsoniae;

<220>
 <223> Tyrosine ammonia lyase enzyme from Flavobacterium johnsoniae
 (FjTAL) (codon optimised)

<400> 6
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cagaaggtta ccatctccga tgtggttg aaccgtgtta acgagtcctt caacttcctc	120
aaggagtctt ccggcaacaa ggtcatctac ggtgtgaaca ccggcttcgg cccaatggca	180
caataccgta ttaaggaatc cgatcagatc cagcttcagt acaatctgat ccgttccac	240
tcttcgggca ccggaaaacc actctcccca gtttgtgcta aggcagcaat cttggctcgc	300
ctgaacaccc tgtccctcgg taactccggc gtgcatccat ctgtcatcaa cctgatgtcg	360
gaactgatca acaaagacat taccctcctc atcttcgagc acggtggcgt cggagcatcc	420
ggtgacctgg ttcagctttc tcacctggct ttggtttctca tcggcgaagg cgaagtgttc	480
tacaagggtg aacgccgccc aactccagaa gttttcgaaa ttgagggtt gaagccaatc	540
caggttgaga tccgtgaggg cctcgccttg attaacggta ctagcgtgat gaccggtatt	600
ggagtgggtca acgtgtacca cgcaaagaag ctgctggact ggtccctgaa gtcctcctgc	660
gccatcaatg aacttgttca ggcttacgat gatcattca gcgcagagct gaaccagacg	720
aagcgccaca agggccagca ggaaatcgct ctgaagatgc gtcagaacct ctctgacagc	780
accctgatcc gcaagcgca ggaccacctg tattccggcg aaaacaccga ggagattttc	840
aaggagaagg tgcaggagta ctactccctg cgctgcgttc cacagattct cggcccggtc	900
ctcgaaacta tcaataacgt cgctccatc ctggaagatg agttcaactc cgctaacgat	960
aacccaatca tcgacgtgaa gaaccagcac gtgtaccatg gcggcaactt ccacggtgac	1020
tacatctctc tggaaatgga caagttgaaa atcgttatca ccaaactgac catgcttgca	1080
gaacgccagc ttaactatct tctcaactcc aagatcaacg aacttctgcc accattcgtg	1140
aacctcggca ccctgggttt caacttcggc atgcagggcg ttcagttcac cgcgacctcc	1200
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aacgataacc aggacatcgt ctccatgggc accaactccg cagtgatcac gtccaaggtt	1320
atcgagaacg ctttcgaagt cctggctatc gaaatgatca ccacgttca ggccatcgat	1380
tacctcggcc agaaggataa gatctcctcc gtttccaaga agtggtacga tgaaatccgc	1440
aacattatcc ctaccttcaa ggaggatcag gttatgtacc cattcgtgca gaaggttaag	1500
gatcacctca tcaacaacta a	1521

<210> 7

<211> 542
<212> PRT
<213> Nicotiana tabacum

<220>
<221> misc_feature
<222> (287)..(287)
<223> Xaa can be any naturally occurring amino acid

<220>
<223> 4-coumarate-CoA ligase from Nicotiana tabacum (Nt4CL)

<400> 7

Met Glu Lys Asp Thr Lys Gln Val Asp Ile Ile Phe Arg Ser Lys Leu
1 5 10 15

Pro Asp Ile Tyr Ile Pro Asn His Leu Pro Leu His Ser Tyr Cys Phe
20 25 30

Glu Asn Ile Ser Glu Phe Ser Ser Arg Pro Cys Leu Ile Asn Gly Ala
35 40 45

Asn Lys Gln Ile Tyr Thr Tyr Ala Asp Val Glu Leu Asn Ser Arg Lys
50 55 60

Val Ala Ala Gly Leu His Lys Gln Gly Ile Gln Pro Lys Asp Thr Ile
65 70 75 80

Met Ile Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ala Phe Ile Gly
85 90 95

Ala Ser Tyr Leu Gly Ala Ile Ser Thr Met Ala Asn Pro Leu Phe Thr
100 105 110

Pro Ala Glu Val Val Lys Gln Ala Glu Ala Ser Ser Ala Lys Ile Ile
115 120 125

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

Asn Asp Val Lys Ile Ile Cys Ile Asp Ser Ala Pro Glu Gly Cys Leu

145		150		155		160
His Phe Ser Val	Leu Thr Gln Ala Asn Glu His Asp Ile Pro Glu Val					
	165			170		175
Glu Ile Gln Pro Asp Asp Val Val	Ala Leu Pro Tyr Ser Ser Gly Thr					
	180		185		190	
Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Leu Val Thr						
	195		200		205	
Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His						
	210		215		220	
Ser Glu Asp Val Met Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser						
	225		230		235	240
Leu Asn Ser Val Leu Leu Cys Gly Leu Arg Val Gly Ala Ala Ile Leu						
	245		250		255	
Ile Met Gln Lys Phe Asp Ile Val Ser Phe Leu Glu Leu Ile Gln Ser						
	260		265		270	
Tyr Lys Val Thr Ile Gly Pro Phe Val Pro Pro Ile Val Leu Xaa Ile						
	275		280		285	
Ala Lys Ser Pro Met Val Asp Asp Tyr Asp Leu Ser Ser Val Arg Thr						
	290		295		300	
Val Met Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Thr Val						
	305		310		315	320
Arg Ala Lys Phe Pro Asn Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr						
	325		330		335	
Glu Ala Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Pro						
	340		345		350	
Phe Glu Ile Lys Ser Gly Ala Cys Gly Thr Val Val Arg Asn Ala Glu						
	355		360		365	

Met Lys Ile Val Asp Pro Lys Thr Gly Asn Ser Leu Pro Arg Asn Gln
370 375 380

Ser Gly Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu
385 390 395 400

Asn Asp Pro Glu Ala Thr Ala Arg Thr Ile Asp Lys Glu Gly Trp Leu
405 410 415

Tyr Thr Gly Asp Ile Gly Tyr Ile Asp Asp Asp Asp Glu Leu Phe Ile
420 425 430

Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala
435 440 445

Pro Ala Glu Leu Glu Ala Leu Leu Leu Asn His Pro Asn Ile Ser Asp
450 455 460

Ala Ala Val Val Pro Met Lys Asp Glu Gln Ala Gly Glu Val Pro Val
465 470 475 480

Ala Phe Val Val Arg Ser Asn Gly Ser Thr Ile Thr Glu Asp Glu Val
485 490 495

Lys Asp Phe Ile Ser Lys Gln Val Ile Phe Tyr Lys Arg Ile Lys Arg
500 505 510

Val Phe Phe Val Asp Ala Ile Pro Lys Ser Pro Ser Gly Lys Ile Leu
515 520 525

Arg Lys Asp Leu Arg Ala Lys Leu Ala Ala Gly Leu Pro Asn
530 535 540

<210> 8

<211> 1629

<212> DNA

<213> Nicotiana tabacum

<220>

<223> 4-coumarate-CoA ligase from *Nicotiana tabacum* (Nt4CL)

<400> 8

atggagaaag atacaaaaca ggttgacata attttccgat caaaactccc tgatatttac	60
atccctaacc atcttccttt acactcctac tgtttcgaaa acatttccga gttcagttct	120
cgtccttggt taatcaatgg cgccaacaaa caaatttata cgtatgctga tgttgaactc	180
aattcaagaa aagttgctgc tggctctcac aaacaaggga ttcaacaaa ggatacaata	240
atgatcctat tgcctaactc cccagaattt gtgtttgctt tcattggtgc atcgtacctc	300
ggagctatth ctacaatggc caatcctttg tttactcctg ctgaggttgt gaagcaagcc	360
gaggcttcta gtgctaagat cattgtcaca caagcgtgtc atgttaacaa agtgaaagat	420
tatgcatttg agaatgatgt gaagatcata tgcacgact cggcgccgga gggttgtctc	480
cacttctccg tgctaactca ggctaattgag cacgatattc ctgaggttga aattcaacct	540
gacgatgtgg tggcgttgcc atactcctcc gggacgacgg gattacctaa aggagtgatg	600
ttgacgcaca agggacttgt gacaagcgtc gcacaacaag tcgacggtga aaatccgaat	660
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ctcaactccg ttttgctttg tggattaagg gtgggagcag cgattttgat tatgcagaaa	780
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gtaccaccta ttgttttggy cattgctaag agtcctatgg ttgatgatta tgatctttca	900
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ggaacagttg tgagaaatgc tgaaatgaaa attgtggatc ctaaaactgg taattctctt	1140
cccagaaatc aatctggaga aatttgcatt agaggagacc agatcatgaa aggctacctg	1200
aatgatccag aggccacagc aagaacaata gacaaagaag ggtggttata tactggtgac	1260
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aaatacaaaag gatttcaagt cgcacctgct gagctcgaag ctctccttct caaccatccc	1380
aacatttctg atgctgctgt tgtcccatg aaggacgagc aagcaggaga agttccagtg	1440
gcttttgttg ttagatccaa cggatccacc attactgaag atgaagtcaa agattttatt	1500

tcaaagcagg tgatatttta taagaggata aagcgggtat ttttcgtgga tgctattcct 1560
 aaatctccat ctggcaaaat ccttcgaaaa gatttgagag ctaaactggc tgctgggctt 1620
 ccaaattaa 1629

<210> 9
 <211> 561
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> 4-coumarate-CoA ligase from Arabidopsis thaliana (At4CL)

<400> 9

Met Ala Pro Gln Glu Gln Ala Val Ser Gln Val Met Glu Lys Gln Ser
 1 5 10 15

Asn Asn Asn Asn Ser Asp Val Ile Phe Arg Ser Lys Leu Pro Asp Ile
 20 25 30

Tyr Ile Pro Asn His Leu Ser Leu His Asp Tyr Ile Phe Gln Asn Ile
 35 40 45

Ser Glu Phe Ala Thr Lys Pro Cys Leu Ile Asn Gly Pro Thr Gly His
 50 55 60

Val Tyr Thr Tyr Ser Asp Val His Val Ile Ser Arg Gln Ile Ala Ala
 65 70 75 80

Asn Phe His Lys Leu Gly Val Asn Gln Asn Asp Val Val Met Leu Leu
 85 90 95

Leu Pro Asn Cys Pro Glu Phe Val Leu Ser Phe Leu Ala Ala Ser Phe
 100 105 110

Arg Gly Ala Thr Ala Thr Ala Ala Asn Pro Phe Phe Thr Pro Ala Glu
 115 120 125

Ile Ala Lys Gln Ala Lys Ala Ser Asn Thr Lys Leu Ile Ile Thr Glu
 130 135 140

Ala Arg Tyr Val Asp Lys Ile Lys Pro Leu Gln Asn Asp Asp Gly Val
 145 150 155 160

Val Ile Val Cys Ile Asp Asp Asn Glu Ser Val Pro Ile Pro Glu Gly
 165 170 175

Cys Leu Arg Phe Thr Glu Leu Thr Gln Ser Thr Thr Glu Ala Ser Glu
 180 185 190

Val Ile Asp Ser Val Glu Ile Ser Pro Asp Asp Val Val Ala Leu Pro
 195 200 205

Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met Leu Thr His
 210 215 220

Lys Gly Leu Val Thr Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro
 225 230 235 240

Asn Leu Tyr Phe His Ser Asp Asp Val Ile Leu Cys Val Leu Pro Met
 245 250 255

Phe His Ile Tyr Ala Leu Asn Ser Ile Met Leu Cys Gly Leu Arg Val
 260 265 270

Gly Ala Ala Ile Leu Ile Met Pro Lys Phe Glu Ile Asn Leu Leu Leu
 275 280 285

Glu Leu Ile Gln Arg Cys Lys Val Thr Val Ala Pro Met Val Pro Pro
 290 295 300

Ile Val Leu Ala Ile Ala Lys Ser Ser Glu Thr Glu Lys Tyr Asp Leu
 305 310 315 320

Ser Ser Ile Arg Val Val Lys Ser Gly Ala Ala Pro Leu Gly Lys Glu
 325 330 335

Leu Glu Asp Ala Val Asn Ala Lys Phe Pro Asn Ala Lys Leu Gly Gln
 340 345 350

Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met Ser Leu Gly
355 360 365

Phe Ala Lys Glu Pro Phe Pro Val Lys Ser Gly Ala Cys Gly Thr Val
370 375 380

Val Arg Asn Ala Glu Met Lys Ile Val Asp Pro Asp Thr Gly Asp Ser
385 390 395 400

Leu Ser Arg Asn Gln Pro Gly Glu Ile Cys Ile Arg Gly His Gln Ile
405 410 415

Met Lys Gly Tyr Leu Asn Asn Pro Ala Ala Thr Ala Glu Thr Ile Asp
420 425 430

Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Ile Asp Asp Asp
435 440 445

Asp Glu Leu Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys
450 455 460

Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu Ile Gly His
465 470 475 480

Pro Asp Ile Thr Asp Val Ala Val Val Ala Met Lys Glu Glu Ala Ala
485 490 495

Gly Glu Val Pro Val Ala Phe Val Val Lys Ser Lys Asp Ser Glu Leu
500 505 510

Ser Glu Asp Asp Val Lys Gln Phe Val Ser Lys Gln Val Val Phe Tyr
515 520 525

Lys Arg Ile Asn Lys Val Phe Phe Thr Glu Ser Ile Pro Lys Ala Pro
530 535 540

Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys Leu Ala Asn Gly
545 550 555 560

Leu

<210> 10
 <211> 1686
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> 4-coumarate-CoA ligase from Arabidopsis thaliana (At4CL)
 (codon optimised)

<400> 10
 atggcaccac aggaacaggc agtctcccag gttatggaaa agcagtccaa caacaacaac 60
 tccgatgtta tcttccgctc caagttgcct gacatctaca tcccaaacca tctgtccctg 120
 cacgattaca ttttccagaa catctccgaa tttgctacta agccatgcct gatcaacggc 180
 ccaaccggtc acgtgtacac ctactctgac gtccacgtga tcagccgcca gatcgcagct 240
 aacttccaca agctgggctg gaaccagaac gacgtagtga tgctgctgct ccctaactgc 300
 cctgagttcg tcctgtcctt cctggccgcc tccttccgcg gtgcaaccgc gaccgcggcc 360
 aacccattct tcacgccagc agagatcgct aagcaggcta aggcttctaa caccaagctg 420
 atcatcaccg aagcgcgcta cgtggacaag atcaagccac tccagaacga cgatggcggtt 480
 gtgatcgtgt gcatcgacga caacgagtcc gttccaatcc cagagggctg tctgaggttc 540
 accgagctga cccaatcgac caccgaagcg tccgaggtta tcgactccgt tgaaatctcc 600
 cctgacgatg tcgtcgccct gccatactcc agcggcacca ccggcttgcc aaagggtgtg 660
 atgctgaccc acaagggact cgttacctcc gtggcacagc aggtcgatgg tgaaaacccc 720
 aacctgtact tccattccga tgacgtcatc ctgtgcgtcc tgccgatgtt ccacatctac 780
 gctctgaact ccatcatgct gtgcggcctc cgcgtcggtg cagcaatcct gatcatgcca 840
 aagttcgaat tcaacctgct gctggagttg atccagcgct gcaaggtgac cgtggcaccc 900
 atggtgcccc cgatcgtgct ggcaatcgcg aagtcagcg aaaccgaaaa gtacgacctg 960
 tcatccatcc gcgtcgtcaa gtcgggcgcc gcaccactcg gcaaggagct ggaggacgct 1020
 gtcaacgcta agttccctaa cgcgaagctc ggccagggtg acggtatgac cgaggccggc 1080
 ccagtcctgg ccatgtccct gggcttcgca aaggagccat tcccggtgaa gtccggcgca 1140
 tgcggcaccg ttgtgcgcaa cgcagagatg aagatcggtg accagatac cggtgactcc 1200

ctgtcccgta accagcccgg cgagatctgc atccgcggcc accagatcat gaagggctac 1260
 ctgaacaacc ctgctgtctac cgccgaaacc atcgataagg atggctggct ccacaccggc 1320
 gacatcgggtc tgatcgacga cgacgatgaa ctgttcatcg tcgatcgctt taaggagttg 1380
 atcaagtaca agggcttcca ggtggccccc gcagaactgg aagcactgct catcggccac 1440
 cctgatatca ccgatgtcgc cgtcgtggcc atgaaggagg aagcagcagg cgaagtgcca 1500
 gtcgcttttcg tgggtgaagtc caaggattcc gagttgtccg aggatgatgt gaagcagttc 1560
 gtgtccaagc aggtcgtgtt ctacaagcgc atcaacaagg tgttcttcac cgaatccatc 1620
 ccaaaggcac catccggcaa gtcctgcgc aaggacctgc gcgctaagct ggctaacggc 1680
 ctgtaa 1686

<210> 11
 <211> 585
 <212> PRT
 <213> Physcomitrella patens

<220>
 <223> 4-coumarate-CoA ligase from Physcomitrella patens (Pp4CL)

<400> 11

Met Ser Pro Ser Leu Leu Pro Gln Pro Ile Val Ser Glu Ser Thr Gly
 1 5 10 15

Glu Ser Val Met Lys Met Ser Leu Gln Ser Glu Val Arg Glu Ala Ser
 20 25 30

Leu Ala Thr Gly Glu Asn Pro Glu Pro Phe Leu Leu Glu Thr Asp Ala
 35 40 45

Glu Ser Gln Ile Met Glu Pro Val His Ala Glu Val His Asp Phe Ile
 50 55 60

Tyr Arg Ser Lys Leu Pro Asp Ile Asp Ile Pro Asn His Met Pro Leu
 65 70 75 80

Ala Asp Tyr Cys Leu Glu Lys Ser Ser Gln Trp Pro Asp Lys Val Cys
 85 90 95

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

Leu Ser Ser Arg Arg Val Ala Ala Gly Leu Asp Lys Ile Gly Val Lys
115 120 125

Gln Gly Asp Val Ile Ala Leu Leu Leu Pro Asn Cys Ala Glu Phe Val
130 135 140

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

Asn Pro Phe Tyr Thr Ala Ala Glu Leu Glu Lys Gln Ile Glu Ala Ser
165 170 175

Gly Ala Gly Ile Val Ile Thr Gln Ser Ser Tyr Ile Glu Lys Leu Ala
180 185 190

Gly Leu Asn Val Gln Ile Ile Thr Val Asp Gln His Val Ala Asn Cys
195 200 205

Met His Ile Ser Val Leu Leu Asn Ala Cys Glu Asp Glu Cys Pro Gln
210 215 220

Val Arg Ile His Pro Asp Asp Leu Val Cys Leu Pro Tyr Ser Ser Gly
225 230 235 240

Thr Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Ser Leu Val
245 250 255

Ser Ser Val Ser Gln Gln Val Asp Gly Glu Ala Pro Asn Phe Asn Ile
260 265 270

Thr Val Glu Asp Thr Leu Met Cys Val Leu Pro Met Phe His Ile Tyr
275 280 285

Ser Leu Asn Ser Ile Leu Leu Cys Gly Leu Arg Val Gly Ala Thr Leu
290 295 300

Val Ile Met Pro Lys Phe Glu Leu Pro Lys Leu Leu Asp Leu Ile Gln
305 310 315 320

Arg His Lys Val Thr Met Gly Pro Phe Val Pro Pro Ile Val Leu Ala
325 330 335

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

Met Val Met Ser Gly Ala Ala Pro Leu Gly Arg Glu Leu Glu Asp Ala
355 360 365

Phe Arg Ala Arg Leu Pro Asn Ala Val Leu Gly Gln Gly Tyr Gly Met
370 375 380

Thr Glu Ala Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Thr
385 390 395 400

Pro Phe Ser Val Lys Pro Gly Ser Cys Gly Thr Val Val Arg Asn Ala
405 410 415

Glu Val Lys Ile Val Asp Thr Glu Thr Gly Met Ser Leu Pro Tyr Asn
420 425 430

Gln Pro Gly Glu Ile Cys Ile Arg Gly Pro Gln Ile Met Lys Gly Tyr
435 440 445

Leu Lys Asn Pro Glu Ala Thr Ala Asn Thr Ile Asp Lys Asp Gly Phe
450 455 460

Leu His Thr Gly Asp Val Ala Phe Ile Asp Glu Asp Glu Glu Met Phe
465 470 475 480

Ile Val Asp Arg Val Lys Glu Ile Ile Lys Phe Lys Gly Phe Gln Val
485 490 495

Pro Pro Ala Glu Leu Glu Ala Leu Leu Leu Ser His Lys Glu Ile Gln
500 505 510

Asp Ala Ala Val Val Ser Arg Lys Asp Asp Val Ala Gly Glu Val Pro
515 520 525

Val Ala Phe Val Val Arg Ala Thr Ser Ser Thr Ile Thr Glu Asp Glu
530 535 540

Val Lys Asp Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Lys Ile His
545 550 555 560

Asn Val Tyr Phe Val Asp Ser Val Pro Lys Ser Pro Ser Gly Lys Ile
565 570 575

Leu Arg Lys Asp Leu Arg Asn Lys Val
580 585

<210> 12
<211> 1758
<212> DNA
<213> Physcomitrella patens

<220>
<223> 4-coumarate-CoA ligase from Physcomitrella patens (Pp4CL)
(codon optimised)

<400> 12
atgtcaccat cgctccttcc ccagccaatc gtgtccgaat ccaccggtga atccgtgatg 60
aagatgtccc tccagtccga agtgcgcgaa gcatccctgg caaccggtga aaaccctgaa 120
ccattcctgc tggaaaccga tgctgaatcc cagatcatgg aacctgtgca cgctgaagtt 180
cacgatttca tctaccgttc taagctgcct gatatcgata tcccaaacca catgcctctg 240
gctgattact gcctggagaa gtcctcccag tggcctgata aggtgtgcct gatcgatggt 300
gtgaccggtc gcgaacaccg ctacggcgaa attgagctgt cctcccgccg cgtggcagca 360
ggccttgata agatcggcgt gaagcagggc gatgtcatcg cactgctctt gcctaactgc 420
gctgagttcg tcctgggtgtt cctggggcgca gcgaagcgcg gcgccgttgt caccaccgct 480
aaccatttct acaccgccgc cgagttggag aagcaaatcg aggcctccgg tgcgggcatt 540
gttatcactc agagcagcta catcgagaag ctgcaggcc ttaacgtcca gatcatcacc 600
gttgatcagc acgtggctaa ttgcatgcac atctccgtgc tgctgaacgc atgcgaagat 660

gaatgccctc aggtgcgtat ccaccctgac gatctggtct gcctgccata ctctccggc	720
accaccggct tgccaaaggg cgtgatgctg acccacaagt cccttggtgc atccgtgtcc	780
caacaggtgg acggcgaagc accaaacttc aacatcactg tcgaggacac cctgatgtgc	840
gtgctgcca tggtccacat ctattccctc aactccatcc tgctgtgcgg cctccgtgtg	900
ggcgccaccc tcgttattat gccgaagttc gaactgcaa agctgttgga cctgatccag	960
cgtcacaagg tgaccatggg cccattcgtg ccgccaatcg tcctggccat cgcaaagaac	1020
ccaatcgtcg agaattacga tctctcctcc atgcgcatgg ttatgtccgg cgctgcacct	1080
ctgggtcggg agctggagga cgctttccgt gcccgttgcc caaacgccgt tctgggccag	1140
ggctacggga tgactgaagc cggcccagtc ctggctatgt gcctcgcatt cgcaaagacc	1200
ccattctccg tgaagccagg ctctgcggc accgtggtgc gcaacgctga agtgaaaatc	1260
gtcgataccg aaaccggcat gtccctgcca tacaaccagc caggcgagat ctgcatccgc	1320
ggcccacaga tcatgaaggg ctacctgaag aaccagaag ctaccgctaa caccatcgat	1380
aaggatggct tcctgcacac cggcgatgtc gcattcatcg atgaggatga ggagatgttc	1440
atcgttgatc gcgtcaagga gatcatcaag ttcaagggtc tccaggtgcc tcctgcggag	1500
ctggaagctc tcctgctgtc ccacaaggag atccaggacg ctgctgtcgt gtcccgtaa	1560
gatgacgtgg cgggcgaagt tccagtggca ttcgtggtcc gcgctaccag ctccaccatc	1620
accgaggatg aagtcaagga ttacatcgca aagcaggtcg ttttctacaa gaagatccac	1680
aacgtatact tcgtggattc cgtgccaaag tctccatccg gcaagatcct gcgtaaggat	1740
ctccgtaaca aggtgtaa	1758

<210> 13
 <211> 522
 <212> PRT
 <213> Streptomyces coelicolor

<220>
 <223> 4-coumarate-CoA ligase from Streptomyces coelicolor (Sc4CL)
 <400> 13

Met	Phe	Arg	Ser	Glu	Tyr	Ala	Asp	Val	Pro	Pro	Val	Asp	Leu	Pro	Ile
1				5					10				15		

His Asp Ala Val Leu Gly Gly Ala Ala Ala Phe Gly Ser Thr Pro Ala
20 25 30

Leu Ile Asp Gly Thr Asp Gly Thr Thr Leu Thr Tyr Glu Gln Val Asp
35 40 45

Arg Phe His Arg Arg Val Ala Ala Ala Leu Ala Glu Thr Gly Val Arg
50 55 60

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

Leu Ala Phe Tyr Ala Ala Thr Arg Ala Gly Ala Ser Val Thr Thr Val
85 90 95

His Pro Leu Ala Thr Ala Glu Glu Phe Ala Lys Gln Leu Lys Asp Ser
100 105 110

Ala Ala Arg Trp Ile Val Thr Val Ser Pro Leu Leu Ser Thr Ala Arg
115 120 125

Arg Ala Ala Glu Leu Ala Gly Gly Val Gln Glu Ile Leu Val Cys Asp
130 135 140

Ser Ala Pro Gly His Arg Ser Leu Val Asp Met Leu Ala Ser Thr Ala
145 150 155 160

Pro Glu Pro Ser Val Ala Ile Asp Pro Ala Glu Asp Val Ala Ala Leu
165 170 175

Pro Tyr Ser Ser Gly Thr Thr Gly Thr Pro Lys Gly Val Met Leu Thr
180 185 190

His Arg Gln Ile Ala Thr Asn Leu Ala Gln Leu Glu Pro Ser Met Pro
195 200 205

Ser Ala Pro Gly Asp Arg Val Leu Ala Val Leu Pro Phe Phe His Ile
210 215 220

Tyr Gly Leu Thr Ala Leu Met Asn Ala Pro Leu Arg Leu Gly Ala Thr
 225 230 235 240

Val Val Val Leu Pro Arg Phe Asp Leu Glu Gln Phe Leu Ala Ala Ile
 245 250 255

Gln Asn His Arg Ile Thr Ser Leu Tyr Val Ala Pro Pro Ile Val Leu
 260 265 270

Ala Leu Ala Lys His Pro Leu Val Ala Asp Tyr Asp Leu Ser Ser Leu
 275 280 285

Arg Tyr Ile Val Ser Ala Ala Ala Pro Leu Asp Ala Arg Leu Ala Ala
 290 295 300

Ala Cys Ser Gln Arg Leu Gly Leu Pro Pro Val Gly Gln Ala Tyr Gly
 305 310 315 320

Met Thr Glu Leu Ser Pro Gly Thr His Val Val Pro Leu Asp Ala Met
 325 330 335

Ala Asp Ala Pro Pro Gly Thr Val Gly Arg Leu Ile Ala Gly Thr Glu
 340 345 350

Met Arg Ile Val Ser Leu Thr Asp Pro Gly Thr Asp Leu Pro Ala Gly
 355 360 365

Glu Ser Gly Glu Ile Leu Ile Arg Gly Pro Gln Ile Met Lys Gly Tyr
 370 375 380

Leu Gly Arg Pro Asp Ala Thr Ala Ala Met Ile Asp Glu Glu Gly Trp
 385 390 395 400

Leu His Thr Gly Asp Val Gly His Val Asp Ala Asp Gly Trp Leu Phe
 405 410 415

Val Val Asp Arg Val Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val
 420 425 430

Ala Pro Ala Glu Leu Glu Ala His Leu Leu Thr His Pro Gly Val Ala

435

440

445

Asp Ala Ala Val Val Gly Ala Tyr Asp Asp Asp Gly Asn Glu Val Pro
 450 455 460

His Ala Phe Val Val Arg Gln Pro Ala Ala Pro Gly Leu Ala Glu Ser
 465 470 475 480

Glu Ile Met Met Tyr Val Ala Glu Arg Val Ala Pro Tyr Lys Arg Val
 485 490 495

Arg Arg Val Thr Phe Val Asp Ala Val Pro Arg Ala Ala Ser Gly Lys
 500 505 510

Ile Leu Arg Arg Gln Leu Arg Glu Pro Arg
 515 520

<210> 14
 <211> 1569
 <212> DNA
 <213> Streptomyces coelicolor

<220>
 <223> 4-coumarate-CoA ligase from Streptomyces coelicolor (Sc4CL)
 (codon optimised)

<400> 14
 atgttccgtt ccgagtacgc agatgtgcct ccagtggacc tccctatcca cgatgctgtc 60
 ctgggtggcg cggccgcatt cggcagcacc ccagctctga tcgatggcac cgatggcacc 120
 accctgacct acgaacaggt cgatcgcttc caccgtcgcg tcgctgctgc tctggcggaa 180
 accggcgtgc gcaagggcga tgtcctggcc ctgcactctc caaacaccgt tgctttccct 240
 ctggcattct acgctgcaac ccgcgctggg gcatccgtga ccactgttca ccctctcgct 300
 accgcagaag agtttgctaa gcagctgaag gattcggctg cacgttggat cgtcaccgtt 360
 tccccactgc tgtccaccgc acgccgcgcc gcagagttgg caggcggcgt gcaggaaatt 420
 ttggtctgcg attctgctcc aggtcaccgt tctctcgtcg atatgctggc tagcaccgca 480
 cccgaaccat ccgtcgctat cgatccagca gaagatgtgg ctgcccttcc gtactcctct 540
 ggccaccacc gcaccccaaa ggggtgtgat ctgaccacc gccagattgc aaccaacctg 600

gctcagctgg aaccttccat gccatccgct ccaggtgacc ggggtgctggc tgttctgcca	660
ttcttccaca tctacggctt gaccgcactc atgaacgctc ctttgcgctt ggggtgctacc	720
gtgggtgggtgc tccctcgctt cgacctggag cagttccttg cagccatcca gaaccaccgt	780
atcaccagtt tgtacgtcgc cccaccaatc gttttggcac tggctaagca ccctctggtg	840
gccgactatg acctttcctc cctccgttac atcgtgagcg ccgcggcacc gctcgacgcg	900
cgcctggcag ccgcttgctt ccagcgtctg ggcctgcccc cgggtggggca agcgtacggt	960
atgaccgagc tgtctcctgg caccacgctc gtgccgctcg atgcaatggc agatgccccca	1020
cccggcaccg tgggtcgcct gatagctggc accgagatgc gcatcgtgtc cctgaccgac	1080
ccaggcaccg acctgccggc aggcgaatcc ggcgaaatcc tgatccgcgg cccccagatt	1140
atgaagggct acctcggccg cccagatgct accgcagcaa tgatcgatga ggagggttg	1200
ctgcacaccg gcgatgtggg ccacgtggac gctgatgggtt ggttggttcgt cgtggatcgc	1260
gttaaggagc tgatcaagta caagggtttc caggttgctc ccgcggagct tgaagcacac	1320
ttgctcacc acccaggtgt tgcagatgca gctgtcgtcg gcgcatacga cgacgacggt	1380
aacgaggtgc cgcacgcctt tgtgggtccgc cagccggctg caccaggcct cgcggagtcc	1440
gaaatcatga tgtacgtggc tgaacgcgtt gctccataca agcgcgtgcg ccgcgtgacc	1500
ttcgtcgatg ccgtgccacg cgcagcatcc ggcaagatcc tgcgtcgcca gctgcgcgag	1560
ccacgctaa	1569

<210> 15
 <211> 383
 <212> PRT
 <213> Rubus idaeus

<220>
 <223> benzalacetone synthase from Rubus idaeus (RiPKS)

<400> 15

Met	Val	Thr	Val	Glu	Glu	Val	Arg	Lys	Ala	Gln	Arg	Ala	Glu	Gly	Pro
1				5					10					15	

Ala	Thr	Val	Leu	Ala	Ile	Gly	Thr	Ala	Thr	Pro	Pro	Asn	Cys	Val	Gly
			20					25					30		

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Ile Glu Leu Lys Gln Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Ile Val Glu Ile Pro Lys Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Val
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

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

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Ile Thr Val Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Cys
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Val Ala Ser Ile Ile Val
210 215 220

Gly Ala Asp Pro Leu Pro Glu Ile Glu Lys Pro Leu Phe Glu Leu Val
225 230 235 240

Ser Ala Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Glu Gly
245 250 255

His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Glu Asn Val Pro
260 265 270

Ala Leu Ile Ser Lys Asn Ile Glu Lys Ser Leu Asn Glu Thr Phe Lys
275 280 285

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

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

Pro Glu Lys Leu Glu Ala Thr Gly His Ile Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Val Val Arg Arg Lys
340 345 350

Ser Ala Ala Asn Gly Val Thr Thr Arg Ile Leu Ser Ile Gly Gln Ile
355 360 365

Ser Lys Ser Leu Leu Ile Leu Ala Trp Phe Leu Phe Ser Leu Val
370 375 380

<210> 16
<211> 1152
<212> DNA
<213> Rubus idaeus

<220>
<223> benzalacetone synthase from Rubus idaeus (RiPKS)
(codon optimised)

<400> 16
atggttaccg ttgaagaagt ccgcaaggct cagcgcgcag aaggccctgc aaccgttctg 60
gcaatcggca ccgcaacccc accaaactgc gtcggccagt ccacctaccc agattattat 120
ttccgtatca ccaactctga acacaagatt gaactgaagc agaagttcca gaggatgtgc 180

gataagtcca tgatcaagaa gcgttacatg taccttaccg aagagatcct gaaggagaac 240
 ccatccatgt gcgagtacat ggctccatcc cttgatgctc gccaggacat ggtcatcgtg 300
 gaaatcccaa agctgggcaa ggaagcagcc accaaggcaa tcaaggagtg gggccagccg 360
 aagtcgaaga tcacccacct tgttttctgc accaccagcg gtgtggatat gcctggcgcc 420
 gactaccagc tgatcaagct cttcggcctg cgcccatccg tcaagcgctt catgatgtac 480
 cagcagggct gcttcgccgg cggcaccgtt ctgcgcctgg ctaaggatct ggcagaaaac 540
 aaccgcggtg cccgcgttct cgtcgtgtgc tccgagatca ccgtggtcac cttccgcggc 600
 ccatccgaca cccaccttga ctgtctgggt ggccaggcac tcttcggcga tggcgtggca 660
 tccatcatcg tcggcgca tctctcctt gaaatcgaaa agccactttt cgaacttgtc 720
 agcgcagcac agaccatcct gccagattct gagggcgcaa tcgagggccca cctccgcgag 780
 gtgggtctta ccttccatct gctcgaaaac gtgccagcac tgatctcaa gaacatcgaa 840
 aagtcctga acgaaacctt caagccactg gacatcatgg actggaactc cctgttctgg 900
 atcgctcacc caggcgggtc ggctatcctg gatcaggtcg aggctaagct gggctctgaag 960
 ccggagaagt tggaggctac cggccacatc ctgtccgaat acggcaacat gtcctccgca 1020
 tgcgttctct tcattcctga cgtggtgcgg cgcaagtccg cagccaacgg tgtgaccacc 1080
 cgtatcctga gcatcgggtc gatctccaag tccctgctga tcctggcatg gttcctcttc 1140
 tccctggtgt aa 1152

<210> 17
 <211> 384
 <212> PRT
 <213> Rheum palmatum

<220>
 <223> benzalacetone synthase from Rheum palmatum (RpBAS)

<400> 17

Met Ala Thr Glu Glu Met Lys Lys Leu Ala Thr Val Met Ala Ile Gly
 1 5 10 15

Thr Ala Asn Pro Pro Asn Cys Tyr Tyr Gln Ala Asp Phe Pro Asp Phe
 20 25 30

Tyr Phe Arg Val Thr Asn Ser Asp His Leu Ile Asn Leu Lys Gln Lys
35 40 45

Phe Lys Arg Leu Cys Glu Asn Ser Arg Ile Glu Lys Arg Tyr Leu His
50 55 60

Val Thr Glu Glu Ile Leu Lys Glu Asn Pro Asn Ile Ala Ala Tyr Glu
65 70 75 80

Ala Thr Ser Leu Asn Val Arg His Lys Met Gln Val Lys Gly Val Ala
85 90 95

Glu Leu Gly Lys Glu Ala Ala Leu Lys Ala Ile Lys Glu Trp Gly Gln
100 105 110

Pro Lys Ser Lys Ile Thr His Leu Ile Val Cys Cys Leu Ala Gly Val
115 120 125

Asp Met Pro Gly Ala Asp Tyr Gln Leu Thr Lys Leu Leu Asp Leu Asp
130 135 140

Pro Ser Val Lys Arg Phe Met Phe Tyr His Leu Gly Cys Tyr Ala Gly
145 150 155 160

Gly Thr Val Leu Arg Leu Ala Lys Asp Ile Ala Glu Asn Asn Lys Gly
165 170 175

Ala Arg Val Leu Ile Val Cys Ser Glu Met Thr Thr Thr Cys Phe Arg
180 185 190

Gly Pro Ser Glu Thr His Leu Asp Ser Met Ile Gly Gln Ala Ile Leu
195 200 205

Gly Asp Gly Ala Ala Ala Val Ile Val Gly Ala Asp Pro Asp Leu Thr
210 215 220

Val Glu Arg Pro Ile Phe Glu Leu Val Ser Thr Ala Gln Thr Ile Val
225 230 235 240

Pro Glu Ser His Gly Ala Ile Glu Gly His Leu Leu Glu Ser Gly Leu
245 250 255

Ser Phe His Leu Tyr Lys Thr Val Pro Thr Leu Ile Ser Asn Asn Ile
260 265 270

Lys Thr Cys Leu Ser Asp Ala Phe Thr Pro Leu Asn Ile Ser Asp Trp
275 280 285

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

Gln Val Thr Ala Lys Val Gly Leu Glu Lys Glu Lys Leu Lys Val Thr
305 310 315 320

Arg Gln Val Leu Lys Asp Tyr Gly Asn Met Ser Ser Ala Thr Val Phe
325 330 335

Phe Ile Met Asp Glu Met Arg Lys Lys Ser Leu Glu Asn Gly Gln Ala
340 345 350

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

Gly Ile Thr Val Glu Thr Val Val Leu Arg Ser Val Pro Val Ile Ser
370 375 380

<210> 18
<211> 1155
<212> DNA
<213> Rheum palmatum

<220>
<223> benzalacetone synthase from Rheum palmatum (RpBAS)
(codon optimised)

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<210> 19
 <211> 348
 <212> PRT
 <213> Rubus idaeus

<220>
 <223> benzalacetone reductase from Rubus idaeus (RiBAR)

<400> 19

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

Thr Arg Ser Ile Thr Leu Lys Leu Pro Gln Gly Ser Thr Gly Leu Leu
35 40 45

Leu Lys Asn Leu Tyr Leu Ser Cys Asp Pro Tyr Met Arg Ala Arg Met
50 55 60

Thr Asn His His Arg Leu Ser Tyr Val Asp Ser Phe Lys Pro Gly Ser
65 70 75 80

Pro Ile Ile Gly Tyr Gly Val Ala Arg Val Leu Glu Ser Gly Asn Pro
85 90 95

Lys Phe Asn Pro Gly Asp Leu Val Trp Gly Phe Thr Gly Trp Glu Glu
100 105 110

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

Asp Val Pro Leu Ser Tyr Tyr Thr Gly Leu Leu Gly Met Pro Gly Met
130 135 140

Thr Ala Tyr Ala Gly Phe Tyr Glu Ile Cys Ser Pro Lys Lys Gly Glu
145 150 155 160

Thr Val Tyr Val Ser Ala Ala Ser Gly Ala Val Gly Gln Leu Val Gly
165 170 175

Gln Phe Ala Lys Leu Thr Gly Cys Tyr Val Val Gly Ser Ala Gly Ser
180 185 190

Lys Glu Lys Val Asp Leu Leu Lys Asn Lys Phe Gly Phe Asp Glu Ala
195 200 205

Phe Asn Tyr Lys Glu Glu Ala Asp Leu Asp Ala Ala Leu Arg Arg Tyr
210 215 220

Phe Pro Asp Gly Ile Asp Ile Tyr Phe Glu Asn Val Gly Gly Lys Met
225 230 235 240

Leu Asp Ala Val Leu Pro Asn Met Arg Pro Lys Gly Arg Ile Ala Val
245 250 255

Cys Gly Met Ile Ser Gln Tyr Asn Leu Glu Gln Pro Glu Gly Val Arg
260 265 270

Asn Leu Met Ala Leu Ile Val Lys Gln Val Arg Met Glu Gly Phe Met
275 280 285

Val Phe Ser Tyr Tyr His Leu Tyr Gly Lys Phe Leu Glu Thr Val Leu
290 295 300

Pro Tyr Ile Lys Gln Gly Lys Ile Thr Tyr Val Glu Asp Val Val Asp
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Gly Leu Asp Asn Ala Pro Ala Ala Leu Ile Gly Leu Tyr Ser Gly Arg
325 330 335

Asn Val Gly Lys Gln Val Val Val Val Ser Arg Glu
340 345

<210> 20
<211> 1047
<212> DNA
<213> Rubus idaeus

<220>
<223> benzalacetone reductase from Rubus idaeus (RiBAR)
(codon optimised)

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<210> 21

<211> 11497

<212> DNA

<213> Artificial Sequence

<220>

<223> plasmid RiPKS-At4CL-RcTAL-pECXK (pECXK_A)

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<211> 4494

<212> DNA

<213> Artificial Sequence

<220>

<223> operon RiPKS-At4CL-RcTAL

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 <211> 11422
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<212> DNA

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<220>

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<211> 4497

<212> DNA

<213> Artificial Sequence

<220>

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<211> 11425

<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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<210> 56

<211> 4506

<212> DNA

<213> Artificial Sequence

<220>

<223> operon RpBAS-Pp4CL-SeSam8

<400> 56

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<210> 57

<211> 11383

<212> DNA

<213> Artificial Sequence

<220>

<223> plasmid RpBAS-Sc4CL-RcTAL-pECXK (pECXK_S)

<400> 57

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<212> DNA

<213> Artificial Sequence

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