

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

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

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

<400> 2
atgacctgc aatcccagac tgcaaaggac tgcctggcgc tggatggtgc actgacactg 60
gttcagtgcg aagcaattgc cactcaccgc tcacggatct ccgtcacacc agcattgcgg 120
gaacgctgcg cccgcgcgca cgcacgtctg gagcacgcta tcgcagaaca gcgtcacatc 180
tatggtatca ccaccggctt cggaccactg gctaatacgcc tgatcggtgc agatcagggc 240
gccgaactcc agcagaacct catctaccac cttgctactg gcgtgggccc aaaactctcc 300
tgggctgaag cacgtgcact catgctggct cgtctcaact ccatacctca gggcgcactt 360
ggtgcatcac cagaaacat cgaccgtatc gttgccgttc tgaacgctgg cttcgcccca 420
gaagtcccag ctacagggcac cgttggtgca tctggcgatc tgacccact ggctcacatg 480
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ggcgcagtga tggatcgctt gtgcggtggc ccactgacct tggcagcccg tgacggtctg 600
gctctggtca acggtacttc cgctatgacc gcaatcgctg ctttgaccgg tgtggaggct 660
gcgcgcgcaa tcgacgccgc attgcgccac tccgctgtgc tcatggaggt tctctccggc 720
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gcaaccgaac gtctggccca ggctctcgat ggccggtgc gcgtttgccg caccttgacc 840
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tactccctgc gcgtggtgcc acagctggtt ggcgctgtct gggacaccct cgattggcac 960
gatcgctcg tgacctgcga actcaactct gtgaccgaca acccaatctt cccggaaggc 1020
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gacgccctga acgctgcatt ggttaccctg gcaggtctgg tggagcgcca gatcgcacgc 1140
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cttcagtccg gcttcattggg cgcgcaggtc accgcaaccg cgctccttgc tgaaatgcgc 1260
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ggccaggctg gctgggtcct taccgcacgc gacctgcgcg atcgcacccg cgctgtctcg 1500
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 gaataacctga agtctgataa gccgatctac	180
ggcctcacc agggcttcgg tccactggtc ctgttcgatg cagattccga actggaacag	240
ggcggctctc tcatctccca tctgggcacc ggccagggtg caccgcttgc accggaagtg	300
tccgcctga ttctgtggct ccgcattcaa aacatgcgca agggctattc ggctgtcagt	360
cctgtgttct ggcaaaaact ggccgacctc tggaacaagg gcttcacccc tgctatccct	420
cgccacggca ccgtgtccgc cagcggcgat ctccagcctc tggcacacgc tgccctggct	480
tttaccggcg tgggcgaggc atggaccctg gatgcagacg gccgttggtc caccgtgcc	540
gccgtggacg cattagcagc actgggtgca gagccgttcg attggccagt gcgcgaggct	600
ttggccttcg tgaacggtac gggcgcatca ctgcgggtgg cagttctcaa ccacagatcc	660
gctctccgtc tcgtacgagc atgtgcagtc ttgtctgccc gtttggttac cttgctagga	720
gctaatactg 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 agatcggctc ggcatgcac atggcagctt atctggctga acgccagctc	1080
ggcctgctgg tgagcccgtg 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 tgtgggcca gttggcaggc atctgcccac cactggatgc tgaccgcca	1440
ctgggcgcgg aggtccgcgc tgctcgcgat ctctctccg cacacgctga ccagctgctc	1500
gttgacgagg ctgatggcaa agacttcggc taa	1533

<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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aaggagttct ccggcaacaa ggtcatctac ggtgtgaaca ccggcttcgg cccaatggca	180
caataccgta ttaaggaatc cgatcagatc cagcttcagt acaatctgat ccgttcccac	240
tcttcgggca ccggaaaacc actctcccca gtttgtgcta aggcagcaat cttggctcgc	300
ctgaacaccc tgtccctcgg taactccggc gtgcatccat ctgtcatcaa cctgatgtcg	360

gaactgatca acaaagacat taccccactc 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 gatcacttca 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 cgcctccatc ctggaagatg agttcaactc cgctaacgat	960
aaccaatca 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
accaccgag aatctcagat gctgtccaac cctatgtacg ttcactccat tccaaacaac	1260
aacgataacc aggacatcgt ctccatgggc accaactccg cagtgatcac gtccaaggtt	1320
atcgagaacg ctttcgaagt cctggctatc gaaatgatca ccatcgttca 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 tggctttcac aaacaaggga ttcaacaaa ggatacaata 240
atgatcctat tgcctaactc ccagaattt gtgtttgctt tcattggtgc atcgtacctc 300
ggagctatct 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 gattacctaaggagtgatg	600
ttgacgcaca agggacttgt gacaagcgtc gcacaacaag tcgacggtga aaatccgaat	660
ttgtatatcc atagcgagga cgtgatgctt tgtgtccttg ccttgttcca tatctattca	720
ctcaactccg ttttgctttg tggattaagg gtgggagcag cgattttgat tatgcagaaa	780
tttgatattg tttctttctt ggagttgata caaagttaca aggtgacaat agggccgttt	840
gtaccaccta ttgttttggg cattgctaag agtcctatgg ttgatgatta tgatctttca	900
tcagtaagaa ccgtcatgtc tggggctgca ccattaggaa aggagcttga agatactgtt	960
cgagccaaat ttcctaatagc taaacttggg cagggttatg gtatgacaga agctggacca	1020
gtgttggcta tgtgcttggc atttgcaaaa gaaccctttg aaataaaatc aggggcatgt	1080
ggaacagttg tgagaaatgc tgaaatgaaa attgtggatc ctaaaactgg taattctctt	1140
cccagaaatc aatctggaga aatttgcatt agaggagacc agatcatgaa aggctacctg	1200
aatgatccag aggccacagc aagaacaata gacaaagaag ggtggttata tactggtgac	1260
attggctaca ttgatgatga cgacgagctt ttcattgttg atcgattaaa ggaactgac	1320
aaatacaaag 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 tctgtcctg 120
cacgattaca ttttccagaa catctccgaa tttgctacta agccatgcct gatcaacggc 180

ccaaccggtc acgtgtacac ctactctgac gtccacgtga tcagccgcca gatcgcagct	240
aacttccaca agctgggcgt gaaccagaac gacgtagtga tgctgctgct ccctaactgc	300
cctgagttcg tcctgtcctt cctggccgcc tccttcgcg gtgcaaccgc gaccgcggcc	360
aaccatttct 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 cgcgtcgggtg cagcaatcct gatcatgcca	840
aagttcgaat tcaacctgct gctggagttg atccagcgct gcaaggtgac cgtggcacc	900
atggtgcccc cgatcgtgct ggcaatcgcg aagtccagcg aaaccgaaaa gtacgacctg	960
tcatccatcc gcgtcgtcaa gtcgggcgcc gcaccactcg gcaaggagct ggaggacgct	1020
gtcaacgcta agttccctaa cgcgaagctc ggccagggtc acggtatgac cgaggccggc	1080
ccagtcctgg ccatgtccct gggcttcgca aaggagccat tcccggtgaa gtccggcgca	1140
tgccggcaccg ttgtgcgcaa cgcagagatg aagatcggtg acccagatac cggtgactcc	1200
ctgtcccgta accagcccgg cgagatctgc atccgcggcc accagatcat gaagggtac	1260
ctgaacaacc ctgctgctac cgccgaaacc atcgataagg atggctggct ccacaccggc	1320
gacatcggtc tgatcgacga cgacgatgaa ctgttcacg tcgatcgct taaggagttg	1380
atcaagtaca agggcttcca ggtggcccc gcagaactgg aagcactgct catcgccac	1440
cctgatatca ccgatgtcg cgtcgtggcc atgaaggagg aagcagcagg cgaagtcca	1500
gtcgctttcg tggatgaagtc caaggattcc gagttgtccg aggatgatgt gaagcagttc	1560
gtgtccaagc aggtcgtgtt ctacaagcgc atcaacaagg tgttcttcac cgaatccatc	1620
ccaaaggcac catccggcaa gatcctgcgc 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 cctcccgcg cgtggcagca	360
ggccttgata agatcggcgt gaagcagggc gatgtcatcg cactgctctt gcctaactgc	420
gctgagttcg tcctggtgtt cctgggcgca gcgaagcgcg gcgccgttgt caccaccgct	480
aaccatttct acaccgccgc cgagttggag aagcaaatcg aggcctccgg tgcgggcatt	540
gttatcactc agagcagcta catcgagaag ctgcgaggcc 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 ccatttcgtg ccgccaatcg tcctggccat cgcaaagaac	1020
ccaatcgtcg agaattacga tctctcctcc atgcgcatgg ttatgtccgg cgctgcacct	1080
ctgggtcggg agctggagga cgctttccgt gcccgttgct caaacgccgt tctgggccag	1140
ggctacggga tgactgaagc cggcccagtc ctggctatgt gcctcgcat 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 gcgtaagga gatcatcaag ttcaagggtc tccaggtgcc tcctgcggag 1500
ctggaagctc tcctgctgtc ccacaaggag atccaggacg ctgctgtcgt gtcccgttaag 1560
gatgacgtgg cgggcgaagt tccagtggca ttcgtggtcc gcgctaccag ctccaccatc 1620
accgaggatg aagtcaagga ttacatcgca aagcaggtcg ttttctacaa gaagatccac 1680
aacgtatact tcgtggattc cgtgcctaaag 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
ttggctctgcg attctgctcc aggtcaccgt tctctcgctg atatgctggc tagcaccgca	480
cccgaaccat ccgtcgctat cgatccagca gaagatgtgg ctgcccttcc gtactcctct	540
ggcaccaccg gcaccccaaa ggggtgtgatg ctgaccacc gccagattgc aaccaacctg	600
gctcagctgg aaccttccat gccatccgct ccaggtgacc ggggtgctggc tgttctgcca	660
ttcttccaca tctacggctt gaccgcactc atgaacgctc ctttgccgct gggtgctacc	720
gtggtggtgc tccctcgctt cgacctggag cagttccttg cagccatcca gaaccaccgt	780
atcaccagtt tgtacgtcgc cccaccaatc gttttggcac tggctaagca ccctctgggtg	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
atgaagggtc acctcggccg cccagatgct accgcagcaa tgatcgatga ggagggttg	1200
ctgcacaccg gcgatgtggg ccacgtggac gctgatgggt gggtgttcgt 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
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 gcaatcggca ccgcaacccc accaaactgc gtcggccagt ccacctacc 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 tcaccacact tgttttctgc accaccagcg gtgtggatat gcctggcgcc 420
 gactaccagc tgatcaagct cttcggcctg cgcccatccg tcaagcgcct catgatgtac 480
 cagcagggct gcttcgccgg cggcaccgtt ctgcgcctgg ctaaggatct ggcagaaaac 540
 aaccgcggtg cccgcgttct cgtcgtgtgc tccgagatca ccgtggtcac cttccgcggc 600
 ccatccgaca cccaccttga ctgtctggtt ggccaggcac tcttcggcga tggcgtggca 660
 tccatcatcg tcggcgcaga tcctctccct gaaatcgaaa agccactttt cgaacttgtc 720
 agcgcagcac agaccatcct gccagattct gagggcgcaa tcgagggccca cctccgcgag 780
 gtgggtctta ccttccatct gctcgaaaac gtgccagcac tgatctcaa gaacatcgaa 840
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<210> 17

<211> 384

<212> PRT

<213> Rheum palmatum

<220>

<223> benzalacetone synthase from Rheum palmatum (RpBAS)

<400> 17

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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

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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
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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
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Asn Val Gly Lys Gln Val Val Val Val Ser Arg Glu
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<210> 20

<211> 1047

<212> DNA

<213> Rubus idaeus

<220>

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

<400> 20

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<210> 21

<211> 11497

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 21

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<213> Artificial Sequence

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<213> Artificial Sequence

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<223> operon RpBAS-At4CL-RcTAL

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<212> DNA

<213> Artificial Sequence

<220>

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<211> 11437

<212> DNA

<213> Artificial Sequence

<220>

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<211> 4569

<212> DNA

<213> Artificial Sequence

<220>

<223> operon RpBAS-Pp4CL-RcTAL

<400> 52

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<211> 11497

<212> DNA

<213> Artificial Sequence

<220>

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<211> 4506

<212> DNA

<213> Artificial Sequence

<220>

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<400> 56

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<211> 11383

<212> DNA

<213> Artificial Sequence

<220>

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

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<213> Artificial Sequence

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<211> 4440

<212> DNA

<213> Artificial Sequence

<220>

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41