

SEQUENCE LISTING

<110> AGRONUTRI TION
Institut National Polytechnique de Toulouse

<120> Nouvelle souche streptomyces barakatei, ses composés actifs
dérivés et leur utilisation dans le traitement des plantes

<130> INPACT01

<160> 11

<170> PatentIn version 3.3

<210> 1
<211> 1467
<212> DNA
<213> Streptomyces barakatei - ADNr 16S - SEQ n°1

<400> 1

| | |
|---------------------------------------------------------------------|------|
| cgaacgctgg ccgcgtgctt aacacatgca agtcgaacga tgaaccactt cgggtggggat | 60 |
| tagtggcgaa cgggtgagta acacgtgggc aatctgccct tcactctggg acaagccctg | 120 |
| gaaacgggggt ctaataccgg atacaacact ctcgggcatac cgatgagtgt ggaaagctcc | 180 |
| ggcgggtgaag gatgagcccg cggcctatca gcttgttggt gaggtaacgg ctcaccaagg | 240 |
| cgacgacggg tagccggcct gagagggcga ccggccacac tgggactgag acacggccca | 300 |
| gactcctacg ggaggcagca gtggggaata ttgcacaatg ggcgaaagcc tgatgcagcg | 360 |
| acgccgcgtg agggatgacg gccttcgggt tgtaaacctc tttcagcagg gaagaagcga | 420 |
| aagtgcgggt acctgcagaa gaagcgccgg ctaactacgt gccagcagcc gcggtataac | 480 |
| gtagggcgcg agcgttgtcc ggaattattg ggcgtaaaga gctcgtaggc ggtctgtcgc | 540 |
| gtcggatgtg aaagcccggg gcttaacccc gggctctgcat tcgatacggg cagactagag | 600 |
| tgtggtaggg gagatcgaa ttcctggtgt agcggtgaaa tgcgcagata tcaggaggaa | 660 |
| caccggtggc gaaggcggat ctctgggcca ttactgacgc tgaggagcga aagcgtgggg | 720 |
| agcgaacagg attagatacc ctggtagtcc acgccgtaaa cgggtgggaac taggtgttgg | 780 |
| cgacattcca cgtcgtcgggt gccgcagcta acgcattaag ttccccgcct ggggagtagc | 840 |
| gccgcaaggc taaaactcaa aggaattgac gggggcccg cacaagcagcg gagcatgtgg | 900 |
| cttaattcga cgcaacgcga agaaccttac caaggcttga catacaccgg aaacggccag | 960 |
| agatggctgc ccccttgtgg tcggtgtaca ggtggtgcat ggctgtcgtc agctcgtgtc | 1020 |
| gtgagatgtt ggggttaagtc ccgcaacgag cgcaaccctt gttctgtgtt gccagcatgc | 1080 |
| ccttcgggggt gatggggact cacaggagac tgccgggggtc aactcggagg aagggtggga | 1140 |
| cgacgtcaag tcacatgcc ccttatgtct tgggctgcac acgtgctaca atggcaggta | 1200 |
| caatgagctg cgaagccgtg aggcggagcg aatctcaaaa agcctgtctc agttcggatt | 1260 |
| ggggtctgca actcgacccc atgaagtcgg agttgctagt aatcgcagat cagcagtgct | 1320 |
| gcggtgaata cgttcccggg ccttgtacac accgcccgtc acgtcacgaa agtcggtaac | 1380 |
| acccgaagcc ggtggcccaa ccccttgtgg gagggagctg tcgaaggtgg gactggcgat | 1440 |
| tgggacgaag tcgtaacaag gtagccg | 1467 |

| | | |
|-------|------------------------------------|----|
| <210> | 2 | |
| <211> | 20 | |
| <212> | DNA | |
| <213> | amorce universelle 27f - SEQ n°2 | |
| <400> | 2 | |
| | agagtttgat cctggctcag | 20 |
| <210> | 3 | |
| <211> | 19 | |
| <212> | DNA | |
| <213> | amorce universelle 1492r - SEQ n°3 | |
| <400> | 3 | |
| | ggttaccttg ttacgactt | 19 |
| <210> | 4 | |
| <211> | 24 | |
| <212> | DNA | |
| <213> | amorce PR1 f - SEQ n°4 | |
| <400> | 4 | |
| | ctggctattc tcgattttta atcg | 24 |
| <210> | 5 | |
| <211> | 24 | |
| <212> | DNA | |
| <213> | amorce PR1 r - SEQ n°5 | |
| <400> | 5 | |
| | tcctgcatat gatgctcctt attg | 24 |
| <210> | 6 | |
| <211> | 30 | |
| <212> | DNA | |
| <213> | amorce PDF1 f - SEQ n°6 | |
| <400> | 6 | |
| | tcattggctaa gtttgcttcc atcatcaccc | 30 |
| <210> | 7 | |
| <211> | 24 | |
| <212> | DNA | |
| <213> | amorce PDF1 r - SEQ n°7 | |
| <400> | 7 | |
| | gtagatttaa catgggactg cgac | 24 |
| <210> | 8 | |
| <211> | 21 | |
| <212> | DNA | |
| <213> | amorce PAL1 f - SEQ n°8 | |
| <400> | 8 | |
| | cggaggagga gtggacgcta t | 21 |
| <210> | 9 | |
| <211> | 21 | |
| <212> | DNA | |
| <213> | amorce PAL1 r - SEQ n°9 | |
| <400> | 9 | |

tgcgacaccg tttttggttc t 21

<210> 10
<211> 24
<212> DNA
<213> amorce EF1 f - SEQ n°10

<400> 10
atgccccagg acatcgtgat ttca 24

<210> 11
<211> 24
<212> DNA
<213> amorce EF1 r - SEQ n°11

<400> 11
ttggcggcac ccttagctgg atca 24