

SEQUENCE LISTING

<110> BIOGAIA AB

<120> SELECTION AND USE OF MELATONIN SUPPORTING BACTERIA TO REDUCE INFANTILE COLIC

<130> 69.139115/02

<150> GB 1905470.9

<151> 2019-04-17

<150> GB 1812079.0

<151> 2018-07-24

<160> 9

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

<220>

<221> MISC_FEATURE

<222> (3) .. (3)

<223> any amino acid

<400> 1

Leu Pro Xaa Thr Gly

1 5

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer LrNuc1f

<400> 2

ggaactttgg gaaacctga

20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer LrNuc1r

<400> 3

cgggcaactt taccatcact

20

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer LrNuc2f

 <400> 4
 tactcgtgaa aatgccgttg 20

 <210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer LrNuc2r

 <400> 5
 gtgcccctgt catttcaact 20

 <210> 6
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer LrNuc3f

 <400> 6
 agctttacca aattgaccct ga 22

 <210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer LrNuc3r

 <400> 7
 ttgatattag gcgcatacctt tt 22

 <210> 8
 <211> 2259
 <212> DNA
 <213> Lactobacillus reuteri SD112

 <400> 8
 atgaagaata atagttcaaa atattgttta ttgtaggga cagcgtggtt aggactatat 60
 ttccaagcta atagtgttca tgcggatgcg actggtatca cagctaattgg agaaactacc 120
 catagcaatg ttactccaat gggttcagact aataaggatg aggcaagtac accgcaaaca 180
 actactgatt ggtctgaccc ggccaaatat caaagtgaca ttccagttca gatttttagga 240
 atcaatgact tgcattggtgg gttagaaacg actggatcag ctacgattgg agataagact 300

tattcgaatg ccggaacagt tgcacgccta gctggtaacc ttgatgcggc ggaggaaagt	360
tttaagaacg ctaatccgac gggaagctca attcgggtag aagccggaga tatggttggg	420
gcttctccag caaattctgc tcttctccaa gacgaatcaa ccatgcatgc tttagacgca	480
atgcattttg aaataggaac tttgggaaac catgagttcg atgaaggttt agctgagtat	540
atgcggattg ttaatggtgg tgaacctact aaacaatata atgaagctga gatggcctat	600
cctcatgtga aaacagggat taatatcatt actgccaatg ttgtaaataa atctgatggt	660
caaatcccat ttggaatgca accatacttg attaaagaaa ttcatactag tgatggtaaa	720
gttgcccgga tcggatttat tgggattgaa actacttccc taccaatttt aaccttatac	780
gataattaca aagattatga tgttttagac gaggctgaaa caattgcaaa atatgatcaa	840
attttacgca aaaaagggtgt taacgcaatt gtagttcttg ccatacagg ggtttcaact	900
gataaagatg gcagcactaa aggtaatgct gttgatatca ttaagaagct ttaccaaatt	960
gaccctgata attctgtcga cctttatatt gctggctact cccaccaata tgctaattgct	1020
actgttggaa gtgtaaaatt agtgcaagcc atttacacgg gtaaagctta cgatgatatt	1080
atcggttaca tcgatccaac aactaatgat tttgcgcca atagtctcgt ttcacatgtc	1140
tttccggtac tatctgaaaa ggatgcgcct aatatcaaaa cggatgcaaa tgttacagca	1200
attgttgaag atgcgaacaa ccgagtagca ccgattatta acaagaaaat aggggaagct	1260
gctacaacag gcgatattct tggacgactt cataatactc ctactcgtga aaatgccgtt	1320
ggtgaattag ttgtcgatgg tcaattatat gccgctcata aagtaggctt accagctgat	1380
tttgcgatga ctaatacagg gggcgttcgt gcagatctgc atgttaatcc tgatcgttcc	1440
attacatggg ggagtgccca agcagttcaa ccatttggtg atattttgcg ggtagttgaa	1500
atgacagggg cacaaatcgt tgaagccttg aatcaacaat acgacgaaga tcaagcttac	1560
tacttacaga tttccgggct acattatact tatactgacc aaaacgatcc taaccaacca	1620
tataaggctcg ttcaagttta tgaccaacat aatcaaccgc ttgatatgaa taagacttac	1680
aatgttgtta ttaatgactt tttagcagggt ggcgagatg gcttttctgc atttaagggt	1740
actaaagttg tcgggattgt tggccaagat acagacgcgt ttattgacta tattactgat	1800
atgactaatg atggtaaacc aattactgcg ccaacaatga accgtaagat ttacttgact	1860
gctgaacaag tagcgaaggc tgactcagat tcacagttac aaacaggaac taatcagaac	1920
actcaaaacg atgctaattc ccagactgaa ggaaatcagc ttcaagaagt tccgagccaa	1980
ccggtatctc caacagtaac cttgccaaaca acagctgggtc aacccgccga aactgttaca	2040
ctacatgctc aatctaagca acaaaccgta gctgctaata atcaattaat taatttgacg	2100
cctacatcaa ttaatggcca aaaacaaaaa gcagctgacc agcaagcagc tttaccacaa	2160

actagtaacg atgaagatct tgcattactt cttctcggaa gttcattaat ggcagcaacc 2220

ggattgacaa ttattgatcg caagcgtaaa catgcttaa 2259

<210> 9

<211> 752

<212> PRT

<213> Lactobacillus reuteri SD112

<400> 9

Met Lys Asn Asn Ser Ser Lys Tyr Cys Leu Leu Leu Gly Thr Ala Leu
1 5 10 15

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

Ile Thr Ala Asn Gly Glu Thr Thr His Ser Asn Val Thr Pro Met Val
35 40 45

Gln Thr Asn Lys Asp Glu Ala Ser Thr Pro Gln Thr Thr Thr Asp Trp
50 55 60

Ser Asp Pro Ala Lys Tyr Gln Ser Asp Ile Pro Val Gln Ile Leu Gly
65 70 75 80

Ile Asn Asp Leu His Gly Gly Leu Glu Thr Thr Gly Ser Ala Thr Ile
85 90 95

Gly Asp Lys Thr Tyr Ser Asn Ala Gly Thr Val Ala Arg Leu Ala Gly
100 105 110

Asn Leu Asp Ala Ala Glu Glu Ser Phe Lys Asn Ala Asn Pro Thr Gly
115 120 125

Ser Ser Ile Arg Val Glu Ala Gly Asp Met Val Gly Ala Ser Pro Ala
130 135 140

Asn Ser Ala Leu Leu Gln Asp Glu Ser Thr Met His Ala Leu Asp Ala
145 150 155 160

Met His Phe Glu Ile Gly Thr Leu Gly Asn His Glu Phe Asp Glu Gly
165 170 175

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

Tyr Asn Glu Ala Glu Met Ala Tyr Pro His Val Lys Thr Gly Ile Asn
195 200 205

Ile Ile Thr Ala Asn Val Val Asn Lys Ser Asp Gly Gln Ile Pro Phe
 210 215 220

Gly Met Gln Pro Tyr Leu Ile Lys Glu Ile His Thr Ser Asp Gly Lys
 225 230 235 240

Val Ala Arg Ile Gly Phe Ile Gly Ile Glu Thr Thr Ser Leu Pro Ile
 245 250 255

Leu Thr Leu Tyr Asp Asn Tyr Lys Asp Tyr Asp Val Leu Asp Glu Ala
 260 265 270

Glu Thr Ile Ala Lys Tyr Asp Gln Ile Leu Arg Lys Lys Gly Val Asn
 275 280 285

Ala Ile Val Val Leu Ala His Thr Gly Val Ser Thr Asp Lys Asp Gly
 290 295 300

Ser Thr Lys Gly Asn Ala Val Asp Ile Ile Lys Lys Leu Tyr Gln Ile
 305 310 315 320

Asp Pro Asp Asn Ser Val Asp Leu Tyr Ile Ala Gly His Ser His Gln
 325 330 335

Tyr Ala Asn Ala Thr Val Gly Ser Val Lys Leu Val Gln Ala Ile Tyr
 340 345 350

Thr Gly Lys Ala Tyr Asp Asp Ile Ile Gly Tyr Ile Asp Pro Thr Thr
 355 360 365

Asn Asp Phe Ala Pro Asn Ser Leu Val Ser His Val Phe Pro Val Leu
 370 375 380

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

Ile Val Glu Asp Ala Asn Asn Arg Val Ala Pro Ile Ile Asn Lys Lys
 405 410 415

Ile Gly Glu Ala Ala Thr Thr Gly Asp Ile Leu Gly Arg Leu His Asn
 420 425 430

Thr Pro Thr Arg Glu Asn Ala Val Gly Glu Leu Val Val Asp Gly Gln
 435 440 445

Leu Tyr Ala Ala His Lys Val Gly Leu Pro Ala Asp Phe Ala Met Thr
 450 455 460

Asn Thr Gly Gly Val Arg Ala Asp Leu His Val Asn Pro Asp Arg Ser
 465 470 475 480

Ile Thr Trp Gly Ser Ala Gln Ala Val Gln Pro Phe Gly Asn Ile Leu
 485 490 495

Arg Val Val Glu Met Thr Gly Ala Gln Ile Val Glu Ala Leu Asn Gln
 500 505 510

Gln Tyr Asp Glu Asp Gln Ala Tyr Tyr Leu Gln Ile Ser Gly Leu His
 515 520 525

Tyr Thr Tyr Thr Asp Gln Asn Asp Pro Asn Gln Pro Tyr Lys Val Val
 530 535 540

Gln Val Tyr Asp Gln His Asn Gln Pro Leu Asp Met Asn Lys Thr Tyr
 545 550 555 560

Asn Val Val Ile Asn Asp Phe Leu Ala Gly Gly Gly Asp Gly Phe Ser
 565 570 575

Ala Phe Lys Gly Thr Lys Val Val Gly Ile Val Gly Gln Asp Thr Asp
 580 585 590

Ala Phe Ile Asp Tyr Ile Thr Asp Met Thr Asn Asp Gly Lys Pro Ile
 595 600 605

Thr Ala Pro Thr Met Asn Arg Lys Ile Tyr Leu Thr Ala Glu Gln Val
 610 615 620

Ala Lys Ala Asp Ser Asp Ser Gln Leu Gln Thr Gly Thr Asn Gln Asn
 625 630 635 640

Thr Gln Asn Asp Ala Asn Ser Gln Thr Glu Gly Asn Gln Leu Gln Glu
 645 650 655

Val Pro Ser Gln Pro Val Ser Pro Thr Val Thr Leu Pro Thr Thr Ala
 660 665 670

Gly Gln Pro Ala Glu Thr Val Thr Leu His Ala Gln Ser Lys Gln Gln
 675 680 685

Thr Val Ala Ala Asn Asn Gln Leu Ile Asn Leu Thr Pro Thr Ser Ile
 690 695 700

Asn Gly Gln Lys Gln Lys Ala Ala Asp Gln Gln Ala Ala Leu Pro Gln

705

710

715

720

Thr Ser Asn Asp Glu Asp Leu Ala Leu Leu Leu Leu Gly Ser Ser Leu
725 730 735

Met Ala Ala Thr Gly Leu Thr Ile Ile Asp Arg Lys Arg Lys His Ala
740 745 750