0037001PCT-seql-000001

SEQUENCE LISTING

<110> INTRON BIOTECHNOLOGY, INC.

<120> An Antibacterial Composition and A Method of Treating Staphylococcal Infections With the Antibacterial Composition

<130> 0037-001PCT

<150> US 62/277,506
<151> 2016-01-12

<160> 3

<170> PatentIn version 3.5

<210> 1
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> antibacterial composition

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


Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
        35                  40                  45


Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
    50                  55                  60


Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65                  70                  75                  80


Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
                85                  90                  95
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Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
            100                 105                 110

Gln Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
        115                 120                 125

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
    130                 135                 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
145                 150                 155                 160

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
                165                 170                 175

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
            180                 185                 190

Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro
        195                 200                 205

Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln
    210                 215                 220

Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly
225                 230                 235                 240

Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp
                245                 250                 255

Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
            260                 265                 270

Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
        275                 280                 285
```

```
Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
    290                 295                 300

Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
305                 310                 315                 320

Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
                325                 330                 335

Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
            340                 345                 350

Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
        355                 360                 365

Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
    370                 375                 380

Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
385                 390                 395                 400

Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr
                405                 410                 415

Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
            420                 425                 430

Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
        435                 440                 445

Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
    450                 455                 460

Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly
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Val Pro Pro Asn His Ile Pro Gly Val Ala Trp Gly Val Phe Lys
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<213>  Artificial Sequence

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Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala Lys
1               5                   10                  15


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


Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr
        35                  40                  45


Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu
    50                  55                  60


Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys
65                  70                  75                  80


Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser Thr
                85                  90                  95


Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr Gln
            100                 105                 110


Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser Thr
        115                 120                 125
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```
Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro
    130                 135                 140

Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile
145                 150                 155                 160

Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys Ser
                165                 170                 175

Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val Ser
            180                 185                 190

Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro Glu
        195                 200                 205

Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln Tyr
    210                 215                 220

Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly Ile
225                 230                 235                 240

Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp Ala
                245                 250                 255

Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn Ser
            260                 265                 270

Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser Ala
        275                 280                 285

Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe Thr
    290                 295                 300

Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr Val
305                 310                 315                 320
```

```
Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser Met
                325                 330                 335

Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser Gln
            340                 345                 350

Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys Asn
        355                 360                 365

Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly Lys
    370                 375                 380

Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser Trp
385                 390                 395                 400

Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr Phe
                405                 410                 415

Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe Leu
            420                 425                 430

Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val Tyr
        435                 440                 445

Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn Ala
    450                 455                 460

Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly Val
465                 470                 475                 480

Pro Pro Asn His Ile Pro Gly Val Ala Trp Gly Val Phe Lys
                485                 490
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<212> DNA
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gcaggagcaa ttgacgcaga tggttactat catgcacagt gccaagactt aattactgat 180

tatgtattat ggttaacaga taataaagtt agaacttggg gtaatgctaa agaccaaatc 240

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gtatatgatg gaggtaatac ttctacattt actattttag agcaaaactg gaacggttac 420

gctaataaaa aacctacaaa acgtgtagat aattattacg gattaactca ttttattgag 480

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acacctgcac ctaaaaagaa agcaacacta aaagtttcta agaaccatat taactataca 600

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