SEQUENCE LISTING

<110> Lusomedicamenta S.A.

<120> ANTIBACTERIAL PHAGE PEPTIDES AND METHODS OF USE THEREOF

<130> PPI 41012/09

<160> 6

<170> PatentIn version 3.5

<210> 1
<211> 756
<212> DNA
<213> Bacteriophage F87s/06

<400> 1
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tttgacggtt ggtatggtta ccaatgtgca gatttagcag ttgattacat ttattggttg 120

ttagaaatta gaatgtgggg aaatgcaaaa gatgcaatca ataacgattt taaaaacatg 180

gcaacagtat atgaaaacac accatcgttt gttccacaaa taggtgatgt ggctgtattt 240

accaaaggaa tatataaaca atacggtcat attggtttag tgtttaatgg tggtaataca 300

aaccaatttt taattttgga acagaactat gacggtaacg caaatacgcc tgcaaagtta 360

cgttgggata attattacgg ctgtactcac tttattagac ctaagtataa aagtgagggc 420

ttaatgaata agatcacaaa taaagttaaa ccacctgctc aaaaagcagt cggtaaatct 480

gcaagtaaaa taacagttgg aagtaaagcg ccttataacc ttaaatggtc aaaaggtgct 540

tattttaatg cgaaaatcga cggcttaggt gctacttcag ccactagata cggtgataat 600

cgtactaact atagattcga tgttggacag gctgtatacg cgcctggaac attaatatat 660

gtgtttgaaa ttatagatgg ttggtgtcgc atttattgga acaatcataa tgagtggata 720

tggcatgaga gattgattgt gaaagaagtg ttttaa 756

<210> 2
<211> 251
<212> PRT
<213> Bacteriophage F87s/06

<400> 2

Met Lys Thr Tyr Ser Glu Ala Arg Ala Arg Leu Arg Trp Tyr Gln Gly
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Arg Tyr Ile Asp Phe Asp Gly Trp Tyr Gly Tyr Gln Cys Ala Asp Leu
20 25 30

Ala Val Asp Tyr Ile Tyr Trp Leu Leu Glu Ile Arg Met Trp Gly Asn
35 40 45

Ala Lys Asp Ala Ile Asn Asn Asp Phe Lys Asn Met Ala Thr Val Tyr
50 55 60

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Glu Asn Thr Pro Ser Phe Val Pro Gln Ile Gly Asp Val Ala Val Phe
65                  70                  75                  80

Thr Lys Gly Ile Tyr Lys Gln Tyr Gly His Ile Gly Leu Val Phe Asn
                85                  90                  95

Gly Gly Asn Thr Asn Gln Phe Leu Ile Leu Glu Gln Asn Tyr Asp Gly
            100                 105                 110

Asn Ala Asn Thr Pro Ala Lys Leu Arg Trp Asp Asn Tyr Tyr Gly Cys
        115                 120                 125

Thr His Phe Ile Arg Pro Lys Tyr Lys Ser Glu Gly Leu Met Asn Lys
    130                 135                 140

Ile Thr Asn Lys Val Lys Pro Pro Ala Gln Lys Ala Val Gly Lys Ser
145                 150                 155                 160

Ala Ser Lys Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp
                165                 170                 175

Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr
            180                 185                 190

Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val
        195                 200                 205

Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val Phe Glu Ile
    210                 215                 220

Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile
225                 230                 235                 240

Trp His Glu Arg Leu Ile Val Lys Glu Val Phe
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<210> 3
<211> 894
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic - Lysin 170-87

<400> 3

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ggtagccgta atggtatcac tatcgacacc attatcctac atcacaatgc aacaacaaat     120

aaagatgttg ctatgaacac atggctatta ggtggtggcg caggtacatc tgctcattat     180

gaatgtacac caacagaaat tattggatgt gtcggtgagc agtattcagc attccatgcc     240

ggaggtacag gtggtataga cgttcctaag attgctaacc ctaatcaacg ttcaataggt     300

attgaaaatg taaactcgtc aggagcacct aattggtctg tagaccctag aacaattaca     360
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aattgtgctc gtttagtggc agatatttgt acacgttatg gtattccgtg tgaccgacaa 420

catgtgttag gacataacga agtaactgca acagcatgtc ccggaggtat ggatgtagac 480

gaagttgtac gtcaagctca acagttcatg gcaggaggct ctaacaatgc agttaagccg 540

gagccaaaag ttaaaccacc tgctcaaaaa gcagtcggta aatctgcaag taaaataaca 600

gttggaagta aagcgcctta taaccttaaa tggtcaaaag gtgcttattt taatgcgaaa 660

atcgacggct taggtgctac ttcagccact agatacggtg ataatcgtac taactataga 720

ttcgatgttg gacaggctgt atacgcgcct ggaacattaa tatatgtgtt tgaaattata 780

gatggttggt gtcgcattta ttggaacaat cataatgagt ggatatggca tgagagattg 840

attgtgaaag aagtgtttcc cgggggggt tctcatcatc atcatcatca ttaa 894

<210> 4
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct - Lysin 170-87

<400> 4

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

Leu His His Asn Ala Thr Thr Asn Lys Asp Val Ala Met Asn Thr Trp
35 40 45

Leu Leu Gly Gly Gly Ala Gly Thr Ser Ala His Tyr Glu Cys Thr Pro
50 55 60

Thr Glu Ile Ile Gly Cys Val Gly Glu Gln Tyr Ser Ala Phe His Ala
65 70 75 80

Gly Gly Thr Gly Gly Ile Asp Val Pro Lys Ile Ala Asn Pro Asn Gln
85 90 95

Arg Ser Ile Gly Ile Glu Asn Val Asn Ser Ser Gly Ala Pro Asn Trp
100 105 110

Ser Val Asp Pro Arg Thr Ile Thr Asn Cys Ala Arg Leu Val Ala Asp
115 120 125

Ile Cys Thr Arg Tyr Gly Ile Pro Cys Asp Arg Gln His Val Leu Gly
130 135 140

His Asn Glu Val Thr Ala Thr Ala Cys Pro Gly Gly Met Asp Val Asp
145 150 155 160

Glu Val Val Arg Gln Ala Gln Gln Phe Met Ala Gly Gly Ser Asn Asn
165 170 175

Ala Val Lys Pro Glu Pro Lys Val Lys Pro Pro Ala Gln Lys Ala Val
180 185 190

Gly Lys Ser Ala Ser Lys Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn
195 200 205

Leu Lys Trp Ser Lys Gly Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu
210 215 220

Gly Ala Thr Ser Ala Thr Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg
225 230 235 240

Phe Asp Val Gly Gln Ala Val Tyr Ala Pro Gly Thr Leu Ile Tyr Val
245 250 255

Phe Glu Ile Ile Asp Gly Trp Cys Arg Ile Tyr Trp Asn Asn His Asn
260 265 270

Glu Trp Ile Trp His Glu Arg Leu Ile Val Lys Glu Val Phe Pro Gly
275 280 285

Gly Gly Ser His His His His His His
290 295

<210> 5
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic - Lysin 168-87

<400> 5
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gctgatggat ggtatggtac tcaatgtatg gacttgacag tagacgttat gcaacgcttc 120

ttcggatggc gcccgtacgg taatgcaatt gccttggttg accagcctat cccagcaggc 180

ttccaaagaa tccgtaccac aagctctaca caaatcaaag ctggtgacgt tatgatatgg 240

ggcttaggat actatgctca atacggtcac acaggaattg caacggagga tggaagagct 300

gacggaacct ttgtcagtgt tgaccaaaac tggattaacc caagccttga agtaggcagt 360

ccagcagctg ctatccacca caatatggat ggtgtctggg gagttatccg accaccttac 420

gaggctgaat caaagcctaa accacctgca ccaaaaccag ataaaccaaa tctaggacaa 480

aaagttaaac cacctgctca aaaagcagtc ggtaaatctg caagtaaaat aacagttgga 540

agtaaagcgc cttataacct taaatggtca aaaggtgctt attttaatgc gaaaatcgac 600

ggcttaggtg ctacttcagc cactagatac ggtgataatc gtactaacta tagattcgat 660

gttggacagg ctgtatacgc gcctggaaca ttaatatatg tgtttgaaat tatagatggt 720

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aaagaagtgt ttcccggggg gggttctcat catcatcatc atcattaa 828

<210> 6
<211> 275
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct - Lysin 168-87

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Met Val Lys Leu Asn Asp Val Leu Ser Tyr Val Asn Gly Leu Val Gly
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Lys Gly Val Asp Ala Asp Gly Trp Tyr Gly Thr Gln Cys Met Asp Leu
20 25 30

Thr Val Asp Val Met Gln Arg Phe Phe Gly Trp Arg Pro Tyr Gly Asn
35 40 45

Ala Ile Ala Leu Val Asp Gln Pro Ile Pro Ala Gly Phe Gln Arg Ile
50 55 60

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

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

Asp Gly Arg Ala Asp Gly Thr Phe Val Ser Val Asp Gln Asn Trp Ile
100 105 110

Asn Pro Ser Leu Glu Val Gly Ser Pro Ala Ala Ala Ile His His Asn
115 120 125

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

Lys Pro Lys Pro Pro Ala Pro Lys Pro Asp Lys Pro Asn Leu Gly Gln
145 150 155 160

Lys Val Lys Pro Pro Ala Gln Lys Ala Val Gly Lys Ser Ala Ser Lys
165 170 175

Ile Thr Val Gly Ser Lys Ala Pro Tyr Asn Leu Lys Trp Ser Lys Gly
180 185 190

Ala Tyr Phe Asn Ala Lys Ile Asp Gly Leu Gly Ala Thr Ser Ala Thr
195 200 205

```
Arg Tyr Gly Asp Asn Arg Thr Asn Tyr Arg Phe Asp Val Gly Gln Ala
    210                 215                 220

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

Trp Cys Arg Ile Tyr Trp Asn Asn His Asn Glu Trp Ile Trp His Glu
                245                 250                 255

Arg Leu Ile Val Lys Glu Val Phe Pro Gly Gly Gly Ser His His His
            260                 265                 270

His His His
        275
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