SEQUENCE LISTING

<110> Ferring B.V.
Institut Pasteur

<120> BACTERIOPHAGE THERAPY

<130> HE 171 371

<150> EP 13305568.1
<151> 2013-04-30

<160> 45

<170> BiSSAP 1.3

<210> 1
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<213> Bacteriophage wV8

<400> 1

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Gly Leu Phe Arg Ser Ala Pro Ile Thr Gln Thr Thr Phe Leu Met Asp
        35                  40                  45
Leu Thr Asp Trp Asp Val Ser Leu Leu Asp Ala Val Asp Arg Asp Ser
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Arg Lys Ala Glu Thr Ser Ala Pro Glu Arg Val Arg Gln Ile Ser Phe
65                  70                  75                  80
Pro Met Met Tyr Phe Lys Glu Val Glu Ser Ile Thr Pro Asp Glu Ile
                85                  90                  95
Gln Gly Val Arg Gln Pro Gly Thr Ala Asn Glu Leu Thr Thr Glu Ala
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Val Val Arg Ala Lys Lys Leu Met Lys Ile Arg Thr Lys Phe Asp Ile
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Thr Arg Glu Phe Leu Phe Met Gln Ala Leu Lys Gly Lys Val Val Asp
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Ala Arg Gly Thr Leu Tyr Ala Asp Leu Tyr Lys Gln Phe Asp Val Glu
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Lys Lys Thr Val Tyr Phe Asp Leu Asp Asn Pro Asn Ala Asp Ile Asp
                165                 170                 175
Ala Ala Ile Glu Glu Leu Arg Met His Met Glu Asp Glu Ala Lys Thr
            180                 185                 190
Gly Thr Val Ile Asn Gly Glu Glu Ile His Val Val Val Asp Arg Leu
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Phe Phe Ser Lys Leu Val Lys His Pro Lys Ile Arg Asp Ala Tyr Leu
    210                 215                 220
Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln Ile Thr Gly Ser Leu Arg
225                 230                 235                 240
Thr Gly Gly Thr Asp Gly Val Gln Ala His Met Asn Thr Phe Tyr Tyr
                245                 250                 255
Gly Gly Val Lys Phe Val Gln Tyr Asn Gly Lys Phe Lys Asp Lys Arg
            260                 265                 270
Gly Lys Val His Thr Leu Val Ser Ile Asp Ser Val Ala Ala Thr Val
        275                 280                 285
Gly Val Gly His Ala Phe Pro Asn Val Ser Met Leu Gly Glu Ala Asn
    290                 295                 300
Asn Ile Phe Glu Val Ala Tyr Gly Pro Cys Pro Lys Met Gly Tyr Ala
305                 310                 315                 320
Asn Thr Leu Gly Gln Glu Leu Tyr Val Phe Glu Tyr Glu Lys Asp Arg
                325                 330                 335
Asp Glu Gly Ile Asp Phe Glu Ala His Ser Tyr Met Leu Pro Tyr Cys
            340                 345                 350
Thr Arg Pro Gln Leu Leu Val Asp Val Arg Ser Asp Ala Lys Pro Asp
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<210> 2
<211> 27
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<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1 aligning with position 10-36 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 2
Phe Phe Leu Ala Asp Leu Thr Gly Glu Val Gln Ser Ile Pro Asn Thr
1 5 10 15
Tyr Gly Tyr Ile Ser Asn Leu Gly Leu Phe Arg
20 25

<210> 3
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<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P2 aligning with position 8-62 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 3
Ser Arg Phe Phe Leu Ala Asp Leu Thr Gly Glu Val Gln Ser Ile Pro
1 5 10 15
Asn Thr Tyr Gly Tyr Ile Ser Asn Leu Gly Leu Phe Arg Ser Ala Pro
20 25 30
Ile Thr Gln Thr Thr Phe Leu Met Asp Leu Thr Asp Trp Asp Val Ser
35 40 45
Leu Leu Asp Ala Val Asp Arg
50 55

<210> 4
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1-P6 aligning with position 77-115 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 4
Gln Ile Ser Phe Pro Met Met Tyr Phe Lys Glu Val Glu Ser Ile Thr
1 5 10 15
Pro Asp Glu Ile Gln Gly Val Arg Gln Pro Gly Thr Ala Asn Glu Leu
20 25 30
Thr Thr Glu Ala Val Val Arg
35

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1-P6 aligning with position 124-139 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 5
Thr Lys Phe Asp Ile Thr Arg Glu Phe Leu Phe Met Gln Ala Leu Lys
1 5 10 15

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1-P5 aligning with position 147-155 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 6
Gly Thr Leu Tyr Ala Asp Leu Tyr Lys
1 5

<210> 7
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P6 aligning with position 147-161 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 7
Gly Thr Leu Tyr Ala Asp Leu Tyr Lys Gln Phe Asp Val Glu Lys
1 5 10 15

<210> 8
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1 aligning with position 162-183 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 8
Lys Thr Val Tyr Phe Asp Leu Asp Asn Pro Asn Ala Asp Ile Asp Ala
1 5 10 15
Ser Ile Glu Glu Leu Arg
20

<210> 9
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P3 aligning with position 163-183 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 9
Thr Val Tyr Phe Asp Leu Asp Asn Pro Asn Ala Asp Ile Asp Ala Ser
1 5 10 15
Ile Glu Glu Leu Arg
20

<210> 10
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P5-P6 aligning with position 163-183 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 10
Thr Ile Tyr Phe Asp Leu Asp Asn Pro Asn Ala Asp Ile Asp Ala Ser
1 5 10 15
Ile Glu Glu Leu Arg
20

<210> 11
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1 and P3-P6 aligning with position 192-207 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 11
Thr Gly Thr Val Ile Asn Gly Glu Glu Ile His Val Val Val Asp Arg
1 5 10 15

<210> 12
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P2 aligning with position 192-212 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 12
Thr Gly Thr Val Ile Asn Gly Glu Glu Ile His Val Val Val Asp Arg
1 5 10 15
Leu Phe Phe Ser Lys
20

<210> 13
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1 aligning with position 219-240 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 13
Ile Arg Asp Ala Tyr Leu Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln
1 5 10 15
Ile Thr Gly Ser Leu Arg
20

<210> 14
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P2 aligning with position 219-267 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 14
Ile Arg Asp Ala Tyr Leu Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln
1 5 10 15
Ile Thr Gly Ser Leu Arg Thr Gly Gly Thr Asp Gly Val Gln Ala His
20 25 30
Met Asn Thr Phe Tyr Tyr Gly Gly Val Lys Phe Val Gln Tyr Asn Gly
35 40 45
Lys

<210> 15
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P3-P4 aligning with position 221-240 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 15
Asp Ala Tyr Leu Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln Ile Thr
1 5 10 15
Gly Ser Leu Arg
20

<210> 16
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P5 aligning with position 221-267 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 16
Asp Ala Tyr Leu Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln Ile Thr
1 5 10 15
Gly Ser Leu Arg Thr Gly Gly Ala Asp Gly Val Gln Ala His Met Asn
20 25 30
Thr Phe Tyr Tyr Gly Gly Val Lys Phe Val Gln Tyr Asn Gly Lys
35 40 45

<210> 17
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P6 aligning with position 221-260 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 17
Asp Ala Tyr Leu Ala Gln Gln Thr Pro Leu Ala Trp Gln Gln Ile Thr
1 5 10 15
Gly Ser Leu Arg Thr Gly Gly Ala Asp Gly Val Gln Ala His Met Asn
20 25 30
Thr Phe Tyr Tyr Gly Gly Val Lys
35 40

<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1, P3 and P4 aligning with position 261-267 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 18
Phe Val Gln Tyr Asn Gly Lys
1 5

<210> 19
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1-P2 aligning with position 317-336 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 19
Met Gly Tyr Ala Asn Thr Leu Gly Gln Glu Leu Tyr Val Phe Glu Tyr
1 5 10 15
Glu Lys Asp Arg
20

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P1-P6 aligning with position 355-362 of the major capsid protein of bacteriophage wV8 (SEQ ID NO: 1)

<400> 20
Pro Gln Leu Leu Val Asp Val Arg
1 5

<210> 21
<211> 522
<212> PRT
<213> Bacteriophage RB69

<400> 21
Met Thr Thr Ile Lys Thr Lys Ala Gln Leu Val Asp Lys Trp Lys Glu
1 5 10 15
Leu Leu Glu Gly Glu Gly Leu Pro Glu Ile Ala Asn Ser Lys Gln Ala
20 25 30
Ile Ile Ala Lys Ile Phe Glu Asn Gln Glu Lys Asp Phe Glu Val Ser
35 40 45
Pro Glu Tyr Lys Asp Glu Lys Ile Ala Gln Ala Phe Gly Ser Phe Leu
50 55 60
Thr Glu Ala Glu Ile Gly Gly Asp His Gly Tyr Asn Ala Gln Asn Ile
65 70 75 80
Ala Ala Gly Gln Thr Ser Gly Ala Val Thr Gln Ile Gly Pro Ala Val
85 90 95
Met Gly Met Val Arg Arg Ala Ile Pro Asn Leu Ile Ala Phe Asp Ile
100 105 110
Cys Gly Val Gln Pro Met Asn Ser Pro Thr Gly Gln Val Phe Ala Leu
115 120 125
Arg Ala Val Tyr Gly Lys Asp Pro Ile Ala Ala Gly Ala Lys Glu Ala
130 135 140
Phe His Pro Met Tyr Ala Pro Asp Ala Met Phe Ser Gly Gln Gly Ala
145 150 155 160
Ala Lys Lys Phe Pro Ala Leu Ala Ala Ser Thr Gln Thr Lys Val Gly
165 170 175
Asp Ile Tyr Thr His Phe Phe Gln Glu Thr Gly Thr Val Tyr Leu Gln

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            180                 185                 190
Ala Ser Ala Gln Val Thr Ile Ser Ser Ser Ala Asp Asp Ala Ala Lys
        195                 200                 205
Leu Asp Ala Glu Ile Ile Lys Gln Met Glu Ala Gly Ala Leu Val Glu
    210                 215                 220
Ile Ala Glu Gly Met Ala Thr Ser Ile Ala Glu Leu Gln Glu Gly Phe
225                 230                 235                 240
Asn Gly Ser Thr Asp Asn Pro Trp Asn Glu Met Gly Phe Arg Ile Asp
                245                 250                 255
Lys Gln Val Ile Glu Ala Lys Ser Arg Gln Leu Lys Ala Ala Tyr Ser
            260                 265                 270
Ile Glu Leu Ala Gln Asp Leu Arg Ala Val His Gly Met Asp Ala Asp
        275                 280                 285
Ala Glu Leu Ser Gly Ile Leu Ala Thr Glu Ile Met Leu Glu Ile Asn
    290                 295                 300
Arg Glu Val Val Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys Ser
305                 310                 315                 320
Gly Met Thr Asn Ile Val Gly Ser Lys Ala Gly Val Phe Asp Phe Gln
                325                 330                 335
Asp Pro Ile Asp Ile Arg Gly Ala Arg Trp Ala Gly Glu Ser Phe Lys
            340                 345                 350
Ala Leu Leu Phe Gln Ile Asp Lys Glu Ala Val Glu Ile Ala Arg Gln
        355                 360                 365
Thr Gly Arg Gly Glu Gly Asn Phe Ile Ile Ala Ser Arg Asn Val Val
    370                 375                 380
Asn Val Leu Ala Ser Val Asp Thr Gly Ile Ser Tyr Ala Ala Gln Gly
385                 390                 395                 400
Leu Ala Ser Gly Phe Asn Thr Asp Thr Thr Lys Ser Val Phe Ala Gly
                405                 410                 415
Val Leu Gly Gly Lys Tyr Arg Val Tyr Ile Asp Gln Tyr Ala Lys Gln
            420                 425                 430
Asp Tyr Phe Thr Val Gly Tyr Lys Gly Ala Asn Glu Met Asp Ala Gly
        435                 440                 445
Ile Tyr Tyr Ala Pro Tyr Val Ala Leu Thr Pro Leu Arg Gly Ser Asp
    450                 455                 460
Pro Lys Asn Phe Gln Pro Val Met Gly Phe Lys Thr Arg Tyr Gly Ile
465                 470                 475                 480
Gly Val Asn Pro Phe Ala Glu Ser Ser Leu Gln Ala Pro Gly Ala Arg
                485                 490                 495
Ile Gln Ser Gly Met Pro Ser Ile Leu Asn Ser Leu Gly Lys Asn Ala
            500                 505                 510
Tyr Phe Arg Arg Val Tyr Val Lys Gly Ile
        515                 520
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<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 143-162 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 22
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Glu Ala Phe His Pro Met Tyr Ala Pro Asp Ala Met Phe Ser Gly Gln
1               5                   10                  15
Gly Ala Ala Lys
            20
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<210> 23
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 269-280 of the major capsid protein of bacteriophage RB69 (SEQ ID

NO: 21)

<400> 23
Ala Ala Tyr Ser Ile Glu Leu Ala Gln Asp Leu Arg
1 5 10

<210> 24
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 306-319 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 24
Glu Val Val Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys
1 5 10

<210> 25
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 330-342 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 25
Ala Gly Val Phe Asp Phe Gln Asp Pro Ile Asp Ile Arg
1 5 10

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 346-352 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 26
Trp Ala Gly Glu Ser Phe Lys
1 5

<210> 27
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 368-381 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 27
Gln Thr Gly Arg Gly Glu Gly Asn Phe Ile Ile Ala Ser Arg
1 5 10

<210> 28
<211> 50
<212> PRT
<213> Artificial Sequence

<220>

<223> Peptide from bacteriophage strain P8 aligning with position 412-461 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 28
Ser Val Phe Ala Gly Val Leu Gly Gly Lys Tyr Arg Val Tyr Ile Asp
1 5 10 15
Gln Tyr Ala Lys Gln Asp Tyr Phe Thr Val Gly Tyr Lys Gly Ala Asn
20 25 30
Glu Met Asp Ala Gly Ile Tyr Tyr Ala Pro Tyr Val Ala Leu Thr Pro
35 40 45
Leu Arg
50

<210> 29
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain P8 aligning with position 467-510 of the major capsid protein of bacteriophage RB69 (SEQ ID NO: 21)

<400> 29
Asn Phe Gln Pro Val Met Gly Phe Lys Thr Arg Tyr Gly Ile Gly Val
1 5 10 15
Asn Pro Phe Ala Glu Ser Ser Leu Gln Ala Pro Gly Ala Arg Ile Gln
20 25 30
Ser Gly Met Pro Ser Ile Leu Asn Ser Leu Gly Lys
35 40

<210> 30
<211> 18
<212> DNA
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<220>
<223> All bacteria 16S gene forward primer

<400> 30
cggtgaatac gttcccgg 18

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> All bacteria 16S gene reverse primer

<400> 31
tacggctacc ttgttacgac tt 22

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> E. coli 16S gene forward primer

<400> 32
catgccgcgt gtatgaagaa 20

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> E. coli 16S gene reverse primer

<400> 33
cgggtaacgt caatgagcaa a 21

<210> 34
<211> 519
<212> PRT
<213> Bacteriophage JS98

<400> 34
Met Lys Lys Asn Ala Leu Val Gln Lys Trp Ser Ala Leu Leu Glu Asn
1 5 10 15
Glu Ala Leu Pro Glu Ile Val Gly Ala Ser Lys Gln Ala Ile Ile Ala
20 25 30
Lys Ile Phe Glu Asn Gln Glu Gln Asp Ile Leu Thr Ala Pro Glu Tyr
35 40 45
Arg Asp Glu Lys Ile Ser Glu Ala Phe Gly Ser Phe Leu Thr Glu Ala
50 55 60
Glu Ile Gly Gly Asp His Gly Tyr Asp Ala Thr Asn Ile Ala Ala Gly
65 70 75 80
Gln Thr Ser Gly Ala Val Thr Gln Ile Gly Pro Ala Val Met Gly Met
85 90 95
Val Arg Arg Ala Ile Pro His Leu Ile Ala Phe Asp Ile Cys Gly Val
100 105 110
Gln Pro Leu Asn Asn Pro Thr Gly Gln Val Phe Ala Leu Arg Ala Val
115 120 125
Tyr Gly Lys Asp Pro Ile Ala Ala Gly Ala Lys Glu Ala Phe His Pro
130 135 140
Met Tyr Ala Pro Asn Ala Met Phe Ser Gly Gln Gly Ala Ala Glu Thr
145 150 155 160
Phe Glu Ala Leu Ala Ala Ser Lys Val Leu Glu Val Gly Lys Ile Tyr
165 170 175
Ser His Phe Phe Glu Ala Thr Gly Ser Ala His Phe Gln Ala Val Glu
180 185 190
Ala Val Thr Val Asp Ala Gly Ala Thr Asp Ala Ala Lys Leu Asp Ala
195 200 205
Ala Val Thr Ala Leu Val Glu Ala Gly Gln Leu Ala Glu Ile Ala Glu
210 215 220
Gly Met Ala Thr Ser Ile Ala Glu Leu Gln Glu Gly Phe Asn Gly Ser
225 230 235 240
Thr Asp Asn Pro Trp Asn Glu Met Gly Phe Arg Ile Asp Lys Gln Val
245 250 255
Ile Glu Ala Lys Ser Arg Gln Leu Lys Ala Ser Tyr Ser Ile Glu Leu
260 265 270
Ala Gln Asp Leu Arg Ala Val His Gly Met Asp Ala Asp Ala Glu Leu
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Ser Gly Ile Leu Ala Thr Glu Ile Met Leu Glu Ile Asn Arg Glu Val
290 295 300
Ile Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys Ser Gly Met Thr
305 310 315 320
Asn Thr Val Gly Ala Lys Ala Gly Val Phe Asp Phe Gln Asp Pro Ile
325 330 335
Asp Ile Arg Gly Ala Arg Trp Ala Gly Glu Ser Phe Lys Ala Leu Leu
340 345 350
Phe Gln Ile Asp Lys Glu Ala Ala Glu Ile Ala Arg Gln Thr Gly Arg
355 360 365
Gly Ala Gly Asn Phe Ile Ile Ala Ser Arg Asn Val Val Asn Val Leu
370 375 380
Ala Ala Val Asp Thr Ser Val Ser Tyr Ala Ala Gln Gly Leu Gly Gln
385 390 395 400

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Gly Phe Asn Val Asp Thr Thr Lys Ala Val Phe Ala Gly Val Leu Gly
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Gly Lys Tyr Arg Val Tyr Ile Asp Gln Tyr Ala Arg Ser Asp Tyr Phe
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Thr Ile Gly Tyr Lys Gly Ser Asn Glu Met Asp Ala Gly Ile Tyr Tyr
435 440 445
Ala Pro Tyr Val Ala Leu Thr Pro Leu Arg Gly Ser Asp Pro Lys Asn
450 455 460
Phe Gln Pro Val Met Gly Phe Lys Thr Arg Tyr Gly Ile Gly Ile Asn
465 470 475 480
Pro Phe Ala Asp Pro Ala Ala Gln Ala Pro Thr Lys Arg Ile Gln Asn
485 490 495
Gly Met Pro Asp Ile Val Asn Ser Leu Gly Leu Asn Gly Tyr Phe Arg
500 505 510
Arg Val Tyr Val Lys Gly Ile
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<210> 35
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 127-139 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 35
Ala Val Tyr Gly Lys Asp Pro Ile Ala Ala Gly Ala Lys
1 5 10

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 266-277 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 36
Ala Ser Tyr Ser Ile Glu Leu Ala Gln Asp Leu Arg
1 5 10

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 303-316 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 37
Glu Val Ile Asp Trp Ile Asn Tyr Ser Ala Gln Val Gly Lys
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 327-339 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 38
Ala Gly Val Phe Asp Phe Gln Asp Pro Ile Asp Ile Arg
1 5 10

<210> 39
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 343-364 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 39
Trp Ala Gly Glu Ser Phe Lys Ala Leu Leu Phe Gln Ile Asp Lys Glu
1 5 10 15
Ala Ala Glu Ile Ala Arg
20

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 369-378 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 40
Gly Ala Gly Asn Phe Ile Ile Ala Ser Arg
1 5 10

<210> 41
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 409-428 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 41
Ala Val Phe Ala Gly Val Leu Gly Gly Lys Tyr Arg Val Tyr Ile Asp
1 5 10 15
Gln Tyr Ala Arg
20

<210> 42
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 438-458 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 42
Gly Ser Asn Glu Met Asp Ala Gly Ile Tyr Tyr Ala Pro Tyr Val Ala
1 5 10 15
Leu Thr Pro Leu Arg
20

<210> 43

<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide from bacteriophage strain CLB_P2 aligning with position 464-512 of the major capsid protein of bacteriophage JS98 (SEQ ID NO: 34)

<400> 43
Asn Phe Gln Pro Val Met Gly Phe Lys Thr Arg Tyr Gly Ile Gly Ile
1 5 10 15
Asn Pro Phe Ala Asp Pro Ala Ala Gln Ala Pro Thr Lys Arg Ile Gln
20 25 30
Asn Gly Met Pro Asp Ile Val Asn Ser Leu Gly Leu Asn Gly Tyr Phe
35 40 45
Arg

<210> 44
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer to amplify a specific gene (pMT1) from LF82

<400> 44
ccattcatgc agcagctctt t 21

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer to amplify a specific gene (pMT1) from LF82

<400> 45
atcggacaac attagcggtg t 21