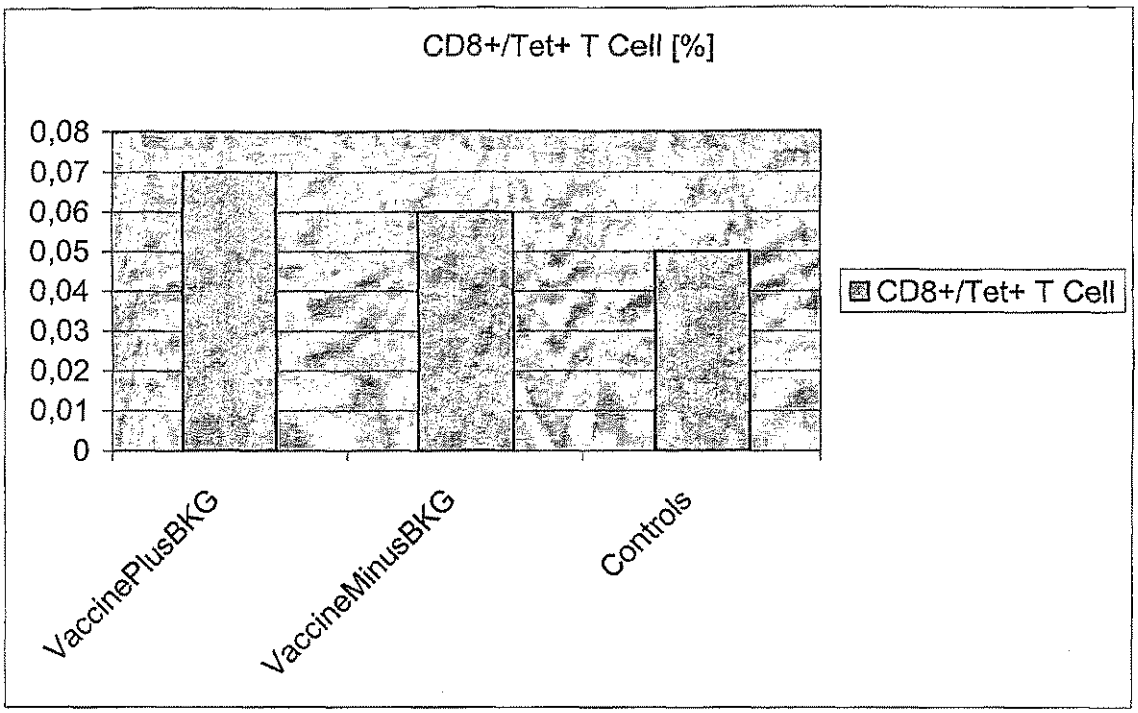

CD8+/Tet+ T Cell [%]
0,08
0,07
0,06
0,05
0,04
0,03
0,02
0,01
0
VaccinePlusBKG
VaccineMinusBKG
Controls
CD8+/Tet+ T Cell

Fig. 1

Experiment 3: Immunisation scheme 1: Gr. HV3.2 - HV3.4 and HV3.11 – HV3.13

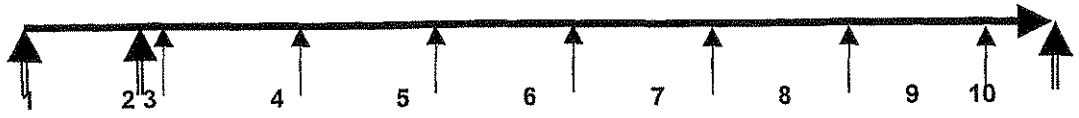


Fig. 2

Experiment 3: Immunisation scheme 2: Gr. HV3.5 – HV3.7 as well as HV3.14 – HV3.16

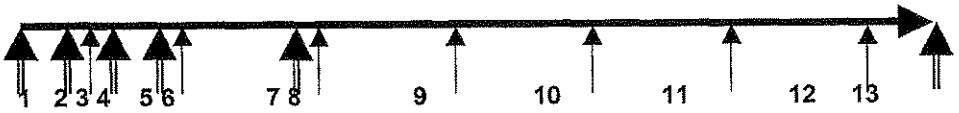


Fig. 3

Experiment 3: Immunisation scheme 3: Gr. HV3.8 – HV3.10 as well as HV3.17 – HV3.19



Fig. 4

Experiment 4: Immunisation scheme 1: Gr. HV4.2 – HV4.4 and HV4.11 – HV4.13

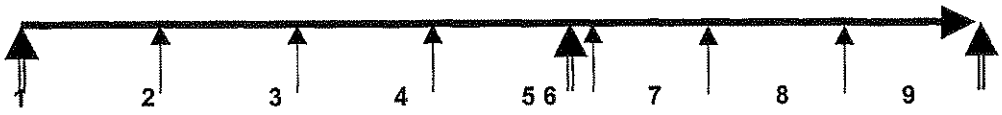


Fig. 5

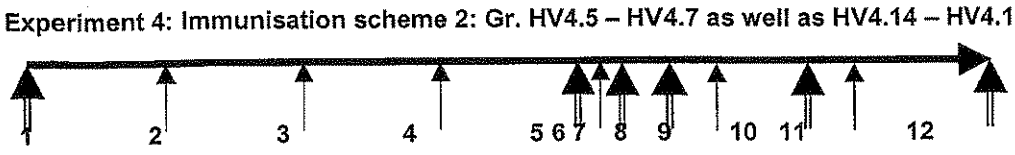

Experiment 4: Immunisation scheme 2: Gr. HV4.5 – HV4.7 as well as HV4.14 – HV4.16
1
2
3
4
5 6 7
8
9
10
11
12

Fig. 6

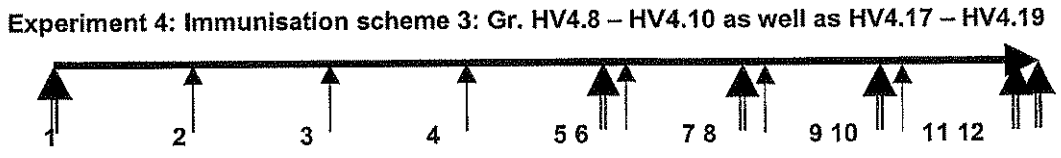

Experiment 4: Immunisation scheme 3: Gr. HV4.8 – HV4.10 as well as HV4.17 – HV4.19
1
2
3
4
5 6
7 8
9 10
11 12

Fig. 7

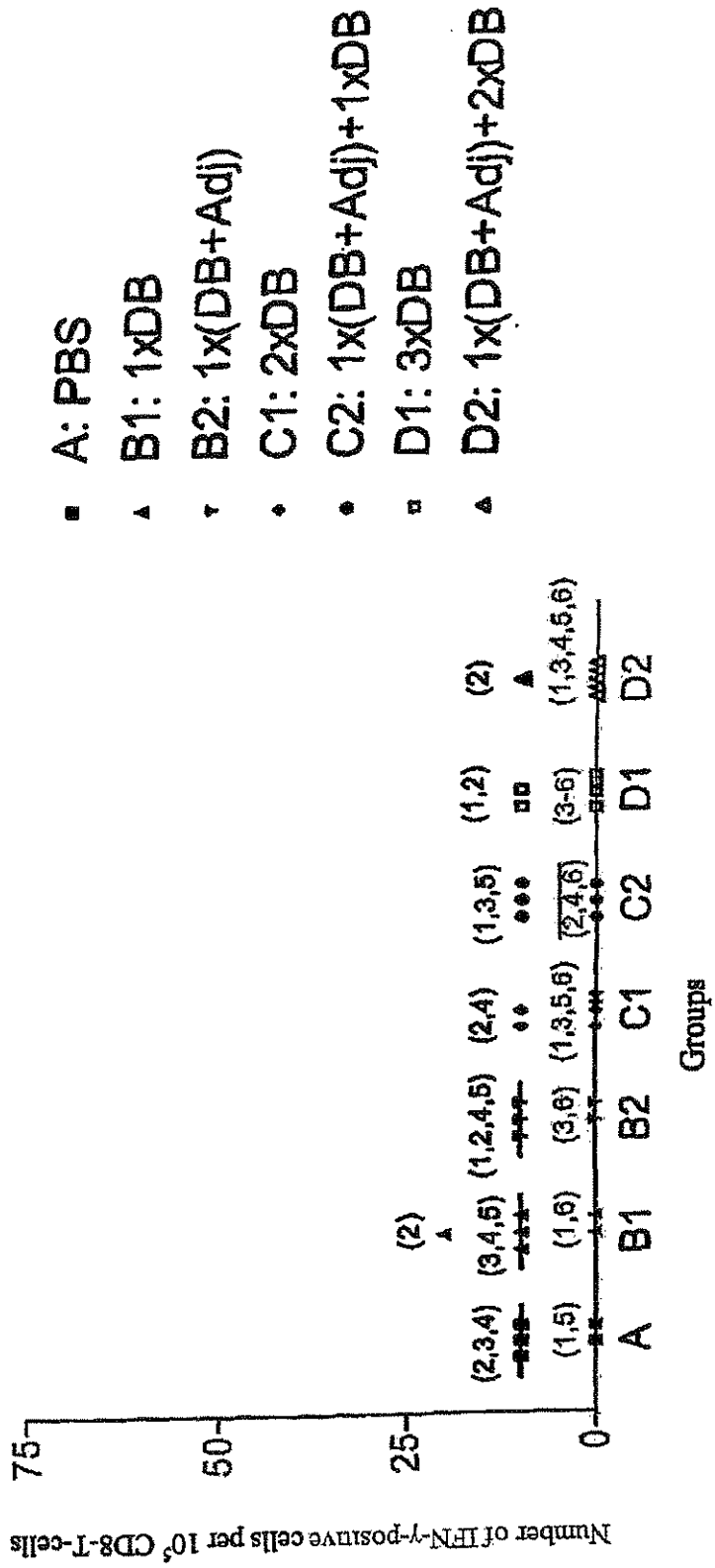

A: PBS
B1: 1xDB
B2: 1x(DB+Adj)
C1: 2xDB
C2: 1x(DB+Adj)+1xDB
D1: 3xDB
D2: 1x(DB+Adj)+2xDB
Number of IFN-γ-positive cells per 10⁵ CD8-T-cells
75
50
25
0
(2,3,4)
(1,5)
(2)
(3,4,5)
(1,6)
(1,2,4,5)
(3,6)
(2,4)
(1,3,5,6)
(1,3,5)
(2,4,6)
(1,2)
(3-6)
(2)
(1,3,4,5,6)
A
B1
B2
C1
C2
D1
D2
Groups

Fig. 8

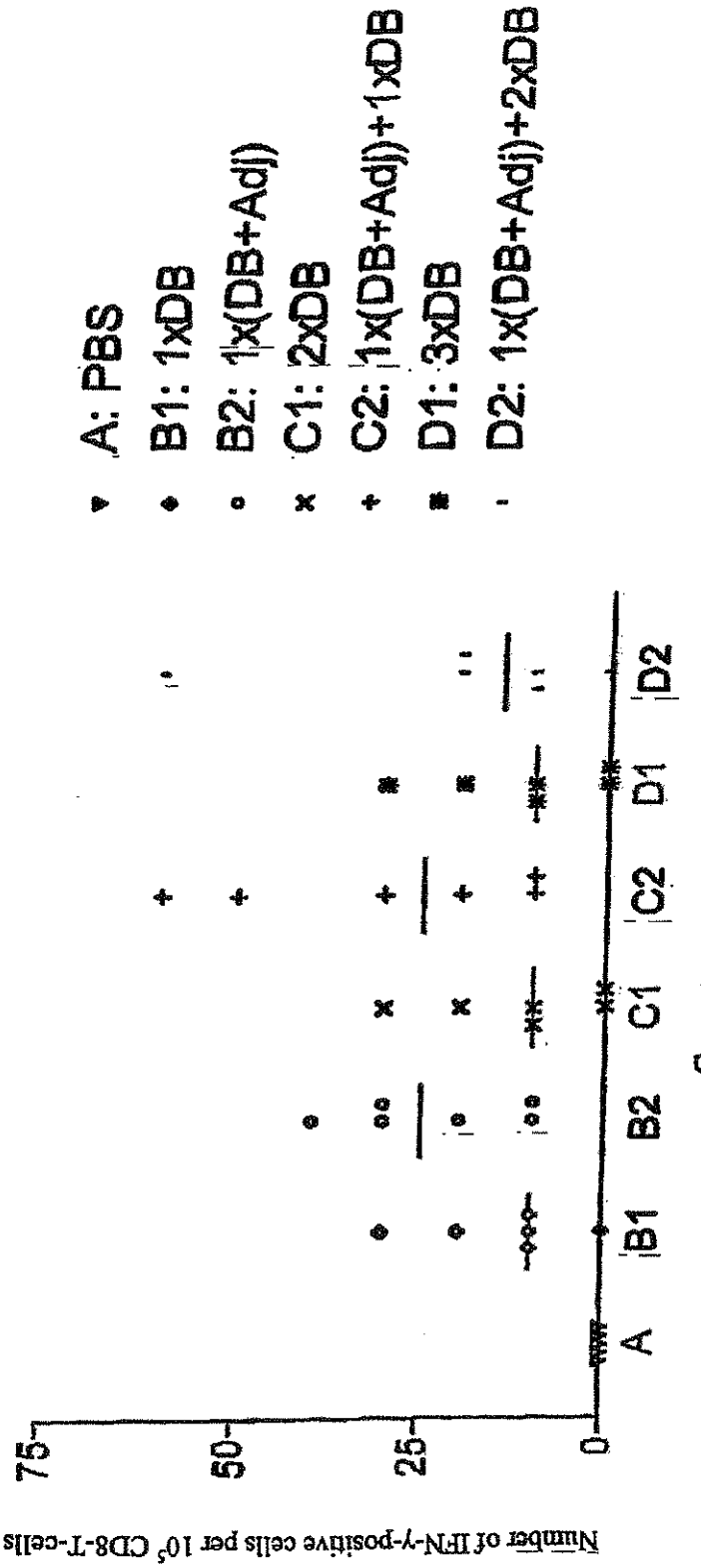

A: PBS
B1: 1xDB
B2: 1x(DB+Adj)
C1: 2xDB
C2: 1x(DB+Adj)+1xDB
D1: 3xDB
D2: 1x(DB+Adj)+2xDB
75
50
25
0
A
B1
B2
C1
C2
D1
D2
Groups
Number of IFN-γ-positive cells per 10^5 CD8-T-cells

Fig. 9

SEQUENCE LISTING

<110> Vakzine Projekt Management GmbH

<120> Combination of bacterial cell and a biologically acitve agent

<130> V 10001 PCT

<140>
<141>

<150>
<151>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: recombinant nucleic acid molecule

<220>
<223> CDS comprising a phagolysosomal domain (211-1722 nt) and a stop codon (1879-1881)

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gcggctgtag tccttccggg cctggtgggg cttgccggcg gagcggcaac cgcgggcgcg 120
ttctcccggc cggggctgcc ggtcgagtac ctgcagtctg caaagcaatc cgctgcaaat 180
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aatgaatata ttgttgtgga gaaaaagaag aaatccatca atcaaaataa tgcagacatt 480
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gcttatccaa atgtaagtgc aaaaattgat tatgatgacg aaatggctta cagtgaatca 780
caattaattg cgaaatttgg tacagcattt aaagctgtaa ataatagctt gaatgtaaac 840
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gatgaagtaa attatgatcc tgaaggtaac gaaattgttc aacataaaaa ctggagcgaa 1500
aacaataaaa gcaagctagc tcatttcaca tcgtccatct atttgccagg taacgcgaga 1560
aatattaatg tttacgctaa agaatgcact ggtttagctt gggaatggtg gagaacggta 1620
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agcttatcga tgtcgacgta g 1881

<210> 2
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: corresponding amino acid sequence of nucleic acid sequence 1

<400> 2

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  1               5                  10                  15

Ile Gly Thr Ala Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala
             20                  25                  30

Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val
         35                  40                  45

Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser
     50                  55                  60

Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser
 65                  70                  75                  80

Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr
                 85                  90                  95

Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly
            100                 105                 110

Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val
        115                 120                 125

Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile
    130                 135                 140

Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile
145                 150                 155                 160

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

Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val
            180                 185                 190

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

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

Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln
225                 230                 235                 240

Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala
                245                 250                 255

Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala
            260                 265                 270
```

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Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys
        275                 280                 285

Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn
    290                 295                 300

Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr
305                 310                 315                 320

Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala
                325                 330                 335

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

Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val
        355                 360                 365

Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys
    370                 375                 380

Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu
385                 390                 395                 400

Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys
                405                 410                 415

Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr
            420                 425                 430

Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn
        435                 440                 445

Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile
    450                 455                 460

Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp
465                 470                 475                 480

Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys
                485                 490                 495

Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser
            500                 505                 510

Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu
        515                 520                 525

Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg
    530                 535                 540

Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr
545                 550                 555                 560

Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala
                565                 570                 575

Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile
            580                 585                 590

Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu
        595                 600                 605
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Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met
610 615 620

Ser Thr
625