

SEQUENCE LISTING

<110> Vakzine Projekt Management GmbH

<120> Recombinant Mycobacterium as vaccine for use in humans

<130> 49047P WO

<150> US61/384375

<151> 2010-09-20

<160> 2

<170> BiSSAP 1.0

<210> 1

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<222> 1..1881

<223> /mol_type="DNA"
 /note="recombinant nucleic acid molecule"
 /organism="Artificial Sequence"

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<221> source

<222> 1..1881

<223> /mol_type="DNA"
 /note="CDS comprising a phagolysosomal domain (211-1722nt) and a
 stop codon (1879-1881)"
 /organism="Artificial Sequence"

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tttcccggc cggggctgcc ggtcgagtac ctgcagtctg caaagcaatc cgctgcaaat 180

aaattgcact cagcaggaca aagcacgaaa gatgcatctg cattcaataa agaaaattca 240

attcatcca tggcaccacc agcatctccg cctgcaagtc ctaagacgcc aatcgaaaag 300

aaacacgcgg atgaaatcga taagtatata caaggattgg attacaataa aaacaatgta 360

ttagtatacc acggagatgc agtgacaaat gtgccgcaa gaaaagggtta caaagatgga 420

aatgaatata ttgtgtgga gaaaaagaag aaatccatca atcaaaataa tgcagacatt 480

caagttgtga atgcaattc gagcctaacc tatccagggtg ctctcgtaaa agcgaattcg 540

gaattagtag aaaatcaacc agatgttctc cctgtaaaac gtgattcatt aacactcagc 600

attgatttgc caggtatgac taatcaagac aataaaatcg ttgtaaaaaa tgccactaaa 660

tcaaacgtta acaacgcagt aaatacatta gtggaaagat ggaatgaaaa atatgctcaa 720

gcttatccaa atgtaagtgc aaaaattgat tatgatgacg aaatggctta cagtgaatca 780

eolf-seql

caattaattg cgaatttgg tacagcattt aaagctgtaa ataatagctt gaatgtaaac 840
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<211> 626

<212> PRT

<213> Artificial Sequence

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<221> SOURCE

<222> 1..626

<223> /mol_type="protein"

/note="CORRESPONDING AMINO ACID SEQUENCE OF SEQ ID NO: 1."

/organism="Artificial Sequence"

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Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met

1 5 10 15

Ile Gly Thr Ala Ala 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

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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
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

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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
 Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met
 610 615 620
 Ser Thr
 625