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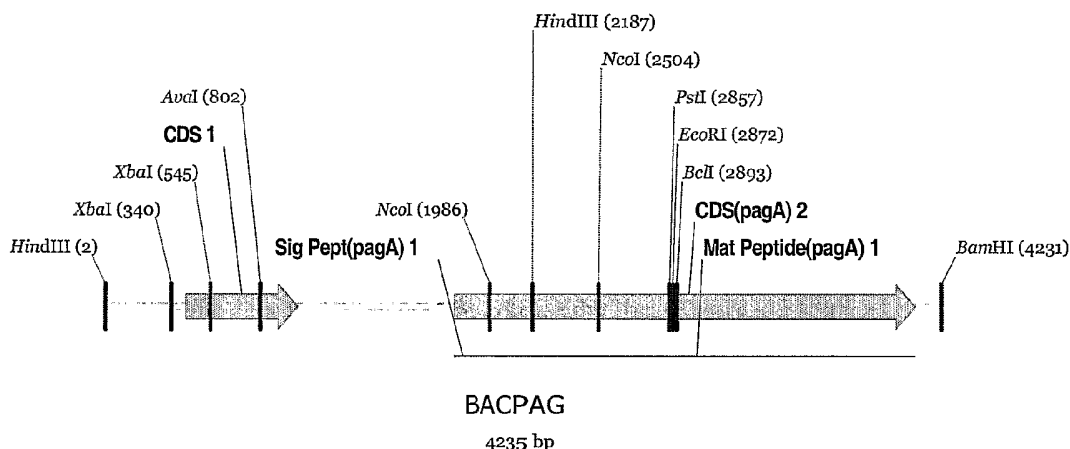
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(54) Title: ANTHRAX VACCINE



(57) Abstract: This invention provides DNA sequences that encode Bacillus anthracis Protective Antigen (PA) proteins that can be used for prophylactic immunization against anthrax infections. The codon usage in the sequence is optimized for expression in the yeast, including strains of *Saccharomyces cerevisiae*, a known safe fermentation source for vaccine products. The invention also includes vaccines and methods of vaccination against *B. anthracis*.

TITLE OF THE INVENTION
ANTHRAX VACCINE

CROSS-REFERENCE TO RELATED APPLICATIONS

- 5 This application claims the benefits of U.S. Provisional Applications Serial Number 60/470563 filed May 14, 2003.

FIELD OF THE INVENTION

The invention relates to the field of vaccination.

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BACKGROUND

Anthrax infection, a disease caused by the spore-forming bacterium Bacillus anthracis, is highly lethal in the pulmonary or inhalation form (For general reviews see Friedlander, 2000; Little and
15 Ivins, 1999; Mock and Fouet, 2001). With an increased awareness of the potential of this pathogen as a weapon, the need for a readily available, safe and effective vaccine for wide public use has grown (See, e.g., Ibrahim *et al.*, 1999). Current vaccine preparations for human use are typically attenuated live spores or cell-free secretion products of B. anthracis adsorbed to alum (AVA). The former preparation was reportedly used in the Soviet Union and had a number of toxicities and production issues. In the US,
20 AVA is reported to be used exclusively. Neither vaccine has the characteristics preferred for broad distribution in the event of an emergency or for general public prophylaxis, *i.e.*, long term protection, high level efficacy with limited number of immunizations, low reactogenicity, and reliable, safe production. Thus, there is a need for new vaccines that provide a better fit to these criteria.

The cytotoxicity of germinating anthrax spores is mediated by two toxins, lethal factor and
25 edema factor. Lethal factor (LF) is a 90-kD protein with catalytic activity which combines with an activated form of protective antigen, PA, an 83-kD protein, to produce an active toxin in macrophages. Edema factor is of similar molecular weight (89 kD) and combines in a separate complex with activated PA to enter its target cell, the neutrophil. Each of the three components are non-toxic individually.

Recent studies have shown that during infection, PA83 is cleaved by mammalian cells at amino
30 acid position 167 of the mature peptide to yield a 63-kD component that binds to either lethal factor (LF) or edema factor (EF). Mutated PA83 that can not be cleaved is not functional for the production of toxin because it fails to form the heptameric pore that facilitates LF or EF to enter mammalian cells (Leppla, 2000). Under fermentation conditions and presumably during infection, B. anthracis synthesizes PA83 with a leader sequence that is responsible for its secretion into the medium and into tissues.

35 Although there are limited data in humans correlating protection against B. anthracis infection to specific immune responses, the available evidence suggests that neutralizing antibodies against the 83-

kD uncleaved protective antigen (PA83) is a surrogate marker for protective immunity (Baillie, 2001; Turnbull *et al.*, 1988). The data are more extensive in animal protection models using guinea pigs, rabbits, mice and rhesus monkeys (Fellows *et al.*, 2001; Ivins *et al.*, 1998). Immunization with purified PA or recombinant PA reportedly confers protection against challenge in rhesus macaques (Ivins *et al.*, 1998). Passive protection was also reportedly demonstrated with anti-PA antibodies. It is believed that there is a rough correlation between anti-PA titer and protection against lethal challenge with B. anthracis spores. Reuveny *et al.* reported a more quantitative correlate with neutralization of *in vitro* macrophage killing for the guinea pig model (Reuveny *et al.*, 2001). The cumulative evidence supports the concept that PA, whether obtained from B. anthracis or as a recombinant protein, can be an effective immunogen for anthrax prophylaxis. Published data also purport to show that the reactive epitopes are found within the cleaved, activated 63-kD form of PA (Flick-Smith *et al.*, 2002; Little and Ivins, 1999; Singh *et al.*, 1991).

One of the current anthrax vaccines is produced from a culture filtrate of germinating B. anthracis spores (Puziss, 1962; Puziss, 1963). The major component of this formulation is PA83 with some LF and EF. No further enrichment or purification of the protective component is reportedly performed. Minor, but highly potent reactogenic substances could also be present. Trace amounts of LF and EF purified from the B. anthracis fermentation could theoretically combine with PA cleaved after administration to yield toxins.

A variety of alternative preparations designed to address the toxicity issues raised above have been reported in the literature. These range from the use of attenuated B. anthracis strains with enhanced PA production, to acellular recombinant protein products to naked DNA preparations. A summary of these approaches are listed below:

Replicating vector strategies:

Bacillus anthracis – An attenuated, non-capsular strain has been reported that produces recombinant PA constitutively from a replicating vector. The heterologous constitutive promoter from α -amylase expressed as much as 10-fold higher titers of rPA than the native pagA promoter. The spores from the recombinant strains were stated to have elicited good anti-PA antibody titers and protected guinea pigs in a lethal challenge model (Cohen *et al.*, 2000). Appropriate containment for production of a live, attenuated spore vaccine is an important consideration for large-scale production.

Bacillus subtilis – This related non-pathogenic, sporulating bacillus is a good vehicle for expressing secreted proteins. It has been under investigation as a substitute production vehicle for production of PA for decades (Ivins and Welkos, 1986). The limitations of this system are safety concerns that require the development of non-sporulating strains and more importantly, degradation of PA by B. subtilis proteases (Baillie *et al.*, 1998a; Baillie *et al.*, 1998b). The maximal reported yield using this system was 2 mg/L. The introduction of mutations affecting catabolite repression and growth

phase regulation reportedly resulted in an increase in the yield of PA but a multiply protease-negative background to improve PA yield is still needed (Baillie *et al.*, 1998a).

Salmonella typhimurium – The PA gene was cloned into S. typhimurium with the aim of using the ability of this non-pathogenic (for humans) bacterium as a vector to introduce the PA antigen. A high copy plasmid with the *placd* promoter was used. The resultant strain was stated to have the ability to colonize the host and it was necessary to passage to regain colonization ability. The plasmid in the colonizing strain had lower copy number, suggesting that less PA antigen may be produced. This strain was reported to afford some protection against lethal challenge in mice (Coulson *et al.*, 1994).

Vaccinia virus – PA was cloned into vaccinia virus to use a replicating vector as an immunization strategy. Some protection was reported when using particular vector constructs (60% and 50% of mice and guinea pigs respectively), but anti-PA titers were produced only in mice (Iacono-Connors *et al.*, 1990). The relevance for humans is not known.

Lactobacillus casei – Lactobacilli are commensals of the gut and are generally regarded as safe (Zegers *et al.*, 1999). L. casei strains expressing PA internally have been reported with the aim of developing a live oral vaccine with a high level of mucosal immunity, an unproven strategy.

Acellular antigen production:

Baculovirus – The PA gene was cloned into baculovirus for the production of PA (Iacono-Connors *et al.*, 1990). The material produced was larger (86 kD vs. 83.5 kD) than authentic PA83 because it still had a secretory leader sequence. The preparations were reported to have produced high titer anti-PA responses in mice and to have protected mice and guinea pigs from lethal challenge when administered with an adjuvant. Production by baculovirus requires tissue culture growth – a costly protocol for large-scale production.

Escherichia coli – Several laboratories have reported production of recombinant wild-type PA in E. coli and have made mutated PA in this organism. One potential limitation of bacterially produced material is the requirement to purify the antigen from the lipopolysaccharide component of E. coli, an extremely potent pyrogen. Using the E. coli signal sequence on PA causes the material to accumulate in the periplasmic space (yield - 500 µg/L) (Sharma *et al.*, 1996). A his-tagged fusion accumulated as inclusion bodies and was denatured in urea and refolded (Gupta *et al.*, 1999). This change improved the yield to 2 mg/L. Until very recently, yields from inducible vectors were relatively low but constitutive overexpression has been reported to give yields of biologically active material at 125 mg/L (Chauhan *et al.*, 2001). Metal chelate chromatography was used for purification.

DNA plasmid – A DNA plasmid encoding PA63 was reported to have elicited a humoral immune response in mice. Mice immunized with the PA DNA vaccine were said to have been protected against lethal challenge with a combination of anthrax PA plus LF (Gu *et al.*, 1999).

Saccharomyces cerevisiae – Baker's yeast is generally recognized as safe for the production of heterologous protein. This yeast has been shown to be easily and rapidly cultivated under minimal

containment conditions and to lack toxic secreted or intracellular materials. Antigens isolated from yeast fermentations have good safety profiles. Small peptides and large proteins have been produced successfully. It has been proven to be a safe and commercially viable production vehicle for recombinant DNA derived hepatitis B vaccine. However, the current state of understanding of protein production in yeast does not allow one to predict which proteins will be made in sufficient quantities for commercial production. Variables that are not yet foreseeable or controllable are the degree of glycosylation, either O or N, the extent of protein degradation, and correct polypeptide folding. Potential glycosylation sites can be determined by sequence analysis, but the presence of such a consensus site does not guarantee that it will be glycosylated. Furthermore, addition of a yeast leader sequence does not by itself guarantee that a given protein will be secreted. Neither can one predict whether a protein will be toxic for the producing yeast cells. The parameters that are understood and can be controlled include the presence or absence of yeast non-translated leader sequences, mutations that reduce, but do not eliminate N-glycosylation, mutations that reduce protein degradation, promoter sequences that permit tightly regulated control of synthesis, plasmid copy number, and strain to strain variations. For any given protein, the outcome depends on the correct combination of sequence, expression vector, host strain, fermentation conditions and the intrinsic nature of the protein to be expressed, none of which can be predicted or guaranteed in the absence of empirical results. Thus, it is not possible to predict whether the sequence of a gene of interest will be translated into the desired functional protein in yeast or, if it is produced, whether it will be made in quantities sufficient for commercial application.

One report of a B. anthracis gene expressed in S. cerevisiae is a study designed to identify the substrates of the LF component via the yeast two-hybrid system (Vitale *et al.*, 1999). The experiment employed an inactive mutated LF as bait. This approach reportedly led to the identification of the MAP kinase kinases (MAPKKs) Mek1 and Mek2 as proteins capable of specific interaction with LF.

SUMMARY OF THE INVENTION

This invention relates to polynucleotides encoding a Bacillus anthracis Protective Antigen (also referred to herein as "PA") protein wherein the coding sequence of the polynucleotide has been codon-optimized for efficient expression in a yeast host cell. Preferably, the polynucleotides are DNA. In one preferred embodiment, the polynucleotide encodes a protein which retains its wild-type amino acid sequence. In one preferred embodiment the polynucleotide encodes a 63-kD form of the PA protein, referred to as PA63.

In another preferred embodiment, the polynucleotide encodes an 83-kD form of PA, referred to as PA83. In an alternate embodiment, the polynucleotides encode a mutated form of a PA protein which has reduced protein function as compared to wild-type protein, but which retains the immunogenicity of the wild-type protein such as the chymotrypsin processing site. A preferred mutated

form of the PA protein is a PA83 which has been mutated to prevent processing of the protein to the PA63 form of PA. This invention also relates to the PA proteins produced using the polynucleotides.

Another aspect of this invention is a vector carrying the polynucleotides encoding a codon-optimized PA protein. Yet another aspect of this invention are host cells containing these vectors.

5 In a preferred embodiment, the vector is a plasmid vector. In a particularly preferred embodiment, the vector is a plasmid vector comprising an insert wherein the insert comprises an expression cassette comprising:

a) a polynucleotide encoding a codon-optimized PA protein for expression in a yeast host cell; and

10 b) a promoter operably linked to the polynucleotide.

Another type of vector which is envisioned by this invention is a shuttle plasmid vector comprising a yeast origin of replication, a bacterial origin of replication and a polynucleotide insert, wherein the insert comprises an expression cassette comprising:

a) a polynucleotide encoding a codon-optimized PA protein for expression in a yeast host cell; and

b) a promoter which functions in yeast operably linked to the polynucleotide; and

c) a yeast-active transcriptional terminator.

An aspect of this invention is a yeast host cell carrying a polynucleotide of this invention. In a preferred embodiment, the polynucleotide is carried on a plasmid vector. In alternative 20 embodiments, the polynucleotide is integrated into the chromosomal DNA of the yeast host cell. In a preferred embodiment, the synthetic PA gene is under the control of a promoter from the yeast galactose gene cluster (a GAL promoter) and the yeast host cell has been genetically engineered for controlled induction of genes regulated by GAL promoters. In alternative embodiments, the controlled induction is high level, mid level or low level induction of genes regulated by GAL promoters.

25 This invention also relates to a method of making a PA protein comprising expressing in a yeast host cell a polynucleotide encoding a PA protein, or mutated form of a PA protein which has reduced protein function as compared to wild-type protein, but which maintains immunogenicity, the sequence of the polynucleotide encoding PA comprising codons optimized for expression in a yeast host. In a preferred embodiment, the synthetic PA gene is under the control of a GAL promoter and the yeast 30 host cell has been genetically engineered for controlled induction of genes regulated by GAL promoters. In a preferred method, the PA protein is produced as an intracellular product. In another preferred method, the PA protein is produced as a product secreted from the yeast host cell.

An aspect of this invention provides a vaccine against disease, cellular toxicity or death caused by B. anthracis. A vaccine of this invention includes an effective amount of a PA protein that was

expressed in yeast through the use of a polynucleotide of this invention. A vaccine of this invention also includes pharmaceutically acceptable excipients.

An aspect of this invention is a method of vaccinating a patient against disease, toxicity or death caused by B. anthracis. A vaccine of this invention is administered to a patient in a manner
5 appropriate for the induction in the patient of an immune response against the PA protein of B. anthracis.

An aspect of this invention provides a method for purification of the PA protein expressed in yeast. In the method a homogenate of yeast cells is formed. Yeast proteases are inactivated in the homogenate by addition of a series of protease inhibiting compounds, and the PA protein is separated from yeast cellular proteins by a series of chromatographic separations.

10 An aspect of this invention is a process of isolating the 63 kilodalton form of Protective Antigen from a culture of yeast cells expressing a recombinant polynucleotide. In particular embodiments, the polynucleotide is carried on an expression vector in the cells, for example, a plasmid or artificial chromosome. The expression of the polynucleotide can be regulated by an inducible promoter. After expression of the polynucleotide, the yeast cells are disrupted to create a suspension which is
15 subsequently clarified. The cells can be disrupted using methods known in the art including a press, homogenizer or microfluidizer. Clarification is commonly performed by low speed centrifugation. The clarified solution is mixed with a denaturant. In preferred embodiments the denaturant is a non-ionic denaturant, e.g., 6M urea. Thereafter the PA63 is purified from the solution by chromatography on cation exchange resin followed by chromatography on an anion exchange resin, in a denaturing buffer.
20 In preferred embodiments, the PA63 is eluted from each column using a linear gradient of NaCl and 6M urea. The fractions containing the PA63 are then dialyzed against an appropriate buffer and, optionally, concentrated.

A polynucleotide according to this invention comprises a sequence encoding a B. anthracis PA protein, such coding sequence having been "codon optimized" for expression in yeast by
25 substituting wild-type codons with codons that are preferred by a yeast host. Because the coding sequences used in this invention are not found in nature, we sometimes refer to polynucleotides having such codon optimized sequences as "synthetic" polynucleotides, as having a "synthetic" sequence encoding a PA protein, or simply as having a "synthetic" PA gene. In each case, the use herein of the term "synthetic" means that the gene has been modified so that it contains codons which are preferred
30 for expression in a non-native host, e.g., a yeast or other eukaryote. In many cases, the amino acids encoded by the synthetic PA gene remain the same as the wild-type. In some embodiments, the synthetic gene may encode a modified protein.

The term "promoter" as used herein refers to a recognition site on a DNA strand to which the RNA polymerase binds. The promoter forms an initiation complex with RNA polymerase to initiate

and drive transcriptional activity. The complex can be modified by activating sequences termed "enhancers" or inhibiting sequences termed "silencers."

The term "cassette" refers to the sequence of the present invention which contains the nucleic acid sequence which is to be expressed and may also include regulatory sequences. Each cassette will have its own sequence. Thus by interchanging the cassette the vector will express a different sequence. Because of the restriction sites at the 5' and 3' ends, the cassette can be easily inserted, removed or replaced with another cassette.

The term "vector" refers to some means by which DNA fragments can be introduced into and maintained in a host organism or host tissue. Various types of vectors are known in the art including plasmid, virus (including adenovirus), bacteriophages, artificial chromosomes, linear DNA and cosmids. Vectors can replicate autonomously or integrate into the host cell genome.

The term "effective amount" means sufficient vaccine composition is administered to a patient so that an immune response results. One skilled in the art recognizes that this level may vary.

In reference to a nucleic acid or protein sequence, the term "native" means that the sequence is the same as it is found occurring in nature. It is also referred to as a "wild type" sequence.

The term "patient" means a mammal, particularly domesticated livestock including but not limited to dogs, cats, cows, bulls, steers, pigs, horses, sheep, goats, mules, donkeys, etc. Most preferably, a patient is a human.

BRIEF DESCRIPTIONS OF THE DRAWINGS

FIGS. 1A&B. FIG. 1A. Diagram of B. anthracis PA gene. FIG. 1B. DNA sequence (SEQ ID NO:47) and amino acid translation product (SEQ ID NO:48) of portion of B. anthracis PA83 gene corresponding to PA63.

FIGS. 2A&B. Yeast codon-optimized DNA sequence (SEQ ID NO:49) and amino acid translation product (SEQ ID NO:50) of synthetic B. anthracis PA63 gene.

FIGS. 3A&B. FIG. 3A. Yeast secretion vector pHK4 α 2 used for expression of secreted PA63. FIG. 3B. pAGT1 – pKH4 α 2 with PA63.

FIG. 4. Yeast expression vector pGAL110 used for internal expression of PA63 (PA63pGAL10#2).

FIG. 5. Time course of intracellular PA63 expression from transformant L-1 in S. cerevisiae strain 1849. Equal volumes of cell lysate were loaded on the gel. A and B indicate duplicate fermentations of transformant L-1 and vector control transformant K-1. Samples of L-1A and L-1B are shown for 0, 48, and 72 h in lanes 3-5 and 6-8, respectively. A 72 h sample of K-1A alone is shown in lane 2. A 48 h sample of K-1A and a 72 h sample of K-1B mixed with 10 ng PA63 standard are shown in lanes 1 and 9, respectively. Molecular size standards are also shown.

FIG. 6. An exemplary Western blot used for quantitation of internally expressed PA63 by transformant 8-3 (*S. cerevisiae* host strain 1260). Samples are from two independent experiments: lanes 12-15 are samples of cell lysates of 8-3 from one experiment, and lanes 4-7 and 8-11 represent duplicate sample preparations of cell lysates of 8-3 from another experiment. Replicate fermentations of 8-3 within the same experiment are represented by 4,5; 6,7; 8,9; 10,11; 12,13; 14,15. Odd and even-numbered lanes contain 0.25 and 0.5 μ g total protein of 8-3 loaded, respectively. For the samples of the vector control transformant, 0.5 μ g total protein was loaded. Lane 1 is a sample of vector control transformant 7-1A alone. Lanes 2, 3 and 16, 17 contain samples from vector control transformant 7-1A and -B mixed with 10 and 20 ng PA83, respectively. Molecular size standards are also shown.

FIG. 7. Time course for induction of secreted PA63 by strain 14A (*S. cerevisiae* host strain 1849). Equal volumes of supernatants were loaded in each lane. T0, T24, T48, and T72 are shown for 14A in lanes 1, 3, 5, and 7, respectively. T48 and T72 are shown for vector control transformant 12B alone in lanes 4 and 6. 10 ng PA63 standard is shown alone in lane 9 and mixed with vector control 12B from 24 h in lane 2. Lane 8 contains a supernatant from an independent 72 h fermentation of strain 14A. Molecular size standards are shown.

FIGS. 8A&8B. FIG. 8A. DNA sequence (SEQ ID NO:53) and FIG. 8B. Amino acid translation product (SEQ ID NO: 54) of native bacterial PA83 gene without its leader sequence.

FIG. 9. DNA sequence (SEQ ID NO: 51) and amino acid translation product (SEQ ID NO: 52) of yeast codon-optimized domain 4 of *B. anthracis* PA gene.

FIGS. 10A&B. FIG. 10A. DNA sequence (SEQ ID NO: 55) and FIG. 10B. Amino acid translation product (SEQ ID NO: 56) of yeast codon-optimized *B. anthracis* PA83 gene.

FIGS. 11A&B. FIG. 11A. FIG. 11A DNA sequence (SEQ ID NO: 57) and FIG. 11B. Amino acid translation product (SEQ ID NO: 58) of yeast codon-optimized *B. anthracis* PA83 with a mutation at the furin cleavage site.

FIG. 12. Exemplary Western blot comparing production of codon-optimized and native PA63 from transformants fermented for 72 h in complex YEHDG medium. Lane 1, MW size standards mixed with 100 ng cell-lysate protein from yeast transformant 8-3 which produces PA63 intracellularly (see Example 2). Lane 2, 20 ng purified *E. coli*-produced rPA83. Lanes 3-7 and 13 contain 25 μ L medium supernatant from yeast transformants: lane 3, vector control transformant 12B; lanes 4 and 5 "native" PA63 transformants b-2 and b-3, respectively; lanes 6 and 7, "rebuilt" PA63 transformants 14A and 14C, respectively; lane 13, transformant 14A fermented in a previous experiment. Lanes 8-12 contain 500 ng protein cell lysate from yeast transformants: lane 8, 12B (vector control); lane 9, b-2; lane 10, b-3; lane 11, 14A; lane 12, 14C. Positions of molecular weight markers are indicated.

FIG. 13. Western blot depicting intracellular expression of uncleavable PA83 (lacking Furin cleavage site) from *S. cerevisiae* transformant Q-3 (yeast host 1558) and uncleavable PA83 from transformants 9-1 through 9-8 of yeast host strain 1260. Lanes 1-8 contain 4 μ g cell lysate protein from transformants 9-1

through 9-8 and lane 9 contains 4 µg cell lysate protein from transformant Q-3. Lane 10 contains 1 µg of recombinant PA83 purified from *E. coli*.

FIG. 14. Western blot depicting intracellular expression of uncleavable PA83, from *S. cerevisiae* transformant 9-1, and cleavable PA83 from *S. cerevisiae* strain 5-C: lane 1, 200 ng *E. coli*-purified recombinant PA83; lanes 2-8 contain 250 ng of cell lysate protein; lane 2, vector control transformant fermented in shake flask; lanes 3 and 4, strain 9-1 (uncleavable PA83) fermented in shake flask; lanes 5 and 6, strain 5C (cleavable PA83) fermented in shake flask; lanes 7 and 8, strain 5C (cleavable PA83) fermented in culture tube.

FIG. 15. Western blot depicting intracellular expression of PA63 from large-scale fermentation of strain 8-3. Lanes 1 and 11: 10 ng PA63 mixed with 500 ng protein cell lysate of vector transformant 7-1. Lanes 2 and 12: 20 ng PA63 mixed with 500 ng protein cell lysate of vector transformant 7-1. Lanes 3 and 9: 10 ng PA83 mixed with 500 ng protein cell lysate from vector transformant 7-1. Lanes 4 and 10: 20 ng PA83 mixed with 500 ng protein cell lysate from vector transformant 7-1. Lanes 5 and 6, 250 and 500 ng protein of cell lysate, respectively from large-scale fermentation of 8-3. Lanes 7 and 8, 250 and 500 ng protein of cell lysate, respectively from tube fermentation of 8-3.

FIG. 16. Flow chart of a process for purification of PA63 protein from a yeast cell homogenate.

FIG. 17. SDS-PAGE gel analysis and Western blot of purified PA63 product and process retains. (A). SDS-PAGE analysis of 50HS chromatography; lane 1, load to 50HS column; lane 2, non-retained pool; lane 3, gradient fractions 12-21 (load to source Q); lane 4, gradient fractions 22-30; lane 5, high salt wash. (B). SDS-PAGE analysis of source Q chromatography. Lane 1, gradient fractions 17-18 (product); lane 2, gradient fractions 31-32; lane 3, gradient fractions 52-53.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a synthetic polynucleotide sequence that encodes for a PA protein of *Bacillus anthracis*. The invention also provides a synthetic polynucleotide sequence that encodes for an 83-kD form of the PA protein that is identical to the mature 83-kD PA protein of *Bacillus anthracis* or a 63-kD form of the PA protein. The invention also relates to synthetic sequences that encode mutated or truncated versions of PA63 or PA83 which, upon introduction into a patient, elicit antibodies that are protective against disease, cellular toxicity, debilitation or death due to anthrax infections or ameliorate such symptoms. These mutations include alterations that prevent the formation of activated PA63, such as alterations in the furin cleavage site.

The codon usage in the sequences for PA proteins have been optimized for expression in the yeast *Saccharomyces cerevisiae*, a known safe fermentation source for vaccine products. The invention also provides plasmids that are suitable for expression in yeast of the desired product intracellularly and

plasmids that are suitable for production in yeast of extracellular protein using a S. cerevisiae secretory leader sequence, an example of which is the alpha factor-based pre-pro-leader sequence. The invention also provides the 63-kD protein, PA63, the 83-kD protein PA83, and mutant proteins produced by expressing the synthetic DNA sequence in S. cerevisiae. The invention also includes methods of

5 inducible and constitutive production of yeast produced PA.

The present invention provides a method for generating a polynucleotide sequence of B. anthracis PA that has been optimized for expression in yeast cells. In particular preferred embodiments, use of the polynucleotides results in the expression of authentic 63-kD PA as a secreted protein or as protein that accumulates within the yeast cell. It is readily apparent to those skilled in the art that

10 portions of polynucleotide sequence can be used to generate larger PA proteins including polypeptides such as PA83 or smaller PA proteins that display domains of PA that induce an immunoprotective response in a patient. The polynucleotide sequence can also be used to create plasmids that will express PA in bacteria such as E. coli as native protein, or peptides derived from PA63. The bacterially expressed proteins can also be tagged proteins with groups such as 6X his, HA or GST, to facilitate

15 purification. The present invention also provides a method for producing PA in recombinant yeast host strains which are genetically deficient in their ability to glycosylate proteins and/or carry a mutation in the *prb1* and or *pep4* protease genes.

The wild-type sequence containing the coding region of PA63 (BACPAG) is known. FIGs. 1 A and B. PA63 is a post-translational protein cleavage product of full-length PA83. In accordance with

20 this invention, PA63 segments were converted to sequences having identical translated amino acid sequences, but with alternative codon usage as defined by Lathe (Lathe, 1985) and selected for yeast codons for highly expressed genes (Sharp and Cowe, 1991). The methodology may be summarized as follows:

1. Identify placement of codons for proper open reading frame.
- 25 2. Compare wild-type codon for observed frequency of use by yeast genes.
3. If codon is not one of those commonly employed by yeast, replace it with an optimal codon for high expression in yeast cells.
4. Repeat this procedure until the entire gene segment has been replaced.
5. Inspect new gene sequence for undesired sequences generated by these codon replacements
- 30 (e.g. unwanted restriction enzyme sites, splice sites, promoters, undesirable palindrome or repeat sequences, etc.) and substitute codons that eliminate these sequences. See FIG. 2.
6. Assemble synthetic gene segments and test for expression in yeast cells.

Once the desired sequence is designed, the gene fragment encoding PA63 can be prepared by annealing and extension of oligomers designed to encode the final desired sequence.

Using the present invention, one can produce an immunogenic PA protein in a yeast host

35 cell. It should be understood that the PA protein need not retain the functional activity of a wild-type

PA63 protein as produced by B. anthracis. The key concept is that the yeast produced protein is immunogenic and, when used as a vaccine, can stimulate an immune response that is fully or partially protective against the disease, debilitation, cellular toxicity or death caused by infection with B. anthracis. Therefore, because when making a PA protein of this invention, one is only concerned with retaining the immunogenic properties of the protein, and not the functional properties, one is free to modify the protein. Modified proteins can lack some or all of the functional characteristics of the wild-type PA63 protein and be equivalent, immunologically, to the wild-type protein. It can be useful to modify the protein in the process of designing yeast codon optimized versions of the protein, *i.e.*, changed amino acids, full length uncleavable PA83, or to produce PA63 protein that is less than full length.

It is known that epitopes within Domain 4 can stimulate antibodies against the PA63 protein that can protect against the disease, cellular toxicity, debilitation or death caused by anthrax infection. Therefore, when designing mutant forms of the PA protein, it is most preferred that one attempt to maintain the wild-type sequence of domain 4. Changes can be introduced in other areas of the PA protein, especially in the N-terminal domain between the N-terminus and the cleavage site for processing PA83 to the PA63 form of PA. In general, it can be useful to modify the PA protein sequence to prevent cleavage of the protein by proteases and/or protein processing enzymes in yeast and/or mammals. For example, one may choose to alter the amino acid sequence of the cleavage site located at the furin cleavage site, amino acids 163-167. This change is useful to prevent potential cleavage of the PA protein by the yeast Kex2 protease. Another example of a change is to alter the amino acid sequence of the chymotrypsin cleavage site located at amino acids 312-313.

Vectors

In accordance with this invention, a synthetic polynucleotide sequence encoding a PA protein can be inserted into a vector. The vector is preferably a plasmid, although other vectors including linear DNA linked to a promoter, integrative vectors, Yeast Artificial Chromosomes, phages or cosmid vectors may also be used. For convenience in manipulating the vector, the vector may be in a shuttle plasmid form, that is, may contain origins of replication for both yeast and bacterial hosts.

An expression cassette can be used. An expression cassette includes a synthetic sequence encoding a PA protein operably linked to a promoter and, optionally, other regulatory sequences such as an enhancer or a terminator. The regulatory sequences are from yeast genes, are from non-yeast genes or are hybrid regulatory sequences derived by assembling regulatory elements from different organisms. In the latter two cases, the regulatory sequences are recognized by the protein and genetic expression systems of yeast.

It is preferred that the vector contain one or more promoters that are active in yeast or other host cells. For example, the vector could contain only a promoter active in yeast or, if expression is desired in another host, also or alternatively contain a promoter active in such host. Alternatively, a promoter could be used that is active in both yeast and an alternate host. In a preferred embodiment where expression is desired in yeast, the plasmid would contain a promoter that is active in yeast. Yeast promoters such as the ADH1, GAL1, GAL10, GAL7, PGK or GAP(TDH) promoters are commonly used in the art. However, numerous other promoters including other yeast promoters, eukaryotic promoters that are active in yeast and even hybrid promoters made from portions of promoters from two different organisms are known, and will become known. So long as the promoter is active in yeast, such promoters can be used interchangeably for expressing a synthetic PA gene in yeast. It is preferred that the synthetic codon-optimized sequence encoding the PA protein is operably linked to such a promoter.

In preferred embodiments, there are restriction sites flanking the expression cassette portion of the plasmid so that the cassette can easily be removed or replaced. The shuttle plasmid may be replicated in prokaryotic cells or eukaryotic cells.

Standard techniques of molecular biology for preparing and purifying DNA constructs enable the preparation of the plasmids, phages, shuttle plasmids and other recombinant nucleic acid molecules of this invention.

Expression of Synthetic PA Protein

A vector carrying a synthetic PA gene is introduced into a yeast host cell. Preferred yeast hosts include strains of Saccharomyces cerevisiae, Saccharomyces carlsbergensis and Kluyveromyces lactis. Other yeasts, including but not limited to Pichia pastoris, Hansenula sp., Schizosaccharomyces pombe and Candidia sp. may also be useful. The cell is used to establish a yeast cell culture using standard techniques known in the art. To produce PA protein, the culture is incubated and allowed to ferment in an appropriate manner as known in the art. The synthetic PA gene can be expressed throughout the period of incubation or, preferably, the expression of the gene is induced at a particular time during the incubation. In the latter case, the time of induction can be chosen taking into consideration the age, cell density, metabolic state, growth phase or other measures or combinations of measures of the cell culture as deemed appropriate by the skilled artisan or as known and practiced in the art.

Production of PA using a synthetic DNA sequence can be strain-dependent and is expected to vary with culture conditions. Other known sources of variation in production are known to arise from mechanical conditions, local water and air. Therefore, one of skill in the art will be aware that when production of PA is performed using strains or culture conditions other than those exemplified

herein, one should perform routine testing and optimization of production conditions for the equipment and conditions employed.

The present methods can produce PA as an intracellular product or as a secreted product. Of the exemplified constructs, the constructs designed to produce secreted PA do not produce yields as large as the constructs designed to produce internal PA. However, it is believed that a secreted product will serve better in a production scale process because of ease of harvest and purification.

Recombinant Protective Antigen has been purified from various sources (*E. coli*, *B. subtilis*) in the 83-kilodalton form using both native and denaturing purification processes. We are not aware of literature reports on the purification of the 63-kilodalton form of protective antigen.

Once the synthetic PA gene has been expressed for an appropriate period of time the PA protein can be harvested from the culture using standard methods of protein isolation and purification known and practiced in the art. If the PA was expressed in a fashion that produced secreted PA protein, the protein is isolated from the culture fluid. If all or a portion of the protein exists in refractile or inclusion bodies within yeast cells, the protein can be isolated, denatured and refolded using standard techniques.

If recombinant protein is produced and retained in an intracellular compartment of the host yeast cell, a cell pellet can be isolated from the culture medium by centrifugation, washed, and lysed by a variety of known physical or chemical methods. The crude lysate can be further clarified to remove cellular debris components. Purification of recombinant protein is undertaken from either the supernatant liquid or the pellet, depending on the solubility of the expressed protein. A variety of known techniques including, but not limited to, membrane filtration, centrifugation, chromatography, and differential extraction may be employed to purify the recombinant protein from host cell contaminants. In the case of poorly soluble or aggregated proteins, a variety of known techniques may be employed to improve solubilization, including, but not limited to, detergent extraction, solvent extraction, and use of denaturants and refolding techniques.

Formulations

The vaccine of the present invention can be formulated according to methods known and used in the art. Guidelines for pharmaceutical administration in general are provided in, for example, *Modern Vaccinology*, Ed. Kurstak, Plenum Med. Co. 1994; *Remington's Pharmaceutical Sciences* 18th Edition, Ed. Gennaro, Mack Publishing, 1990; and *Modern Pharmaceutics* 2nd Edition, Eds. Banker and Rhodes, Marcel Dekker, Inc., 1990.

PA protein of the present invention can be prepared as acidic or basic salts. Pharmaceutically acceptable salts (in the form of water- or oil-soluble or dispersible products) include conventional non-toxic salts or the quaternary ammonium salts that are formed, e.g., from inorganic or organic acids or

bases. Examples of such salts include acid addition salts such as acetate, adipate, alginate, aspartate, benzoate, benzenesulfonate, bisulfate, butyrate, citrate, camphorate, camphorsulfonate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptanoate, glycerophosphate, hemisulfate, heptanoate, hexanoate, hydrochloride, hydrobromide, hydroiodide, 2-hydroxyethanesulfonate, lactate, maleate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, oxalate, pantoate, pectinate, persulfate, 3-phenylpropionate, picrate, pivalate, propionate, succinate, tartrate, thiocyanate, tosylate, and undecanoate; and base salts such as ammonium salts, alkali metal salts such as sodium and potassium salts, alkaline earth metal salts such as calcium and magnesium salts, salts with organic bases such as dicyclohexylamine salts, N-methyl-D-glucamine, and salts with amino acids such as arginine and lysine.

It is preferred that the adjuvant is chosen as appropriate for use with the particular protein used as well as the ionic composition of the final formulation. Consideration should also be given to whether the PA protein alone will be formulated into a vaccine or whether the protein will be formulated into a combination vaccine. In the latter instance one should consider the buffers, adjuvants and other formulation components that will be present in the final combination vaccine.

Aluminum based adjuvants are commonly used in the art and include aluminum phosphate, aluminum hydroxide, aluminum hydroxy-phosphate and aluminum hydroxy-sulfate-phosphate. Trade names of adjuvants in common use include ADJUPHOS, MERCK ALUM and ALHYDROGEL. The conjugate can be bound to or co-precipitated with the adjuvant as desired and as appropriate for the particular adjuvant used.

Non-aluminum adjuvants can also be used if approved for use in the expected patient population. Non-aluminum adjuvants include QS21, Lipid-A and derivatives or variants thereof, Freund's complete or incomplete adjuvant, neutral liposomes, liposomes containing vaccine, microparticles and cytokines or chemokines.

It is preferred that the vaccine be formulated with an aluminum adjuvant. In other preferred embodiments, the vaccine is formulated with both an aluminum adjuvant and QS21.

It is preferable, in certain embodiments, to formulate the PA protein with immunogens from Haemophilus influenza, hepatitis viruses A, B, or C, human papilloma virus, measles, mumps, rubella, varicella, influenza virus, polio virus, smallpox, rotavirus, Streptococcus pneumoniae and Staphylococcus aureus. Combination vaccines have the advantages of increased patient comfort and lower costs of administration due to the fewer inoculations required.

When formulating combination vaccines one should be mindful of the various buffers and adjuvants used with the other immunogens. Some buffers may be appropriate for some immunogen-adjuvant pairs and not appropriate for others. In particular, one should assess the effects of phosphate levels on the various immunogen-adjuvant pairs to assure compatibility in the final formulation.

Vaccination

The vaccine of the present invention can be administered to a patient by different routes such as intravenous, intraperitoneal, subcutaneous, intranasal or intramuscular. A preferred route is intramuscular. Suitable dosing regimens are preferably determined taking into account factors well known in the art including age, weight, sex and medical condition of the subject; the route of administration; the desired effect; and the particular PA protein and formulation employed. The vaccine can be used in multi-dose vaccination formats. It is expected that a dose would consist of the range of 1 μ g to 1.0 mg total protein. In an embodiment of the present invention the range is 0.1 mg to 1.0 mg. However, one may prefer to adjust dosage based on the amount of protein delivered. In either case these ranges are guidelines. More precise dosages should be determined by assessing the immunogenicity of the PA protein produced so that an immunologically effective dose is delivered. An immunologically effective dose is one that stimulates the immune system of the patient to establish a level immunological memory sufficient to provide long term protection against disease, cellular toxicity, debilitation or death caused by infection with B. anthracis. The PA protein is preferably formulated with an adjuvant.

The timing of doses depend upon factors well known in the art. After the initial administration one or more booster doses may subsequently be administered to maintain antibody titers. An example of a dosing regime would be day 1, 1 month, a third dose at either 4, 6 or 12 months, and additional booster doses at distant times as needed.

A patient or subject, as used herein, is a mammal, particularly domesticated livestock and animals including but not limited to dogs, cats, cows, bulls, steers, pigs, horses, sheep, goats, mules, donkeys, etc. Most preferably a patient is a human. A patient can be of any age at which the patient is able to respond to inoculation with the present vaccine by generating an immune response. The immune response so generated can be completely or partially protective against disease, cellular toxicity, debilitation or death caused by infection with B. anthracis.

The following examples are offered by way of illustration and are not intended to limit the invention in any manner.

EXAMPLE 1:

Design and Synthesis of a Synthetic PA Sequence

The wild-type sequence for the PA gene encoding PA63 as part of PA83 (BACPAG) is known (See FIGs. 1A and B). In accordance with this invention, PA63 segments were converted to sequences having identical translated amino acid sequences, but with alternative codon usage as using the methodology described above. The yeast codon-optimized sequence is shown in FIGs. 2A and B.

The gene fragment encoding PA63 was prepared by the annealing and extension of 24 oligomers (91-110 bp in length) designed to encode the final desired sequence.

5' GACGTCGACGGTGTAACCTTCGACTTCCAAGGAGTCTGGAATACCGTCGTTGTCTCTGTCTGGAACAG
TTGGACCAGCGGAGGTGGA (SEQ ID NO:1)

5 5' CCTTGGAAGTCGAAGGTTACACCGTCGACGTCAAGAACAAGAGAACCTTCTTGTCTCCATGGATCTCC
AACATTCACGAAAAGAAGGGTTTGACCAAG (SEQ ID NO:2)

5' CGGTGACCTTTTCGAAGTCGGAGTATGGGTGGAAGCAGTAGACCACTTTTCTGGGGAAGACTTGTTAC
TTGGTCAAACCCTTCTTTTCGTGAATGTTGGAG (SEQ ID NO:3)

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5' CCGACCCATACTCCGACTTCGAAAAGGTCACCGGTAGAATCGACAAGAACGTCTCCCCAGAAGCTAGA
CACCCATTGGTTGCTGCTTACCCAATTGTCCACGT (SEQ ID NO:4)

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5' CTGGTTTCGGAGTCCGTGTTTTGGGTGGATTGGTCTTCGTTCTTGGACAAAATGATGTTTTCCATGTC
AACGTGGACAATTGGGTAAGCAGCAACCAATGG (SEQ ID NO:5)

5' ATCCACCCAAAACACGGACTCCGAAACCAGAACTATCTCTAAGAACACCTCCACTTCTAGAACCCACA
CTTCCGAAGTCCACGGTAACGCTGAAGTTCACGC (SEQ ID NO:6)

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5' CGATAGCGACGGTGGAGGAGTTGGAGTTGGAGAAACCAGCAGAGACGGAACCACCAATGTCTGAAGAAA
GAAGCGTGAACCTCAGCGTTACCGTGGACTTCG (SEQ ID NO:7)

5' CTCCAATCCTCACTCCTCCACCGTCGCTATCGACCACTCTTTGTCTCCTTGGCTGGTGAAAGAACTTGGG
CTGAAACCATGGGTTTGAACACTGCTGACACCGC (SEQ ID NO:8)

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5' GGAGGTGGTTGGCAAGACGTTGTAGATTGGAGCGGTACCAGTGTTGACGTATCTAATGTTAGCGTTCA
ATCTAGCGGTGTCAGCAGTGTTCAAACCCATGG (SEQ ID NO:9)

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5' CTCCAATCTACAACGTCTTGCCAACCACCTCCTTGGTCTTGGGTAAAGAACCAAACCTTGGCTACTATC
AAGGCTAAGGAAAACCAATTGTCCCAAATCTTGGC (SEQ ID NO:10)

5' GGAGAAGTCGTCTTGAGCGTTCAAAGCGATTGGAGCCAAGTCTTGGATGGGTAGTAGTTGTTTGGAG
CCAAGATTTGGGACAATTGGTTTTCTTAGCC (SEQ ID NO:11)

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5' CCAATCGCTTTGAACGCTCAAGACGACTTCTCCTCTACTCCAATCACCATGAACTACAACCAATTCTT
GGAATTGGAAAAGACTAAGCAATTGCGTTTGGACACC (SEQ ID NO:12)

5 ' CCGGTGTCGACTCTGACTCTACCGTTTTTCGAAGTTGTAAGTAGCAATGTTACCGTAAACTTGGTCGGT
GTCCAAACGCAATTGCTTAGTCTTTTCCAATT (SEQ ID NO:13)

5 5 ' CTTCGAAAACGGTAGAGTCAGAGTCGACACCGGTTCCAAC TGGTCTGAAGTCTTGCCACAAATCCAAG
AAACCACCGCTAGAATCATCTTCAACGGTAAGGACTTG (SEQ ID NO:14)

5 ' GTCTGGCTTGGTGGTTTCCAATGGGTCCGATGGGTGACAGCAGCAATTCTTCTTTCAACCAAGTTCA
AGTCCTTACCGTTGAAGATGATTCTAGCGGTGG (SEQ ID NO:15)

10

5 ' CCGACCCATTGGAAACCACCAAGCCAGACATGACCTTGAAGGAAGCTTTGAAGATCGCTTTCGGTTTC
AACGAACCAAACGGTAACTTGCAATACCAAGGTAAGG (SEQ ID NO:16)

15

5 ' GCCAATTGGTTCTTGATGTTTTGAGAGGTTTGTGTCGAAGTTGAAGTCGAATTCGGTGATGTCCTT
ACCTTGGTATTGCAAGTTACCGTTTGGTTCG (SEQ ID NO:17)

5 ' CCAACAAACCTCTCAAAACATCAAGAACCAATTGGCTGAATTGAACGCTACCAACATTTACACTGTTT
TGGACAAGATCAAGTTGAACGCCAAGATGAACATCTTGATCAGAGAC (SEQ ID NO:18)

20

5 ' GGGCTTCCTTGACAACGGATTTCGTCAGCACCGACAGCAATGTTGTTTCTGTCGTAGTGGAATCTCTTG
TCTCTGATCAAGATGTTTCATCTTGGCGTTCAACTTG (SEQ ID NO:19)

5 ' GCTGACGAATCCGTTGTCAAGGAAGCCACAGAGAAGTCATCAACTCCTCCACCGAAGGTTTGTGTT
GAACATCGACAAGGACATCAGAAAGATCTTGTCCGG (SEQ ID NO:20)

25

5 ' GAGGAAATGTTCAACATGTCGTATCTGTCGTTGATGACTTCCTTCAAACCTTCGGTGTCCTTCAATTC
GACGATGTAACCGGACAAGATCTTCTGATGTCCTTGTTCGATG (SEQ ID NO:21)

30

5 ' GTCATCAACGACAGATACGACATGTTGAACATTTCTCTTTGAGACAAGACGGTAAGACCTTCATCGA
CTTCAAGAAGTACAACGACAAGTTGCC (SEQ ID NO:22)

5 ' GGGTTGATGATGGTGTTTTCTTAGTGACAGCGTAAACGTTGACCTTGAGTTTGGGTGGAAATGTA
CAATGGCAACTTGTCGTTGTACTTCTTGAAGTCGATGAAGG (SEQ ID NO:23)

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5 ' CGCTGTCACTAAGGAAAACACCATCATCAACCCATCCGAAAACGGTGACACTTCCACCAACGGTATCA
AGAAGATTTTGATCTTCTCTAAGAAGGGTTACGAAATTGGT (SEQ ID NO:24)

The oligomers were alternating, overlapping sense and antisense sequences that spanned the entire length of the optimized PA63 coding sequence. Each oligomer had a complementary overlap of 28-38 bp with the adjoining oligomer (duplex had a T_m of 72-78 C° as calculated by VECTOR NTI

Six separate extension reactions were performed using four adjoining overlapping oligomers and sense and antisense PCR primers (28-32 nt in length with duplex T_m =62-68 C°). Appropriate conditions for PCR are those described in International Publication number WO 01/14416A2. As a result of these PCR reactions, 6 colinear fragments of the gene were created (referred to herein for convenience as C+, D, E, F, G, H).

The fragments were gel-separated on agarose and the appropriately-sized products excised were purified using the GENE CLEAN Spin Column method (QBIogene, Carlsbad, CA) as recommended by the manufacturer. Colinear fragments C+, D, and E and colinear fragments F, G, and H were combined in subsequent PCR reactions with the appropriate primers to yield fragments II+ and III, respectively. The complete gene for PA63 was then assembled by an additional PCR reaction in which fragments II+ and III were combined using distal sense and antisense primers which incorporated *Bam*HI sites to allow cloning of the final product into a yeast vector. The sense primer incorporated additional upstream sequences to permit in frame cloning with a yeast secretion leader including its cleavage site via the Kex2 protease. The resulting 1.7-kb product (designated PA63 +L) was gel-isolated and cloned into pCR-Blunt II-TOPO (INVITROGEN, Carlsbad, CA) as recommended by the manufacturer. The sequence was obtained and errors identified. The gene was subcloned into pGEM3zf+ (PROMEGA, Madison, WI) and the errors sequentially corrected by site-directed mutagenesis using the QUIK-CHANGE Site-directed Mutagenesis Kit (STRATAGENE, La Jolla, CA) using the manufacturer's recommendations. A final PCR reaction with HIGH FIDELITY PCR Supermix (INVITROGEN, Carlsbad, CA) using an antisense primer

(5'CGCGGATCCTTAACCAATTTTCGTAACCCTTCTTAGAGAA) (SEQ ID NO: 25)

which incorporated a stop codon upstream of the *Bam*HI site and a sense primer which contained a *Bam*HI site as listed below (SEQ ID NO:26) plus a convenient portion of the gene sequence amplified the corrected sequence. The reaction product was subcloned into a TA cloning vector (INVITROGEN, Carlsbad, CA) using the manufacturer's protocol.

The DNA was purified from the final clone and the *Bam*HI fragment subcloned in the proper orientation into a yeast secretion vector (pHK4 α 2, FIG. 3) to construct pAGT1. The sequence of the insert was verified by DNA sequencing.

It is readily apparent to those skilled in the art that this invention extends to the use of DNA sequence data and its deduced amino acid sequence from naturally occurring modifications of the PA protein and from recombinant sequences that confer improved properties such as increased

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liter of distilled water: agar, 20 g; sorbitol, 182 g; and SD medium minus leucine, 27.4 g (QBIogene #4811-015) (Carlsbad, CA). Clonal Leu⁺ isolates were obtained by serial growth on Leu⁻ plates.

Five-ml seed cultures were grown at 30° C in 5X minus leucine medium containing 4.0 % glucose and 0.1 M sorbitol medium for 18-24 h to OD₆₀₀ of 1.5-3.0/ml. 5X minus leucine medium contains the following components per liter: Yeast Nitrogen Base without added amino acids or ammonium sulfate, 8.5 g; adenine, 0.40 g; L-tyrosine, 0.25 g; uracil, 0.20 g, succinic acid, 10.0 g, ammonium sulfate, 5.0 g and 50 ml of Leucine-Minus Solution #3. Leucine-Minus Solution #3 contains per liter of distilled water, L-arginine, 2 g; L-histidine, 1.0 g; L-isoleucine, 6 g; L-lysine 4.0 g; L-methionine, 1.0 g; L-phenylalanine, 6.0 g; L-tryptophan, 4.0 g. A 0.3 ml aliquot was transferred to either 5.0 ml of 5X minus leucine medium containing 2 % glucose, 4 % galactose or YEHDG medium for 72 h to a final OD₆₀₀ of 5-16.0/ml. YEHDG medium contains per liter: L-Hy-Soy peptone-Sheffield, 10 g; Yeast extract, 20 g; L-dextrose, 16 g; D(+) galactose, 40 g.

After harvesting a total of 10 ODs per sample, the cell pellets were broken with glass beads in 0.3 mL lysis buffer (0.1 M sodium phosphate buffer, pH 7.2, 0.5 M NaCl, 1 mM PMSF). The lysate was recovered by centrifugation, the unbroken cells/beads were washed with 0.3 mL of lysate buffer and the clarified supernatants were combined. The clarified lysate was assayed for protein by the BIO-RAD Protein Assay Dye Reagent system (cat#500-0006) (BIORAD, Hercules, CA) according to the manufacturer's instructions. The cell lysates were analyzed for the expression of PA63 by immunoblot analysis after electrophoresis on either 4-15 % gradient Tris-HCl gels (BIORAD #161-1158) or 10-20% gradient Tris-HCl Criterion gels (BIORAD # 345-0043) in 1X Tris glycine SDS buffer (cat#161-0732) (BIORAD, Hercules, CA) under reducing and denaturing conditions. When equal amounts of protein lysate were subjected to electrophoresis, the samples contained 0.25-0.5 µg of total cellular protein. Sometimes equal volumes of cell lysate were analyzed and in this case, 0.05-1.0 µg total protein were loaded on the gels. The gels were electroblotted onto 0.2 micron PVDF membrane filters. To estimate protein size, prestained standards between 10 and 250 kDa were run in parallel with the lysates (cat # 161-0372) (BIORAD, Hercules, CA).

Recombinant PA83 prepared from *E. coli* BL21 as described by Roberts, J.E. et al. (Roberts *et al.*, 1998) was used as size standard. PA63 was derived from PA83 by treatment with trypsin as described by Miller et al. (Miller *et al.*, 1999) using Trypsin, type XI (SIGMA # T1005) (SIGMA CHEMICAL CO., St. Louis, MO) and Trypsin soybean inhibitor (SIGMA #T9003) (SIGMA CHEMICAL CO., St. Louis, MO). Either PA63 or PA83 were run as standards on every gel. For both qualitative and quantitative purposes, PA63 and PA83 standard were mixed with cell lysates prepared from a vector control transformant. Proteins were immunodetected using a monoclonal antibody to PA83 obtained from BIODESIGN (Clone C3 #C86613M) (BIODESIGN INTERNATIONAL, Saco, ME) as primary antibody and goat anti-mouse IgG (H+L) horseradish peroxidase-linked whole antibody (ZYMEX #81-6520) (ZYMED LABORATORIES, South San Francisco, CA, City, State) as the

secondary antibody. The filters were processed using the "WESTERN LIGHTNINGTM Chemiluminescence Reagent Plus kit (PERKIN ELMER, Wellesley, MA).

A time course of induction of PA63 by transformant L-1 (strain 1849) fermented in duplicate, A and B, in complex YEHDG medium showed a major protein band that had the same mobility as the PA63 standard (FIG. 5). No expression was detected with a vector control transformant, K-1A (lane 2). Optimal expression was obtained at 48 hours (lanes 4 and 7). Production of internal PA63 was greater in complex medium than in a defined medium. Isolate 8-3 was chosen as the best producer of internally-produced PA63 in yeast strain 1260 based on Western analysis using PA63 and PA83 as standards and ELISAs using PA83 as standard.

EXAMPLE 3:

Quantitation of Internal Yields

To estimate the yield of PA per culture volume, 5 mL culture of strain 8-3 which produces PA63 intracellularly, and vector control transformant 7-1 (both transformants of strain 1260) were processed either for quantitative ELISAs or for semi-quantitative Westerns. Two independent fermentation experiments designated one and two, were conducted with duplicate fermentations, A and B, for each transformant. For each experiment, the samples were analyzed by both techniques using authentic recombinant PA83 from *E. coli* as standard. ELISA and Westerns were performed using standard techniques. The antibodies used to capture and detect PA63 in the ELISA were monoclonal antibodies to PA83 (clone BAP0103, #C86301M,) and (clone C3, #C86613M,), respectively, (BIODESIGN INTERNATIONAL, Saco, ME). The antibody used in the Western blots was clone C3. A typical Western blot for quantitation is shown in FIG. 6. The results from ELISA determinations and semi-quantitative Westerns from the two independent experiments with culture 8-3 are shown in Table 1. These yields are within the range of the best yields reported for PA production from *B. anthracis* (Leppla, 1988) and recombinant PA production in *E. coli* (Chauhan *et al.*, 2001) without the potential of contamination with toxic bacterial components.

Table 1 $\mu\text{g PA/mL culture (tube)}$
-transformants of 1260

Analysis Method	Isolate 8-3 ^a titer($\mu\text{g PA/mL}$)
Experiment 1	
ELISA-1 ^b	71
ELISA-2 ^b	58
Western-1	47
Western-3	52
Experiment 2	
ELISA-3 ^b	144
Western-2	99
Western-3	82
Average ^c	79

^a Avg. of duplicate fermentations-Avg. variation, 1.4 and 1.2-fold for ELISA and Western, respectively

^b Underestimate due to inhibition of PA detection by cell lysate

5 ^c Average of all values from both experiments

EXAMPLE 4:

Expression of Secreted PA63 in Yeast Strain 1849

10 The synthetic DNA encoding the PA63 protein and with codons optimized for yeast expression was purified from the clone described in Example 1 and the *Bam*HI fragment subcloned in the proper orientation into a yeast secretion vector (pHK4 α 2, FIG. 3) to construct pAGT1. The sequence of the insert was verified by DNA sequencing. For secretion, the vector of choice is pHK4 α 2, which utilizes the yeast *GAL10* promoter and contains a unique *Bam*HI site for fusion (in-frame) of the ORF of interest to

15 the yeast alpha factor (MF α 1) pre-pro secretory leader. The 5'-end of the synthetic PA63 was modified to add the last 7 amino acids of the pro-leader including the cloning site and Lys-Arg cleavage site for the

*Bam*HI KEX2 site

5 Ile Leu Ser Leu Asp Lys Arg (SEQ ID NO:30)

10 protocol (Hinnen et al., 1978). Transformants were selected on synthetic agar medium lacking leucine and containing 1 M sorbitol. The synthetic medium contained per liter of distilled water: agar, 20 g; sorbitol, 182 g; and SD medium minus leucine, 27.4 g (QBIogene #4811-015)(Q BIO, Carlsbad, CA). Clonal Leu⁺ isolates were obtained by serial growth on Leu⁻ plates.

15 glucose and 0.1 M sorbitol medium for 18-24 h to OD₆₀₀ of 1.5-3.0/mL. 5X minus leucine medium contains the following components per liter: Yeast Nitrogen Base w/o amino acids or ammonium sulfate, 8.5 g; adenine, 0.40 g; L-tyrosine, 0.25 g; uracil, 0.20 g, succinic acid, 10.0 g, ammonium sulfate, 5.0 g and 50 ml of Leucine-Minus Solution #3. Leucine-Minus Solution #3 contains per liter of distilled water, L-arginine, 2 g; L-histidine, 1.0 g; L-isoleucine, 6 g; L-lysine 4.0 g; L-methionine, 1.0 g; L-phenylalanine, 6.0 g; L-tryptophan, 4.0 g. A 0.3 mL aliquot was transferred to either 5.0 mL of 5X minus
20 leucine medium containing 2 % glucose, 4 % galactose or YEHDG medium for 72 h to a final OD₆₀₀ of 5-16.0/ml. YEHDG medium contains per liter: L-Hy-Soy peptone-Sheffield, 10 g; Yeast extract, 20 g; L-dextrose, 16 g; D(+) galactose, 40 g.

25 PA63 by immunoblot analysis. Twenty-five microliter samples were subjected to electrophoresis on 4-15 % gradient Tris-HCl gels (cat #161-1158)(BIORAD, Hercules, CA) in 1X Tris glycine SDS buffer (cat #161-0732) (BIORAD, Hercules, CA) under reducing and denaturing conditions. The gels were electroblotted onto 0.2 micron PVDF membrane filters. To estimate protein size, prestained standards between 10 and 250 kDa were run in parallel with the samples (cat # 161-0372) (BIORAD, Hercules, 30 CA). Recombinant PA83 from *E. coli* BL21 as described by Roberts, J.E. et al. (Roberts *et al.*, 1998) was used as size standard. PA63 was derived from PA83 by treatment with trypsin as described by Miller et al. (Miller *et al.*, 1999) using Trypsin, type XI (cat # T1005)(SIGMA CHEMICAL CO., St. Louis, MO) and Trypsin soybean inhibitor (cat #T9003) (SIGMA CHEMICAL CO., St Louis, MO). Either PA63 or PA83 were run as standards on every gel. For both qualitative and quantitative purposes, 35 PA63 and PA83 standard were mixed with cell lysates prepared from a vector control transformant.

Proteins were immunodetected using a monoclonal antibody to PA83 obtained from BIODESIGN INTERNATIONAL, Saco, ME (Clone C3 #C86613M) as primary antibody and goat anti-mouse IgG (H+L) horseradish peroxidase-linked whole antibody (Zymed #81-6520) (ZYMED LABORATORIES, South San Francisco, CA) as the secondary antibody. The filters were processed using the "WESTERN LIGHTNING[™] Chemiluminescence Reagent Plus kit (PERKIN ELMER, Wellesley, MA).

Multiple isolates were screened using small scale shake flask fermentations or roller tube fermentations. Culture 14A in strain 1849 was determined to yield the most secreted PA63 as determined by semi-quantitative Western blots. A time course of production of secreted PA from strain 14A is shown in FIG. 7. A protein band of ~75 kDa was detected minutely at 24 h, increased at 48 h, and was maximally produced at 72 h (see lanes 3, 5 and 7, respectively). No protein was detected in the supernatant of a transformant containing the vector control alone, 12B, shown at 48 and 72 h as shown in lanes, 4 and 6, respectively. There were some smaller proteins that could be degradation products. These proteins appear as early as 24 h and appear to get smaller with time. The ~75-kDa protein is larger than the PA63 control. There are several possibilities for the altered mobility of the secreted protein including N- or O-linked core glycosylation and uncleaved leader sequence. A protein band of ~75 kDa was detected in all three of the transformed *S. cerevisiae* strains tested. Production of secreted PA was greater in complex medium than in a defined medium. Assays on cellular lysates indicated that some PA63 was retained intracellularly.

PA63 secretion was not improved in 2 different *pep4* mutants (deficient in vacuolar proteases) incubated for various times.

EXAMPLE 5:

Domain 4 Construct

Native PA63 has a cellular receptor binding site within domain 4 that has been implicated in vaccine-induced immunity. Domain 4, a 140-amino acid protein corresponding to bacterial amino acids 596-735 of SEQ ID NO: 54, is capable of inducing antibodies that protect mice from infection with *B. anthracis* (Flick-Smith *et al.*, 2002). Further evidence that domain 4 has a key role was shown by neutralization of toxin with affinity-enhanced recombinant antibodies directed to an epitope within domain 4. Thus, it can be readily seen that expression of recombinant domain 4 in yeast would yield a small protein in a safe expression host. It is expected that this domain and other appropriate immunogenic domains of PA expressed in yeast would offer the advantage of increased immunogenicity, easier purification and higher yields than the entire protein.

The wild-type sequence for the gene encoding the uncleaved PA83 (BACPAG) is known (See FIG. 8). In accordance with this invention, domain 4 sequence without the bacterial signal sequence having identical translated amino acid sequences, but with alternative codon usage as defined by Lathe (Lathe, 1985) and selected for yeast codons for highly expressed genes (Sharp and Cowe, 1991) was

amplified by PCR from a plasmid containing PA63 DNA sequence optimized for yeast codon usage. The 5' primer (GTCACGGATCCTGTCTTTGGATAAGAGATTCCACTACGACAGAAA CAACATT) (SEQ ID NO: 31)

contained the desired yeast leader sequence for secretion and the 3' primer

(CGCGGATCCTTAACCAATTTTCGTAACCCTTCTTAGAGAA) (SEQ ID NO: 32)

contained a *Bam*HI restriction site and TAA as a stop codon. The PCR fragment was digested with *Bam*HI and cloned into secretory vector. The yeast codon optimized domain 4 sequence without the leader is shown in Figure 9A and its translation in 9B.

EXAMPLE 6:

PA83 Construct and Expression

The wild-type sequence for the gene encoding the uncleaved PA83 (BACPAG) is known (See FIG.8). In accordance with this invention, PA83 segments without the bacterial signal sequence were converted to sequences having identical translated amino acid sequences, but with alternative codon usage as defined by Lathe (Lathe, 1985) and selected for yeast codons for highly expressed genes (Sharp and Cowe, 1991). See FIG. 11. The methodology was the same as for Example 1.

Native, mature PA83 binds to cellular receptors and requires activation by endoproteolytic cleavage to interact with either LF and EF to form active toxin (Reviewed by Mock and Fouet, 2001). A mutated form of PA83 that has the amino acid sequence RKKK (SEQ ID NO: 33) instead of the wild-type RKKR (SEQ ID NO: 34) sequence within the furin cleavage site at amino acids 164-167 does not form active toxins with EF and LF (Beauregard et al, 2000). Proteolytic cleavage is rate-limiting for internalization of the protein and the mutated protein remains on the surface. Yet this mutated protein still contains the immunoprotective domains implicated in vaccine-induced immunity such as domain 4 (Flick-Smith *et al.*, 2002). This mutant form of PA83 and other appropriate immunogenic domains of PA expressed in yeast can offer the advantages of increased immunogenicity, easier purification and higher yields.

The gene fragment encoding PA83 with a mutation of R to K at amino acid 167 to alter the furin and potential Kex2p cleavage site was prepared by the annealing and extension of 31 oligomers (91-110 bp in length) designed to encode the final desired sequence. The oligomers were alternating, overlapping sense and antisense sequences that spanned the entire length of the optimized PA83 coding sequence. Each oligomer had a complementary overlap of 28-38 bp with the adjoining oligomer (duplex had a T_m of 72-78 C° as calculated by Vector NTI program, version 7, INFORMAX, Bethesda, MD). Eight separate extension reactions were performed using four adjoining overlapping oligomers and sense and antisense PCR primers (28-32 nt in length with duplex T_m=62-68 C°). The actual conditions of PCR were similar to those described in International Publication number WO 01/14416A2.

The oligomers and resulting fragments D,E,F,G, and representing the PA63 portion of the molecule are the same as in Example 1. The N-terminal portion were created from the following oligomers which were used to create fragments A, B and C. The 12 oligomers for A, B, and C are the following:

5 ' GAAGTTAAGCAAGAAAACAGATTGTTGAACGAATCTGAATCCTCTTCCCAAGGTTTGTGTTGGGTTA
CTACTTCTCCGACTTGAACCTTCCAAGCTCCAATGGTCGTCACC-3 ' (SEQ ID NO: 35)

5 ' CGGATGGGATGTTCTCTAATTCGGAGGATGGGATGGACAAGTC
ACCGGTAGTAGAGGAGGTGACGACCATTTGGAGCTTGGAAAGTTCAAGTCGG-3 ' (SEQ ID NO: 36)

5 ' TCCCATCCTCCGAATTAGAGAACATCCCATCCGAAAACCAATACTTCCAATCCGCTATCTGGTCC
GGCTTCATCAAGGTCAAGAAGTCCGACG-3 ' (SEQ ID NO: 37)

5 ' GGAAGCCTTGTTGATGACTTCTTGGTCGTCGACCCACATAGTAACGTGGTTGTCAGCGGAGGTAG
CGAAAGTGTATTCGTCGGACTTCTTGACCTTGATGAAGCCGG-3 ' (SEQ ID NO: 38)

5 ' GGGTCGACGACCAAGAAGTCATCAACAAGGCTTCCAACCTCCAACAAGATCAGATTGGAAAAGGGT
AGATTGTACCAAATTAAGATCCAATACCAAAGAGAAAACCCAACCG-3 ' (SEQ ID NO: 39)

5 ' GAGATGACTTCCTTCTTGTGTTTGGGAGTCGGTCCAGTACAACCTTGAAGTCCAAACCCCTTTTCGGT
TGGGTTTTCTCTTTGGTATTGGATCTTAATTTGG-3 ' (SEQ ID NO: 40)

5 ' GGACCGACTCCCCAAAACAAGAAGGAAGTCATCTCYTCTGACAACTTGCAATTGCCAGAAATTGAAG
CAAAAGTCYTCCAACCTCCAGAAAGAAGAAGTCCACCTCCGCTGG (SEQ ID NO: 41)

5 ' GACGTCGACGGTGTAACCTTCGACTTCCAAGGAGTCTGGAATACCGTCGTTGTCTCTGTCTGGAA
CAGTTGGACCAGCGGAGGTGGACcttCTTCTTCTGGAGTTGG-3 ' (SEQ ID NO: 42)

5 ' CCTTGAAGTCGAAGGTTACACCGTCGAGTCAAGAACAAGAGAACCTTCTTGTCTCCAATGGATC
TCCAACATTCACGAAAAGAAGGGTTTGACCAAG-3 ' (SEQ ID NO: 43)

5 ' CGGTGACCTTTTCGAAGTCGGAGTATGGGTGCGAAGCAGTAGACCACTTTTCTGGGGAAGACTTG
TACTTGGTCAAACCCCTTCTTTTCGTGAATGTTGGAG-3 ' (SEQ ID NO: 44)

5 ' CCGACCCATACTCCGACTTCGAAAAGGTACCCGGTAGAATCGACAAGAACGTCTCCCCAGAAGCT
AGACACCCATTGGTTGCTGCTTACCCAATTGTCCACGT-3 ' (SEQ ID NO: 45)

5 ' CTGGTTTCGGAGTCCGTGTTTTGGGTGGATTGGTCTTCGTTCTTGGACAAAATGATGTTTCCAT
GTCAACGTGGACAATTGGGTAAGCAGCAACCAATGG-3 ' (SEQ ID NO: 46)

- 5 As a result of these PCR reactions, the following 8 fragments of the gene were created: A, B, C, D, E, F,G, H. Fragment C contains the mutation which results in a lysine in place of the arginine at amino acid 167.

- 10 The fragments were gel separated on agarose with the appropriately-sized products excised and purified using the Gene Clean Spin Column method (QBIOSGENE, Carlsbad, CA) as recommended by the manufacturer. Fragments A and B, fragments C, D, and E, and fragments F, G, and H were combined in a subsequent PCR reaction with the appropriate primers to yield the fragments I, II and III, respectively. The complete gene for PA83 was then assembled by an additional PCR reaction in which

fragments I, II and III were combined using distal sense and antisense primers which incorporated *Bam*HI sites to allow cloning of the final product into a yeast vector. The sense primer incorporated additional upstream sequences that permit in-frame cloning with a yeast secretion leader and its Kex2 protease cleavage site as in Example 1. The resulting 2.2-kb product (designated PA83 U +L) was gel isolated and cloned into pCR-Blunt II-TOPO (INVITROGEN, Carlsbad, CA) as recommended by the manufacturer. The sequence was obtained and errors identified. The final DNA sequence and encoded protein sequence are shown in Figure 11. The gene was subcloned into pGEM3zf+ (PROMEGA, Madison, WI) and the errors sequentially corrected by site-directed mutagenesis using the Quik-Change Site-directed Mutagenesis Kit (STRATAGENE, La Jolla, CA) using the manufacturer's recommendations. It can be readily seen by those skilled in the art that the sequence of the PA83 can be changed to produce wild-type and altered forms of PA83 in response to mutated versions made by man or naturally occurring modifications.

EXAMPLE 7:

Preparation of Immunogenic Compositions

Purified PA63 is formulated according to known methods, such as by the admixture of pharmaceutically acceptable carriers, stabilizers, or a vaccine adjuvant. The immunogenic PA63 of the present invention may be prepared for vaccine use by combining with a physiologically acceptable composition such as, e.g. PBS, saline or distilled water. The immunogenic PA63 are administered in a dosage range of about 0.1 to 100 mcg, preferably about 1 to about 20 mcg, in order to obtain the desired immunogenic effect. The amount of PA63 per formulation may vary according to a variety of factors, including but not limited to the individual's condition, weight, age and sex. Administration of the PA63 formulation may be by a variety of routes, including but not limited to oral, subcutaneous, topical, mucosal and intramuscular.

An antimicrobial preservative, e.g. thimerosal, optionally may be present. The immunogenic antigens of the present invention may be employed, if desired, in combination with vaccine stabilizers and vaccine adjuvants. Typical stabilizers are specific compounds, e.g. polyanions such as heparin, inositol hexasulfate, sulfated beta- cyclodextrin, less specific excipients, e.g. amino acids, sorbitol, mannitol, xylitol, glycerol, sucrose, dextrose, trehalose, and variations in solution conditions, e.g. neutral pH, high ionic strength (ca. 0.5-2.0M salts), divalent cations (Ca^{2+} , Mg^{2+}). Examples of adjuvants are $\text{Al}(\text{OH})_3$, $\text{Al}(\text{OH})_x(\text{SO}_4)_y(\text{PO}_4)_z$ and $\text{Al}(\text{PO}_4)$. The vaccine of the present invention may be stored under refrigeration or in lyophilized form.

EXAMPLE 8:

S. cerevisiae codon usage required for optimal production of PA63 in yeast

To determine whether the alteration of codons used in Examples 1-4 provided for optimal production in yeast, the authentic bacterial sequence of PA63, which is the 1.7-kb furin cleavage product of authentic native PA83, was amplified by PCR from authentic native bacterial PA83 isolated from B. anthracis. The authentic native bacterial PA83 had been cloned and the sequence subsequently corrected so that the amino acid sequence matched that of codon-optimized PA83. The native PA63 sequence as inserted into the same yeast secretory expression vector as the codon-optimized sequence (see Example 4). The amount of secreted and internal PA63 was determined by semi-quantitative Western analysis.

DNA from B. anthracis ATCC strain 14578 was obtained from a 5.0-mL culture. The culture was inactivated and total DNA was purified by the addition of 0.5 mL 20 % SDS, 5.0 mL of phenol-chloroform and 0.75 mL 5.0 M NaCl. The DNA was purified by standard procedures and resuspended in TE for use in PCR.

The full-length PA83 (2.2 kb) was amplified with *Bam*HI restriction enzyme sites by PCR using the following primers (*Bam*HI sites underlined): 83 sense,

5'CGCGGATCCGAAGTTAAACAGGAGAACCG3' (SEQ ID NO: 59), 83 antisense -

5'CGCGGATCCTTATCCTATCTCATAGCCTT 3'(SEQ ID NO: 60).

Two rounds of PCR were used to amplify the desired regions. The first round used PFU turbo DNA polymerase, genomic DNA according to the manufacturer's recommendations and the following PCR conditions: 1 min 95 °C, 1 X; 95 °C 45 sec, 55 °C 45 sec, 72 °C 2.5 min 30X; 72 °C 10 min, 1 X; 4 °C hold. The second round was performed with 1 µL of product from the first round, and PCR SUPERMIX HIGH FIDELITY (cat # 10790-020)(INVITROGEN, Carlsbad, CA) according to the manufacturer's recommendations. The PCR conditions were as follows: 30 sec 94° C, 1 X; 94° C 30 sec, 55° C, 30 sec, 68° C, 2.5 min, 25X; 68° C, 7 min, 1X; 4° C hold. The PCR product was purified and concentrated on a Gene Clean Spin column according to the manufacturer's recommendation (QBIOSGENE, Carlsbad, CA). The PCR products were cut with *Bam*HI, purified by Gene Clean Spin columns and ligated to the vector pKH4alpha2 that had been digested with *Bam*HI and treated with alkaline phosphatase to prevent self-ligation. The orientation of the insert was confirmed by restriction digest and the DNA sequence of plasmid pba83PAG#11 analyzed. Four bp that differed from the published sequence, used to construct the yeast codon-optimized version, were found.

To facilitate correction of the sequence, the *Bam*HI fragment of pba83PAG#11 was gel isolated and concentrated on a Gene Clean Spin column according to the manufacturer's recommendation (QBIOSGENE, Carlsbad, CA). The *Bam*HI fragment was ligated to pGEM3zf that had been digested with *Bam*HI and treated with alkaline phosphatase to construct pba83#13. The sequence was corrected using QUICK CHANGE MULTI-SITE-DIRECTED mutagenesis kit (STRATAGENE, La Jolla, CA) according to the manufacturer's instructions and the DNA sequence of the resultant plasmid, pba83multi#5, was verified.

In order to clone the 1.7-kb furin cleavage product of authentic native PA83, and to facilitate cloning into the yeast secretory vector with the appropriate leader sequence, the following sense and antisense primers (*Bam*HI sites underlined), respectively,

5'CGCGGATCCTGTCTTTGGATAAGAGAAGTACAAGTGCTGGACCTAC3' (SEQ ID NO: 61) and

5'CGCGGATCCTTATCCTATCTCATAGCCTT3' (SEQ ID NO: 62) were used for PCR with pba83multi#5 as template. The PCR conditions were as described above using PCR SUPERMIX HIGH FIDELITY (cat # 10790-020)(INVITROGEN®, Carlsbad, CA). The *Bam*HI fragment was isolated as described above and cloned into pCR2.1TOPO (INVITROGEN, Carlsbad, CA) according to the manufacturer's recommendation. Subsequently, the *Bam*HI fragment was gel-isolated again and ligated into pKH4α2 that had been digested with *Bam*HI and treated with alkaline phosphatase. The correct orientation and sequence was confirmed by DNA sequencing of plasmid pba63pKH4α2#11.

The plasmid pba63pKH4α2#11 was used to transform *S. cerevisiae* strain #1849 as in Examples 2 and 4. Leu⁺ transformants obtained with pba63pKH4α2, pAGT1 (codon-optimized PA63, Example 4), and pKH4α2 (vector control) were fermented in complex medium YEHDG as described in Examples 2 and 4. Supernatants of cultures of twenty-four independent Leu⁺ transformants obtained with pba63pKH4α2 were screened for the production of secreted PA63 as described in Example 4. No PA63 was detected from any of the transformants containing the authentic native sequence, even after prolonged exposure of the blot. Secreted PA63 was however, detected from transformants containing the yeast codon-optimized sequence (data not shown).

We had previously found both secreted and intracellular PA63 produced by transformants containing the plasmid pAGT1, designed to secrete codon-optimized PA63 (Example 4). To ensure that PA63 was not produced inside the cell from a transformant containing "authentic native" PA63 sequence, we evaluated selected transformants for both intracellular and extracellular production of PA63. Fermentations and assessment of PA63 production were conducted as described in Examples 2 and 4. The amount of PA63 produced in yeast from the authentic native bacterial sequence was compared to that of the "codon-optimized" gene by Western blot analysis as shown in FIG. 12. PA63 was detected in both the medium supernatants and cell lysates of transformants containing the codon-optimized gene as shown in lanes 6, 7 and 11, 12, respectively. In both cases, the PA63 detected was larger than 63 kDa. It was also larger than PA63 produced from a transformant constructed to produce PA63 intracellularly (see Example 2) as shown in lane 1 and described in Example 4. In contrast, PA63 was not detected in either cell lysates (lanes 9 and 10) or medium supernatants (lanes 4 and 5) from transformants containing the "native" construct, even after a very long exposure of the blot. No protein was detected in either supernatants (lane 3) or cell lysates (lane 8) of the vector control transformant.

EXAMPLE 9:

Intracellular Expression of Uncleavable PA83 with Altered Furin Cleavage Site in *S. cerevisiae*

The DNA encoding the PA83 protein with codons optimized for yeast expression was amplified from the final corrected clone (lacking the Furin cleavage site) as carried in the pGEM3Zf+ vector described in Example 6 using the following sense and antisense primers, respectively,

5'CGCGGATCCCACAAAACAAAATGGAAGTTAAGCAAGAAACAGA 3' (SEQ ID NO: 63) and

5'CGCGGATCCTTAACCAATTTCGTAACCCCTTCTTAGAGAA3' (SEQ ID NO: 29) containing a *Bam*HI restriction site and TAA as a stop codon. The *Bam*HI fragment was subcloned in the proper orientation into a yeast vector (pGAL110, FIG. 4) to construct PA83pGAL10#24. The sequence of the insert was verified by DNA sequencing. The plasmid was used to transform *S. cerevisiae* strains #1260 (*MATa*, *leu2-2, 112*, *mn9*, *ura3Δ*, *can1*, *his3Δ::GAL10p-GAL4-URA3*, *prb1Δ::HIS3*, *cir^o*), #1558 (*MATa*, *leu2-04*, *prb1Δ::HIS3*, *mn9::ura3*, *ade1*, *his3::URA3*, *cir^o*) and #1849 (*MATa*, *leu2-04*, *prb1Δ::HIS3*, *mn9::ura3*, *ade1*, *his3::GAL10p-GAL4-URA3*, *cir^o*) to leucine prototrophy (*Leu⁺*) as described in Examples 2 and 4.

For screening multiple transformants of strains 1849 and 1558, small-scale trial fermentations were conducted in complex YEHDG medium and evaluated for expression of PA83 by Western blot as described in Example 2. A major protein that co-migrated with the *E. coli* PA83 standard was detected by Western blotting in cell lysates of transformants of both strains 1849 and 1558. No proteins were detected in lysates of vector control transformants. The best internal producer of PA83 was a transformant of 1558, strain Q-3, with a volumetric productivity of 12.0 μg PA83 produced per mL of culture medium with PA83 comprising 7.0 % of the total cell protein. Production of internal PA83 was greater in complex than in a defined medium. Media compositions were described in Example 2.

Production of uncleavable PA83 was evaluated from strain Q-3 and several transformants of strain 1260, 9-1 through 9-8, that were fermented in 50 mL of medium in 250-mL shake flasks. Inoculum development began by thawing the frozen vials and transferring 1.0 mL inoculum to 50 mL of medium contained in a 250-mL flask. Strain Q-3 was transferred into 5X minus leucine + 4% Dextrose medium and strains 9-1 through 9-8 were transferred into 5X minus leucine minus adenine + 4% Dextrose medium. The composition of 5X minus leucine medium was described in Example 2. The flasks were incubated at 28° C and agitated at 250 rpm. For each strain, samples were removed aseptically after ~ 24 h to determine the glucose concentration and OD₆₀₀.

When the glucose in the 250-mL flask reached between 5 and 25 g/L, 1.0 mL of culture was transferred to another 250-mL Erlenmeyer flask containing YEHDG medium. YEHDG medium was described in Example 2. Again, the flasks were incubated at 28° C and agitated at 250 rpm. For each strain, samples were removed aseptically after 48 h and 72 h to determine the glucose and galactose concentration and OD₆₀₀.

The flasks were harvested after 72 h and pellets corresponding to 25 OD₆₀₀ units were collected for each strain. The cell-pellets were broken with 0.5 g of 0.45 mm acid washed glass beads in 0.3 mL of 0.2 M HEPES, pH 7.3 containing 0.5 mg/mL Pefabloc (ROCHE DIAGNOSTICS, Mannheim,

Germany), 1x Complete Protease Inhibitor Cocktail (Roche), 3.5 μ g/mL pepstatin (ROCHE), 20 mM benzamidine (SIGMA, St. Louis MO), 5 mM EDTA, and 5 mM EGTA. Breakage was performed at 4° C using a vortex mixer for 15 minutes. Cellular debris and beads were collected by centrifugation in a microcentrifuge and the supernatant was transferred to a second microcentrifuge tube that was again centrifuged to remove debris. Aliquots were removed and assayed for total protein using the BCA assay (PIERCE, Rockford, Illinois). Four μ g of each lysate were then loaded on a 4-12 % NUPAGE BIS TRIS gel and subjected to electrophoresis in MOPS SDS running buffer (INVITROGEN, Carlsbad, CA). The gel was transferred to PVDF membrane (INVITROGEN, Carlsbad, CA) for Western blotting using MAb 86613M (BIODESIGN INTERNATIONAL, Saco, ME) as primary antibody and goat anti-mouse-IgG peroxidase conjugate (PERKIN ELMER, Boston, MA) as secondary antibody. Detection was performed using CN/DAB peroxidase substrate (PIERCE, Rockford, Illinois). Purified recombinant *E. coli* PA83 (see Examples 2 and 4) was used as standard.

The results are shown in FIG. 13. Transformant 9-1 of *S. cerevisiae* strain 1260 (lane 1) was one of the best producers of internally-produced rPA83 and was chosen for large-scale fermentation.

EXAMPLE 10:

Intracellular Expression of PA83 with Intact Furin Cleavage Site (cleavable PA83) in *S. cerevisiae*

The DNA encoding the PA83 protein with a mutated Furin cleavage site (Example 6) and with codons optimized for yeast expression was subcloned into pCR4-TOPO (INVITROGEN, Carlsbad, CA). The PA83 coding sequence was altered to encode an arginine at amino acid 167 of the cleavage site using the QUICKCHANGE Site-directed mutagenesis kit (STRATAGENE, La Jolla, CA). The primers used for mutating the site were:

Sense 5' CAACTCCAGAAAGAAGAGATCCACCTCCGCTGGTC - SEQ ID NO: 64 and antisense 5' GACCAGCGGAGGTGGATCTCTTCTTTCTGGAGTTG - SEQ ID NO: 65

The sequence of the modified plasmid was verified by DNA sequencing. The DNA for the cleavable construct was amplified from pCR4-TOPO as a *Bam*HI fragment using the sense primer described in the previous example, 5'CGCGGATCCACAAAACAAAATGGAAGTTAAGCAAGAAAACAGA (SEQ ID NO: 63), and the antisense primer described in Examples 1 and 2.

5'CGCGGATCCCTTAACCAATTTTCGTAACCCTTCTTAGAGAA3' (SEQ ID NO: 29) The *Bam*HI fragment was subcloned in the proper orientation into a yeast expression vector (pGAL110, FIG. 4) to construct pPA83clGAL10#6. The sequence of the insert was verified by DNA sequencing. The plasmid was used to transform *S. cerevisiae* strain 1260 to leucine prototrophy as described in Examples 2 and 4. Production of cleavable PA83 was evaluated from several transformants of strain 1260 and uncleavable PA83 was produced from transformant 9-1 in small-scale fermentations conducted in YEHDG medium as described in Examples 2 and 4. Cell-pellets corresponding to 10 OD₆₀₀ units were broken in the

presence of 0.5 g of 0.45 mm glass beads and 0.5 mL of breaking buffer (20 mM HEPES, pH 8.2, 5 mM EDTA, 1x "Complete" protease inhibitor cocktail (ROCHE DIAGNOSTICS, Mannheim, Germany) by continuous vortexing at high speed at 4° C for 10 minutes. Cellular debris and glass beads were collected by centrifugation in a microcentrifuge at 4° C for 10 minutes. The clarified supernatants were transferred to new tubes and assayed for total protein using the BCA assay (Pierce, Rockford, Illinois). Two and one half μ g of each sample was loaded onto a 4-12 % NUPAGE BIS TRIS gel and run in MOPS SDS running buffer (INVITROGEN, Carlsbad, CA). The gel was transferred to PVDF membrane (INVITROGEN, Carlsbad, CA) and Western blotted using Mab 86613M (BIODESIGN, Saco, ME) as primary antibody and goat anti-mouse-IgG peroxidase conjugate (PERKIN ELMER, Boston, MA) as secondary antibody. Detection was performed using CN/DAB peroxidase substrate (PIERCE, Rockford, IL). Purified recombinant *E. coli* PA83 (see Examples 2 and 4) was used as standard. No detection was obtained with a cell lysate containing the vector control. Cleavable PA83 was detected in all three yeast transformants tested and co-migrated with uncleavable PA83 produced in *S. cerevisiae*. Transformant 5C was chosen as one of the best producers of cleavable PA83.

Subsequently, production of uncleavable PA83 by yeast strain 9-1 and cleavable PA83 produced by strain 5-C, fermented in shake flasks in YEHDG medium, was assessed. Strain 5-C was also fermented in YEHDG in a culture tube. The tube fermentations were conducted as described in Examples 2 and 4. The shake-flask fermentations were conducted as described in Example 2, except that the galactose induction was conducted in 50 mL YEHDG medium in a 250-mL flask with inocula scaled-up proportionately. Cell lysates were prepared and evaluated by Western blot as described in Example 2. The results are shown in FIG. 14. Purified recombinant *E. coli* PA83 (lane 1) was used as standard. The additional protein detected below rPA83 is a degradation product that is sometimes observed. No detection was obtained with a cell lysate containing the vector control (lane 2). Production of uncleavable PA83 was greater than cleavable PA83 (compares lanes 3 and 4 to 5 and 6). Production of cleavable PA83 was greater in culture tube (5-mL volume) than in a shake flask (compare lanes 7 and 8 to 5 and 6).

EXAMPLE 11:

Fermentation and Purification of Internally-Expressed PA63

Frozen seed stock of yeast strain 8-3 (strain 1260 transformed with plasmid p63GAL10#2) was used for large-scale fermentation and purification. The vial of seed stock was thawed and 1.0 mL was used to inoculate a 250-mL Erlenmeyer flask containing 50 mL of a leucine-free selective medium (5X Leu⁻ medium. Bayne et al., 1988.) containing 4 % dextrose. The flask was incubated at 28° C, 250 rpm on a rotary shaker. After 24 hours (residual glucose 22.3 g/L), a culture volume of 11 mL was added to a 2-L flask containing 877 mL of the same medium. Again, the flask was incubated at 28° C and agitated at 250 rpm. After 24.5 hours (residual glucose 12.9 g/L), the contents of the 2-L flask were used to

inoculate a 20-L reactor containing a chemically defined medium (Oura, E., 1974) optimized for our strains. This medium contained 20 g/L glucose followed by 40 g/L galactose for induction. The reactor was operated at 28° C, 4.7 L/min, 15 psig, and 300 rpm. Under these conditions, dissolved oxygen levels were maintained at greater than 30 % of saturation. Cellular growth was monitored by glucose
5 consumption, optical density (A₆₀₀ nm, 1-cm cuvettes), dry cell weight, galactose utilization and ethanol production. Cultivation continued for 90 h reaching an OD₆₀₀ of 35 and a dry cell weight of 19.7 g/L.

The culture was harvested via hollow fiber tangential flow filtration (AMICON H5MP01-43 cartridge) using an AMICON DC-10 harvest skid (MILLIPORE, Billerica, MA). The permeate was discarded and the cells were concentrated down to 1.35 L. Cells were then diafiltered with PBS, and
10 collected by centrifugation at 8000 rpm, 4° C for 20 minutes using a Sorvall Evolution RC (SLA-3000 rotor). Cells were stored at -70° C.

To evaluate production of PA63 by strain 8-3 in large-scale fermentation, cell lysates were prepared from 10 OD₆₀₀ units of the harvested culture and evaluated as detailed in Examples 2 and 3. Production of PA63 from a small-scale culture tube fermentation (72 h, complex YEHDG medium) was
15 also assessed. The results of a Western blot are shown in FIG. 15. It can be seen that the protein produced from the large-scale fermentation, lanes 5 and 6, comigrated with PA63 produced in a tube fermentation, lanes 7, and 8 and with the control PA63 shown in lanes 1, 2, 11 and 12. It is apparent that the yield of PA63 from the large-scale fermentation is greater than that of the tube fermentation. The titer of PA63 from the large-scale fermentation was estimated to be 220 µg per mL and the % total
20 protein, 12 %, compared to 65 µg/mL and 8.0 % of the total protein for the tube fermentation (using the semi-quantitative Western method described in Example 3).

The quantitation of expression in the large-scale fermentation was confirmed by ELISA as described in Example 3. Volumetric titers of 360 and 80 µg per mL were determined for the large-scale and tube fermentations, respectively. The enhanced yields from the large-scale fermentation can
25 probably be attributed to both decoupling of cell growth from induction of PA63 expression, and selective pressure for plasmid maintenance.

The purification process for PA63 from yeast is presented in FIG. 16. Frozen yeast cells were thawed in a cold-water bath for several hours. The cells were resuspended in five times the volume of cold breaking buffer (0.2 M HEPES, pH 7.4, 2 mM MgCl₂, 0.5 mg/mL PEFABLOC (Roche Applied
30 Science, Indianapolis, IN), 1x "complete" EDTA free protease inhibitor mix (ROCHE APPLIED SCIENCE, Indianapolis, IN), 3.5 µg/mL pepstatin (ROCHE APPLIED SCIENCE, Indianapolis, IN), 20 mM benzamidine (SIGMA, St. Louis, MO), and 1 µL benzonase (EM INDUSTRIES, Hawthorne, NY) per gram of cells.

The yeast cells were ruptured by 4 sequential passes through a microfluidizer apparatus (Model
35 110S, MICROFLUIDICS, Newton, MA) at a pressure of 18,000 psi. The temperature of the lysate was

maintained at <15° C throughout the procedure by cooling between passes in an ice water bath. The pH of the lysate remained at 7.4 throughout the procedure.

Following the cell breakage, EDTA and EGTA were added to the lysate at final concentrations of 5 mM each. Insoluble material was removed from the lysate by low speed centrifugation (10,000 x g) in a Sorvall RC-5C refrigerated centrifuge with a GS3 rotor for 20 minutes at 4° C.

The supernatant of the low speed spin was clarified by filtration through a series of 47 mm diameter filters (AP15, AP25, and 5 µM (DURAPORE White Hydrophilic Disc SVLP, MILLIPORE, Billerica, MA). The clarified lysate was divided into aliquots and stored at -70° C.

Preliminary attempts were made to purify PA63 under non-denaturing conditions using a variety of column chemistries. None of the chemistries were able to resolve a single defined PA63 peak. In all cases investigated, the PA63 bled slowly off of the columns across the entire elution gradient. We believe this may be due in part to the active nature of PA63, which is designed to self-assemble into heptamers. This activity may be responsible for the formation of multimeric PA63 structures or PA63-yeast protein aggregates in the lysate, which prevents isolation of a single enriched PA63 fraction under non-denaturing conditions.

Therefore, further processing of the lysate was performed under denaturing conditions because the PA63 was not amenable to purification under non-denaturing conditions. Non-ionic denaturants are preferred because ionic denaturants would not be compatible with the chromatography resins employed in subsequent steps. Specifically, the lysate was made 6 M in urea and was applied to a 1 L POROS 50HS column (APPLIED BIOSYSTEMS, Foster City, CA) equilibrated in 6 M urea/20 mM HEPES, pH 7.3 at a flow rate of 35 mL/min using a WATERS 650 Prep system with a Linear UV/VIS detector (WATERS, Milford, MA). Proteins were eluted from the column using a 0-1 M NaCl gradient in 6 M urea/HEPES buffer.

Total protein in column fractions was determined using a commercial bicinchoninic acid (BCA) assay (PIERCE CHEMICAL, Rockford, IL) and SDS-PAGE with Western blotting. The PA63-containing fractions were pooled and concentrated over a 10-kDa tangential flow membrane (PREPSCALE TFF, MILLIPORE, Billerica, MA). The concentrated pool was diluted with 6 M urea-containing 20 mM HEPES buffer and then applied to a 50 mL SOURCE Q (AMERSHAM BIOSCIENCES, Piscataway, NJ) anion exchange column equilibrated in 6 M urea/HEPES and again purified with a 0-1 M NaCl gradient in the presence of 6 M urea. The PA63 containing fractions were pooled and dialyzed extensively against 20 mM HEPES, pH 7.3 containing 0.15 M NaCl and 16 µM CaCl₂. The product of the Source Q step was >90 % pure PA63 by SDS-PAGE analysis. The pooled product was filtered at 0.2 µm and stored in aliquots at -70° C.

FIG. 17 presents the results of SDS-PAGE analysis by Coomassie staining and Western blotting for the final product and intermediate process retains. Table 2 summarizes the material balance of protein through the process.

Table 2. Material balance and protein recovery at research-scale

Process Retain	Volume (mL)	Protein Concentration ($\mu\text{g/mL}$)	Total Protein (mg)
Clarified Lysate	320	13200	4224
50HS Pool	420	1000	420
Source Q Pool (product)	240	589	141

EXAMPLE 12:

Immunogenicity of Recombinant PA63

5 An aspect of this invention indicates that the purified yeast recombinant PA63 protein (purified as described in Example 11) can induce in mammals a robust immune response that is cross-reactive to PA83 (the precursor form of PA63). Mice (five per group) were vaccinated on days 0, 7 and 21 with antigens formulated on Merck aluminum adjuvant (MAA), *E. coli* recombinant PA83, or yeast recombinant PA63. One group of mice received MAA alone. Mice were bled on day 29 to measure
 10 antibody titers to recombinant antigens (Table 3). Titers were measured by coating 96 well plates with 0.1 $\mu\text{g/well}$ of either rPA63 or rPA83. The secondary antibody was goat anti-mouse IgG-HRP (SOUTHERN BIOTECHNOLOGY, Birmingham, AL) used at 1:6000 dilution. The plate was developed with TMB (PIERCE CHEMICALS, Rockford, IL) and read at OD₄₅₀.

15 Table 3. Mouse end point titers to recombinant proteins, GMT of five mice per group

<u>Group</u>	<u>GMT to rPA63</u>	<u>GMT to rPA83</u>
50 μg rPA83	1,350,519	3,103,372
50 μg rPA63	588,128	588,128
20 MAA	<100	<100

Rabbits (ten per group) were vaccinated on days 0, 1 month, 2 months, and 3 months with recombinant yeast PA63 formulated on MAA. One group of rabbits received adjuvant alone, and one group of five rabbits received two 125 μL doses of the currently licensed vaccine Anthrax Vaccine
 25 Adsorbed (AVA) (BIOPORT CORP., Lansing, MI). All rabbits were bled at 2 weeks post last vaccination to measure antibody titers to recombinant PA83 (Table 4). Titers were measured as described above but the secondary antibody was goat anti-rabbit IgG-HRP (SOUTHERN BIOTECHNOLOGY, Birmingham, AL) used at 1:6000.

Table 4. Rabbit end point titers to recombinant PA83, GMT of ten rabbits per group, except for the AVA group in which there were five rabbits

	<u>Group</u>	<u>GMT to rPA83</u>
5	0.5 μ g rPA63	166,491
	5.0 μ g rPA63	455,795
	50 μ g rPA63	649,507
	AVA	799,882
	MAA	<100

10

Monkeys (three per group) were vaccinated on days 0, 2 months, and 6 months with recombinant yeast PA63 formulated on MAA. One group of monkeys received adjuvant alone, and one group of monkeys received three human doses (500 μ L) of the currently licensed AVA vaccine. Monkeys were bled at two weeks post dose three to measure antibody titers to recombinant PA83 (Table 5). End point titers were measured as described above except that the secondary antibody was goat anti-monkey IgG-HRP (SOUTHERN BIOTECHNOLOGY, Birmingham, AL) used at 1:5000 dilution.

15

Table 5. Monkey end point titers to recombinant PA83, GMT of three monkeys per group

20	<u>Group</u>	<u>GMT to rPA83</u>
	5 μ g rPA63	63,496
	50 μ g rPA63	100,793
	AVA	100,793
	MAA	1,000

25

EXAMPLE 13:

Protection against exposure to B. anthracis by yeast recombinant PA63

The immune response induced by the vaccine formulated with recombinant PA63 produced in yeast confers protection against a lethal aerosol exposure of the deadly B. anthracis. Rabbits were vaccinated as described above and exposed to a lethal aerosol challenge of B. anthracis Ames strain. Spores of the B. anthracis Ames strain were grown in Leighton and Doi medium (Leighton, T. J. and Doi, R. H., 1971), purified by centrifugation through 58% HYPACUE-76 (NYCODED, INC., Princeton, NJ) and resuspended in sterile water containing 1% phenol, and stored at 2-8° C until used. Immediately before aerosol challenge, the spores were diluted in sterile water for injection to 2.2-2.8 X 10⁹ CFU/ml and heat-shocked at 60° C for 45 min. After respiratory minute volumes were measured, animals were exposed in a head-only chamber to a spore aerosol generated by a three-jet collision

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nebulizer. For each animal, the concentration of spores in the aerosol inhaled dose (expressed as LD₅₀) was determined by plating a sample from an all glass impinger onto tryptic soy agar plates (DIFCO, Detroit, MI). Animals were observed for a period of two weeks and deaths from anthrax recorded (Table 6).

5

Table 6. Rabbit survival data after lethal challenge of *B. anthracis* Ames strain

	<u>Group</u>	<u>% Mortality</u>	<u>Spore Dose (LD₅₀)</u>
	0.5 µg rPA63, 10 animals	50	733
10	5 µg rPA63, 9 animals	11	673
	50 µg rPA63, 10 animals	40	611
	AVA, 5 animals	0	591
15	MAA, 10 animals	100	624

Monkeys were vaccinated as described above, and given a booster dose of either 5 µg or 50 µg or MAA alone, and exposed to a lethal aerosol challenge of *B. anthracis* Ames strain, as described above, two weeks after the booster injection. The challenge dose was approximately 1000 LD₅₀ per animal. Animals were observed for a period of four weeks and deaths from anthrax recorded (Table 7).

20

Table 7. Monkey survival data after lethal challenge of *B. anthracis* Ames strain

	<u>Group (groups of 3)</u>	<u>% Mortality</u>
25	5 µg rPA63	0
	50 µg rPA63	30
	AVA	30
	MAA	100

30

The results from these single monkey and rabbit protection studies indicate that yeast-expressed rPA63 is a very promising candidate for a component of an anthrax vaccine. The data also suggest that rPA63 has the potential to be as effective as AVA, the current vaccine.

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WHAT IS CLAIMED IS:

1. A method for the production of recombinant Bacillus anthracis Protective Antigen protein, comprising:
 - 5 a) providing an expression vector including a polynucleotide comprising a nucleotide sequence encoding a Bacillus anthracis Protective Antigen protein, said nucleotide sequence being codon-optimized for expression in yeast,
 - b) transforming a yeast with the vector,
 - c) fermenting the transformed yeast under conditions appropriate for the expression of
 - 10 the Protective Antigen protein, and
 - d) isolating the Protective Antigen protein.
2. The method according to Claim 1 wherein the Protective Antigen protein is PA63.
- 15 3. The method according to Claim 1 wherein the Protective Antigen protein is PA83.
4. The method according to Claim wherein the Protective Antigen protein encompasses a portion of the protein that, upon introduction into a patient, stimulates an immunoprotective response against Bacillus anthracis.
- 20 5. The method according to Claim 1 wherein the yeast is selected from the group consisting of Pichia pastoris, Hansenula sp., Candidia sp., Saccharomyces cerevisiae, Saccharomyces carlsbergensis and Kluyveromyces lactis.
- 25 6. The process according to Claim 1 wherein the yeast host comprises at least one genetic alteration selected from the group comprising alterations to prevent proteolysis, improve removal of the secretory leader and to promote proper glycosylation.
7. The process according to Claim 2 wherein the PA83 protein is modified to prevent
- 30 protease cleavage of the PA83 at the cleavage site recognized by furin.
8. A synthetic polynucleotide comprising a sequence encoding a Bacillus anthracis Protective Antigen protein, the amino acid sequence of said Protective Antigen protein maintaining wild-type Protective Antigen protein immunogenicity, wherein said polynucleotide sequence encoding the
- 35 Protective Antigen protein is comprised of codons optimal for expression in a yeast host.

9. A polynucleotide according to Claim 8 wherein the protein is selected from the group consisting of a PA63 protein having a wild type amino acid sequence, a PA83 protein having a wild type amino acid sequence and a PA83 protein modified to prevent protease cleavage of the PA83 at the cleavage site recognized by furin and/or other mammalian processing enzymes.

5

10. A polynucleotide according to Claim 8 which is DNA.

11. A polynucleotide according to Claim 8 which comprises a sequence selected from the group consisting of SEQ ID NOs: 49, 51, 55 and 57.

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12. A yeast expression vector comprising a polynucleotide according to Claim 8.

13. The vector of Claim 12 wherein the polynucleotide is operably associated with at least one regulatory sequence recognized by a yeast host cell.

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14. The vector according to Claim 13 wherein the regulatory sequences comprise a GAL10 promoter and a yeast transcriptional terminator.

15. The vector according to Claim 13 wherein the regulatory sequences comprise a GAL1 promoter and a yeast transcriptional terminator.

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16. A yeast host cell harboring a vector according to Claim 12.

17. A yeast host cell harboring a vector according selected from the group consisting of the vectors of Claim 14 and Claim 15.

25

18. A vaccine comprising a recombinant Bacillus anthracis Protective Antigen protein wherein said Protective Antigen protein was produced in yeast by expression of a yeast codon-optimized nucleotide sequence.

30

19. A method of vaccination of a patient against Bacillus anthracis comprising administering of a vaccine of Claim 18 to the patient.

20. The method of Claim 19 wherein the patient is a human.

35

21. The method of Claim 19 wherein the patient is selected from the group consisting of domesticated animals and livestock.

22. The method of Claim 19 wherein the vaccine is administered by injection.

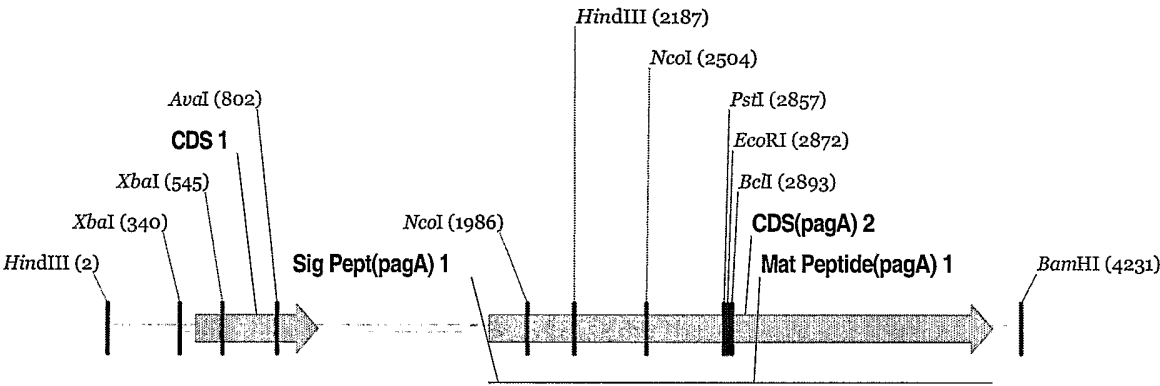
23. The method of Claim 1 wherein the Protective Antigen protein is secreted from the yeast.

24. The method of Claim 1 wherein the Protective Antigen protein is isolated from the cytoplasm of the yeast.

25. The expression vector of Claim 12 wherein a polynucleotide encoding a secretion signal recognized by a yeast is operably linked to the polynucleotide encoding the Protective Antigen protein.

26. A process of isolating the 63 kilodalton form of Protective Antigen from a culture of yeast cells expressing a recombinant PA63 gene comprising,
disrupting the yeast cells to create a suspension and clarifying the suspension,
adding a denaturant to the suspension,
applying the suspension to a column containing a cation exchange resin in a denaturing buffer,
eluting the PA63 from the cation exchange resin with a salt gradient in the denaturing buffer,
applying the PA63 to a column containing an anion exchange resin in a denaturing buffer,
eluting the PA63 from the anion exchange resin with a salt gradient in the denaturing buffer, and
dialyzing the PA63 to remove the denaturant.

27. The process of Claim 26 wherein the denaturant and denaturing buffer contains a sufficient amount of urea to denature the PA63.



BACPAG
4235 bp

FIGURE 1A

Bacterial sequence (PA63)

agtacaagtgctggacctacgggttccagaccgtgacaatgatggaatccctga
ttcattagaggttagaaggatatacggttgatgtcaaaaataaaagaacttttc
tttcaccatggattttctaataattcatgaaaagaaaggattaaccaaatataaa
tcattctcctgaaaaatggagcacggccttctgatccgtacagtgatttcgaaaa
ggttacaggacggattgataagaatgtatcaccagaggcaagacaccccccttg
tggcagcttatccgattgtacatgtagatatggagaatattattctctcaaaa
aatgaggatcaatccacacagaatactgatagtgaacgagacaataagtaa
aaatacttctacaagtaggacacatactagtgaagtacatggaaatgcagaag
tgcattgcgtcgttctttgatattgggtgggagtgtatctgcaggatttagtaat
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aacttgggctgaaacaatgggttttaataaccgctgatacagcaagattaaatg
ccaatattagatatgtaaatactgggacggctccaatctacaacgtgttacca
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ggaaaaccaattaagtcaaatacttgcacctaataattattatccttctaaaa
acttggcgccaatcgcattaaatgcacaagacgatttcagttctactccaatt
acaatgaattacaatcaatttcttgagttagaaaaaacgaaacaattaagatt
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aacttacaatatcaagggaagacataaccgaatttgatttttaatttcgatca
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tatatactgtattagataaaatcaaattaaatgcaaaaatgaatattttaata
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gaaattgaagatactgaagggttaagaagttataaatgacagatatgatat
gttgaatatatttctagtttacggcaagatggaaaaacatttatagattttaaaa
aatataatgataaattaccgttatatatataagtaatcccaattataaggtaaat
gtatatgctgttactaaagaaaacactattattaatcctagtgagaatgggga
tactagtaccaacgggatcaagaaaattttaatcttttctaaaaaaggctatg
agatagga

Translation

STSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYK
SSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSK
NEDQSTQNTDSETRTISKNTSTSRHTTSEVHGNAEVHASFFDIGGSVSAGFSN
FIGSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYN
VLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYP SKNLAPIALNAQDDFSS
TPITMNYNQFLELEKTKQLRLDTDQVYGNIAITYNFENGRVRVDTGSNWSEVLP
QIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNE
PNGNLQYQGDITEFDNFNDQQT SQNIKNQLAELNATNIYTVLDKIKLNAKMN
ILIRDKRFHYDRNNI AVGADES VVKEAHREVIN S STEGLLLNIDKDIRKILSG
YIVEIEDTEGLKEVIN DRYDMLNISSLRQDGKTFIDFKKYNDKLPYIISPNY
KVN VYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYEIG

FIGURE 1B

PA63 Yeast codon optimized

TCCACCTCCGCTGGTCCAACCTGTTCCAGACAGAGACAACGACGGTATTCCAGA
CTCCTTGGAAGTCGAAGGTTACACCGTCGACGTCAAGAACAAGAGAACCTTCT
TGTCTCCATGGATCTCCAACATTACGAAAAAGGGTTTGACCAAGTACAAG
TCTTCCCCAGAAAAGTGGTCTACTGCTTCCGACCCATACTCCGACTTCGAAAA
GGTCACCGGTAGAATCGACAAGAACGTCTCCCCAGAAAGCTAGACACCCATTGG
TTGCTGCTTACCCAATTGTCCACGTTGACATGGAAAAACATCATTTTTGTCCAAG
AACGAAGACCAATCCACCCAAAACACGGACTCCGAAACCAGAACTATCTCTAA
GAACACCTCCACTTCTAGAACCCACACTTCCGAAGTCCACGGTAACGCTGAAG
TTCACGCTTCTTTCTTCGACATTGGTGGTTCCGTCTCTGCTGGTTTTCTCCAAC
TCCAACCTCCTCCACCGTCGCTATCGACCACTCTTTGTCTTGGCTGGTGAAAG
AACTTGCGCTGAAACCATGGGTTTGAACACTGCTGACACCGCTAGATTGAACG
CTAACATTAGATACGTCAACACTGGTACCGCTCCAATCTACAACGTCTTGCCA
ACCACCTCCTTGGTCTTGGGTAAGAACCACCTTGGCTACTATCAAGGCTAA
GGAAAACCAATTGTCCCAAATCTTGGCTCCAAACAACACTACTACCCATCCAAGA
ACTTGGCTCCAATCGCTTTGAACGCTCAAGACGACTTCTCCTCTACTCCAATC
ACCATGAACTACAACCAATTCTTGGAAATTGGAAAAGACTAAGCAATTGCGTTT
GGACACCGACCAAGTTTACGGTAACATTGCTACTTACAACCTTCGAAAACGGTA
GAGTCAGAGTCGACACCGGTTCCAACCTGGTCTGAAGTCTTGCCACAAATCCAA
GAAACCACCGCTAGAATCATCTTCAACGGTAAGGACTTGAACCTTGGTTGAAAG
AAGAATTGCTGCTGTCAACCCATCCGACCCATTGGAAACCACCAAGCCAGACA
TGACCTTGAAGGAAGCTTTGAAGATCGCTTTCGGTTTCAACGAACCAAACGGT
AACTTGCAATACCAAGGTAAGGACATCACCGAATTGCACTTCAACTTCGACCA
ACAAACCTCTCAAAACATCAAGAACCAATTGGCTGAATTGAACGCTACCAACA
TTTACACTGTTTTTGGACAAGATCAAGTTGAACGCCAAGATGAACATCTTGATC
AGAGACAAGAGATTCCACTACGACAGAAACAACATTGCTGTCGGTGCTGACGA
ATCCGTTGTCAAGGAAGCCACAGAGAAGTCATCAACTCCTCCACCGAAGGTT
TGTTGTTGAACATCGACAAGGACATCAGAAAGATCTTGTCGGTTACATCGTC
GAAATTGAAGACACCGAAGGTTTGAAGGAAGTCATCAACGACAGATACGACAT
GTTGAACATTTCTCTTTTGAAGACAAGACGGTAAGACCTTCATCGACTTCAAGA
AGTACAACGACAAGTTGCCATTGTACATTTCCAACCCAACTACAAGGTCAAC
GTTTACGCTGTCACTAAGGAAAACACCATCATCAACCCATCCGAAAACGGTGA
CACTTCCACCAACGGTATCAAGAAGATTTTGATCTTCTCTAAGAAGGGTTACG
AAATTGGT

Translation

STSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYK
SSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSK
NEDQSTQNTDSETRTISKNTSTSRHTTSEVHGNAEVHASFFDIGGSVSAGFSN
SNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLP
TTSLVLGKNQTLATIKAKENQLSQILAPNNYYP SKNLAPIALNAQDDFSSTPI
TMNYNQFLELEKTKQLRLD TDQVYGN IATYNF ENGRVRVDTGSNWSEVL PQIQ
ETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNG
NLQYQGKDI TEFDNF DQOTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILI
RDKRFHYDRNNIAVGADES VVKEAHREVINSSTEGLLLNIDKDIRKILSGYIV
EIEDTEGLKEVIN DRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVN
VYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYEIG

FIGURE 2

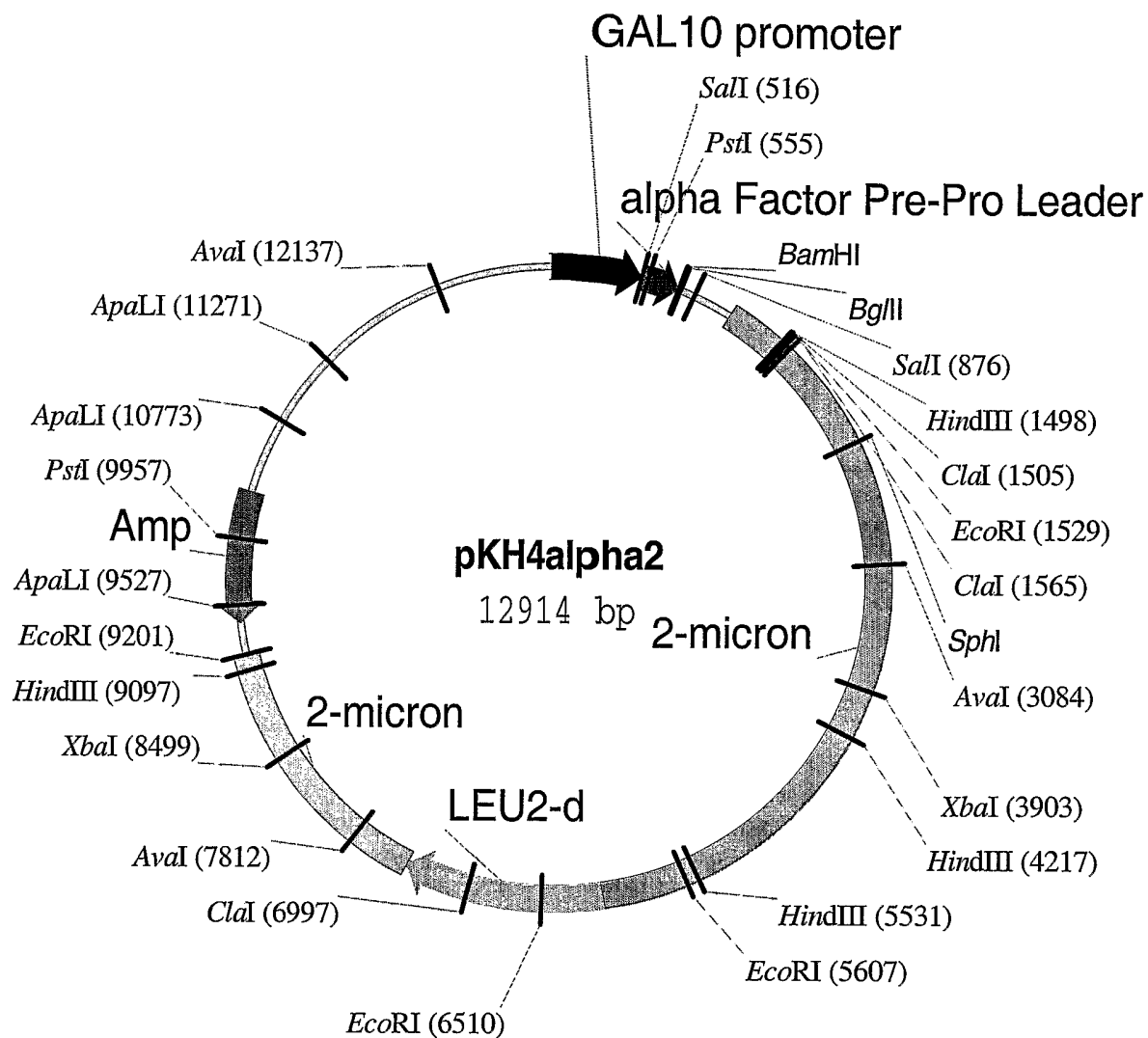


FIGURE 3A

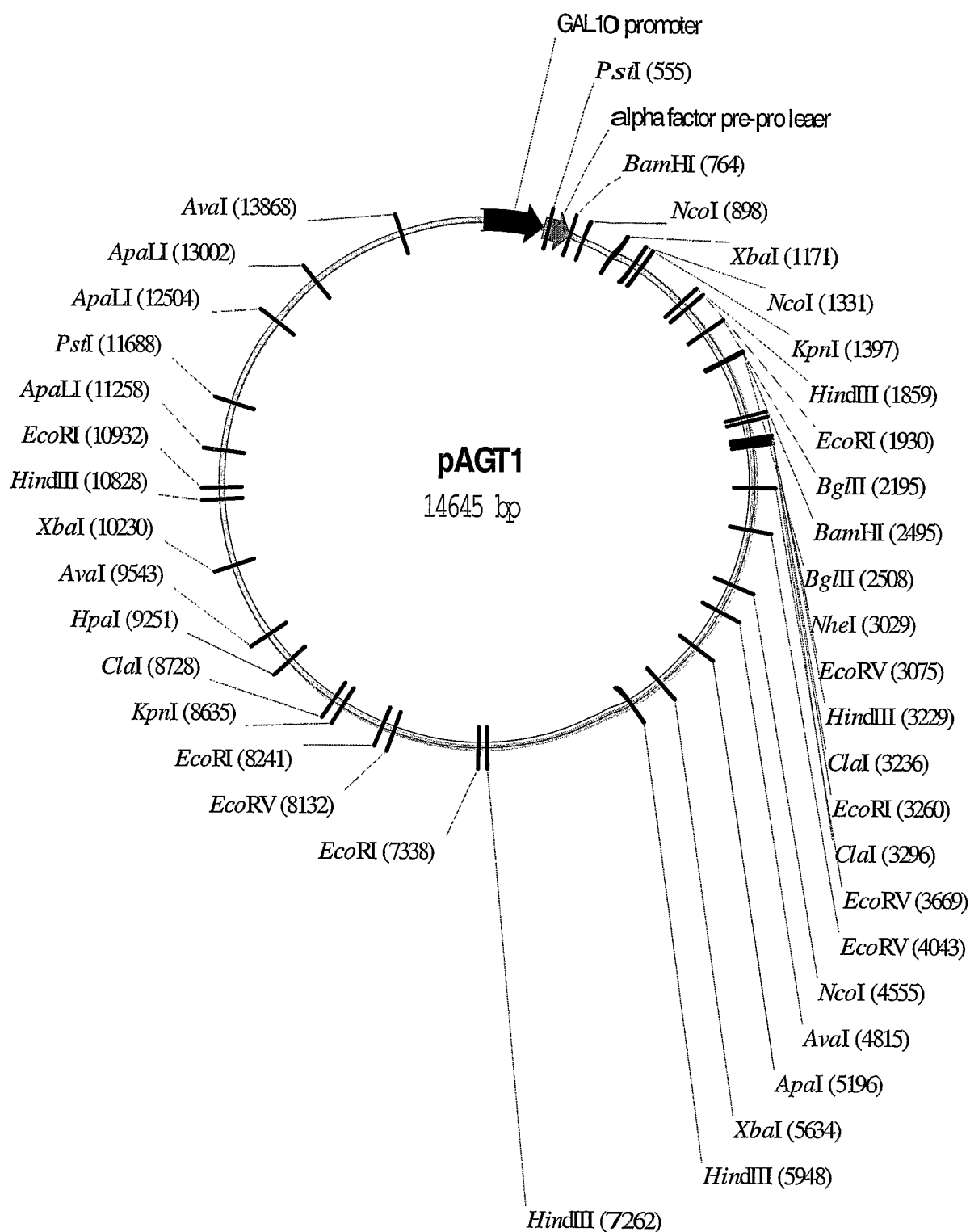


FIGURE 3B

pGAL110

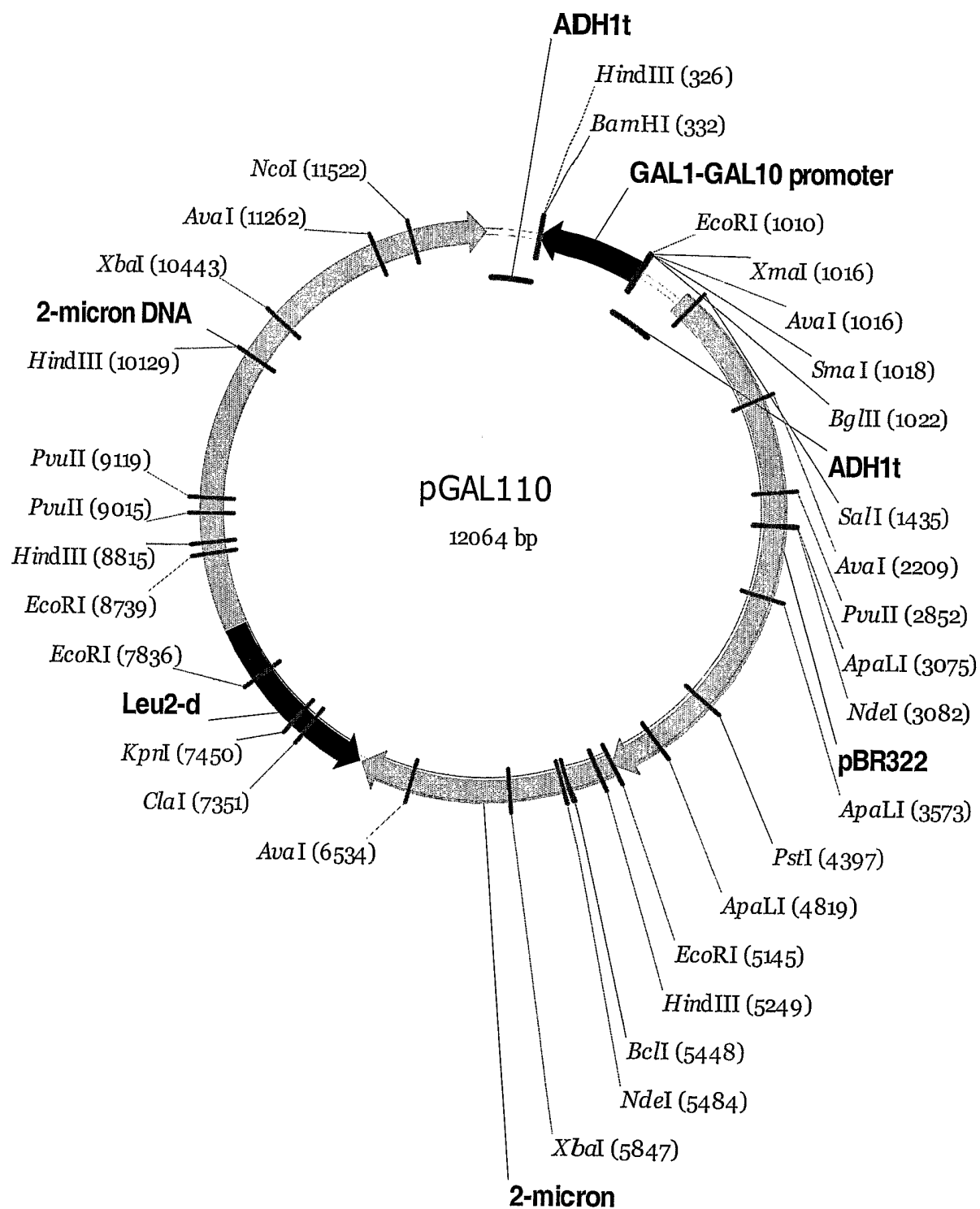


FIGURE 4

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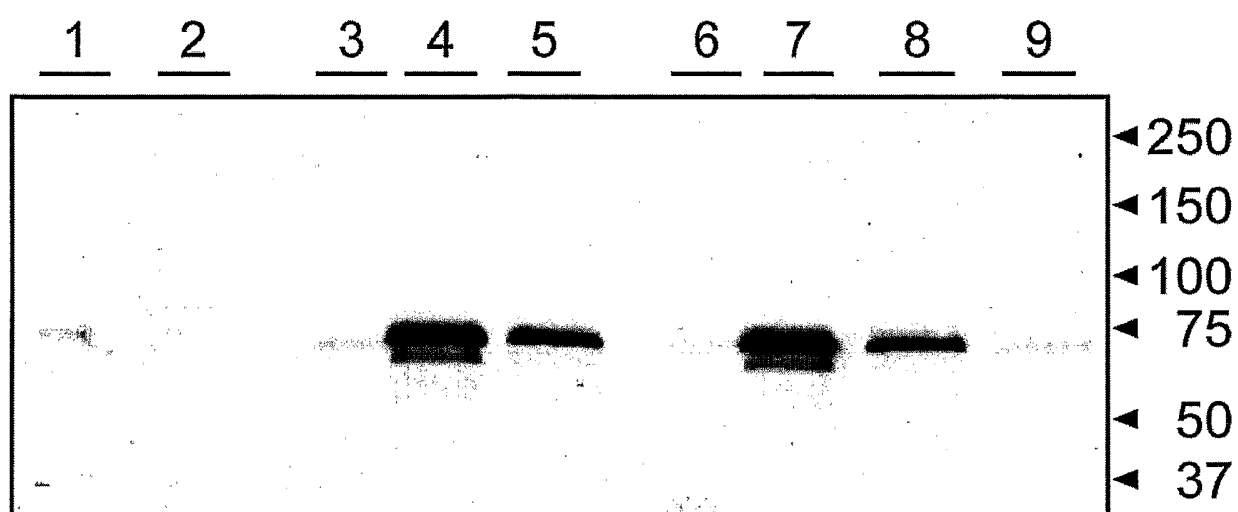


FIGURE 5

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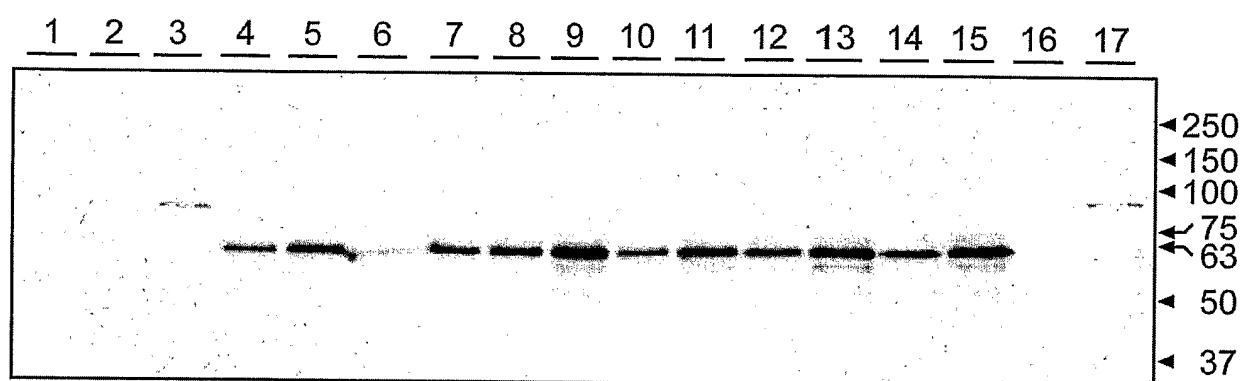


FIGURE 6

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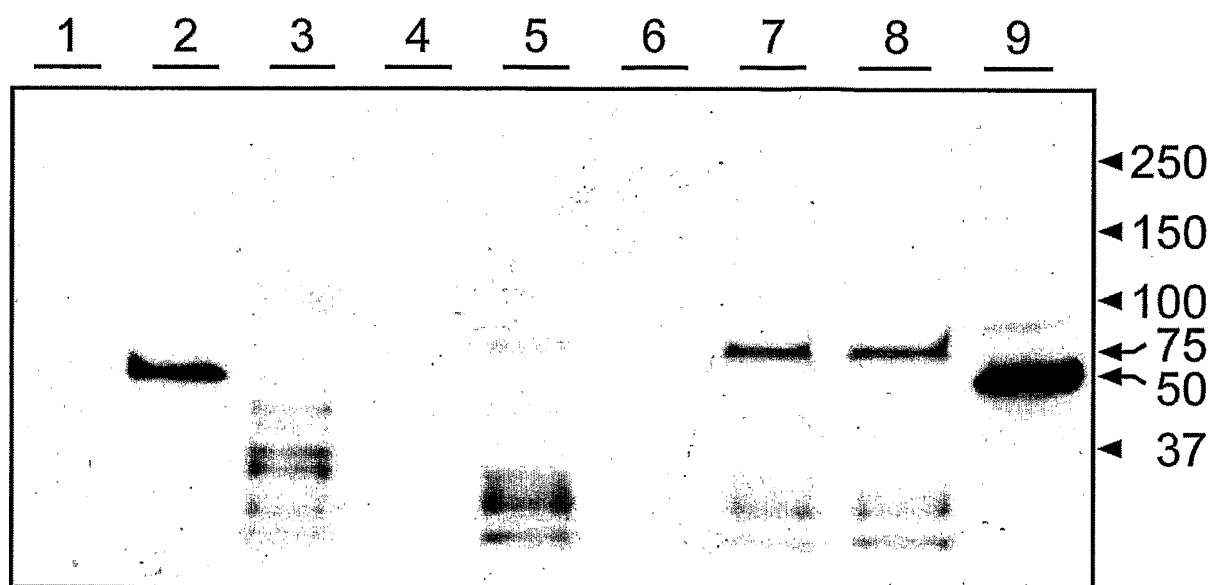


FIGURE 7

gaagttaaacaggagaaccggttattaaatgaatcagaatcaagttcccaggggttactag
gatactattttagtgatttgaattttcaagcacccatgggtgggtacctcttctactacagg
ggatttatctattcctagttctgagttagaaaatattccatcggaaaaccaatattttcaa
tctgctatttgggtcaggatttatcaaagttaagaagagtgatgaatatacatatttgctactt
ccgctgataatcatgtaacaatgtgggttagatgaccaagaagtgattaataaagcttctaa
ttctaacaaaatcagattagaaaaaggaagattatatcaaataaaaattcaatatcaacga
gaaaatcctactgaaaaaggattggatttcaagttgtactggaccgatttctcaaaaataaaa
aagaagtgatttctagtgataacttacaattgccagaattaaaaaataaatcttcgaactc
aagaaaaaagcgaagtacaagtgtgacctacgggttcagaccgtgacaatgatggaatc
cctgattcattagaggtagaaggatatacgggttgatgtcaaaaataaaagaacttttcttt
caccatggatttctaataattcatgaaaagaaaggattaaccaaatataaatcatctcctga
aaaatggagcacggcttctgatccgtacagtgatttgcgaaaaggttacaggacggattgat
aagaatgtatcaccagaggcaagacaccccccttggtggcagcttatccgattgtacatgtag
atatggagaatattattctctcaaaaaatgaggatcaatccacacagaatactgatagtga
aacgagaacaataagtaaaaaatacttctacaagtaggacacatactagtgaagtacatgga
aatgcagaagtgcattgcgtcgttctttgatattgggtgggagtgtatctgcaggatttagta
attcgaattcaagtacgggtcgcaattgatcattcactatctctagcaggggaaagaacttg
ggctgaaacaatgggtttaataaccgctgatacagcaagattaaatgccaatattagatat
gtaataactgggacggctccaatctacaacgtgttaccaacgacttcgttagtgtaggaa
aaaatcaaacactcgcgacaattaaagctaaggaaaaccaattaagtcaaatacttgcacc
taataattattatccttctaaaaacttggcgccaatcgcattaaattgcacaagacgatttc
agttctactccaattacaatgaattacaatcaatttcttgagttagaaaaaacgaaacaat
taagattagatacggatcaagtatatgggaatatagcaacatacaatttttgaaaatggaag
agtgaggggtggatacaggctcgaactggagtgaagtgttaccgcaaatcaagaaacaact
gcacgtatcatttttaattggaaaagattttaaattctggtagaaaaggcggatagcggcgggtta
atcctagtgtatccattagaaacgactaaaccggatatgacattaaagaagccctttaaata
agcatttggatttaacgaaccgaatggaaacttacaatatcaagggaagacataaccgaa
tttgatttttaatttcgatcaacaaacatctcaaaaatatcaagaatcagtttagcggaaattaa
acgcaactaacatatatactgtattagataaaaatcaaattaaatgcaaaaat
gaatatttttaataagagataaacgtttttcattatgatagaaataacatagcagttggggcg
gatgagtcagtagttaaggaggctcatagagaagtaattaattcgtcaacagaggggattat
tgttaaatattgataaggatataagaaaaatattatcagggttataattgtagaaattgaaga
tactgaagggcttaagaagttataaatgacagatatgatattgtgaatatttctagttta
cggcaagatggaaaaacattttatagatttttaaaaaatataatgataaattaccgttatata
taagtaatcccaattataaggtaaatgtatatgctgttactaaagaaaacactattattaa
tcctagtgagaatggggatactagtagccaacgggatcaagaaaattttaatcttttctaaa
aaaggctatgagatagga

FIGURE 8A

Translation with Domain 4 underlined

1	EVKQENRLLN	ESESSSQGLL	GYFSDLNFQ	APMVVTSSTT	GDLSIPSSEL
51	ENIPSENQYF	QSAIWSGFIK	VKKSDEYTFA	TSADNHVTMW	VDDQEVINKA
101	SNSNKIRLEK	GRLYQIKIQY	QRENPTKGL	DFKLYWTD SQ	NKKEVISSDN
151	LQLPELKQKS	SNSRKKRSTS	AGPTVPDRDN	DGIPDSLEVE	GYTVDVKNKR
201	TFLSPWISNI	HEKKGLTKYK	SSPEKWSTAS	DPYSDFEKVT	GRIDKNVSPE
251	ARHPLVAAYP	IVHVDMENII	LSKNEDQSTQ	NTDSETRTIS	KNTSTSRTH T
301	SEVHGNAEVH	ASFFDIGGSV	SAGFSNSNSS	TVAIDHSLSL	AGERTWAETM
351	GLNTADTARL	NANIRYVNTG	TAPIYNVLPT	TSLVLGKNQT	LATIKAKENQ
401	LSQILAPNNY	YPSKNLAPIA	LNAQDDFSST	PITMNYNQFL	ELEKTKQLRL
451	DTDQVYGNIA	TYNFENGRVR	VDTGSNWSEV	LPQIQETTAR	IIFNGKDLNL
501	VERRIAAVNP	SDPLETTKPD	MTLKEALKIA	FGFNEPNGNL	QYQGKDITEF
551	DFNFDQQTSQ	NIKNQLAELN	ATNIYTVLDK	IKLNAKMNIL	IRDKRFHYDR
601	NNIAVGADES	VVKEAHREVI	NSSTEGLLL N	IDKDIRKILS	GYIVEIEDTE
651	GLKEVINDRY	DMLNISSLRQ	DGKTFFIDFKK	YNDKLPLYIS	NPNYKVN VYA
701	VTKENTIINP	SENGDTSTNG	IKKILIFS KK	GYEIG	

FIGURE 8B

Domain 4 - Yeast codon optimized DNA sequence without bacterial signal

ttccactacgacagaaacaacattgctgtcgggtgctgacgaatccgttgt caaggaagccc
acagagaagtcatcaactcctccaccgaagggtttgttggtgaacatcgac aaggacatcag
aaagatccttgtccggttacatcgtcgaaattgaagacaccgaagggtttga aggaagtcatc
aacgacagatacgacatggtgaacatttcctctttgagacaagacggtaa gaccttcacg
acttcaagaagtacaacgacaagttgccattgtacatttccaacccaaac tacaagggtcaa
cgtttacgctgtcactaaggaaaacaccatcatcaacccatccgaaaacg gtagacacttcc
accaacgggtatcaagaagattttgatcttctctaagaagggttacgaaat tgggt

Domain 4- Translated protein without signal sequence

FHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIED
TEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVA
TKENTIINPSENGDTSTNGIKKILIFSKKGYEIG

DNA sequence and amino acid translation product of yeast codon-optimized *B. anthracis* PA83 gene

DNA sequence

1	GAAGTTAAGC	AAGAAAAACAG	ATTGTTGAAC	GAATCTGAAT	CCTCTTCCCA	AGGTTTGTTC
	CTTCAATTTCG	TTCTTTTGTC	TAACAACTTG	CTTAGACTTA	GGAGAAGGGT	TCCAAACAAC
61	GGTTACTACT	TCTCCGACTT	GAACTTCCAA	GCTCCAATGG	TCGTCACCTC	CTCTACTACC
	CCAATGATGA	AGAGGCTGAA	CTTGAAGGTT	CGAGGTTACC	AGCAGTGGAG	GAGATGATGG
121	GGTGACTTGT	CCATCCCATC	CTCCGAATTA	GAGAACATCC	CATCCGAAAA	CCAATACTTC
	CCACTGAACA	GGTAGGGTAG	GAGGCTTAAT	CTCTTGTAAG	GTAGGCTTTT	GGTTATGAAG
181	CAATCCGCTA	TCTGGTCCGG	CTTCATCAAG	GTCAAGAAGT	CCGACGAATA	CACTTTCGCT
	GTTAGGCGAT	AGACCAGGCC	GAAGTAGTTC	CAGTTCCTCA	GGCTGCCTAT	GTGAAAGCGA
241	ACCTCCGCTG	ACAACCACGT	TACTATGTGG	GTCGACGACC	AAGAAGTCAT	CAACAAGGCT
	TGGAGGCGAC	TGTTGGTGCA	ATGATACACC	CAGCTGCTGG	TTCTTCAGTA	GTGTTCCTCA
301	TCCAATCCCA	ACAAGATCAG	ATTGGAAGAG	GGTAGATTGT	ACCAAATTAA	GATCCAATAC
	AGGTTGAGGT	TGTTCTAGTC	TAACCTTTTC	CCATCTAACA	TGGTTTAATT	CTAGGTTATG
361	CAAAGAGAAA	ACCCAACCGA	AAAGGGTTTG	GACTTCAAGT	TGTACTGGAC	CGACTCCCCA
	GTTTCTCTTT	TGGGTTGGCT	TTTCCCAAAC	CTGAAGTTCA	ACATGACCTG	GCTGAGGGTT
421	AACAAGAAGG	AAGTCATCTC	CTCTGACAAC	TTGCAATTGC	CAGAATTGAA	GCAAAAGTCC
	TTGTTCTTCC	TTCAGTAGAG	GAGACTGTTG	AACGTTAACG	GTCTTAACCT	CGTTTTTCAGG
481	TCCAATCCCA	GAAAGAAGAG	ATCCACCTCC	GCTGGTCCAA	CTGTTCAGTA	CAGAGACAAC
	AGGTTGAGGT	CTTCTTCTTT	CAGGTGGAGG	CGACCAGGTT	GACAAGGTC	GTCTCTGTTG
541	GACGGTTATC	CAGACTCCCT	GGAAGTCGAA	GGTTACACCG	TCGACGTCAA	GAACAAGAGA
	CTGCCATAAG	GTCTGAGGAA	CCTTCAGCTT	CCAATGTGGC	AGCTGCAGTT	CTTGTTCTCT
601	ACCTTCTTGT	CTCCATGGAT	CTCCAACATT	CACGAAAAGA	AGGGTTTGAC	CAAGTACAAG
	TGGAAGAACA	GAGGTACCTA	GAGGTTGTAA	GTGCTTTTCT	TCCCAAACCT	GTTTCATGTT
661	TCTTCCCCAG	AAAAGTGGTC	TACTGCTTCC	GACCCATACT	CCGACTTCGA	AAAGGTCACC
	AGAAGGGGTC	TTTTCACCAG	ATGACGAAGG	CTGGGTATGA	GGCTGAAGCT	TTTCCAGTGG
721	GGTAGAATCG	ACAAGAACGT	CTCCCCAGAA	GCTAGACACC	CATTGGTTGC	TGCTTACCCA
	CCATCTTATC	TGTTCTTGCA	GAGGGGTCTT	CGATCTGTGG	GTAACCAACG	ACGAATGGGT
781	ATTGTCCACG	TTGACATGGA	AAACATCATT	TTGTCCAAGA	ACGAAGACCA	ATCCACCCAA
	TAACAGGTGC	AACTGTACCT	TTTGTAGTAA	AACAGGTTCT	TGCTTCTGGT	TAGGTGGGTT
841	AACACGGACT	CCGAAACCAG	AACTATCTCT	AAGAACACCT	CCACTTCTAG	AACCCACACT
	TTGTGCCTGA	GGCTTTGGTC	TTGATAGAGA	TTCTTGTGGA	GGTGAAGATC	TTGGGTGTGA
901	TCCGAAGTCC	ACGGTAACGC	TGAAGTTCAC	GCTTCTTTCT	TCGACATTGG	TGGTTCGGTC
	AGGCTTCAGG	TGCCATTGCG	ACTTCAAGTG	CGAAGAAAAG	AGCTGTAACC	ACCAAGCCAG
961	TCTGCTGGTT	TCTCCAATCT	CAACTCCTCC	ACCGTCGCTA	TCGACCACCT	TTTGTCTGGT
	AGACGACCAA	AGAGGTTGAG	GTTGAGGAGG	TGGCAGCGAT	AGCTGGTGAG	AAACAGGAAC
1021	GCTGGTGAAA	GAACTTGGGC	TGAAACCATG	GGTTTGAACA	CTGCTGACAC	CGCTAGATTG
	CGACCACTTT	CTTGAACCCG	ACTTTGGTAC	CCAAACTTGT	GACGACTGTG	GCGATCTAAC
1081	AACGCTAACA	TTAGATACGT	CAACACTGGT	ACCGCTCCAA	TCTACAACGT	CTTGCCAACC
	TTGCGATTGT	AATCTATGCA	GTTGTGACCA	TGGCGAGGTT	AGATGTTGCA	GAACGGTTGG
1141	ACCTCCTTGG	TCTTGGGTAA	GAACCAAACC	TTGGCTACTA	TCAAGGCTAA	GGAAAACCAA
	TGGAGGAACC	AGAACCCATT	CTTGGTTTGG	AACCGATGAT	AGTTCCGATT	CCTTTTGGTT
1201	TTGTCCCAAA	TCTTGGCTCC	AAACAACCTA	TACCCATCCA	AGAACTTGGC	TCCAATCGCT
	AACAGGGTTT	AGAACCAGAG	TTTGTTGATG	ATGGGTAGGT	TCTTGAACCG	AGGTTAGCGA
1261	TTGAACGCTC	AAGACGACTT	CTCCTCTACT	CCAATCACCA	TGAACACAA	CCAATTCTTG
	AACTTGCGAG	TTCTGCTGAA	GAGGAGATGA	GGTTAGTGGT	ACTTGATGTT	GGTTAAGAAC
1321	GAATTGGAAG	AGACTAAGCA	ATTGCGTTTG	GACACCGACC	AAGTTTACGG	TAACATTGCT
	CTTAACCTTT	TCTGATTCGT	TAACGCAAAC	CTGTGGCTGG	TTCAAATGCC	ATTGTAACGA
1381	ACTTACAAC	TCGAAAACCG	TAGAGTCAGA	GTCGACACCG	GTTCCAACCT	GTCTGAAGTC
	TGAATGTTGA	AGCTTTTGCC	ATCTCAGTCT	CAGCTGTGGC	CAAGGTTGAC	CAGACTTCAG
1441	TTGCCACAAA	TCCAAGAAAC	CACCGCTAGA	ATCATCTTCA	ACGGTAAGGA	CTTGAACCTG
	AACGGTGTTT	AGGTTCTTTG	GTGGCGATCT	TAGTAGAAGT	TGCCATTCTT	GAACCTGAAC
1501	GTTGAAAGAA	GAATTGCTGC	TGTCAACCCA	TCCGACCCAT	TGGAAACCAC	CAAGCCAGAC
	CAACTTTCTT	CTTAACGACG	ACAGTTGGGT	AGGCTGGGTA	ACCTTTGGTG	GTTCCGGTCTG
1561	ATGACCTTGA	AGGAAGCTTT	GAAGATCGCT	TTCGGTTTCA	ACGAACCAAA	CGGTAACCTTG
	TACTGGAAC	TCCTTCGAAA	CTTCTAGCGA	AAGCCAAAGT	TGCTTGGTTT	GCCATTGAAC

FIGURE 10A – 1

```
1621 CAATACCAAG GTAAGGACAT CACCGAATTC GACTTCAACT TCGACCAACA AACC TCTCAA
    GTTATGGTTC CATTCCGTGA GTGGCTTAAG CTGAAGTTGA AGCTGGTTGT TTGGAGAGTT
1681 AACATCAAGA ACCAATTGGC TGAATTGAAC GCTACCAACA TTTACTACTGT TTTGGACAAG
    TTGTAGTTCT TGGTTAACCG ACTTAACCTG CGATGGTTGT AAATGTGACA AAACCTGTTC
1741 ATCAAGTTGA ACGCCAAGAT GAACATCTTG ATCAGAGACA AGAGATTCCA CTACGACAGA
    TAGTTCAACT TGCGGTTCTA CTTGTAGAAC TAGTCTCTGT TCTCTAAGGT GATGCTGTCT
1801 AACAAACATTG CTGTCGGTGC TGACGAATCC GTTGTC AAGG AAGCCCACAG AGAAGTCATC
    TTGTTGTAAC GACAGCCACG ACTGCTTAGG CAACAGTTCC TTCGGGTGTC TCTTCAGTAG
1861 AACTCCTCCA CCGAAGGTTT GTTGTGAAC ATCGACAAGG ACATCAGAAA GATCTTGTC
    TTGAGGAGGT GGCTTCCAAA CAACAACCTG TAGCTGTTCC TGTAAGTCTTT CTAGAACAGG
1921 GGTACATCG TCGAAATTGA AGACACCGAA GGTTTGAAGG AAGTCATCAA CGACAGATAC
    CCAATGTAGC AGCTTTAACT TCTGTGGCTT CCAAACCTTC TTCAGTAGTT GCTGTCTATG
1981 GACATGTTGA ACATTTCTC TTTGAGACAA GACGGTAAGA CCTTCATCGA CTTC AAGAAG
    CTGTACAACT TGTAAGGAG AACTCTGTT CTGCCATTCT GGAAGTAGCT GAAGTTCTTC
2041 TACAACGACA AGTTGCCATT GTACATTTCC AACC CAAACT ACAAGGTCAA CGTTTACGCT
    ATGTTGCTGT TCAACGGTAA CATGTAAAGG TTGGGTTTGA TGTTCCAGTT GCAAATGCGA
2101 GTCATAAGG AAAACACCAT CATCAACCCA TCCGAAAACG GTGACACTTC CACC AACGGT
    CAGTGATTCC TTTTGTGGTA GTAGTTGGGT AGGCTTTTGC CACTGTGAAG GTGGTTGCCA
2161 ATCAAGAAGA TTTTGATCTT CTCTAAGAAG GGTTACGAAA TTGGT
```

FIGURE 10A – 2

Translation of Yeast codon optimized DNA sequence without leader

1	EVKQENRLLN	ESESSSQGLL	GYFSDLNFQ	APMVVTSSTT	GDLSIPSSEL
51	ENIPSENQYF	QSAIWSGFIK	VKKSDEYTFA	TSADNHVTMW	VDDQEVINKA
101	SNSNKIRLEK	GRLYQIKIQY	QRENPTKGL	DFKLYWTDQ	NKKEVISSDN
151	LQLPELKQKS	SNSRKKRSTS	AGPTVPDRDN	DGIPDSLEVE	GYTVDVKNKR
201	TFLSPWISNI	HEKKGLTKYK	SSPEKWSTAS	DPYSDFEKVT	GRIDKNVSPE
251	ARHPLVAAYP	IVHVDMENII	LSKNEDQSTQ	NTDSETRTIS	KNTSTSRTHT
301	SEVHGNAEVH	ASFFDIGGSV	SAGFSNSNSS	TVAIDHSLSL	AGERTWAEATM
351	GLNTADTARL	NANIRYVNTG	TAPIYNVLPT	TSLVLGKNQT	LATIKAKENQ
401	LSQILAPNNY	YPSKNLAPIA	LNAQDDFSST	PITMNYNQFL	ELEKTKQLRL
451	DTDQVYGNIA	TYNFENGRVR	VDTGSNWSEV	LPQIQETTAR	IIFNGKDLNL
501	VERRIAAVNP	SDPLETTKPD	MTLKEALKIA	FGFNEPNGNL	QYQKGDI TEF
551	DFNFDQOTSQ	NIKNQLAELN	ATNIYTVLDK	IKLNAKMNIL	IRDKRFHYDR
601	NNIAVGADES	VVKEAHREVI	NSSTEGLLLN	IDKDIRKILS	GYIVEIEDTE
651	GLKEVINDRY	DMLNISSLRQ	DGKTFIDFKK	YNDKLPLYIS	NPNYKVNVA
701	VTKENTIINP	SENGDTSTNG	IKKILIFSCK	GYEIG	

FIGURE 10B

DNA sequence and amino acid translation product of yeast codon-optimized B. anthracis PA83 gene with modified furin cleavage site

DNA sequence

```

1   GAAGTTAAGC AAGAAAACAG ATTGTTGAAC GAATCTGAAT CCTCTTCCCA AGGTTTGTGTG
   CTTCAATTCTG TTCTTTTGTG TAACAACCTG CTTAGACTTA GGAGAAGGGT TCCAAACAAC
61  GGTACTACT TCTCCGACTT GAACTTCCAA GCTCCAATGG TCGTCACCTC CTCTACTACC
   CCAATGATGA AGAGGCTGAA CTTGAAGGTT CGAGGTTACC AGCAGTGGAG GAGATGATGG
121 GGTGACTTGT CCATCCCATC CTCCGAATTA GAGAACATCC CATCCGAAAA CCAATACTTC
   CCACTGAACA GGTAGGGTAG GAGGCTTAAT CTCTGTAGG GTAGGCTTTT GGTATGAAG
181 CAATCCGCTA TCTGGTCCGG CTTCATCAAG GTCAAGAAGT CCGACGAATA CACTTTCGCT
   GTTAGGCGAT AGACCAGGCC GAAGTAGTTC CAGTTCCTCA GGCTGCTTAT GTGAAZAGCGA
241 ACCTCCGCTG ACAACCACGT TACTATGTGG GTCGACGACC AAGAAGTCAT CAACAAGGCT
   TGGAGGCGAC TGTTGGTGCA ATGATACACC CAGCTGCTGG TTCTTCAGTA GTTGTTCGGA
301 TCCAACCTCA ACAAGATCAG ATTGGAAAAG GGTAGATTGT ACCAAATTAA GATCCAAATAC
   AGGTTGAGGT TGTTCCTAGTC TAACCTTTTC CCATCTAACA TGGTTTAATT CTAGGTTATG
361 CAAAGAGAAA ACCCAACCGA AAAGGGTTTG GACTTCAAGT TGTACTGGAC CGACTCCCAA
   GTTTCTCTTT TGGGTTGGCT TTTCCCAAAC CTGAAGTTCA ACATGACCTG GCTGAGGGTT
421 AACAAGAAGG AAGTCATCTC CTCTGACAAC TTGCAATTGC CAGAATTGAA GCAAAZAGTCC
   TTGTTCTTCC TTCAGTAGAG GAGACTGTGG AACGTTAACG GTCTTAACTT CGTTTTTCAGG
481 TCCAACCTCA GAAAGAAGAA GTCCACCTCC GCTGGTCCAA CTGTTCCAGA CAGAGACAAC
   AGGTTGAGGT CTTTCTTCTT CAGGTGGAGG CGACCAGGTT GACAAGGTCT GTCTCTGTTG
541 GACGGTATTC CAGACTCCTT GGAAGTCGAA GGTACACCG TCGACGTCAA GAACAAGAGA
   CTGCCATAAG GTCTGAGGAA CCTTCAGCTT CCAATGTGGC AGCTGCAGTT CTTGTTCTCT
601 ACCTTCTTGT TCCTCATGGAT CTCCAACATT CACGAAAAGA AGGGTTTGAC CAAGTACAAG
   TGGAAGAACA GAGGTACCTA GAGGTGTGTA GTGCTTTTCT TCCCAAACTG GTTCATGTTC
661 TCTTCCCCAG AAAAGTGGTC TACTGCTTCC GACCCATACT CCGACTTCGA AAAGGTCACC
   AGAAGGGGTC TTTTACCAG ATGACGAAGG CTGGGTATGA GGCTGAAGCT TTTCCAGTGG
721 GGTAAGATCG ACAAGAACGT CTCCCAGAA GCTAGACACC CATTGGTTGC TGCTTACCCA
   CCATCTTAGC TGTTCCTGCA GAGGGGTCTT CGATCTGTGG GTAACCAACG ACGAATGGGT
781 ATTGTCCACG TTGACATGGA AAACATCATT TTGTCCAAGA ACGAAGACCA ATCCACCCAA
   TAACAGGTGC AACTGTACCT TTTGTAGTAA AACAGGTTCT TGCTTCTGGT TAGGTGGGTT
841 AACACGGACT CCGAAACCAG AACTTGGTAC AAGAACACCT CCACCTCTAG AAGCCACACT
   TTGTGCCTGA GGCTTTGGTC TTGATAGAGA TTCTTGTGGA GGTGAAGATC TTGGGTGTGA
901 TCCGAAGTCC ACGGTAACGC TGAAGTTCAC GCTTCTTTCT TCGACATTGG TGTTCCGTC
   AGGCTTCAGG TGCCATTGCG ACTTCAAGTG CGAAGAAAGA AGCTGTAACC ACCAAGGCAG
961 TCTGCTGGTT TCTCCAACCT CAACCTCCTCC ACCGTCGCTA TCGACCACTC TTTGTCTTGT
   AGACGACCAA AGAGGTTGAG GTTGAGGAGG TGGCAGCGAT AGCTGGTGAG AAACAGGAAC
1021 GCTGGTGAAA GAACTTGGGC TGAAACCATG GGTTTGAACA CTGCTGACAC CGCTAGATTG
   CGACCACCTT CTTGAACCCG ACTTTGGTAC CCAAACCTGT GACGACTGTG GCGATCTAAC
1081 AACGCTAACA TTAGATACGT CAACACTGGT ACCGCTCCAA TCTACAACGT CTTGCCAACC
   TTGCGATTGT AATCTATGCA GTTGTGACCA TGGCGAGGTT AGATGTTGCA GAACGGTTGG
1141 ACCTCCTTGG TCTTGGGTAA GAACCAAACC TTGGCTACTA TCAAGGCTAA GGAAACCAA
   TGGAGGAACC AGAACCCATT CTTGGTTTGG AACCGATGAT AGTTCCGATT CCTTTTGGTT
1201 TTGTCCCAA TCTTGGCTCC AAACAACCTAC TACCCATCCA AGAACTTGGC TCCAATCGCT
   AACAGGGTTT AGAACCAGAG TTTGTTGATG ATGGGTAGGT TCTTGAACCG AGGTTAGCGA
1261 TTGAACGCTC AAGACGACTT CTCTCTACT CCAATCACCA TGAACCTACA CCAATCTTG
   AACTTGCGAG TCTTGCTGAA GAGGAGATGA GGTAGTGGT ACTTGATGTT GGTAAAGAAC
1321 GAATTGGAAG AGACTAAGCA ATTGCGTTTG GACACCGACC AAGTTTACGG TAACATTGCT
   CTTAACCTTT TCTGATTCTG TAACGCAAAC CTGTGGCTGG TTCAAATGCC ATTGTAACGA
1381 ACTTACAAC TCGAAAACGG TAGAGTCAGA GTCGACACCG GTTCCAACCTG GTCTGAAGTC
   TGAATGTTGA AGCTTTTGCC ATCTCAGTCT CAGCTGTGGC CAAGGTTGAC CAGACTTCAG
1441 TTGCCACAAA TCCAAGAAAC CACCGCTAGA ATCATCTTCA ACGGTAAGGA CTTGAACTTG
   AACGGTGTTC AGTTCTTTTG TGCGCATCT TAGTAGAAGT TGCCATTCCCT GAACCTGAA
1501 GTTGAAAGAA GAATTGCTGC TGTCAACCCA TCCGACCCAT TGGAAACCCAC AAGCAGAC
   CAACTTTCTT CTTAACGACG ACAGTTGGGT AGGCTGGGTA ACCTTTGGTG GTTCGGTCTG

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FIGURE 11A – 1

```

1561  ATGACCTTGA AGGAAGCTTT GAAGATCGCT TTCGGTTTCA ACGAACCAAA CGGTAACCTG
      TACTGGAACT TCCTTCGAAA CTTCTAGCGA AAGCCAAAGT TGCTTGTTTT GCCATTGAAC
1621  CAATACCAAG GTAAGGACAT CACCGAATTC GACTTCAACT TCGACCAACA AACCTCTCAA
      GTTATGGTTC CATTCCTGTA GTGGCTTAAG CTGAAGTTGA AGCTGGTTGT TTGGAGAGTT
1681  AACATCAAGA ACCAATTGGC TGAATTGAAC GCTACCAACA TTTACACTGT TTTGGACAAG
      TTGTAGTTCT TGGTTAACCG ACTTAACTTG CGATGGTTGT AAATGTGACA AAACCTGTTC
1741  ATCAAGTTGA ACGCCAAGAT GAACATCTTG ATCAGAGACA AGAGATTCCA CTACGACAGA
      TAGTTCAACT TCGGGTTCTA CTTGTAGAAC TAGTCTCTGT TCTCTAAGGT GATGCTGTCT
1801  AACAAACATTG CTGTCGGTGC TGACGAATCC GTTGTCAAGG AAGCCCACAG AGAAGTCATC
      TTGTTGTAAC GACAGCCACG ACTGCTTAGG CAACAGTTCC TTCGGGTGTC TCTTCAGTAG
1861  AACTCCTCCA CCGAAGGTTT GTTGTGAAC ATCGACAAGG ACATCAGAAA GATCTTGTCCT
      TTGAGGAGGT GGCTTCCAAA CAACAACCTG TAGCTGTTCC TGTAGTCTTT CTAGAACAGG
1921  GGTACATCG TCGAAATTGA AGACACCGAA GGTTTGAAGG AAGTCATCAA CGACAGATAC
      CCAATGTAGC AGCTTTAACT TCTGTGGCTT CCAAACCTCC TTCAGTAGTT GCTGTCTATG
1981  GACATGTTGA ACATTTCCCTC TTTGAGACAA GACGGTAAGA CCTTCATCGA CTTCAGAAG
      CTGTACAAC TGTAAAGGAG AAACCTCTGT CTGCCATTCT GGAAGTAGCT GAAGTTCCTC
2041  TACAACGACA AGTTGCCATT GTACATTTCC AACCCAAACT ACAAGGTCAA CGTTTACGCT
      ATGTTGCTGT TCAACGGTAA CATGTAAAGG TTGGGTTTGA TGTTCCAGTT GCAAATGCGA
2101  GTCACATAAGG AAAACACCAT CATCAACCCA TCCGAAAACG GTGACACTTC CACCAACGGT
      CAGTGATTCC TTTTGTGGTA GTAGTTGGGT AGGCTTTTGC CACTGTGAAG GTGGTTGCCA
2161  ATCAAGAAGA TTTTGATCTT CTCTAAGAAG GGTACGAAA TTGGT

```

FIGURE 11A – 2

Translated

```

1  EVKQENRLLN  ESESSSQGLL  GYYFSDLNFQ  APMVVTSSST  GDLSIPSSEL
51  ENIPSENQYF  QSAIWSGFIK  VKKSDEYTFA  TSADNHVTMW  VDDQEVINKA
101 SNSNKIRLEK  GRLYQIKIQY  QRENPTKGL  DFKLYWTD SQ  NKKEVISSDN
151 LQLPELKQKS  SNSRKKKSTS  AGPTVPDRDN  DGIPDSLEVE  GYTVDVKNKR
201 TFLSPWISNI  HEKKGLTKYK  SSPEKWSTAS  DPYSDFEKVT  GRIDKNVSPE
251 ARHPLVAAYP  IVHVDMENII  LSKNEDQSTQ  NTDSETRTIS  KNTSTSRHT
301 SEVHGNAEVH  ASFFDIGGSV  SAGFSNSNSS  TVAIDHSLSL  AGERTWAETM
351 GLNTADTARL  NANIRYVNTG  TAPIYNVLP  TSLVLGKNQT  LATIKAKENQ
401 LSQILAPNNY  YPSKNLAPIA  LNAQDDFSST  PITMNYNQFL  ELEKTKQLRL
451 DTDQVYGNIA  TYNFENGRVR  VDTGSNWSEV  LPQIQETTAR  IIFNGKDLNL
501 VERRIAAVNP  SDPLETTKPD  MTLKEALKIA  FGFNEPNGNL  QYQKGDITEF
551 DFNFDQOTSQ  NIKNQLAELN  ATNIYTVLDK  IKLNAKMNIL  IRDKRFHYDR
601 NNIAVGADES  VVKEAHREVI  NSSTEGLLL  IDKDIRKILS  GYIVEIEDTE
651 GLKEVINDRY  DMLNISSLRQ  DGKTFIDFKK  YNDKLPLYIS  NPNYKVNVA
701 VTKENTIINP  SENGDTSTNG  IKKILIFSKK  GYEIG

```

FIGURE 11B

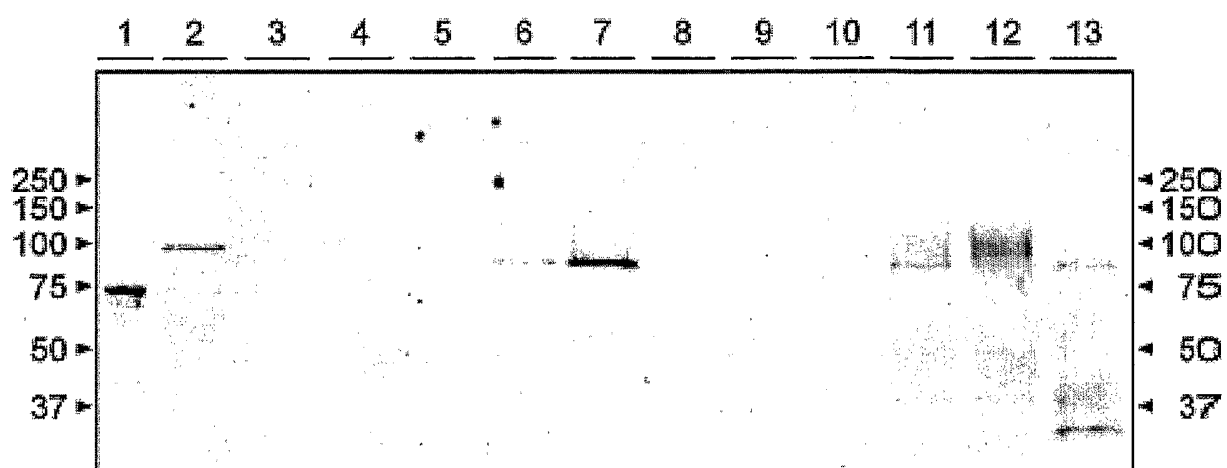


FIGURE 12

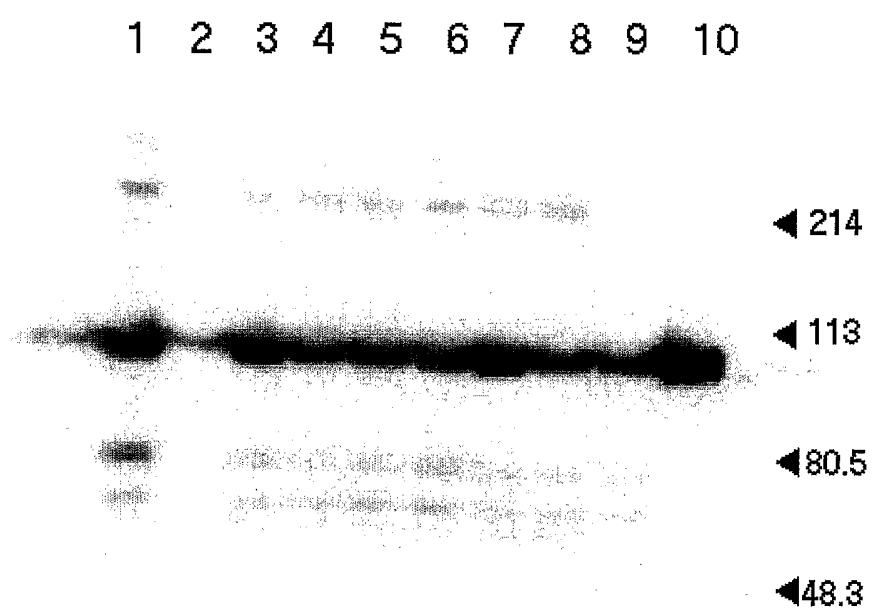


FIGURE 13

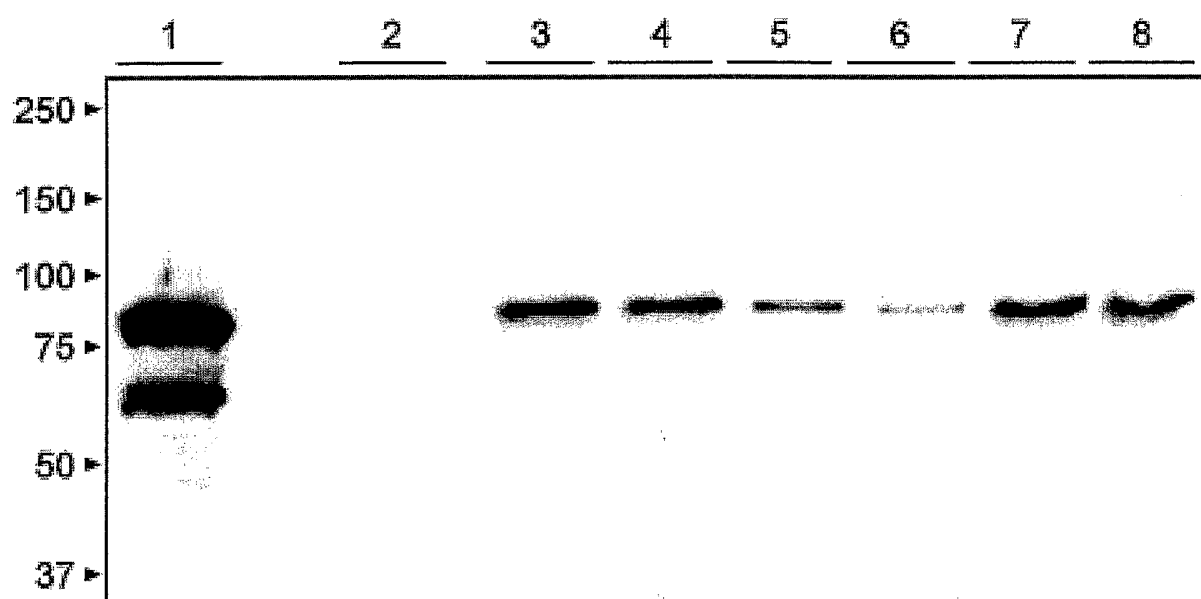


FIGURE 14

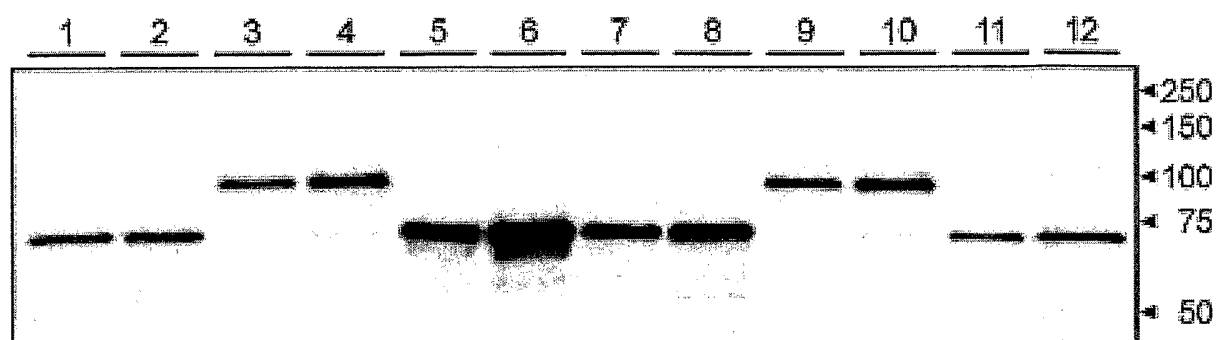


FIGURE 15

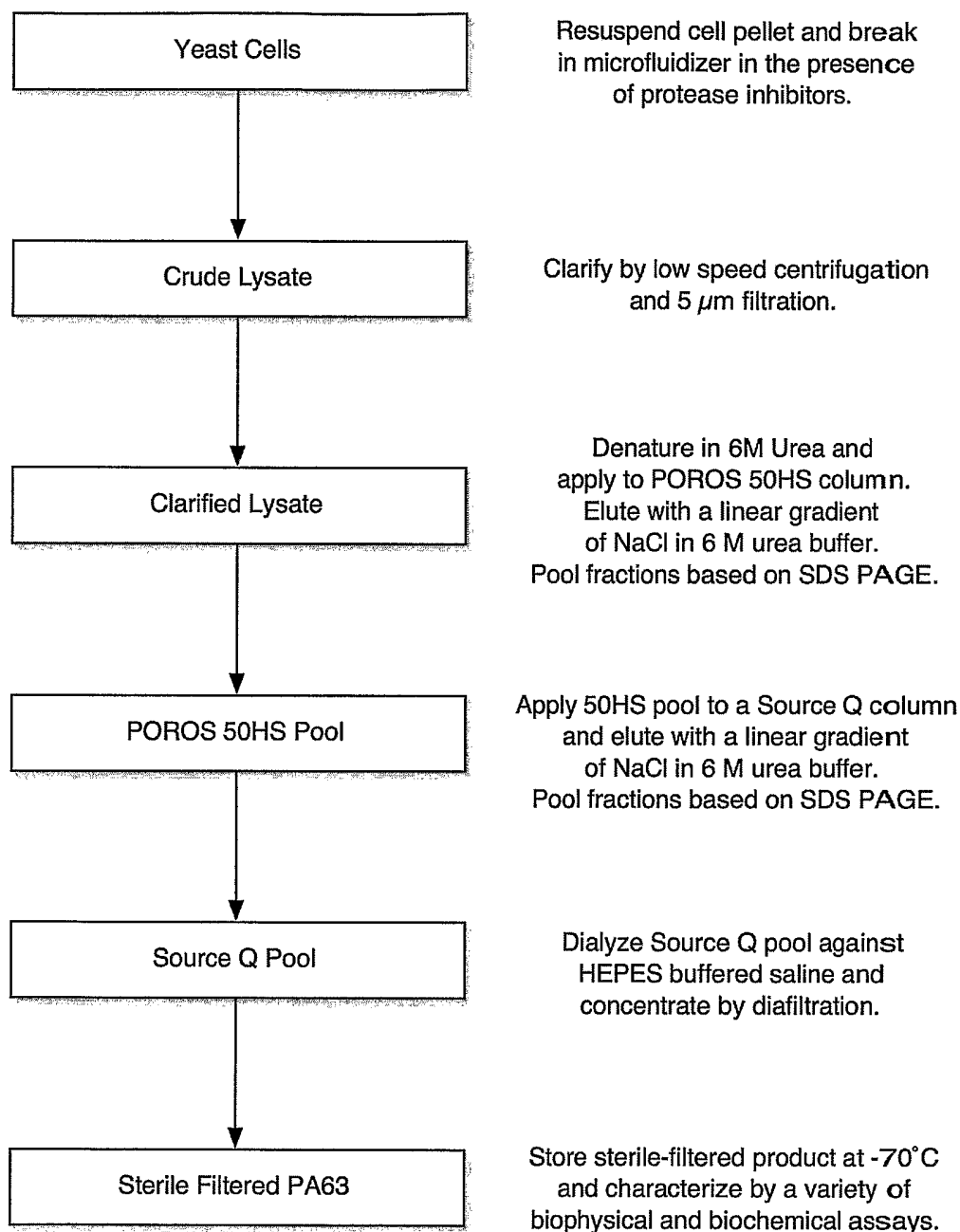


FIGURE 16

A. SDS PAGE Analysis of 50HS Chromatography

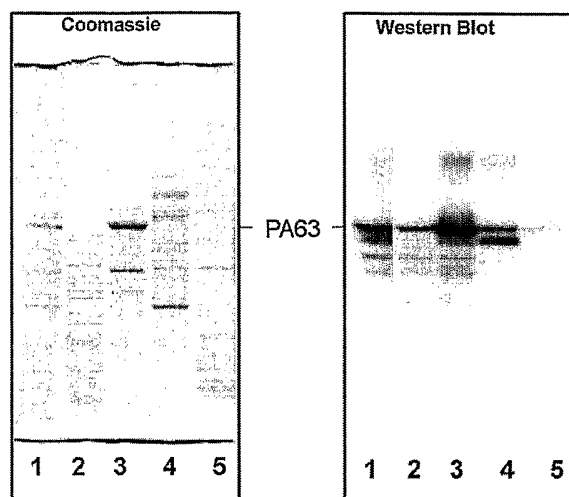


FIGURE 17A

B. SDS PAGE Analysis of Source Q Chromatography

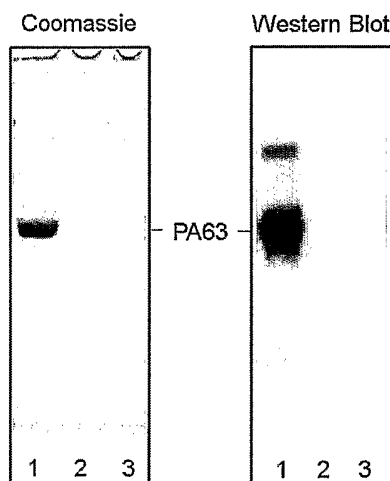


FIGURE 17B

SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> ANTHRAX VACCINE

<130> PCT 21112Y

<150> 60/470,563

<151> 2003-05-14

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 87

<212> DNA

<213> Bacillus anthracis

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tggaacagtt ggaccagcgg aggtgga 87

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<211> 98

<212> DNA

<213> Bacillus anthracis

<400> 2

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ggatctccaa cattcacgaa aagaagggtt tgaccaag 98

<210> 3

<211> 101

<212> DNA

<213> Bacillus anthracis

<400> 3

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acttgtactt ggtcaaacc ttcttttctg gaatgttga g 101

<210> 4

<211> 103

<212> DNA

<213> Bacillus anthracis

<400> 4

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aagctagaca ccattgggtt gctgcttacc caattgtcca cgt 103

<210> 5

<211> 101

<212> DNA

<213> Bacillus anthracis

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tccatgtcaa cgtggacaat tgggtaagca gcaaccaatg g 101

<210> 6
<211> 102
<212> DNA
<213> Bacillus anthracis

<400> 6
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aaccacact tccgaagtcc acggtaacgc tgaagttcac gc 102

<210> 7
<211> 101
<212> DNA
<213> Bacillus anthracis

<400> 7
cgatagcgac ggtggaggag ttggagttgg agaaaccagc agagacggaa ccaccaatgt 60
cgaagaaaga agcgtgaact tcagcgttac cgtggacttc g 101

<210> 8
<211> 102
<212> DNA
<213> Bacillus anthracis

<400> 8
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aacttgggct gaaaccatgg gtttgaacac tgctgacacc gc 102

<210> 9
<211> 101
<212> DNA
<213> Bacillus anthracis

<400> 9
ggaggtgggt ggcaagacgt tgtagattgg agcggtagca gtgttgacgt atctaattgt 60
agcgttcaat ctagcgggtg cagcagtggt caaacccatg g 101

<210> 10
<211> 103
<212> DNA
<213> Bacillus anthracis

<400> 10
ctccaatcta caacgtcttg ccaaccacct ccttggctct gggtaagaac caaaccttgg 60
ctactatcaa ggctaaggaa aaccaattgt cccaaatctt ggc 103

<210> 11
<211> 100
<212> DNA
<213> Bacillus anthracis

<400> 11
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gtttggagcc aagatttggg acaattggtt ttccttagcc 100

<210> 12
<211> 105
<212> DNA
<213> Bacillus anthracis

<400> 12
ccaatcgctt tgaacgctca agacgacttc tcctctactc caatcaccat gaactacaac 60
caattcttgg aattggaaaa gactaagcaa ttgcggttgg acacc 105

<210> 13
<211> 100
<212> DNA
<213> Bacillus anthracis

<400> 13
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tggtcggtgt ccaaacgcaa ttgcttagtc ttttccaatt 100

<210> 14
<211> 106
<212> DNA
<213> Bacillus anthracis

<400> 14
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aatccaagaa accaccgcta gaatcatctt caacggtaag gacttg 106

<210> 15
<211> 101
<212> DNA
<213> Bacillus anthracis

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caagttcaag tccttaccgt tgaagatgat tctagcggtg g 101

<210> 16
<211> 105
<212> DNA
<213> Bacillus anthracis

<400> 16
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tcggtttcaa cgaaccaaac ggtaacttgc aataccaagg taagg 105

<210> 17
<211> 99
<212> DNA
<213> Bacillus anthracis

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atgtccttac cttggtattg caagttaccg tttggttcg 99

<210> 18
<211> 115
<212> DNA
<213> Bacillus anthracis

<400> 18
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cactgttttg gacaagatca agttgaacgc caagatgaac atcttgatca gagac 115

<210> 19
<211> 104
<212> DNA
<213> Bacillus anthracis

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atctcttgtc tctgatcaag atgttcattt tggcgttcaa cttg 104

<210> 20
<211> 104
<212> DNA
<213> Bacillus anthracis

<400> 20
gctgacgaat ccgttgtcaa ggaagccac agagaagtca tcaactcctc caccgaaggt 60
ttgttgttga acatcgacaa ggacatcaga aagatcttgt ccgg 104

<210> 21
<211> 111
<212> DNA
<213> Bacillus anthracis

<400> 21
gaggaaatgt tcaacatgtc gtatctgtcg ttgatgactt ccttcaaacc ttcgggtgtct 60
tcaatttcga cgatgtaacc ggacaagatc tttctgatgt ccttgatgat g 111

<210> 22
<211> 95
<212> DNA
<213> Bacillus anthracis

<400> 22
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ttcatcgact tcaagaagta caacgacaag ttgcc 95

<210> 23
<211> 109
<212> DNA
<213> Bacillus anthracis

<400> 23
gggttgatga tgggtgttttc cttagtgaca gcgtaaactg tgaccttgta gtttgggttg 60
gaaatgtaca atggcaactt gtcgttgtag ttcttgaagt cgatgaagg 109

<210> 24
<211> 109
<212> DNA
<213> Bacillus Anthracis

<400> 24
cgctgtcact aaggaaaaca ccatcatcaa cccatccgaa aacggtgaca cttccaccaa 60
cggatatcaag aagattttga tcttctctaa gaagggttac gaaattggt 109

<210> 25
<211> 39
<212> DNA
<213> Bacillus anthracis

<400> 25
cgcggtatcct taaccaattt cgtaaccctt cttagagaa 39

<210> 26
<211> 28
<212> DNA
<213> Bacillus anthracis

<400> 26
gtcacggatc ctgtcttttg ataagaga 28

<210> 27
<211> 7
<212> PRT
<213> Bacillus anthracis

<400> 27
Ile Leu Ser Leu Asp Lys Arg
1 5

<210> 28
<211> 49
<212> DNA
<213> Bacillus anthracis

<400> 28
cgcggtatccc acaaaacaaa atgtccacct ccgctgggtcc aactgttcc 49

<210> 29
<211> 39
<212> DNA
<213> Bacillus anthracis

<400> 29
cgcggtatcct taaccaattt cgtaaccctt cttagagaa 39

<210> 30
 <211> 7
 <212> PRT
 <213> Bacillus anthracis

 <400> 30
 Ile Leu Ser Leu Asp Lys Arg
 1 5

<210> 31
 <211> 52
 <212> DNA
 <213> Baccillus anthracis

<400> 31
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<210> 32
 <211> 39
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 <213> Bacillus anthracis

<400> 32
 cgcggtatcct taaccaattt cgtaaccctt cttagagaa 39

<210> 33
 <211> 4
 <212> PRT
 <213> Bacillus anthracis

<400> 33
 Arg Lys Lys Lys
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<210> 34
 <211> 4
 <212> PRT
 <213> Bacillus anthracis

<400> 34
 Arg Lys Lys Arg
 1

<210> 35
 <211> 108
 <212> DNA
 <213> Bacillus anthracis

<400> 35
 gaagttaagc aagaaaacag attgttgaac gaatctgaat cctcttccca aggtttgttg 60
 ggttactact tctccgactt gaacttccaa gtcctaatgg tcgtcacc 108

<210> 36
 <211> 93
 <212> DNA

<213> Bacillus anthracis

<400> 36

cggatgggat gttctctaata tcggaggatg ggatggacaa gtcaccggta gtagaggagg 60
tgacgaccat tggagcttgg aagttcaagt cgg 93

<210> 37

<211> 93

<212> DNA

<213> Bacillus anthracis

<400> 37

tcccatcctc cgaattagag aacatcccat ccgaaaacca atacttccaa tccgctatct 60
ggtccgggctt catcaaggtc aagaagtccg acg 93

<210> 38

<211> 107

<212> DNA

<213> Bacillus anthracis

<400> 38

ggaagccttg ttgatgactt cttggtcgtc gaccacata gtaacgtggt tgtcagcgga 60
ggtagcgaag gtgtattcgt cggacttctt gaccttgatg aagccgg 107

<210> 39

<211> 111

<212> DNA

<213> Bacillus anthracis

<400> 39

gggtcgacga ccaagaagtc atcaacaagg cttccaactc caacaagatc agattggaaa 60
agggtagatt gtaccaaatt aagatccaat accaaagaga aaaccaacc g 111

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<211> 99

<212> DNA

<213> Bacillus anthracis

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tcggttgggt tttctctttg gtattggatc ttaatttgg 99

<210> 41

<211> 109

<212> DNA

<213> Bacillus anthracis

<400> 41

ggaccgactc ccaaaacaag aaggaagtca tctcytctga caacttgcaa ttgccagaat 60
tgaagcaaaa gtcytccaac tccagaaaga agaagtccac ctccgctgg 109

<210> 42

<211> 107

<212> DNA

<213> Bacillus anthracis

<400> 42

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tggaacagtt ggaccagcgg aggtggactt cttctttctg gagttgg 107

<210> 43

<211> 98

<212> DNA

<213> Bacillus anthracis

<400> 43

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ggatctccaa cattcacgaa aagaagggtt tgaccaag 98

<210> 44

<211> 101

<212> DNA

<213> Bacillus anthracis

<400> 44

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acttgtactt ggtcaaacc ttcttttctg gaatgttgga g 101

<210> 45

<211> 103

<212> DNA

<213> Bacillus anthracis

<400> 45

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aagctagaca cccattgggt gctgcttacc caattgtcca cgt 103

<210> 46

<211> 101

<212> DNA

<213> Bacillus anthracis

<400> 46

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tccatgtcaa cgtggacaat tgggtaagca gcaaccaatg g 101

<210> 47

<211> 1704

<212> DNA

<213> Bacillus anthracis

<400> 47

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tctaattattc atgaaaagaa aggattaacc aaatataaat catctcctga aaaatggagc 180
acggcttctg atccgtacag tgatttcgaa aagggttacag gacggattga taagaatgta 240
tcaccagagg caagacaccc cttgtggca gcttatccga ttgtacatgt agatatggag 300
aatattattc tctcaaaaaa tgaggatcaa tccacacaga atactgatag tgaaacgaga 360
acaataagta aaaatacttc tacaagtagg acacatacta gtgaagtaca tggaaatgca 420

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gaagtgcattg cgctcgttctt tgatatttggt gggagtggtat ctgcaggatt tagtaattcg 480
aattcaagta cggctcgcaat tgatcattca ctatctctag caggggaaag aacttgggct 540
gaaacaatgg gtttaataac cgctgataca gcaagattaa atgccaatat tagatatgta 600
aatactggga cggctccaat ctacaacgtg ttaccaacga cttcgttagt gttaggaaaa 660
aatcaaacac tcgcgacaat taaagctaag gaaaaccaat taagtcaaat acttgcacct 720
aataattatt atccttctaa aaacttggcg ccaatcgcat taaatgcaca agacgatttc 780
agttctactc caattacaat gaattacaat caatttcttg agttagaaaa aacgaaacaa 840
ttaagattag atacggatca agtatatggg aatatagcaa catacaattt tgaaaatgga 900
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gaattaaacg caactaacat atatactgta ttagataaaa tcaaattaaa tgcaaaaatg 1260
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ttacggcaag atggaaaaac atttatagat tttaaaaaat ataatgataa attaccgta 1560
tatataagta atcccaatta taaggtaa atgtatatgctg ttactaaaga aaacactatt 1620
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tctaaaaaag gctatgagat agga 1704

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<210> 48

<211> 571

<212> PRT

<213> Bacillus anthracis

<400> 48

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 20          25          30
Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His Glu Lys Lys Gly
 35          40          45
Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser Thr Ala Ser Asp
 50          55          60
Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile Asp Lys Asn Val
 65          70          75          80
Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr Pro Ile Val His
 85          90          95
Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu Asp Gln Ser Thr
 100         105         110
Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys Asn Thr Ser Thr
 115         120         125
Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala Glu Val His Ala
 130         135         140
Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly Phe Ser Asn Phe
 145         150         155         160
Ile Gly Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser Leu
 165         170         175
Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala Asp
 180         185         190
Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr Ala
 195         200         205

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Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys Asn
  210                215                220
Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln Ile
  225                230                235                240
Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile Ala
                245                250                255
Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn Tyr
                260                265                270
Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp Thr
                275                280                285
Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly Arg
  290                295                300
Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln Ile
  305                310                315                320
Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn Leu
                325                330                335
Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu Thr
                340                345                350
Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe Gly
                355                360                365
Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile Thr
  370                375                380
Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys Asn
  385                390                395                400
Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp Lys
                405                410                415
Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg Phe
                420                425                430
His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val Val
  435                440                445
Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu Leu
  450                455                460
Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile Val
  465                470                475                480
Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg Tyr
                485                490                495
Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe Ile
                500                505                510
Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn Pro
  515                520                525
Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile
  530                535                540
Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile
  545                550                555                560
Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
                565                570

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<210> 49
 <211> 1704
 <212> DNA
 <213> Bacillus anthracis

<400> 49
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tccaacattc acgaaaagaa gggtttgacc aagtacaagt cttccccaga aaagtgggtct 180
actgcttccg acccatactc cgacttcgaa aaggtcaccg gtagaatcga caagaacgtc 240
tccccagaag ctagacaccc attgggtgct gcttacccaa ttgtccacgt tgacatggaa 300
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gaagttcacg cttcttttctt cgacattggt ggttccgtct ctgctgggtt ctccaactcc 480
aactcctcca ccgtcgctat cgaccactct ttgtccttgg ctggtgaaag aacttgggct 540
gaaaccatgg gtttgaacac tgctgacacc gctagattga acgctaacat tagatacgtc 600
aacactggta ccgtctcaat ctacaacgtc ttgccaacca cctccttggg cttgggtaag 660
aaccaaacct tggctactat caaggctaag gaaaaccaat tgtcccaaat cttgggtcca 720
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<210> 50

<211> 568

<212> PRT

<213> Bacillus anthracis

<400> 50

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

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Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser Leu Ala Gly Glu
      165      170      175
Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala Asp Thr Ala Arg
      180      185      190
Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr Ala Pro Ile Tyr
      195      200      205
Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys Asn Gln Thr Leu
      210      215      220
Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln Ile Leu Ala Pro
225      230      235      240
Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile Ala Leu Asn Ala
      245      250      255
Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn Tyr Asn Gln Phe
      260      265      270
Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp Thr Asp Gln Val
      275      280      285
Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly Arg Val Arg Val
      290      295      300
Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln Ile Gln Glu Thr
305      310      315      320
Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn Leu Val Glu Arg
      325      330      335
Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu Thr Thr Lys Pro
      340      345      350
Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe Gly Phe Asn Glu
      355      360      365
Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile Thr Glu Phe Asp
      370      375      380
Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys Asn Gln Leu Ala
385      390      395      400
Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp Lys Ile Lys Leu
      405      410      415
Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg Phe His Tyr Asp
      420      425      430
Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val Val Lys Glu Ala
      435      440      445
His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu Leu Leu Asn Ile
      450      455      460
Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile Val Glu Ile Glu
465      470      475      480
Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg Tyr Asp Met Leu
      485      490      495
Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe Ile Asp Phe Lys
      500      505      510
Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn Pro Asn Tyr Lys
      515      520      525
Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile Ile Asn Pro Ser
      530      535      540
Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys Ile Leu Ile Phe
545      550      555      560
Ser Lys Lys Gly Tyr Glu Ile Gly
      565

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<210> 51

<211> 420

<212> DNA

<213> *Bacillus anthracis*

<400> 51

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agaaagatct tgtccgggta catcgtcgaa attgaagaca ccgaagggtt gaaggaagtc 180
atcaacgaca gatacgacat gttgaacatt tcctctttga gacaagacgg taagaccttc 240
atcgacttca agaagtacaa cgacaagttg ccattgtaca tttccaaccc aaactacaag 300
gtcaacgttt acgctgtcac taaggaaaac accatcatca acccatccga aaacggtgac 360
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<210> 52

<211> 140

<212> PRT

<213> *Bacillus anthracis*

<400> 52

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Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
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Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
          20           25           30
Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
          35           40           45
Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
          50           55           60
Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
65           70           75           80
Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
          85           90           95
Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
          100          105          110
Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
          115          120          125
Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
          130          135          140

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<210> 53

<211> 2205

<212> DNA

<213> *Bacillus anthracis*

<400> 53

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ggggatttat ctattcctag ttctgagtta gaaaatattc catcggaaaa ccaatatttt 180
caatctgcta tttggtcagg atttatcaaa gttaagaaga gtgatgaata tacatttgct 240
acttccgctg ataatcatgt aacaatgtgg gtagatgacc aagaagtgat taataaagct 300
tctaattcta acaaaatcag attagaaaaa ggaagattat atcaaataaa aattcaatat 360
caacgagaaa atcctactga aaaaggattg gatttcaagt tgtactggac cgattctcaa 420
aataaaaaag aagtgatttc tagtgataac ttacaattgc cagaattaaa acaaaaatct 480
tcgaactcaa gaaaaaagcg aagtacaagt gctggacctc cggttccaga ccgtgacaat 540
gatggaatcc ctgattcatt agaggtagaa ggatatacgg ttgatgtcaa aaataaaaga 600
acttttcttt caccatggat ttctaattatt catgaaaaga aaggattaac caaatataaa 660

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tcacatctcctg aaaaatggag caccggcttct gatccgtaca gtgattttcga aaagggttaca 720
ggacgggattg ataagaatgt atcaccagag gcaagacacc cccttgtggc agcttatccg 780
attgtacatg tagatatgga gaattattatt ctctcaaaaa atgaggatca atccacacag 840
aatactgata gtgaaacgag aacaataagt aaaaatactt ctacaagtag gacacatact 900
agtgaagtac atggaaatgc agaagtgcac gcgtcgttct ttgatattgg tgggagtgta 960
tctgcaggat ttagtaattc gaattcaagt acggctcgcaa ttgatcattc actatctcta 1020
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aatgccata ttagatatgt aaatactggg acggctccaa tctacaacgt gttaccaacg 1140
acttcgttag tgttaggaaa aaatcaaaca ctcgcgacaa ttaaagctaa ggaaaaccaa 1200
ttaagtcaaa tacttgcacc taataattat tatccttcta aaaacttggc gccaatcgca 1260
ttaaatgcac aagacgattt cagttctact ccaattacaa tgaattacaa tcaatttctt 1320
gagttagaaa aaacgaaaca attaagatta gatacggatc aagtatatgg gaatatagca 1380
acatacaatt ttgaaaatgg aagagtggag gtggatacag gctcgaactg gagtgaagtg 1440
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<210> 54

<211> 735

<212> PRT

<213> Bacillus anthracis

<400> 54

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

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Asp	Arg	Asp	Asn	Asp	Gly	Ile	Pro	Asp	Ser	Leu	Glu	Val	Glu	Gly	Tyr	
			180					185					190			
Thr	Val	Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	Pro	Trp	Ile	Ser	
		195					200					205				
Asn	Ile	His	Glu	Lys	Lys	Gly	Leu	Thr	Lys	Tyr	Lys	Ser	Ser	Pro	Glu	
	210					215					220					
Lys	Trp	Ser	Thr	Ala	Ser	Asp	Pro	Tyr	Ser	Asp	Phe	Glu	Lys	Val	Thr	
225					230					235					240	
Gly	Arg	Ile	Asp	Lys	Asn	Val	Ser	Pro	Glu	Ala	Arg	His	Pro	Leu	Val	
				245					250					255		
Ala	Ala	Tyr	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu	Ser	
			260					265					270			
Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg	Thr	
		275					280					285				
Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	
	290					295					300					
Gly	Asn	Ala	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser	Val	
305					310					315					320	
Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	
				325					330					335		
Ser	Leu	Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	
			340					345					350			
Asn	Thr	Ala	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	
		355					360					365				
Thr	Gly	Thr	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	
	370					375					380					
Leu	Gly	Lys	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	
385				390						395					400	
Leu	Ser	Gln	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	
			405						410					415		
Ala	Pro	Ile	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	
			420					425					430			
Thr	Met	Asn	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	
		435					440					445				
Arg	Leu	Asp	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	
	450					455					460					
Glu	Asn	Gly	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	
465					470					475					480	
Leu	Pro	Gln	Ile	Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	
				485					490					495		
Asp	Leu	Asn	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	
		500						505					510			
Pro	Leu	Glu	Thr	Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	
		515					520					525				
Ile	Ala	Phe	Gly	Phe	Asn	Glu	Pro	Asn	Gly	Asn	Leu	Gln	Tyr	Gln	Gly	
	530					535					540					
Lys	Asp	Ile	Thr	Glu	Phe	Asp	Phe	Asn	Phe	Asp	Gln	Gln	Thr	Ser	Gln	
545					550					555					560	
Asn	Ile	Lys	Asn	Gln	Leu	Ala	Glu	Leu	Asn	Ala	Thr	Asn	Ile	Tyr	Thr	
				565					570					575		
Val	Leu	Asp	Lys	Ile	Lys	Leu	Asn	Ala	Lys	Met	Asn	Ile	Leu	Ile	Arg	
		580						585					590			
Asp	Lys	Arg	Phe	His	Tyr	Asp	Arg	Asn	Asn	Ile	Ala	Val	Gly	Ala	Asp	
		595					600					605				

Glu	Ser	Val	Val	Lys	Glu	Ala	His	Arg	Glu	Val	Ile	Asn	Ser	Ser	Thr
610						615					620				
Glu	Gly	Leu	Leu	Leu	Asn	Ile	Asp	Lys	Asp	Ile	Arg	Lys	Ile	Leu	Ser
625					630					635					640
Gly	Tyr	Ile	Val	Glu	Ile	Glu	Asp	Thr	Glu	Gly	Leu	Lys	Glu	Val	Ile
				645					650					655	
Asn	Asp	Arg	Tyr	Asp	Met	Leu	Asn	Ile	Ser	Ser	Leu	Arg	Gln	Asp	Gly
			660					665					670		
Lys	Thr	Phe	Ile	Asp	Phe	Lys	Lys	Tyr	Asn	Asp	Lys	Leu	Pro	Leu	Tyr
		675					680					685			
Ile	Ser	Asn	Pro	Asn	Tyr	Lys	Val	Asn	Val	Tyr	Ala	Val	Thr	Lys	Glu
690						695					700				
Asn	Thr	Ile	Ile	Asn	Pro	Ser	Glu	Asn	Gly	Asp	Thr	Ser	Thr	Asn	Gly
705				710						715					720
Ile	Lys	Lys	Ile	Leu	Ile	Phe	Ser	Lys	Lys	Gly	Tyr	Glu	Ile	Gly	
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<210> 55
 <211> 4365
 <212> DNA
 <213> Bacillus anthracis

<400> 55
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<210> 56

<211> 735

<212> PRT

<213> Bacillus anthracis

<400> 56

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Thr	Ser	Ala	Asp	Asn	His	Val	Thr	Met	Trp	Val	Asp	Asp	Gln	Glu	Val
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Ile	Asn	Lys	Ala	Ser	Asn	Ser	Asn	Lys	Ile	Arg	Leu	Glu	Lys	Gly	Arg
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<211> 4365

<212> DNA

<213> *Bacillus anthracis*

<400> 57

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<211> 735

<212> PRT

<213> Bacillus anthracis

<400> 58

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Met	Val	Val	Thr	Ser	Ser	Thr	Thr	Gly	Asp	Leu	Ser	Ile	Pro	Ser	Ser	35	40	45	
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Thr	Ser	Ala	Asp	Asn	His	Val	Thr	Met	Trp	Val	Asp	Asp	Gln	Glu	Val	85	90	95	
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Leu	Tyr	Gln	Ile	Lys	Ile	Gln	Tyr	Gln	Arg	Glu	Asn	Pro	Thr	Glu	Lys	115	120	125	
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Ser	Asn	Ser	Arg	Lys	Lys	Lys	Ser	Thr	Ser	Ala	Gly	Pro	Thr	Val	Pro	165	170	175	
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Thr	Val	Asp	Val	Lys	Asn	Lys	Arg	Thr	Phe	Leu	Ser	Pro	Trp	Ile	Ser	195	200	205	
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Lys	Asn	Glu	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Glu	Thr	Arg	Thr	275	280	285	
Ile	Ser	Lys	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	290	295	300	
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Ser	Ala	Gly	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	325	330	335	
Ser	Leu	Ser	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	340	345	350	
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Pro Leu Glu Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys
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Lys Asp Ile Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln
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<213> Bacillus anthracis

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