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(54) Titre : DERIVES ANTIGENES ASSOCIES AUX TUMEURS DE LA FAMILLE MAGE, ET SEQUENCES D'ACIDES NUCLEIQUES CODANT CES DERIVES, UTILISES POUR LA PREPARATION DE PROTEINES DE FUSION ET DE COMPOSITIONS DESTINEES A LA VACCINATION

(54) Title: TUMOR-ASSOCIATED ANTIGEN DERIVATIVES FROM THE MAGE FAMILY, AND NUCLEIC ACID SEQUENCES ENCODING THEM, USED FOR THE PREPARATION OF FUSION PROTEINS AND OF COMPOSITIONS FOR VACCINATION

(57) Abrégé/Abstract:

The present invention relates to novel proteins and to their production, from the MAGE family. In particular, to a MAGE protein fused to an immunological fusion partner, such as Lipoprotein D. Such antigens may be formulated to provide vaccines for the treatment of a range of tumours. Novel methods for purifying MAGE proteins are also provided.

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<p>(57) Abstract</p> <p>The present invention relates to novel proteins and to their production, from the MAGE family. In particular, to a MAGE protein fused to an immunological fusion partner, such as Lipoprotein D. Such antigens may be formulated to provide vaccines for the treatment of a range of tumours. Novel methods for purifying MAGE proteins are also provided.</p>		

TUMOR-ASSOCIATED ANTIGEN DERIVATIVES FROM THE MAGE FAMILY, AND NUCLEIC ACID SEQUENCES ENCODING THEM, USED FOR THE PREPARATION OF FUSION PROTEINS AND OF COMPOSITIONS FOR VACCINATION

The present invention relates to protein derivatives, comprising a tumor-associated antigen, that find utility in cancer vaccine therapy. In particular the derivatives of the invention include fusion proteins comprising an antigen encoded by the family of MAGE genes (e.g. MAGE-3, MAGE-1), linked to an immunological fusion partner which provides T helper epitopes, such as, for example the lipidated form of protein D from Haemophilus influenzae B; chemically modified MAGE proteins wherein the antigen's disulphide bridges are reduced and the resulting thiols blocked and genetically modified MAGE proteins provided with an affinity tag and/or genetically modified to prevent disulphide bridge formation. Methods are also described for purifying MAGE proteins and for formulating vaccines for treating a range of cancers, including, but not limited to Melanoma, breast, bladder, lung, NSCLC, head and squamous cell carcinoma, colon carcinoma and oesophagus carcinoma.

Antigens encoded by the family of MAGE genes are predominately expressed on melanoma cells (including malignant melanoma) and some other cancers including NSCLC (non small cell lung cancer), head and neck squamous cell carcinoma, bladder transitional cell carcinoma and oesophagus carcinoma, but are not detectable on normal tissues except in the testis and the placenta (Gaugler, 1994; Weynants, 1994; Patard, 1995). MAGE-3 is expressed in 69% of melanomas (Gaugler, 1994), and can also be detected in 44% of NSCLC (Yoshimatsu 1988), 48% of head and neck squamous cell carcinoma, 34% of bladder transitional cell carcinoma 57% of oesophagus carcinoma 32% of colon cancers and 24% of breast cancers (Van Pel, 1995); Inoue, 1995 Fujie 1997; Nishimura 1997). Cancers expressing MAGE proteins are known as Mage associated tumours.

The immunogenicity of human melanoma cells has been elegantly demonstrated in experiments using mixed cultures of melanoma cells and autologous lymphocytes. These culture often generate specific cytotoxic T lymphocytes (CTLs) able to lyse exclusively the autologous melanoma cells but neither autologous fibroblasts, nor autologous EBV-transformed B lymphocytes (Knuth, 1984;

Anichini, 1987). Several of the antigens recognised on autologous melanoma cells by these CTL clones are now identified, including those of the MAGE family.

The first antigen which could be defined through its recognition by specific CTLs on autologous melanoma cells is termed MZ2-E (Van den Eynde, 1989) and is encoded by the gene MAGE-1 (Van der Bruggen, 1991). CTLs directed against MZ2-E recognise and lyse MZ2-E positive melanoma cells from autologous as well as from other patients provided that these cells have the HLA.A1 allele.

The MAGE-1 gene belongs to a family of 12 closely related genes, MAGE 1, MAGE 2, MAGE 3, MAGE 4, MAGE 5, MAGE 6, MAGE 7, MAGE 8, MAGE 9, MAGE 10, MAGE 11, MAGE 12, located on chromosome X and sharing with each other 64 to 85% homology in their coding sequence (De Plaen, 1994). These are sometimes known as MAGE A1, MAGE A2, MAGE A3, MAGE A4, MAGE A5, MAGE A6, MAGE A7, MAGE A8, MAGE A9, MAGE A 10, MAGE A11, MAGE A 12 (The MAGE A family). Two other groups of proteins are also part of the MAGE family although more distantly related. These are the MAGE B and MAGE C group. The MAGE B family includes MAGE B1 (also known as MAGE Xp1, and DAM 10), MAGE B2 (also known as MAGE Xp2 and DAM 6) MAGE B3 and MAGE B4 - the MAGE C family currently includes MAGE C1 and MAGE C2. In general terms, a MAGE protein can be defined as containing a core sequence signature located towards the C-terminal end of the protein (for example with respect to MAGE A1 a 309 amino acid protein, the core signature corresponds to amino acid 195-279).

The consensus pattern of the core signature is thus described as follows wherein x represents any amino acid, lower case residues are conserved (conservative variants allowed) and upper case residues are perfectly conserved.

Core sequence signature

LixvL (2x) I (3x) g (2x) apEExiWexl (2x) m (3-4x) Gxe (3-4x) gxp (2x) llt (3x) VqexYLxYxqVPxsxP (2x) yeFLWGprA (2x) Et (3x) kv

Conservative substitutions are well known and are generally set up as the default scoring matrices in sequence alignment computer programs. These

programs include PAM250 (Dayhoft M.O. *et al.*, (1978), "A model of evolutionary changes in proteins", In "Atlas of Protein sequence and structure" 5(3) M.O. Dayhoft (ed.), 345-352), National Biomedical Research Foundation, Washington, and Blosum 62 (Steven Henikoft and Jorja G. Henikoft (1992), "Amino acid substitution matrices from protein blocks"), Proc. Natl. Acad. Sci. USA 89 (Biochemistry): 10915-10919.

In general terms, substitution within the following groups are conservative substitutions, but substitutions between groups are considered non-conserved. The groups are:

- 10 i) Aspartate/asparagine/glutamate/glutamine
- ii) Serine/threonine
- iii) Lysine/arginine
- iv) Phenylalanine/tyrosine/tryptophane
- v) Leucine/isoleucine/valine/methionine
- 15 vi) Glycine/alanine

In general and in the context of this invention, a MAGE protein will be approximately 50% identical in this core region with amino acids 195 to 279 of MAGE A1.

20 Several CTL epitopes have been identified on the MAGE-3 protein. One such epitope, MAGE-3.A1, is a nonapeptide sequence located between amino acids 168 and 176 of the MAGE-3 protein which constitutes an epitope specific for CTLs when presented in association with the MHC class I molecule HLA.A1. Recently two additional CTL epitopes have been identified on the peptide sequence of the
25 MAGE-3 protein by their ability to mount a CTL response in a mixed culture of melanoma cells and autologous lymphocytes. These two epitopes have specific binding motifs for the HLA.A2 (Van der Bruggen, 1994) and HLA.B44 (Herman, 1996) alleles respectively.

30 The present invention provides MAGE protein derivatives. Such derivatives are suitable for use in therapeutic vaccine formulations which are suitable for the treatment of a range of tumour types.

In one embodiment of the present invention, the derivative is a fusion proteins comprising an antigen from the MAGE protein family linked to a heterologous partner. The proteins may be chemically conjugated, but are preferably expressed as recombinant fusion proteins allowing increased levels to be produced in an expression system as compared to non-fused protein. Thus the fusion partner may assist in providing T helper epitopes(immunological fusion partner), preferably T helper epitopes recognised by humans, or assist in expressing the protein (expression enhancer) at higher yields than the native recombinant protein. Preferably the fusion partner will be both an immunological fusion partner and expression enhancing partner.

In a preferred form of the invention, the immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium, Haemophilus influenza B (WO91/18926). Preferably the protein D derivative comprises approximately the first 1/3 of the protein, in particular approximately the first N-terminal 100-110 amino acids. Preferably the protein D derivative is lipidated. Preferably the first 109 residues of the Lipoprotein D fusion partner is included on the N-terminus to provide the vaccine candidate antigen with additional exogenous T-cell epitopes and increase expression level in E-coli (thus acting also as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells.

Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically the N terminal 81 amino acids are utilised, although different fragments may be used provided they include T-helper epitopes.

In another embodiment the immunological fusion partner is the protein known as LYTA. Preferably the C terminal portion of the molecule is used. Lyta is derived from Streptococcus pneumoniae which synthesize an N-acetyl-L-alanine amidase, amidase LYTA, (coded by the lytA gene {Gene, 43 (1986) page 265-272} an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of E.coli C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-

LYTA fragment at its amino terminus has been described {Biotechnology: 10, (1992) page 795-798}. As used herein a preferred embodiment utilises the repeat portion of the Lyta molecule found in the C terminal end starting at residue 178. A particularly preferred form incorporates residues 188 - 305.

5 The immunological fusion partners noted above are also advantageous in aiding expression. In particular, such fusions are expressed at higher yields than native recombinant MAGE proteins.

Such constructs in a clinical setting have been shown by the present inventors to be able to treat melanoma. In one case, a patient with stage IV
10 melanoma was cleared of metastases after two doses of unadjuvanted lipo D 1/3 MAGE 3 His protein.

Accordingly, the present invention in the embodiment provides fusion proteins comprising a tumour-associated antigen from the MAGE family linked to an immunological fusion partner. Preferably the immunological fusion partner is
15 protein D or fragment thereof, most preferably lipoprotein D. The MAGE proteins are preferably MAGE A1 or MAGE A3. The Lipoprotein D part preferably comprises the first 1/3 of Lipoprotein D.

The proteins of the present invention preferably are expressed in *E. coli*. In a preferred embodiment the proteins are expressed with an affinity tag, such as for
20 example, a histidine tail comprising between 5 to 9 and preferably six histidine residues. These are advantageous in aiding purification.

The present invention also provides a nucleic acid encoding the proteins of the present invention. Such sequences can be inserted into a suitable expression vector and used for DNA/RNA vaccination or expressed in a suitable host.
25 Microbial vectors expressing the nucleic acid may be used as vaccines. Such vectors include for example, poxvirus, adenovirus, alphavirus, listeria and monarphage.

A DNA sequence encoding the proteins of the present invention can be synthesized using standard DNA synthesis techniques, such as by enzymatic ligation
30 as described by D.M. Roberts *et al.* in Biochemistry 1985, 24, 5090-5098, by chemical synthesis, by *in vitro* enzymatic polymerization, or by PCR technology

utilising for example a heat stable polymerase, or by a combination of these techniques.

Enzymatic polymerisation of DNA may be carried out *in vitro* using a DNA polymerase such as DNA polymerase I (Klenow fragment) in an appropriate buffer containing the nucleoside triphosphates dATP, dCTP, dGTP and dTTP as required at a temperature of 10°-37°C, generally in a volume of 50µl or less. Enzymatic ligation of DNA fragments may be carried out using a DNA ligase such as T4 DNA ligase in an appropriate buffer, such as 0.05M Tris (pH 7.4), 0.01M MgCl₂, 0.01M dithiothreitol, 1mM spermidine, 1mM ATP and 0.1mg/ml bovine serum albumin, at a temperature of 4°C to ambient, generally in a volume of 50ml or less. The chemical synthesis of the DNA polymer or fragments may be carried out by conventional phosphotriester, phosphite or phosphoramidite chemistry, using solid phase techniques such as those described in 'Chemical and Enzymatic Synthesis of Gene Fragments - A Laboratory Manual' (ed. H.G. Gassen and A. Lang), Verlag Chemie, Weinheim (1982), or in other scientific publications, for example M.J. Gait, H.W.D. Matthes, M. Singh, B.S. Sproat, and R.C. Titmas, *Nucleic Acids Research*, 1982, 10, 6243; B.S. Sproat, and W. Bannwarth, *Tetrahedron Letters*, 1983, 24, 5771; M.D. Matteucci and M.H. Caruthers, *Tetrahedron Letters*, 1980, 21, 719; M.D. Matteucci and M.H. Caruthers, *Journal of the American Chemical Society*, 1981, 103, 3185; S.P. Adams *et al.*, *Journal of the American Chemical Society*, 1983, 105, 661; N.D. Sinha, J. Biernat, J. McMannus, and H. Koester, *Nucleic Acids Research*, 1984, 12, 4539; and H.W.D. Matthes *et al.*, *EMBO Journal*, 1984, 3, 801.

The process of the invention may be performed by conventional recombinant techniques such as described in Maniatis *et al.*, *Molecular Cloning - A Laboratory Manual*; Cold Spring Harbor, 1982-1989.

In particular, the process may comprise the steps of :

- i) preparing a replicable or integrating expression vector capable, in a host cell, of expressing a DNA polymer comprising a nucleotide sequence that encodes the protein or an immunogenic derivative thereof;
- ii) transforming a host cell with said vector;

- iii) culturing said transformed host cell under conditions permitting expression of said DNA polymer to produce said protein; and
- iv) recovering said protein.

5 The term 'transforming' is used herein to mean the introduction of foreign DNA into a host cell. This can be achieved for example by transformation, transfection or infection with an appropriate plasmid or viral vector using e.g. conventional techniques as described in Genetic Engineering; Eds. S.M. Kingsman and A.J. Kingsman; Blackwell Scientific Publications; Oxford, England, 1988. The
10 term 'transformed' or 'transformant' will hereafter apply to the resulting host cell containing and expressing the foreign gene of interest.

The expression vectors are novel and also form part of the invention.

The replicable expression vectors may be prepared in accordance with the invention, by cleaving a vector compatible with the host cell to provide a linear
15 DNA segment having an intact replicon, and combining said linear segment with one or more DNA molecules which, together with said linear segment encode the desired product, such as the DNA polymer encoding the protein of the invention, or derivative thereof, under ligating conditions.

Thus, the DNA polymer may be preformed or formed during the
20 construction of the vector, as desired.

The choice of vector will be determined in part by the host cell, which may be prokaryotic or eukaryotic but are preferably E. Coli or CHO cells. Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses.

The preparation of the replicable expression vector may be carried out
25 conventionally with appropriate enzymes for restriction, polymerisation and ligation of the DNA, by procedures described in, for example, Maniatis *et al.* cited above.

The recombinant host cell is prepared, in accordance with the invention, by transforming a host cell with a replicable expression vector of the invention under transforming conditions. Suitable transforming conditions are conventional and are
30 described in, for example, Maniatis *et al.* cited above, or "DNA Cloning" Vol. II, D.M. Glover ed., IRL Press Ltd, 1985.

The choice of transforming conditions is determined by the host cell. Thus, a bacterial host such as *E. coli* may be treated with a solution of CaCl_2 (Cohen *et al.*, Proc. Nat. Acad. Sci., 1973, 69, 2110) or with a solution comprising a mixture of RbCl , MnCl_2 , potassium acetate and glycerol, and then with 3-[N-morpholino]-propane-sulphonic acid, RbCl and glycerol. Mammalian cells in culture may be transformed by calcium co-precipitation of the vector DNA onto the cells. The invention also extends to a host cell transformed with a replicable expression vector of the invention.

Culturing the transformed host cell under conditions permitting expression of the DNA polymer is carried out conventionally, as described in, for example, Maniatis *et al.* and "DNA Cloning" cited above. Thus, preferably the cell is supplied with nutrient and cultured at a temperature below 50°C .

The product is recovered by conventional methods according to the host cell and according to the localisation of the expression product (intracellular or secreted into the culture medium or into the cell periplasm). Thus, where the host cell is bacterial, such as *E. coli* it may, for example, be lysed physically, chemically or enzymatically and the protein product isolated from the resulting lysate. Where the host cell is mammalian, the product may generally be isolated from the nutrient medium or from cell free extracts. Conventional protein isolation techniques include selective precipitation, adsorption chromatography, and affinity chromatography including a monoclonal antibody affinity column.

The proteins of the present invention are provided either soluble in a liquid form or in a lyophilised form.

It is generally expected that each human dose will comprise 1 to 1000 μg of protein, and preferably 30 - 300 μg .

The present invention also provides pharmaceutical composition comprising a protein of the present invention in a pharmaceutically acceptable excipient. A preferred vaccine composition comprises at least Lipoprotein D - MAGE-3. Such vaccine may optionally contain one or more other tumor-associated antigen. For example other members belonging to the MAGE and GAGE families. Suitable other tumour associated antigen include MAGE-1, GAGE-1 or Tyrosinase proteins.

Vaccine preparation is generally described in Vaccine Design ("The subunit and adjuvant approach" (eds. Powell M.F. & Newman M.J). (1995) Plenum Press New York). Encapsulation within liposomes is described by Fullerton, US Patent 4,235,877.

5 The proteins of the present invention are preferably adjuvanted in the vaccine formulation of the invention. Suitable adjuvants include an aluminium salt such as aluminium hydroxide gel (alum) or aluminium phosphate, but may also be a salt of calcium, iron or zinc, or may be an insoluble suspension of acylated tyrosine, or acylated sugars, cationically or anionically derivatised polysaccharides,
10 or polyphosphazenes. Other known adjuvants include CpG containing oligonucleotides. The oligonucleotides are characterised in that the CpG dinucleotide is unmethylated. Such oligonucleotides are well known and are described in, for example WO96/02555.

 In the formulation of the inventions it is preferred that the adjuvant
15 composition induces an immune response preferentially of the TH1 type. Suitable adjuvant systems include, for example a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL) together with an aluminium salt. CpG oligonucleotides also preferentially induce a TH1 response.

 An enhanced system involves the combination of a monophosphoryl lipid A
20 and a saponin derivative particularly the combination of QS21 and 3D- MPL as disclosed in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol as disclosed in WO 96/33739.

 A particularly potent adjuvant formulation involving QS21 3D-MPL & tocopherol in an oil in water emulsion is described in WO 95/17210 and is a
25 preferred formulation.

 Accordingly in one embodiment of the present invention there is provided a vaccine comprising a protein of the present invention, more preferably a Lipoprotein D (or derivative thereof) - MAGE-3 adjuvanted with a monophosphoryl lipid A or derivative thereof.

30 Preferably the vaccine additionally comprises a saponin, more preferably QS21.

Preferably the formulation additionally comprises an oil in water emulsion and tocopherol. The present invention also provides a method for producing a vaccine formulation comprising mixing a protein of the present invention together with a pharmaceutically acceptable excipient, such as 3D-MPL.

5 In one aspect of the invention there is provided a process for purifying a recombinantly produced MAGE-protein. The process comprises solubilising the protein, for example in a strong chaotropic agent (such as for example, urea, guanidium hydrochloride), or in a Zwitterionic detergent, e.g. (Empigen BB - n-dodecyl- N,N-dimethylglycine), reducing the protein's intra and inter molecular
10 disulphide bonds, blocking the resulting thiols to prevent oxidative recoupling, and subjecting the protein to one or more chromatographic steps.

Preferably, the blocking agent is an alkylating agent. Such blocking agents include but are not limited to alpha haloacids or alpha haloamides. For example iodoacetic acid and iodoacetamide which results in carboxymethylation or
15 carboxyamidation (carbamidomethylation) of the protein. Other blocking agents may be used and are described in the literature (See for example, The Proteins Vol II Eds H Neurath, RL Hill and C-L Boeder, Academic press 1976, or Chemical Reagents for Protein modification Vol I eds. RL Lundblad and CM Noyes, CRC Press 1985). Typical examples of such other blocking agents include N -
20 ethylmaleimide, chloroacetyl phosphate, O-methylisourea and acrylonitrile. The use of the blocking agent is advantageous as it prevents aggregation of the product, and ensure stability for downstream purification.

In an embodiment of the invention the blocking agents are selected to induce a stable covalent and irreversible derivative (eg alpha halo acids or alpha
25 haloamides). However other blocking agents may be selected such that after purification the blocking agent may be removed to release the non derivatised protein.

MAGE proteins having derivatised free thiol residues are new and form an aspect of the invention. In particular carboxyamidated or carboxymethylated
30 derivatives are a preferred embodiment of the invention.

In a preferred embodiment of the invention the proteins of the present invention is provided with an affinity tag, such as CLYTA or a polyhistidine tail.

In such cases the protein after the blocking step is preferably subjected to affinity chromatography. For those proteins with a polyhistidine tail, immobilised metal ion affinity chromatography (IMAC) may be performed. The metal ion, may be any suitable ion for example zinc, nickel, iron, magnesium or copper, but is preferably zinc or nickel. Preferably the IMAC buffer contain a zwitterionic detergent such as Empigen BB (hereinafter Empigen) as this results in lower levels of endotoxin in the final product.

If the protein is produced with a Clyta part, the protein may be purified by exploiting its affinity to choline or choline analogues such as DEAE. In an embodiment of the invention the proteins are provided with a polyhistidine tail and a Clyta part. These may purified in a simple two step affinity chromatographic purification schedule.

The invention will be further described by reference to the following examples:

15

EXAMPLE I:**Preparation of the recombinant *E. coli* strain expressing the fusion protein Lipoprotein D-MAGE-3-His (LPD 1/3-MAGE-3-His or LpD MAGE-3-His)**

20

1. The *E. Coli* expression system:

For the production of Lipoprotein D the DNA encoding protein D has been cloned into the expression vector pMG 81. This plasmid utilizes signals from lambda phage DNA to drive the transcription and translation of inserted foreign genes. The vector contains the lambda PL promoter PL, operator OL and two utilization sites (NutL and NutR) to relieve transcriptional polarity effects when N protein is provided (Gross et al., 1985. Mol. & Cell. Biol. 5:1015). Vectors containing the PL promoter, are introduced into an *E. coli* lysogenic host to stabilize the plasmid DNA. Lysogenic host strains contain replication-defective lambda phage DNA integrated into the genome (Shatzman et al., 1983; In Experimental Manipulation of Gene Expression. Inouya (ed) pp 1-14. Academic

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Press NY). The lambda phage DNA directs the synthesis of the cI repressor protein which binds to the OL repressor of the vector and prevents binding of RNA polymerase to the PL promoter and thereby transcription of the inserted gene. The cI gene of the expression strain AR58 contains a temperature sensitive mutation so that PL directed transcription can be regulated by temperature shift, i.e. an increase in culture temperature inactivates the repressor and synthesis of the foreign protein is initiated. This expression system allows controlled synthesis of foreign proteins especially of those that may be toxic to the cell (Shimataka & Rosenberg, 1981. Nature 292:128).

10

2. The E. Coli strain AR58:

The AR58 lysogenic E. coli strain used for the production of the LPD-MAGE-3-His protein is a derivative of the standard NIH E.coli K12 strain N99 (F-su- galK2, lacZ- thr-). It contains a defective lysogenic lambda phage (galE::TN10, 1 Kil- cI857 DH1). The Kil- phenotype prevents the shut off of host macromolecular synthesis. The cI857 mutation confers a temperature sensitive lesion to the cI repressor. The DH1 deletion removes the lambda phage right operon and the hosts bio, uvr3, and chlA loci. The AR58 strain was generated by transduction of N99 with a P lambda phage stock previously grown on an SA500 derivative (galE::TN10, 1 Kil- cI857 DH1). The introduction of the defective lysogen into N99 was selected with tetracycline by virtue of the presence of a TN10 transposon coding for tetracyclin resistance in the adjacent galE gene. N99 and SA500 are E.coli K12 strains derived from Dr. Martin Rosenberg's laboratory at the National Institutes of Health.

25

3. Construction of the vector designed to express the recombinant protein LPD-MAGE-3-His:

The rationale was to express MAGE 3 as a fusion protein using the N-terminal third of the lipidated protein D as fusion partner connected at the N-

30

terminus of MAGE-3 and a sequence of several histidine residues (His tail) placed at its C-terminus.

Protein D is a lipoprotein (a 42 kDa immunoglobulin D binding protein exposed on the surface of the Gram-negative bacterium *Haemophilus influenzae*).
5 The protein is synthesized as a precursor with an 18 amino acid residue signal sequence, containing a consensus sequence for bacterial lipoprotein (WO 91/18926).

When the signal sequence of a lipoprotein is processed during secretion, the Cys (at position 19 in the precursor molecule) becomes the amino terminal residue and is concomitantly modified by covalent attachment of both ester-linked and
10 amide-linked fatty acids.

The fatty acids linked to the amino-terminal cysteine residue then function as membrane anchor.

The plasmid expressing the fusion protein was designed to express a precursor protein containing the 18 amino acids signal sequence and the first 109
15 residues of the processed protein D, two unrelated amino acids (Met and Asp), amino acid residues 2 to 314 of MAGE-3, two Gly residues functioning as a hinge region to expose the subsequent seven His residues.

The recombinant strain thus produces the processed lipidated His tailed fusion protein of 432 amino acid residues long (see Figure 1), with the amino acids
20 sequence described in ID No1 and the coding sequence is described in ID No2.

4. Cloning strategy for the generation of the LPD-MAGE-3-His fusion protein (vector pRIT14477):

25 A cDNA plasmid (from Dr Thierry Boon from the Ludwig Institute) containing the coding sequence for MAGE-3 gene (Gaugler B *et al*, 1994), and the vector PRIT 14586, containing the N terminal portion of the Lipo-D-1/3 coding sequence (prepared as outlined in Figure 2) were used. The cloning strategy included the following steps (Figure 3).

30

a) - PCR amplification of the sequences presented in the plasmid cDNA MAGE 3 using the oligonucleotide sense: 5' gc gcc atg gat ctg gaa cag cgt agt cag

cac tgc aag cct, and the oligonucleotide antisense: 5' gcg tct aga tta atg gtg atg gtg atg gtg atg acc gcc ctc ttc ccc ctc tct caa); this amplification leads to the following modifications at the N terminus: changing of the first five codons to *E. coli* codon usage, replacement of the Pro codon by an Asp codon at position 1, installation of an NcoI site at the 5' extremity and finally addition of two 2 Gly codons and the 7 His codon followed by an XbaI site at the C-terminus.

b) - Cloning into the TA cloning vector of invitrogen of the above amplified fragment and preparation of the intermediate vector pRIT14647.

10

c) - Excision of the NcoI XbaI fragment from plasmid pRIT14647 and cloning into the vector pRIT 14586.

d) - Transformation of the host strain AR58.

15

e) - Selection and characterization of the *E. coli* strain transformants containing the plasmid pRIT 14477, expressing the LPD-MAGE-3-His fusion protein.

20 EXAMPLE II:

Preparation of the LPD1/3 - MAGE-3 -His antigen:

1. Growth and induction of bacterial strain - Expression of LPD1/3

25 -MAGE-3 -His:

Cells of AR58 transformed with plasmid pRIT14477 were grown in 2 litre flasks, each containing 400 mL of LY12 medium supplemented with yeast extract (6.4 g/L) and kanamycin sulphate (50 mg/L). After incubation on a shaking table at 30°C for 8 +/- 1 h, a small sample was removed from each flask for microscopic examination. The contents of the two flasks were pooled to provide the inoculum for the 20 litre fermentor.

The inoculum (about 800 mL) was added to a pre-sterilised 20 litre (total volume) fermentor containing 7 litres of medium, supplemented with 50 mg/L of kanamycin sulphate. The pH was adjusted to and maintained at 6.8 by the periodic addition of NH_4OH (25 % v/v), and the temperature was adjusted to and maintained at 30°C. The aeration rate was adjusted to and maintained at 12 litres of air/min and the dissolved oxygen tension was maintained at 50 % of saturation by feedback control of the agitation speed. The over-pressure in the fermentor was maintained at 500 g/cm² (0.5 bar).

The fed-batch cultivation was carried out by controlled addition of a carbon feed solution. The feed solution was added at an initial rate of 0.04 mL/min, and increased exponentially during the first 42 hours to maintain a growth rate of 0.1 h⁻¹.

After 42 hours, the temperature in the fermentor was rapidly increased to 39°C, and the feeding speed was maintained constant at 0.005 mL/g DCW/min during the induction phase for an additional 22-23 hours, during which time intracellular expression of LPD-MAGE-3-His reached a maximum level.

Aliquots (15 mL) of broth were taken at regular intervals throughout the growth/induction phases and at the end of the fermentation to follow the kinetics of microbial growth and intracellular product expression and in addition, to provide samples for microbial identification/purity tests.

At the end of fermentation, the optical density of the culture was between 80 and 120 (corresponding to a cell concentration of between 48 and 72 g DCW/L), and the total liquid volume was approximately 12 litres. The culture was rapidly cooled to between 6 and 10°C, and the cells of ECK32 were separated from the culture broth by centrifugation at 5000 x g at 4°C for 30 minutes. The concentrated cells of ECK32 were quickly stored in plastic bags and immediately frozen at -80°C.

2. Extraction of the protein:

The frozen concentrated cells of ECK32 were thawed to 4°C before being re-suspended in cell disruption buffer to a final optical density of 60 (corresponding to a cell concentration of approximately 36 g DCW/L).

The cells were disrupted by two passes through a high-pressure homogeniser (1000 bar). The broken cell suspension was centrifuged (x 10 000g at 4°C for 30 minutes) and the pellet fraction was washed twice with Triton X100 (1% w/v) + EDTA (1 mM), followed by a wash with phosphate buffered saline (PBS) + Tween* 20 (0.1% v/v) and finally a wash with PBS. Between each washing stage, the suspension was centrifuged at x 10 000g for 30 minutes at 4°C, the supernatant was discarded and the pellet fraction was retained.

EXAMPLE III:

15

Characterisation of fusion Protein Lipo D - MAGE 3:

1. Purification:

20 LPD-MAGE-3-His was purified from the cell homogenate using a sequence of steps described below:

- a) - Solubilisation of the washed pellet fraction from cell disruption,
- b) - Chemical reduction of intra- and inter-protein disulphide bonds followed by blocking of thiol groups to prevent oxidative re-coupling,
- c) - Microfiltration of the reaction mixture for the removal of particulates and reduction of endotoxins,
- d) - Capture and primary purification of LPD-MAGE-3-His by exploitation of the affinity interaction between the polyhistidine tail and zinc-loaded Chelating Sepharose*,
- e) - Removal of contaminant proteins by anion exchange chromatography.

30

* Trade-mark

The purified LPD-MAGE 3-His was subjected to a number of polishing stages:

- f) - Buffer exchange/urea removal by size exclusion chromatography using Superdex^{*} 75,
- 5 g) - In-process filtration,
- h) - Buffer exchange/desalting by size exclusion chromatography using Sephadex^{*} G25.

Each of these steps is described in more detail below:

10

1.1) - Solubilisation of cell homogenate pellet

The pellet fraction from the final washing stage (as described above) was re-solubilised overnight in 800 mL of a solution of guanidine hydrochloride (6M) and sodium phosphate (0.1 M, pH 7.0) at 4°C.

15

1.2) - Reduction and carboxymethylation

The solubilised material (a pale yellow, turbid suspension) was flushed with argon to purge any remaining oxygen, and a stock solution of 2-mercaptoethanol (14M) was added to provide a final concentration of 4.3M (which corresponded to 20 0.44 mL of 2-mercaptoethanol per mL of solution).

The resulting solution was divided and transferred into two glass flasks which were both heated to 95 °C in a water bath. After 15 minutes at 95 °C, the flasks were removed from the water bath and allowed to cool, whereupon the contents were pooled into a foil-covered beaker (5 L), placed on ice, and solid 25 iodoacetamide added with vigorous mixing to provide a final concentration of 6M (which corresponded to 1.11 g of iodoacetamide per mL of solution). The mixture was held on ice in the dark for 1 hour to ensure complete solubilisation of iodoacetamide, before being neutralised (maintaining vigorous mixing and continuous pH monitoring) by the addition of approximately 1 litre of sodium 30 hydroxide (5 M) to give a final pH of 7.5-7.8.

The resulting mixture was maintained on ice in the dark for a further 30 minutes, after which time the pH was re-adjusted to pH 7.5-7.8.

* Trade-mark

1.3) - Microfiltration

The mixture was microfiltered in an Amicon Proflux M12 tangential-flow unit equipped with a Minikros hollow fibre cartridge (ref. No. M22M-600-01N; area 5,600 cm², 0.2 μm). The permeate was retained for subsequent
5 chromatographic purification.

1.4) - Metal (Zn²⁺) chelate chromatography (IMAC)

Metal chelate chromatography was performed with Chelating Sepharose FF (Pharmacia Biotechnology Cat. No. 17-0575-01) packed into a BPG 100/500
10 column (Pharmacia Biotechnology Cat No. 18-1103-01). The dimensions of the packed bed were: diameter 10 cm; cross-sectional area 79 cm²; bed height 19 cm; packed volume 1,500 mL. The empty column was sanitised with sodium hydroxide (0.5M), then washed with purified water.

The support (delivered in 20 % v/v ethanol) was washed with purified water
15 (8 litres) on a Buchner funnel (under vacuum) and charged with zinc by passing at least 15 litres of a solution of ZnCl₂ (0.1M). Excess zinc was removed by washing the support with 10 litres of purified water, until the pH of the outlet liquid reached the pH of the ZnCl₂ solution (pH 5.0). The support was then equilibrated with 4
litres of a solution containing guanidine hydrochloride (6M) and sodium phosphate
20 (0.1M, pH 7.0).

The permeate from microfiltration, containing LPD-MAGE-3-His, was mixed with the support (batch binding), before loading and packing the BPG column with the solution containing guanidine hydrochloride (6M) and sodium phosphate (0.1M, pH 7.0).

25 The next stages of metal chelate chromatography were conducted at an eluent flow rate of 60 mL/min. The column was washed, first with the solution containing guanidine hydrochloride (6M) and sodium phosphate (0.1M, pH 7.0), then with the solution containing urea (6M) and sodium phosphate (0.1M, pH 7.0), until the column eluent attained zero absorbance at OD₂₈₀ nm (baseline).

30 The semi-pure LPD-MAGE-3-His protein fraction was eluted with 2 column volumes of a solution containing urea (6M), sodium phosphate (0.1M, pH 7.0) and imidazole (0.5M). The conductance of this fraction was approximately 16 mS/cm.

1.5) - Anion exchange chromatography

Before continuing with anion exchange chromatography, the conductance of the semi-pure LPD-MAGE-3-His protein fraction was reduced to approximately 4 mS/cm by dilution with a solution containing urea (6M) and Tris-HCl (20 mM, pH 8.0).

Anion exchange chromatography was performed using Q-Sepharose FF (Pharmacia Biotechnology, Cat. No. 17-0510-01) packed in a BPG 200/500 column (Pharmacia Biotechnology Cat. No. 18-1103-11). The dimensions of the packed bed were: diameter 10 cm; cross-sectional area 314 cm²; bed height 9 cm; packed volume 2,900 mL.

The column was packed (with 20 % v/v ethanol) and washed with 9 litres of purified water at an eluent flow rate of 70 mL/min. The packed column was sanitised with 3 litres of sodium hydroxide (0.5M), washed with 30 litres of purified water, then equilibrated with 6 litres of a solution containing urea (6M) and Tris-HCl (20 mM, pH 8.0). The diluted, semi-purified LPD-MAGE-3-His was loaded onto the column and then washed with 9 litres of a solution containing urea (6M), Tris-HCl (20 mM, pH 8.0), EDTA (1mM) and Tween (0.1 %), until the absorbance (280 nm) of the eluent fell to zero.

A further washing step was performed with 6 litres of a solution containing urea (6M) and Tris-HCl (20 mM, pH 8.0).

The purified LPD-MAGE-3-His was eluted from the column with a solution containing urea (6M), Tris-HCl (20 mM, pH 8.0) and NaCl (0.25M).

1.6) - Size exclusion chromatography

The removal of urea from purified LPD-MAGE-3-His and the buffer exchange were both achieved by size exclusion chromatography. This was performed using Superdex 75 (Pharmacia Biotechnology Cat. No. 17-1044-01) packed in an XK 50/100 column (Pharmacia Biotechnology Cat. No. 18-8753-01). The dimensions of the packed bed were: diameter 5 cm; cross-sectional area 19.6 cm²; bed height 90 cm; packed volume 1,800 mL.

The column was packed in ethanol (20 %) and washed with 5 litres of purified water at an effluent flow rate of 20 mL/min. The column was sanitised with 2 litres of sodium hydroxide (0.5M), washed with 5 litres of purified water, then equilibrated with 5 litres of phosphate-buffered saline containing Tween 80 (0.1 %
5 v/v).

The purified LPD-MAGE-3-His fraction (maximum 500 mL/ desalting run) was loaded onto the column at an eluent flow rate of 20 mL/min. The desalted purified LPD-MAGE-3-His was eluted from the column with 3 litres of PBS containing Tween 80 (0.1 % v/v).

10 The fraction containing LPD-MAGE-3-His eluted at the void volume of the column.

1.7) - In-process filtration

The bulk LPD-MAGE-3-His from size exclusion chromatography was
15 filtered through a 0.22 µm membrane in a laminar flow hood (class 10.000). The filtered bulk was frozen at -80 °C and stored until the desalting step.

1.8) - Desalting chromatography

Since the osmolality of the final bulk should be less than 400 mOsM, a
20 further buffer exchange step was required to reduce the salt concentration. This was performed by a desalting chromatographic step using Sephadex G25 (Pharmacia Biotechnology Cat. No. 17-0033-02) packed in a BPG 100/950 column (Pharmacia Biotechnology Cat. No. 18-1103-03). The dimensions of the packed bed were: diameter 10 cm; cross-sectional area 78.6 cm²; bed height 85 cm; packed volume
25 6,500 mL.

The Sephadex G25 was hydrated with 7 litres of purified water and allowed to swell overnight at 4 °C. The gel was then packed in the column with pure water at an eluent flow rate of 100 mL/min.

The column was sanitised with 6 litres of sodium hydroxide (0.5M), then
30 equilibrated with 10 litres of a solution containing sodium phosphate (10 mM, pH 6.8), NaCl (20 mM) and Tween 80 (0.1 % v/v).

The purified LPD-MAGE-3-His fraction (maximum 1500 mL/desalting run) was loaded onto the column at an eluent flow rate of 100 mL/min. The desalted purified LPD-MAGE-3-His fraction eluted at the void volume of the column, was sterile filtered through a 0.22 μ m membrane and stored at -80°C.

- 5 The final bulk protein is thawed to +4°C before being aliquoted into vials and freeze-dried in a lactose excipient (3.2%).

2. Analysis on Coomassie-stained SDS-polyacrylamide gels:

- 10 The LPD-MAGE-3-His purified antigen was analysed by SDS-PAGE on a 12.5% acrylamide gel in reducing conditions.

The protein load was 50 μ g for Coomassie blue staining and 5 μ g for silver nitrate staining. Clinical lot 96K19 and pilot lot 96J22 were analyzed. One major band corresponding to a molecular weight of 60kDa was visualised. Two minor
15 additional bands of approximately 45kDa and 35 kDa were also seen.

3. Western Blot Analysis:

- 20 The peptides revealed by SDS-PAGE analysis of the LPD-MAGE-3-His protein were identified by Western blot using mouse monoclonal antibodies. These antibodies were developed in-house using a purified preparation of the MAGE-3-His protein (this protein does not contain the LPD part of the LPD-MAGE-3-His).

Two monoclonal antibody preparations (Mab 22 and Mab 54) have been selected on the basis of their suitability for Western blot analysis and used in the
25 identity test for lot release. Figure 4 shows the band patterns obtained for lots 96K19 and 96J22 after staining with Mabs 32 and 54. Six hundred (600) ng of protein were resolved on a 12.5% SDS-PAGE, transferred to a nylon membrane, reacted with Mabs 32 and 54 (60 μ g/ml) and revealed with anti-mouse antibodies coupled to peroxidase.

- 30 The 60 kDa and 30 kDa peptide detected by SDS-PAGE are revealed by both Mabs.

EXAMPLE IV:**1. Vaccine preparation using LPD-MAGE-3-His protein:**

5 The vaccine used in these experiments is produced from a recombinant DNA, encoding a Lipoprotein D 1/3-MAGE-3-His, expressed in *E. coli* from the strain AR58, either adjuvanted or not. As an adjuvant, the formulation comprises a mixture of 3 de -O-acylated monophosphoryl lipid A (3D-MPL) and QS21 in an oil/water emulsion. The adjuvant system SBAS2 has been previously described WO
10 95/17210.

3D-MPL: is an immunostimulant derived from the lipopolysaccharide (LPS) of the Gram-negative bacterium *Salmonella minnesota*. MPL has been deacylated and is lacking a phosphate group on the lipid A moiety. This chemical treatment
15 dramatically reduces toxicity while preserving the immunostimulant properties (Ribi, 1986). Ribi Immunochemistry produces and supplies MPL to SB-Biologicals. Experiments performed at Smith Kline Beecham Biologicals have shown that 3D-MPL combined with various vehicles strongly enhances both the humoral and a
20 TH1 type of cellular immunity.

QS21: is a natural saponin molecule extracted from the bark of the South American tree *Quillaja saponaria* Molina. A purification technique developed to separate the individual saponines from the crude extracts of the bark, permitted the isolation of the particular saponin, QS21, which is a triterpene glycoside
25 demonstrating stronger adjuvant activity and lower toxicity as compared with the parent component. QS21 has been shown to activate MHC class I restricted CTLs to several subunit Ags, as well as to stimulate Ag specific lymphocytic proliferation (Kensil, 1992). Aquila (formally Cambridge Biotech Corporation) produces and supplies QS21 to SB-Biologicals.

30 Experiments performed at SmithKline Beecham Biologicals have demonstrated a clear synergistic effect of combinations of MPL and QS21 in the induction of both humoral and TH1 type cellular immune responses.

The oil/water emulsion is composed an organic phase made of of 2 oils (a tocopherol and squalene), and an aqueous phase of PBS containing Tween 80 as emulsifier. The emulsion comprised 5% squalene 5% tocopherol 0.4% Tween 80
5 and had an average particle size of 180 nm and is known as SB62 (see WO 95/17210).

Experiments performed at SmithKline Beecham Biologicals have proven that the adjunction of this O/W emulsion to 3D-MPL/QS21 (SBAS2) further increases the
10 immunostimulant properties of the latter against various subunit antigens.

2. Preparation of emulsion SB62 (2 fold concentrate):

Tween 80 is dissolved in phosphate buffered saline (PBS) to give a 2%
15 solution in the PBS. To provide 100 ml two fold concentrate emulsion 5g of DL alpha tocopherol and 5ml of squalene are vortexed to mix thoroughly. 90ml of PBS/Tween solution is added and mixed thoroughly. The resulting emulsion is then passed through a syringe and finally microfluidised by using an M110S microfluidics machine. The resulting oil droplets have a size of approximately 180
20 nm.

3. Preparation of Lipoprot. D1/3 - MAGE-3-His QS21/3D MPL oil in water (SBAS2) formulation:

25 The adjuvant is formulated as a combination of MPL and QS21, in an oil/water emulsion. This preparation is delivered in vials of 0.7 ml to be admixed with the lyophilised antigen (vials containing from 30 to 300 μ g antigen).

The composition of the adjuvant diluent for the lyophilised vaccine is as follows :

Ingredients:	Quantity (per dose):
<u>Adjuvants</u>	
SB62 Emulsion:	250 μ l
- Squalene	10.7 mg
- DL α -tocopherol	11.9 mg
- Tween 80	4.8 mg
Monophosphoryl Lipid A	100 μ g
QS21	100 μ g
<u>Preservative</u>	
Thiomersal	25 μ g
<u>Buffer</u>	
Water for injection	q.s. ad 0.5 ml
- Dibasic sodium phosphate	575 μ g
- Monobasic potassium phosphate	100 μ g
- Potassium chloride	100 μ g
- Sodium chloride	4.0 mg

The final vaccine is obtained after reconstitution of the lyophilised
5 LPD-MAGE-3-His preparation with the adjuvant or with PBS alone.

The adjuvants controls without antigen were prepared by replacing the
protein by PBS.

4. Vaccine antigen: Fusion protein Lipoprotein D1/3 - MAGE-3-His:

10

Lipoprotein D is a lipoprotein exposed on the surface of the Gram-negative
bacteria *Haemophilus influenzae*.

The inclusion of the first 109 residues of the processed protein D as fusion partner is incorporated to provide the vaccine antigen with a T-cell epitopes. Besides the LPD moiety, the protein contains two unrelated amino acids (Met and Asp), amino acid residues 2 to 314 of Mage-3, two Gly residues functioning as hinge region to expose the subsequent seven His residues.

EXAMPLE V:

1. Immunogenicity of LPD-MAGE-3-His in mice and monkeys:

10

In order to test the antigenicity and immunogenicity of the human MAGE-3 protein, the candidate vaccine was injected into 2 different mouse strains (C57BL/6 and Balb/C), varying in their genetic background and MHC alleles.

For both mouse strains, potential MHC class-I and MHC class-II peptide motifs were theoretically predicted for the MAGE part of the LPD-MAGE-3-His fusion protein.

15

a) - Immunization protocol:

5 mice of each strain were injected twice at 2 weeks interval in the foot pad with 5 μ g of LPD-MAGE-3-His, formulated or not in SBAS2 at 1/10th of the concentration used in human settings.

20

b) - Proliferation assay:

Lymphocytes were prepared by crushing the spleen or the popliteal lymph nodes from the mice, 2 weeks after the last injection. 2×10^5 cells were placed in triplicate in 96 well plates and the cells were re-stimulated in vitro for 72 hours with different concentrations (1- 0.1 μ g/ml) of His-Mage 3 as such or coated onto latex micro-beads.

25

An increased MAGE-3 specific lymphoproliferative activity was observed with both spleen cells (see Figures 5 and 7) and lymph node cells (see Figures 6 and 8) from either C57BL/6 or Balb/C mice injected with the LPD-MAGE-3-His

30

protein, as compared with the lymphoproliferative response of mice having received the SBAS-2 formulation alone or PBS.

Moreover, a significant higher proliferative response was obtained with lymphocytes from mice immunized with LPD-MAGE-3-His in the adjuvant SBAS2
5 (see Figures 6 and 8).

c) - Conclusion:

LPD-MAGE-3-His is immunogenic in mice, and this immunogenicity can be increased by the use of the SBAS2 adjuvant formulation.

10

2. Antibody response:

a) - Immunization Protocol:

Balb/c or C57BL/6 mice were immunized by 2 intra foot pad injections at 2
15 weeks interval with either PBS, or SBAS2, or 5 μ G of LPD-MAGE-3-His, or 5 μ G of LPD-MAGE-3-His + SBAS2.

Three and five animals were used in the control groups and in the tested groups respectively.

20

b) - Indirect ELISA:

Two weeks after the second injection, individual sera were taken and submitted to an indirect ELISA.

2 μ G/ml of purified His MAGE 3 was used as coated antigen. After saturation during 1 hour at 37°C, in PBS + 1% newborn calf serum, the sera were serially
25 diluted (starting at 1/1000) in the saturation buffer and incubated overnight at 4°C, or 90 minutes at 37°C. After washing in PBS/Tween 20,01%, Biotinylated goat anti-mouse total IgG (1/1000) or goat anti-mouse IgG1, IgG2a, IgG2b antisera (1/5000) were used as second antibodies. After 90 minutes incubation at 37°C. Streptavidin coupled to peroxidase was added, and TMB (tetra-methyl-benzidine
30 peroxide) was used as substrate. After 10 minutes the reaction was blocked by addition of H₂SO₄ 0.5M, and the O.D. was determined.

c) - Results:

Figure 9 compares between the different groups of mice (N=5/group), the relative mean midpoint titer of the sera, which consists in the mean dilution needed to reach the midpoint of the curves.

5 These results show that in both mouse strains tested, a weak Ab response is mounted after 2 injections of LPD-MAGE-3-His alone, but that higher anti-MAGE 3 Ab concentrations are generated when LPD-MAGE-3-His is injected in the presence of SBAS2. Thus, only 2 injections of LPD-MAGE-3-His + SBAS2, at 2 weeks interval, are sufficient to generate the high Ab response observed.

10 The better Ab response observed in the Balb/c mice as compared with the response obtained in the C57BL/6 mice can be explained by differences in haplotypes or in background between these 2 strains, even though the Ab titre achieved in C57BL/6 mice is also higher after injections of LPD-MAGE-3-His + SBAS2 than after injections with LPD-MAGE-3-His alone.

15 The Ig subclasses-specific anti-MAGE-3 responses after vaccinations in the different groups of mice can be seen on the figures 10 and 11, which give a comparison of the mean midpoint dilution of the sera.

 Neither IgA, nor IgM were detected in any of the serum samples even from the mice vaccinated with LPD-MAGE-3-His in the adjuvant SBAS2.

20 On the contrary, the total IgG level was slightly higher in the sera from mice vaccinated with LPD-MAGE-3-His alone, and significantly increased in the sera of animals injected with LPD-MAGE-3-His in SBAS2.

 The analysis of the different IgG-subclasses concentrations show that a mixed Ab response was induced in the mice, since the levels of all IgG subclasses tested (IgG1, IgG2a, IgG2b) were higher in mice vaccinated with the adjuvanted Ag than in mice injected with the Ag or the adjuvant alone.

25 The nature of this mixed Ab response after vaccination with LipoD-MAGE 3 in the presence of SBAS2 seems however to depend on the mouse strain, since IgG1 and IgG2b were predominantly found in the sera of Balb/c and C57BL/6 mice
30 respectively.

3. Immunogenicity of Lipoprotein D 1/3 MAGE-3 - His + SBAS2 adjuvant in Rhesus monkeys

Three groups of five Rhesus (*Macaca Mulatta*) animals were selected. RTS,S and gp120 were used as positive control.

Groups:

Group 1 right leg: RTS,S/SBAS2
left leg: GP120/SBAS2

Group 2 right leg: RTS,S/SB26T
left leg: GP120/SB26T

Group 3 right leg: LipoD1/3 Mage 3 His/SBAS2

The animals received vaccine at day 0 and were boosted at day 28, and 84 and bled to determine their antibody response to both the MAGE 3 and protein D component. The vaccines were administered intramuscularly as a bolus injection (0.5ml) in the posterior part of the right leg.

Small blood samples were taken every 14 days. Unheparinized blood samples of 3 ml were collected from the femoral vein, were allowed to clot for at least 1 hour and centrifuged at room temperature for 10 minutes at 2500 rpm.

Serum was removed, frozen at -20°C and sent for determination of the antibody levels by specific Elisa.

96well microplates (maxisorb Nunc) were either coated with 5 µg of His Mage 3 or Protein D overnight at 4°C. After 1 hour saturation at 37°C with PBS NCS 1%, serial dilution of the rabbit sera were added for 1H 30 at 37°C (starting at 1/10), after 3 washings in PBS Tween, anti rabbit biotinylated serum (Amersham ref RPN 1004 lot 88) was added (1/5000). Plates were washed and peroxydase couple streptavidin (1/5000) was added for 30 minutes at 37°C. After washing, 50 µl TMB (BioRad) was added for 7 minutes and the reaction was stopped with H2S04 0.2M, OD was measured at 450 nm. Midpoint dilutions were calculated by SoftmaxPro.

Antibody response:

Small blood samples were taken every 14 days to follow the kinetic of the antibody response to Mage 3 by ELISA. The results indicates that after one injection of LPD1/3 Mage 3 His + SBAS2, the Mage 3 specific total Ig titer was low, a clear boost was seen in 3 out of 5 animals after a second and a third injection of LipoD1/3 Mage 3 + adjuvant in the same monkeys. The poor responders remained negative even after 3 injections. 28 days post II or post III, the antibody titers has returned to basal levels. The subclass of these antibodies was determined as predominantly IgG and not IgM. The switch to IgG suggests that a T helper response has been triggered . The Protein D specific antibody response, although weaker, is exactly parallel to the Mage 3 antibody response.

EXAMPLE VI:

15

1. LPD - MAGE 1 His

In an analogous fashion - LPD - MAGE 1-His was prepared. The amino acid and DNA sequences are depicted in SEQUENCE ID Nos. 3 and 4. The resulting protein was purified in an analogous manner to the LPD-MAGE-3-His protein. Briefly, the cell culture were homogenated and treated with 4M guanidine HCl and 0.5 M beta mercaptoethanol in the presence of 0.5% Empigen detergent. The product was filtered and the permeate treated with 0.6 M iodoacetamide. The carboxyamidated fractions was subjected to IMAC (zinc Chealate-sepharose FF) chromatography. The column was first equilbrated and washed with a solution containing 4M guanidine. HCl and sodium phosphate (20mM, pH7.5) and 0.5% Empigen, then the column was washed with a solution containing 4M urea in sodium phosphate (20mM, pH7.5) 0.5% Empigen buffer. The protein was eluated in the same buffer, but with increasing concentration of Imidazole (20mM, 400mM and 500 mM).

30

The eluate was diluted with 4M Urea. The Q-sepharose column was equilabrated and washed with 4M Urea in 20mM phosphate buffer (pH7.5) in the presence of 0.5% Empigen. A second wash was performed in the same buffer, but

devoid of the detergent. The protein eluted in the same buffer but with increasing Imidazole (150mM, 400mM, 1M). The eluate was ultra filtered.

EXAMPLE VII:

5

Construction of the expression plasmid pRIT14426 and transformation of the host strain AR58 to produce NS1 - MAGE -3 His:

Protein design:

10 The design of the fusion protein NS₁,-MAGE-3-His to be expressed in E. coli is described in figure 12.

The primary structure of the resulting protein has the sequence set forth in ID No. 5.

The coding sequence(ID No. 6) corresponding to the above protein design was placed under the control of λ pL promoter in a E. coli expression plasmid.

15

The cloning strategy for the generation of NS₁-MAGE-3-His fusion protein:

20 The starting material was a cDNA plasmid received from Dr Thierry Boon from the Ludwig Institute, containing the coding sequence for MAGE-3 gene and the vector PMG81, containing the 81aa of NS₁ (Non structural protein) coding region from Influenza.

The cloning strategy outlined in figure 13 included the following steps:

- 25 a) PCR amplification of the sequences presented in the plasmid cDNA MAGE-3 using the oligonucleotide sense: 5' gc gcc atg gat ctg gaa cag cgt agt cag cac tgc aag cct, and the oligonucleotide antisense: 5' gcg tct aga tta atg gtg atg gtg atg gtg atg acc gcc ctc ttc ccc ctc tct caa.

This amplification leads to the following modifications at the N terminus: changing of the first five codons to the E. coli codon usage, replacement of the

Pro codon by an Asp codon at position 1, installation of an NcoI site at the 5' extremity and finally addition of the 2 Gly codons and the 7 His codon followed by an XbaI site at the C-terminus.

- 5 b) Cloning into the TA cloning vector of invitrogen of the above amplified fragment and preparation of the intermediate vector pRIT14647
- c) Excision of the NcoI XbaI fragment from plasmid pRIT14647 and cloning into the vector pRIT PMG81
- 10 d) Transformation of the host strain AR58
- e) Selection and characterization of the E. coli strain transformants containing the plasmid pRIT14426 (see figure 14) expressing the NS1-MAGE-3-His fusion
- 15 protein

Characterization of the recombinant NS₁-MAGE-3-His (pRIT14426):

Bacteria were grown on LB Medium supplemented with 50 µg/ml kanamycin at 30 °C. When the culture had reached OD= 0.3 (at 620 nm), heat

20 induction was achieved by raising the temperature to 42 °C.

After 4 hours induction, cells were harvested, resuspended in PBS and lysed (by disintegration) by pressing three times in the French press. After centrifugation (60 minutes at 100 ,000 g), pellet supernatant and total extract were analyzed by SDS-PAGE. Proteins were visualized in Coomassie B1 stained gels where the

25 fusion protein represented about 1 % of the total E. coli proteins. The recombinant protein appeared as a single band with an apparent MW of 44,9 K. The fusion protein was identified by Western Blot analysis using anti-NS 1 monoclonal.

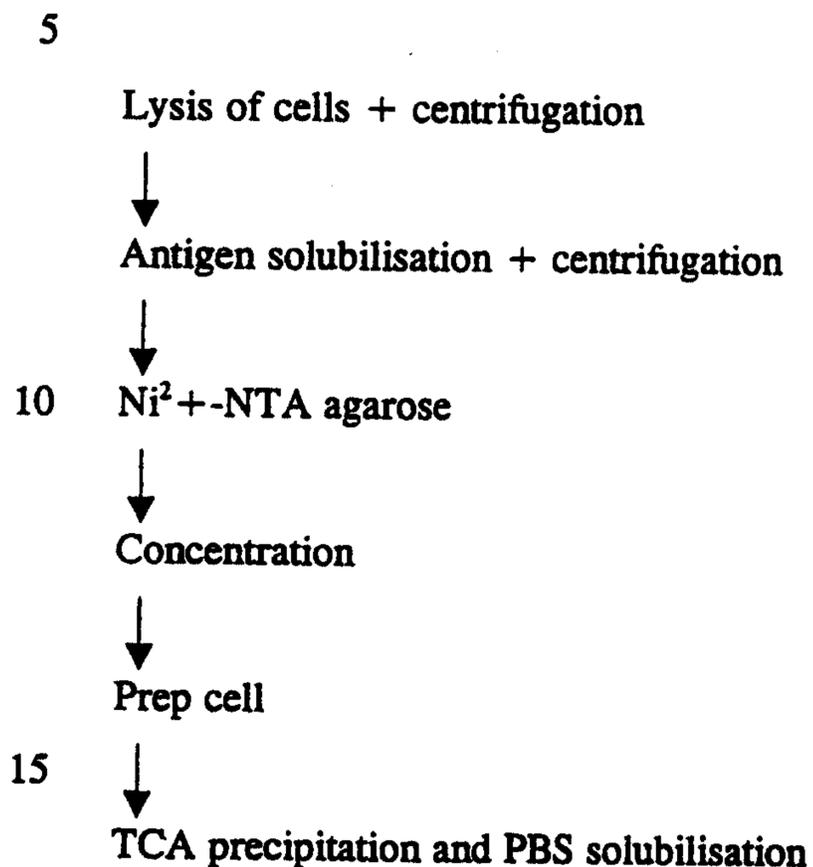
EXAMPLE VIII:

30

Purification of NS1-MAGE 3-His (E. Coli) for Rabbit/Mice Immunization.

Purification Scheme:

The following purification scheme was used to purify the antigen:

**a. Lysis**

20 Bacterial cells (23g) were lysed in 203 ml of a 50 mM PO₄ pH7 buffer by Rannie (homogeniser) and the lysate was centrifuged in a JA 20 rotor at 15,000 rpm during 30 minutes.

The supernatant was discarded.

25 b. Antigen solubilisation

1/3 of the pellet was resolubilised O/N at 4°C in 34 ml of 100 mM PO₄ - 6 M GuHC1 pH7. After centrifugation in a JA 20 rotor at 15,000 rpm for 30 minutes, the pellet was discarded and the supernatant was further purified by IMAC.

30 c. affinity chromatography: Ni²⁺-NTA agarose (Qiagen)

Column volume: 15 ml (16 mm x 7.5 cm)

Packing buffer: 0.1 M PO₄ - 6 M GuHCl pH7

Sample buffer: idem

Washing buffer: 0.1 M PO₄ - 6 M GuHCl pH7

0.1 M PO₄ - 6 M urea pH7

5

Elution: imidazol gradient (0→250 mM) in 0.1 M PO₄ buffer pH7 supplemented with 6 M urea.

Flow rate: 2 ml/min

10

a. Concentration:

15 Antigen positive fractions of the IMAC eluate (160 ml) were pooled and concentrated to 5 ml in an Amicon stirred cell on a Filtron membrane (type Omega cut-off 10,000). The purity at this stage is about 70% as estimated by SDS-PAGE.

b. Preparative electrophoresis (Prep Cell Biorad)

20 2.4 ml of the concentrated sample was boiled in 0.8 ml reducing sample buffer and loaded on a 10% acrylamide gel. The antigen was eluted in a Tris-Glycine buffer pH 8.3 supplemented with 4% SDS and Ns₁ -MAGE 3 His positive fractions were pooled.

a. TCA precipitation:

25

The antigen was TCA precipitated and after centrifugation in a JA 20 rotor at 15,000 rpm for 20 minutes, the supernatant was discarded. The pellet was resolubilised in PBS buffer pH 7.4.

30 The protein is soluble in PBS after freeze/thaw does not show any degradation when stored for 3 hours at 37° C and has an apparent molecular weight of approximately 50,000 Daltons as determined by SDS (12.5% PAGE).

EXAMPLE IX:**Preparation of the E. coli strain expressing a fusion protein CLYTA-MAGE-1-His tail**

- 5 **1. Construction of the expression plasmid pRIT14613 and transformation of the host strain AR58:**

Protein design:

10 The design of the fusion protein Clyta-Mage-1-His to be expressed in E. coli is described in figure 15.

The primary structure of the resulting protein has the sequence set forth in sequence ID No. 7.

15

The coding sequence (see SEQUENCE ID No. 8) corresponding to the above protein design was placed under the control of λ pL promoter in a E. coli expression plasmid.

20

Cloning:

The starting material was the vector PCUZ1 that contains the 117 C-terminal codons of the LytA coding region from Streptococcus pneumoniae and the vector pRIT14518, in which we have previously subcloned the MAGE-1 gene
25 cDNA from a plasmid received from Dr Thierry Boon from the Ludwig Institute.

The cloning strategy for the expression of CLYTA-Mage-1-His protein (see outline in Figure 16) included the following steps:

30

- 2. Preparation of the CLYTA-Mage-1-His coding sequence module:**

a) The first step was a PCR amplification, destined to flank the CLYTA sequences with the NdeI-AflIII restriction sites. The PCR amplification was
35 done using the plasmid PCUZ1as template and as primers the

oligonucleotide sense: 5' tta aac cac acc tta agg agg ata taa cat atg aaa ggg
gga att gta cat tca gac , and the oligonucleotide antisense: 5' GCC AGA
CAT GTC CAA TTC TGG CCT GTC TGC CAG. This leads to the
amplification of a 378 nucleotides long CLYTA sequence.

5

b) The second step was linking of CLYTA sequences to the MAGE-1-His
sequences, to generate the coding sequence for the fusion protein. This step
included the excision of a NdeI-AflIII Clyta fragment and insertion into the
vector pRIT14518 previously opened by NdeI and NcoI (NcoI and AflIII
compatible) restriction enzymes and gave rise to the plasmid pRIT14613.

10

c) Transformation of the host strain AR58

d) Selection and characterization of the E. coli transformant (KAN resistant)
containing the plasmid pRIT14613. (See figure 16)

15

**1. Characterization of the recombinant protein CLYTA-MAGE-1-His
(pRIT14613):**

Bacteria were grown on LB Medium supplemented with 50 µg/ml kanamycin at
30 °C. When the culture had reached OD = 0.3 (at 620 nm), heat induction was
achieved by raising the temperature to 38 °C.

20

After 4 hours induction, cells were harvested, resuspended in PBS and lysed
(by disintegration) by one shot . After centrifugation, pellet supernatant and
total extract were analyzed by SDS-PAGE. Proteins were visualized in
Coomassie B1 stained gels, where the fusion protein represented about 1 % of
the total E. coli proteins. The recombinant protein appeared as a single band
with an apparent MW of about 49 kD. The fusion protein was identified by
Western Blot analysis using anti-Mage-1 polyclonal antibodies.

25

30

Reconstitution of the expression unit composed by the long λ pL promoter (useful for Nalidixic acid induction) and the CLYTA-Mage-1 coding sequence pRIT14614):

5 A EcoRI-NCO₁ restriction fragment containing the long PL promoter and a part of CLYTA sequences was prepared from plasmid pRIT DVA6 and inserted between the EcoRI-NCO₁ sites of plasmid pRIT14613.

The recombinant plasmid pRIT14614 was obtained.

10

The recombinant plasmid pRIT14614 (see figure 17) encoding the fusion protein CLYTA-Mage-1-His was used to transform E. coli AR120. A Kan resistant candidate strain was selected and characterized.

15

Characterization of the recombinant protein:

Bacteria were grown on LB Medium supplemented with 50mg/ ml kanamycin at 30 °C. When the culture had reached OD= 400 (at 620nm) Nalidixic acid was added to a final concentration of 60 mg/ ml.

20

After 4 hours induction, cells were harvested, resuspended in PBS and lysed by desintegration (disintegration CLS "one shot" type). After centrifugation, pellet supernatant and total extract were analyzed by SDS-PAGE. Proteins were visualized in Coomassie Bleu stained gels, where the fusion protein represented about 1 % of the total E. coli proteins. The fusion protein was identified by Western blot analysis using rabbits anti-Mage-1 polyclonal antibodies. The recombinant protein appeared as a single band with an apparent MW of about 49 kD.

25

**EXAMPLE X:
CLYTA - MAGE-3-HIS**

A: Tumour rejection recombinant antigen: a fusion protein CLYTA -Mage-3-His
5 where the C-lyt A fusion partner lead to expression of a soluble protein, act as
affinity tag and provides a useful T-helper.

Preparation of the E. coli strain expressing a fusion protein CLYTA-Mage-3-His
tail

10

Construction of the expression plasmid pRIT14646 and transformation of the host
strain AR 120:

Protein design:

15 The design of the fusion protein Clyta-Mage-3-His to be expressed in E. coli is
described in figure 18.

The primary structure of the resulting protein has the sequence described in
SEQUENCE ID No.9: and the coding sequence in sequence ID No. 10

20

The coding sequence corresponding to the above protein design was placed under
the control of λ pL promoter in a E. coli expression plasmid.

25 **Cloning:**

The starting material was the vector PCUZ1 that contains the 117 C-terminal
codons of the LytA coding region from Streptococcus pneumoniae, described in
Gene 43, (1986) p. 265-272 and the vector pRIT14426, in which we have
30 previously subcloned the MAGE-3 gene cDNA from a plasmid received from Dr
Tierry Boon from the Ludwig Institute.

The cloning strategy for the expression of CLYTA-MAGE-3-His protein (see outline in Figure 19) included the following steps:

1- Preparation of the CLYTA-MAGE-3-His coding sequence module:

5

1.1. The first step was a PCR amplification, destined to flank the CLYTA sequences with the AflII and AflIII restriction sites. The PCR amplification was done using the plasmid PCUZ1as template and as primers the oligonucleotide sense: 5' tta aac cac acc tta agg agg ata taa cat atg aaa ggg gga att gta cat tca gac ,
10 and the oligonucleotide antisense: 5' ccc aca tgt cca gac tgc tgg cca att ctg gcc tgt ctg cca gtg . This leads to the amplification of a 427 nucleotides long CLYTA sequence. The above amplified fragment was cloned into the TA cloning vector of Invitrogen to get the intermediate vector pRIT14661

15 1.2. The second step was linking of CLYTA sequences to the MAGE-3-His sequences, to generate the coding sequence for the fusion protein. This step included the excision of a Afl II-Afl-III Clyta fragment and insertion into the vector pRIT14426 previously opened by Afl II and NcoI (NcoI and AflII compatible) restriction enzymes and gave rise to the plasmid pRIT14662.

20

2.- Reconstitution of the expression unit composed by the long λ pL promoter (useful for Nalidixic acid induction) and the CLYTA-Mage-3 coding sequence:

A BglII - XbaI restriction fragment containing the short pL promoter and the
25 CLYTA-Mage-3-His coding sequences was prepared from plasmid pRIT14662. and inserted between the BglII - XbaI sites of plasmid TCM67 (a pBR322 derivative containing the resistance to ampicillin, and the long λ pL promoter, described in the international application PCT/EP92/O1827). The plasmid pRIT14607 was obtained.

30 The recombinant plasmid pRIT14607 encoding the fusion protein *Clyta-Mage-3 His* was used to transform E. coli AR 120 (Mott et al.1985, Proc. Natl. Acad. Sci, 82: 88). An ampicillin resistant candidate strain was selected and characterized.

3. Preparation of plasmid pRIT 14646:

Finally a plasmid similar to pRIT 14607 but having the Kanamycin selection was constructed (pRIT 14646)

5

Characterization of the recombinant protein:

Bacteria were grown on LB Medium supplemented with 50mg/ ml kanamycin at
10 30°C. When the culture had reached OD = 400 (at 600nm) Nalidixic acid was added to a final concentration of 60?g/ ml.

After 4 hours induction , cells were harvested, resuspended in PBS and lysed by desintegration (desintegration CLS "one shot" type). After centrifugation, pellet supernatant and total extract were analyzed by SDS-PAGE. Proteins were
15 visualized in Coomassie Bleu stained gels, where the fusion protein represented about 1% of the total E. coli proteins. The fusion protein was identified by Western blot analysis using rabbits anti-Mage-3 polyclonal antibodies . The recombinant protein appeared as a single band with an apparent MW of about 58 kD.

20 EXAMPLE XI:

Purification of the recombinant protein CLYTA-Mage-3 His:

The recombinant bacteria AR120 (pRIT 14646) were grown in a 20 Litters
25 fermentor under fed-batch conditions at 30°. The expression of the recombinant protein was induced by adding Nalidixic acid at a final concentration of 60 ?g/ml. Cells were harvested at the end of fermentationand and lyzed at 60 OD/600 by two passages through a French Press disrupter (20 000 psi). Lysed cells were pelleted 20 min at 15 000 g at 4 °C. Supernatant containing the recombinant protein was
30 loaded onto exchange DEAE Sepharose CL6B resin (Pharmacia) pre-equilibrated in 0.3M NaCl, 20 mM Tris HCl pH 7.6 Buffer A. After a column wash with buffer A, fusion protein was eluted by 2 % choline in (Buffer A). Positive antigen

fractions, as revealed by Western blotting analysis using an anti Mage-3 antibody, were pooled. DEAE-eluted antigen was brought to 0.5 % Empigen BB (a zwitterionic detergent) and to 0.5 M NaCl before loading onto an Ion Metal Affinity chromatography column preequilibrated in 0.5 % Empigen BB, 0.5 M NaCl, 50
5 mM phosphate buffer pH 7.6 (Buffer B).

IMAC column was washed with buffer B until 280 nm absorbency reached the base line. A second wash in buffer B without Empigen BB (Buffer C) in order to eliminate the detergent was executed before Antigen elution by an Imidazole gradient 0-250mM Imidazole in buffer C.

10 0.090-0.250 M Imidazole fractions were pooled, concentrated on a 10 kDa Filtron omega membrane before dialysis versus PBS buffer.

CONCLUSION:

15

We have demonstrated that the fused protein LPD-MAGE3-His is immunogenic in mice, and that this immunogenicity (the proliferative response and antibody response) can be further increased by the use of the adjuvant described above. Purification can be enhanced by derivatising the thiols that form disulphide
20 bonds.

We have also demonstrated that a better antibody response was triggered by the vaccination with the LPD-MAGE-3-His in the presence of the adjuvant. The predominant isotype found in the serum of C57BL/6 being IgG2b suggesting that a TH1 type immune response was raised.

25

In the human, clinical setting a patient treated with LPD-MAGE3-His in an unadjuvanted formulation was cleared of melanoma.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT:
 - (A) Smithkline Beecham Biologicals s.a.
 - (B) STREET: rue de l'Institut 89
 - (C) CITY: Rixensart
 - (E) COUNTRY: Belgium
 - (F) POSTAL CODE (ZIP): B-1330

- (ii) TITLE OF THE INVENTION: TUMOR-ASSOCIATED ANTIGEN DERIVATIVES FROM THE MAGE FAMILY, AND NUCLEIC ACID SEQUENCES ENCODING THEM, USED FOR THE PREPARATION OF FUSION PROTEINS AND OF COMPOSITIONS FOR VACCINATION

- (iii) NUMBER OF SEQUENCES: 10

- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Borden Ladner Gervais LLP
 - (B) STREET: 60 Queen Street
 - (C) CITY: Ottawa
 - (D) PROVINCE: Ontario
 - (E) COUNTRY: Canada
 - (F) POSTAL CODE: K1P 5Y7

- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0

- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 2,319,309
 - (B) FILING DATE: 2-FEB-1999

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB/9802543.0
 - (B) FILING DATE: 5-FEB-1998

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB/9802650.3
 - (B) FILING DATE: 6-FEB-1998

- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: John Paxton
 - (B) REGISTRATION NUMBER: 3900
 - (C) REFERENCE/DOCKET NUMBER: PAT 47449W-1

- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (613) 237-5160
 - (B) TELEFAX: (613) 787-3558

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 35          40          45
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 50          55          60
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 65          70          75          80
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 85          90          95
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 100         105         110
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 115         120         125
Asp Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu Glu
 130         135         140
Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala Thr
 145         150         155         160
Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val Thr
 165         170         175
Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser Pro
 180         185         190
Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp Ser
 195         200         205
Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser Thr
 210         215         220
Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys Val
 225         230         235         240
Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu Pro
 245         250         255
Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln Tyr
 260         265         270
Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu Val
 275         280         285
Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr Ile
 290         295         300
Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asn
 305         310         315         320
Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile Ile
 325         330         335

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Ala	Arg	Glu	Gly	Asp	Cys	Ala	Pro	Glu	Glu	Lys	Ile	Trp	Glu	Glu	Leu
			340					345					350		
Ser	Val	Leu	Glu	Val	Phe	Glu	Gly	Arg	Glu	Asp	Ser	Ile	Leu	Gly	Asp
		355					360					365			
Pro	Lys	Lys	Leu	Leu	Thr	Gln	His	Phe	Val	Gln	Glu	Asn	Tyr	Leu	Glu
		370				375					380				
Tyr	Arg	Gln	Val	Pro	Gly	Ser	Asp	Pro	Ala	Cys	Tyr	Glu	Phe	Leu	Trp
385					390					395					400
Gly	Pro	Arg	Ala	Leu	Val	Glu	Thr	Ser	Tyr	Val	Lys	Val	Leu	His	His
			405						410					415	
Met	Val	Lys	Ile	Ser	Gly	Gly	Pro	His	Ile	Ser	Tyr	Pro	Pro	Leu	His
			420					425					430		
Glu	Trp	Val	Leu	Arg	Glu	Gly	Glu	Glu	Thr	Ser	Gly	Gly	His	His	His
		435					440					445			
His	His	His													
		450													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATCCAA	AACTTTAGC	CCTTTCTTTA	TTAGCAGCTG	GCGTACTAGC	AGGTTGTAGC	60
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CGTGGTGCTA	GCGGTTATTT	ACCAGAGCAT	ACGTTAGAAT	CTAAAGCACT	TGCGTTTGCA	180
CAACAGGCTG	ATTATTTAGA	GCAAGATTTA	GCAATGACTA	AGGATGGTCG	TTTAGTGGTT	240
ATTCACGATC	ACTTTTTAGA	TGGCTTGACT	GATGTTGCGA	AAAAATTCCC	ACATCGTCAT	300
CGTAAAGATG	GCCGTTACTA	TGTCATCGAC	TTTACCTTAA	AAGAAATTCA	AAGTTTAGAA	360
ATGACAGAAA	ACTTTGAAAC	CATGGATCTG	GAACAGCGTA	GTCAGCACTG	CAAGCCTGAA	420
GAAGGCCTTG	AGGCCCGAGG	AGAGGCCCTG	GGCCTGGTGG	GTGCGCAGGC	TCCTGCTACT	480
GAGGAGCAGG	AGGCTGCCTC	CTCCTCTTCT	ACTCTAGTTG	AAGTCACCCT	GGGGGAGGTG	540
CCTGCTGCCG	AGTCACCAGA	TCCTCCCCAG	AGTCCTCAGG	GAGCCTCCAG	CCTCCCCACT	600
ACCATGAACT	ACCCTCTCTG	GAGCCAATCC	TATGAGGACT	CCAGCAACCA	AGAAGAGGAG	660
GGCCAAGCA	CCTTCCCTGA	CCTGGAGTCC	GAGTTCCAAG	CAGCACTCAG	TAGGAAGGTG	720
GCCGAATTGG	TTCATTTTCT	GCTCCTCAAG	TATCGAGCCA	GGGAGCCGGT	CACAAAGGCA	780

GAAATGCTGG GGAGTGTCGT CGGAAATTGG CAGTATTTCT TTCCTGTGAT CTTCAGCAAA	840
GCTTCCAGTT CCTTGCAGCT GGTCTTTGGC ATCGAGCTGA TGGAAAGTGA CCCCATCGGC	900
CACTTGTACA TCTTTGCCAC CTGCCTGGGC CTCTCCTACG ATGGCCTGCT GGGTGACAAT	960
CAGATCATGC CCAAGGCAGG CCTCCTGATA ATCGTCCTGG CCATAATCGC AAGAGAGGGC	1020
GACTGTGCCC CTGAGGAGAA AATCTGGGAG GAGCTGAGTG TGTTAGAGGT GTTTGAGGGG	1080
AGGGAAGACA GTATCTTGGG GGATCCCAAG AAGCTGCTCA CCCAACATTT CGTGCAGGAA	1140
AACTACCTGG AGTACCGGCA GGTCCCCGGC AGTGATCCTG CATGTTATGA ATTCCTGTGG	1200
GGTCCAAGGG CCCTCGTTGA AACCAGCTAT GTGAAAGTCC TGCACCATAT GGTAAGATC	1260
AGTGGAGGAC CTCACATTTT CTACCCACCC CTGCATGAGT GGGTTTTGAG AGAGGGGGAA	1320
GAGGGCGGTC ATCACCATCA CCATCACCAT TAA	1353

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CGTGGTGCTA GCGGTTATTT ACCAGAGCAT ACGTTAGAAT CTAAAGCACT TGCCTTTGCA	180
CAACAGGCTG ATTATTTAGA GCAAGATTTA GCAATGACTA AGGATGGTCG TTTAGTGGTT	240
ATTCACGATC ACTTTTTAGA TGGCTTGACT GATGTTGCGA AAAAATTCCC ACATCGTCAT	300
CGTAAAGATG GCCGTTACTA TGTCATCGAC TTTACCTTAA AAGAAATTCA AAGTTTAGAA	360
ATGACAGAAA ACTTTGAAAC CATGGGCTCT CTGGAACAGC GTAGTCTGCA CTGCAAGCCT	420
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TCCTCCTCCT CTCCTCTGGT CCTGGGCACC CTGGAGGAGG TGCCCACTGC TGGGTCAACA	540
GATCCTCCCC AGAGTCCTCA GGGAGCCTCC GCCTTTCCCA CTACCATCAA CTTCACTCGA	600
CAGAGGCAAC CCAGTGAGGG TTCCAGCAGC CGTGAAGAGG AGGGGCCAAG CACCTCTTGT	660

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ATCAAAAATT ACAAGCACTG TTTTCCTGAG ATCTTCGGCA AAGCCTCTGA GTCCTTGACG 840
CTGGTCTTTG GCATTGACGT GAAGGAAGCA GACCCACCCG GCCACTCCTA TGTCCTTGTC 900
ACCTGCCTAG GTCTCTCCTA TGATGGCCTG CTGGGTGATA ATCAGATCAT GCCCAAGACA 960
GGCTTCCTGA TAATTGTCCT GGTCATGATT GCAATGGAGG GCGGCCATGC TCCTGAGGAG 1020
GAAATCTGGG AGGAGCTGAG TGTGATGGAG GTGTATGATG GGAGGGAGCA CAGTGCCTAT 1080
GGGGAGCCCA GGAAGCTGCT CACCCAAGAT TTGGTGCAGG AAAAGTACCT GGAGTACCGG 1140
CAGGTGCCGG ACAGTGATCC CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT 1200
GAAACCAGCT ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT 1260
TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT CGGCGGTCAT 1320
CACCATCACC ATCACCATTA A 1341

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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

```

Glu	Ala	Gln	Gln	Glu	Ala	Leu	Gly	Leu	Val	Cys	Val	Gln	Ala	Ala	Thr
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Ser	Ser	Ser	Ser	Pro	Leu	Val	Leu	Gly	Thr	Leu	Glu	Glu	Val	Pro	Thr
				165					170					175	
Ala	Gly	Ser	Thr	Asp	Pro	Pro	Gln	Ser	Pro	Gln	Gly	Ala	Ser	Ala	Phe
			180					185					190		
Pro	Thr	Thr	Ile	Asn	Phe	Thr	Arg	Gln	Arg	Gln	Pro	Ser	Glu	Gly	Ser
		195					200					205			
Ser	Ser	Arg	Glu	Glu	Glu	Gly	Pro	Ser	Thr	Ser	Cys	Ile	Leu	Glu	Ser
	210					215					220				
Leu	Phe	Arg	Ala	Val	Ile	Thr	Lys	Lys	Val	Ala	Asp	Leu	Val	Gly	Phe
225					230					235					240
Leu	Leu	Leu	Lys	Tyr	Arg	Ala	Arg	Glu	Pro	Val	Thr	Lys	Ala	Glu	Met
			245					250						255	
Leu	Glu	Ser	Val	Ile	Lys	Asn	Tyr	Lys	His	Cys	Phe	Pro	Glu	Ile	Phe
			260					265					270		
Gly	Lys	Ala	Ser	Glu	Ser	Leu	Gln	Leu	Val	Phe	Gly	Ile	Asp	Val	Lys
		275					280					285			
Glu	Ala	Asp	Pro	Thr	Gly	His	Ser	Tyr	Val	Leu	Val	Thr	Cys	Leu	Gly
	290					295						300			
Leu	Ser	Tyr	Asp	Gly	Leu	Leu	Gly	Asp	Asn	Gln	Ile	Met	Pro	Lys	Thr
305					310					315					320
Gly	Phe	Leu	Ile	Ile	Val	Leu	Val	Met	Ile	Ala	Met	Glu	Gly	Gly	His
				325					330					335	
Ala	Pro	Glu	Glu	Glu	Ile	Trp	Glu	Glu	Leu	Ser	Val	Met	Glu	Val	Tyr
			340					345					350		
Asp	Gly	Arg	Glu	His	Ser	Ala	Tyr	Gly	Glu	Pro	Arg	Lys	Leu	Leu	Thr
		355					360					365			
Gln	Asp	Leu	Val	Gln	Glu	Lys	Tyr	Leu	Glu	Tyr	Arg	Gln	Val	Pro	Asp
	370					375					380				
Ser	Asp	Pro	Ala	Arg	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	Leu	Ala
385					390					395					400
Glu	Thr	Ser	Tyr	Val	Lys	Val	Leu	Glu	Tyr	Val	Ile	Lys	Val	Ser	Ala
				405					410					415	
Arg	Val	Arg	Phe	Phe	Phe	Pro	Ser	Leu	Arg	Glu	Ala	Ala	Leu	Arg	Glu
			420					425					430		
Glu	Glu	Glu	Gly	Val	Gly	Gly	His								
		435					440						445		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	Pro	Asn	Thr	Val	Ser	Ser	Phe	Gln	Val	Asp	Cys	Phe	Leu	Trp
1				5					10					15	
His	Val	Arg	Lys	Arg	Val	Ala	Asp	Gln	Glu	Leu	Gly	Asp	Ala	Pro	Phe
			20					25					30		
Leu	Asp	Arg	Leu	Arg	Arg	Asp	Gln	Lys	Ser	Leu	Arg	Gly	Arg	Gly	Ser
		35					40					45			
Thr	Leu	Gly	Leu	Asp	Ile	Glu	Thr	Ala	Thr	Arg	Ala	Gly	Lys	Gln	Ile
	50					55					60				
Val	Glu	Arg	Ile	Leu	Lys	Glu	Glu	Ser	Asp	Glu	Ala	Leu	Lys	Met	Thr
65					70					75					80
Met	Asp	Leu	Glu	Gln	Arg	Ser	Gln	His	Cys	Lys	Pro	Glu	Glu	Gly	Leu
				85					90					95	
Glu	Ala	Arg	Gly	Glu	Ala	Leu	Gly	Leu	Val	Gly	Ala	Gln	Ala	Pro	Ala
			100					105					110		
Thr	Glu	Glu	Gln	Glu	Ala	Ala	Ser	Ser	Ser	Ser	Thr	Leu	Val	Glu	Val
		115					120					125			
Thr	Leu	Gly	Glu	Val	Pro	Ala	Ala	Glu	Ser	Pro	Asp	Pro	Pro	Gln	Ser
	130					135					140				
Pro	Gln	Gly	Ala	Ser	Ser	Leu	Pro	Thr	Thr	Met	Asn	Tyr	Pro	Leu	Trp
145					150					155					160
Ser	Gln	Ser	Tyr	Glu	Asp	Ser	Ser	Asn	Gln	Glu	Glu	Glu	Gly	Pro	Ser
				165					170					175	
Thr	Phe	Pro	Asp	Leu	Glu	Ser	Glu	Phe	Gln	Ala	Ala	Leu	Ser	Arg	Lys
			180					185					190		
Val	Ala	Glu	Leu	Val	His	Phe	Leu	Leu	Leu	Lys	Tyr	Arg	Ala	Arg	Glu
		195					200					205			
Pro	Val	Thr	Lys	Ala	Glu	Met	Leu	Gly	Ser	Val	Val	Gly	Asn	Trp	Gln
	210					215					220				
Tyr	Phe	Phe	Pro	Val	Ile	Phe	Ser	Lys	Ala	Ser	Ser	Ser	Leu	Gln	Leu
225					230					235					240
Val	Phe	Gly	Ile	Glu	Leu	Met	Glu	Val	Asp	Pro	Ile	Gly	His	Leu	Tyr
				245					250					255	
Ile	Phe	Ala	Thr	Cys	Leu	Gly	Leu	Ser	Tyr	Asp	Gly	Leu	Leu	Gly	Asp
			260					265					270		
Asn	Gln	Ile	Met	Pro	Lys	Ala	Gly	Leu	Leu	Ile	Ile	Val	Leu	Ala	Ile
		275					280						285		
Ile	Ala	Arg	Glu	Gly	Asp	Cys	Ala	Pro	Glu	Glu	Lys	Ile	Trp	Glu	Glu
	290					295					300				
Leu	Ser	Val	Leu	Glu	Val	Phe	Glu	Gly	Arg	Glu	Asp	Ser	Ile	Leu	Gly
305					310						315				320
Asp	Pro	Lys	Lys	Leu	Leu	Thr	Gln	His	Phe	Val	Gln	Glu	Asn	Tyr	Leu
				325					330					335	
Glu	Tyr	Arg	Gln	Val	Pro	Gly	Ser	Asp	Pro	Ala	Cys	Tyr	Glu	Phe	Leu
			340					345					350		
Trp	Gly	Pro	Arg	Ala	Leu	Val	Glu	Thr	Ser	Tyr	Val	Lys	Val	Leu	His
		355					360					365			
His	Met	Val	Lys	Ile	Ser	Gly	Gly	Pro	His	Ile	Ser	Tyr	Pro	Pro	Leu
	370					375					380				
His	Glu	Trp	Val	Leu	Arg	Glu	Gly	Glu	Glu	Gly	Gly	His	His	His	His
385					390					395					400
His	His	His													

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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ATGGATCCAA ACACTGTGTC AAGCTTTCAG GTAGATTGCT TTCTTTGGCA TGTCCGCAA 60
CGAGTTGCAG ACCAAGAACT AGGTGATGCC CCATTCCTTG ATCGGCTTCG CCGAGATCAG 120
AAATCCCTAA GAGGAAGGGG CAGCACTCTT GGTCTGGACA TCGAGACAGC CACACGTGCT 180
GGAAAGCAGA TAGTGGAGCG GATTCTGAAA GAAGAATCCG ATGAGGCACT TAAAATGACC 240
ATGGATCTGG AACAGCGTAG TCAGCACTGC AAGCCTGAAG AAGGCCTTGA GGCCCGAGGA 300
GAGGCCCTGG GCCTGGTGGG TGC GCAGGCT CCTGCTACTG AGGAGCAGGA GGCTGCCTCC 360
TCCTCTTCTA CTCTAGTTGA AGTCACCCTG GGGGAGGTGC CTGCTGCCGA GTCACCAGAT 420
CCTCCCCAGA GTCCTCAGGG AGCCTCCAGC CTCCCCACTA CCATGAACTA CCCTCTCTGG 480
AGCCAATCCT ATGAGGACTC CAGCAACCAA GAAGAGGAGG GGCCAAGCAC CTTCCCTGAC 540
CTGGAGTCCG AGTTCCAAGC AGCACTCAGT AGGAAGGTGG CCGAATTGGT TCATTTTCTG 600
CTCCTCAAGT ATCGAGCCAG GGAGCCGGTC ACAAAGGCAG AAATGCTGGG GAGTGTCGTC 660
GGAAATTGGC AGTATTTCTT TCCTGTGATC TTCAGCAAAG CTTCCAGTTC CTTGCAGCTG 720
GTCTTTGGCA TCGAGCTGAT GGAAGTGGAC CCCATCGGCC ACTTGTACAT CTTTGCCACC 780
TGCCTGGGCC TCTCCTACGA TGGCCTGCTG GGTGACAATC AGATCATGCC CAAGGCAGGC 840
CTCCTGATAA TCGTCCTGGC CATAATCGCA AGAGAGGGCG ACTGTGCCCC TGAGGAGAAA 900
ATCTGGGAGG AGCTGAGTGT GTTAGAGGTG TTTGAGGGGA GGAAGACAG TATCTTGGGG 960
GATCCAAGA AGCTGCTCAC CCAACATTTT GTGCAGGAAA ACTACCTGGA GTACCGGCAG 1020
GTCCCCGGCA GTGATCCTGC ATGTTATGAA TTCCTGTGGG GTCCAAGGGC CCTCGTTGAA 1080
ACCAGCTATG TGAAAGTCCT GCACCATATG GTAAAGATCA GTGGAGGACC TCACATTTCC 1140
TACCCACCCC TGCATGAGTG GGTTTTGAGA GAGGGGGAAG AGGGCGGTCA TCACCATCAC 1200
CATCACCATT AA 1212

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Gly	Gly	Ile	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
1				5					10					15	
Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
			20					25					30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
		35					40					45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50					55					60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
65					70					75					80
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
				85					90					95	
Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr	Tyr
			100					105						110	
Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Leu	Asp	Met	Gly
		115					120					125			
Ser	Leu	Glu	Gln	Arg	Ser	Leu	His	Cys	Lys	Pro	Glu	Glu	Ala	Leu	Glu
		130				135					140				
Ala	Gln	Gln	Glu	Ala	Leu	Gly	Leu	Val	Cys	Val	Gln	Ala	Ala	Thr	Ser
145					150					155					160
Ser	Ser	Ser	Pro	Leu	Val	Leu	Gly	Thr	Leu	Glu	Glu	Val	Pro	Thr	Ala
				165					170					175	
Gly	Ser	Thr	Asp	Pro	Pro	Gln	Ser	Pro	Gln	Gly	Ala	Ser	Ala	Phe	Pro
			180					185					190		
Thr	Thr	Ile	Asn	Phe	Thr	Arg	Gln	Arg	Gln	Pro	Ser	Glu	Gly	Ser	Ser
		195					200					205			
Ser	Arg	Glu	Glu	Glu	Gly	Pro	Ser	Thr	Ser	Cys	Ile	Leu	Glu	Ser	Leu
		210				215					220				
Phe	Arg	Ala	Val	Ile	Thr	Lys	Lys	Val	Ala	Asp	Leu	Val	Gly	Phe	Leu
225					230					235					240
Leu	Leu	Lys	Tyr	Arg	Ala	Arg	Glu	Pro	Val	Thr	Lys	Ala	Glu	Met	Leu
				245					250					255	
Glu	Ser	Val	Ile	Lys	Asn	Tyr	Lys	His	Cys	Phe	Pro	Glu	Ile	Phe	Gly
			260					265					270		
Lys	Ala	Ser	Glu	Ser	Leu	Gln	Leu	Val	Phe	Gly	Ile	Asp	Val	Lys	Glu
		275					280					285			
Ala	Asp	Pro	Thr	Gly	His	Ser	Tyr	Val	Leu	Val	Thr	Cys	Leu	Gly	Leu
	290					295						300			
Ser	Tyr	Asp	Gly	Leu	Leu	Gly	Asp	Asn	Gln	Ile	Met	Pro	Lys	Thr	Gly
305					310					315					320
Phe	Leu	Ile	Ile	Val	Leu	Val	Met	Ile	Ala	Met	Glu	Gly	Gly	His	Ala
				325					330					335	
Pro	Glu	Glu	Glu	Ile	Trp	Glu	Glu	Leu	Ser	Val	Met	Glu	Val	Tyr	Asp
			340					345						350	

Gly Arg Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu Thr Gln
 355 360 365
 Asp Leu Val Gln Glu Lys Tyr Leu Glu Tyr Arg Gln Val Pro Asp Ser
 370 375 380
 Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala Leu Ala Glu
 385 390 395 400
 Thr Ser Tyr Val Lys Val Leu Glu Tyr Val Ile Lys Val Ser Ala Arg
 405 410 415
 Val Arg Phe Phe Phe Pro Ser Leu Arg Glu Ala Ala Leu Arg Glu Glu
 420 425 430
 Glu Glu Gly Val Gly Gly His His His His His His
 435 440 445

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC 60
 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG 120
 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG 180
 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC 240
 AAGTACAAGG AACTTTGGTA CTACTIONAGAC GCTAAAGAAG GCGCCATGGT ATCAAATGCC 300
 TTTATCCAGT CAGCGGACGG AACAGGCTGG TACTACCTCA AACCAGACGG AACACTGGCA 360
 GACAGGCCAG AATTGGACAT GGGCTCTCTG GAACAGCGTA GTCTGCACTG CAAGCCTGAG 420
 GAAGCCCTTG AGGCCCAACA AGAGGCCCTG GGCCTGGTGT GTGTGCAGGC TGCCACCTCC 480
 TCCTCCTCTC CTCTGGTCCT GGGCACCTG GAGGAGGTGC CCACTGCTGG GTCAACAGAT 540
 CCTCCCAGA GTCCTCAGGG AGCCTCCGCC TTTCCCCTA CCATCAACTT CACTCGACAG 600
 AGGCAACCCA GTGAGGGTTC CAGCAGCCGT GAAGAGGAGG GGCCAAGCAC CTCTTGTATC 660
 CTGGAGTCCT TGTTCCGAGC AGTAATCACT AAGAAGGTGG CTGATTTGGT TGGTTTTCTG 720
 CTCCTCAAAT ATCGAGCCAG GGAGCCAGTC ACAAAGGCAG AAATGCTGGA GAGTGTCATC 780
 AAAAATTACA AGCACTGTTT TCCTGAGATC TTCGGCAAAG CCTCTGAGTC CTTGCAGCTG 840
 GTCTTTGGCA TTGACGTGAA GGAAGCAGAC CCCACCGGCC ACTCCTATGT CCTTGTCACC 900

TGCCTAGGTC TCTCCTATGA TGGCCTGCTG GGTGATAATC AGATCATGCC CAAGACAGGC 960
TTCCTGATAA TTGTCCTGGT CATGATTGCA ATGGAGGGCG GCCATGCTCC TGAGGAGGAA 1020
ATCTGGGAGG AGCTGAGTGT GATGGAGGTG TATGATGGGA GGGAGCACAG TGCCTATGGG 1080
GAGCCCAGGA AGCTGCTCAC CCAAGATTTG GTGCAGGAAA AGTACCTGGA GTACCGGCAG 1140
GTGCCGGACA GTGATCCCGC ACGCTATGAG TTCCTGTGGG GTCCAAGGGC CCTCGCTGAA 1200
ACCAGCTATG TGAAAGTCCT TGAGTATGTG ATCAAGGTCA GTGCAAGAGT TCGCTTTTTC 1260
TTCCCATCCC TGC GTGAAGC AGCTTTGAGA GAGGAGGAAG AGGGAGTCGG CGGTCATCAC 1320
CATCACCATC ACCATTAA 1338

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Lys Gly Gly Ile Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
1 5 10 15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
20 25 30
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
35 40 45
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
50 55 60
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
65 70 75 80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
85 90 95
Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr Tyr
100 105 110
Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Leu Ala Ser Met
115 120 125
Leu Asp Met Asp Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu
130 135 140
Gly Leu Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala
145 150 155 160
Pro Ala Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val
165 170 175
Glu Val Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro
180 185 190
Gln Ser Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro
195 200 205

Leu Trp Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly
 210 215 220
 Pro Ser Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser
 225 230 235 240
 Arg Lys Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala
 245 250 255
 Arg Glu Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn
 260 265 270
 Trp Gln Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu
 275 280 285
 Gln Leu Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His
 290 295 300
 Leu Tyr Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu
 305 310 315 320
 Gly Asp Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu
 325 330 335
 Ala Ile Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp
 340 345 350
 Glu Glu Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile
 355 360 365
 Leu Gly Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn
 370 375 380
 Tyr Leu Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu
 385 390 395 400
 Phe Leu Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val
 405 410 415
 Leu His His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro
 420 425 430
 Pro Leu His Glu Trp Val Leu Arg Glu Gly Glu Glu Gly Gly His His
 435 440 445
 His His His His His
 450

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAAAGGGG GAATTGTACA TTCAGACGGC TCTTATCCAA AAGACAAGTT TGAGAAAATC 60
 AATGGCACTT GGTACTACTT TGACAGTTCA GGCTATATGC TTGCAGACCG CTGGAGGAAG 120
 CACACAGACG GCAACTGGTA CTGGTTCGAC AACTCAGGCG AAATGGCTAC AGGCTGGAAG 180
 AAAATCGCTG ATAAGTGGTA CTATTTCAAC GAAGAAGGTG CCATGAAGAC AGGCTGGGTC 240

AAGTACAAGG	ACACTTGGTA	CTACTTAGAC	GCTAAAGAAG	GCGCCATGGT	ATCAAATGCC	300
TTTATCCAGT	CAGCGGACGG	AACAGGCTGG	TACTACCTCA	AACCAGACGG	AACACTGGCA	360
GACAGGCCAG	AATTGGCCAG	CATGCTGGAC	ATGGATCTGG	AACAGCGTAG	TCAGCACTGC	420
AAGCCTGAAG	AAGGCCTTGA	GGCCCGAGGA	GAGGCCCTGG	GCCTGGTGGG	TGCGCAGGCT	480
CCTGCTACTG	AGGAGCAGGA	GGCTGCCTCC	TCCTCTTCTA	CTCTAGTTGA	AGTCACCCTG	540
GGGAGGTGC	CTGCTGCCGA	GTCACCAGAT	CCTCCCCAGA	GTCCTCAGGG	AGCCTCCAGC	600
CTCCCCACTA	CCATGAACTA	CCCTCTCTGG	AGCCAATCCT	ATGAGGACTC	CAGCAACCAA	660
GAAGAGGAGG	GGCCAAGCAC	CTTCCCTGAC	CTGGAGTCTG	AGTTCCAAGC	AGCACTCAGT	720
AGGAAGGTGG	CCAAGTTGGT	TCATTTTCTG	CTCCTCAAGT	ATCGAGCCAG	GGAGCCGGTC	780
ACAAAGGCAG	AAATGCTGGG	GAGTGTCGTC	GGAAATTGGC	AGTACTTCTT	TCCTGTGATC	840
TTCAGCAAAG	CTTCCGATTC	CTTGCAGCTG	GTCTTTGGCA	TCGAGCTGAT	GGAAGTGGAC	900
CCCATCGGCC	ACGTGTACAT	CTTTGCCACC	TGCCTGGGCC	TCTCCTACGA	TGGCCTGCTG	960
GGTGACAATC	AGATCATGCC	CAAGACAGGC	TTCCTGATAA	TCATCCTGGC	CATAATCGCA	1020
AAAGAGGGCG	ACTGTGCCCC	TGAGGAGAAA	ATCTGGGAGG	AGCTGAGTGT	GTTAGAGGTG	1080
TTTGAGGGGA	GGGAAGACAG	TATCTTCGGG	GATCCCAAGA	AGCTGCTCAC	CCAATATTTT	1140
GTGCAGGAAA	ACTACCTGGA	GTACCGGCAG	GTCCCCGGCA	GTGATCCTGC	ATGCTATGAG	1200
TTCCTGTGGG	GTCCAAGGGC	CCTCATTGAA	ACCAGCTATG	TGAAAGTCCT	GCACCATATG	1260
GTAAAGATCA	GTGGAGGACC	TCGCATTTCC	TACCCACTCC	TGCATGAGTG	GGCTTTGAGA	1320
GAGGGGGAAG	AGGGCGGTCA	TCACCATCAC	CATCACCATT	AA		1362

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CLAIMS:

1. A process for the purification or production of a MAGE protein, comprising reducing the disulphide bonds of the protein, and blocking the resulting free thiol group with a blocking group and further comprising one or more chromatographic steps, in which the protein is solubilised using a strong chaotropic agent or a zwitterionic detergent.
2. A process according to claim 1 in which the chaotropic agent is urea or guanidium hydrochloride.
3. A process according to claim 1 in which the zwitterionic detergent is Empigen BB –n-dodecyl-N,N-dimethylglycine.
4. A process according to any one of claims 1 to 3 in which the blocking agent is an alkylating agent.
5. A process according to claim 4 in which the blocking agent is alpha haloacid or alpha haloamide.
6. A process according to claim 4 or 5 in which the blocking agent is one or more of iodoacetic acid; iodoacetamide; N-ethylmaleimide; chloroacetyl phosphate; O-methylisourea; or acrylonitrile.
7. A process according to any one of claims 1 to 6 in which the protein comprises an affinity tag.
8. A process according to claim 7 in which the affinity tag is ClytA or a polyhisitidine tail.
9. A process according to claim 7 or 8 in which the protein comprising an affinity tag, after the blocking step, is subjected to affinity chromatography.

10. A process according to claim 9 in which the affinity chromatography is immobilised metal ion affinity chromatography (IMAC).
11. A process according to claim 10 in which the metal ion is zinc, nickel, iron, magnesium or copper.
12. A process according to claim 9, 10 or 11 in which affinity chromatography is performed using buffer containing the zwitterionic detergent Empigen BB.
13. A process according to any one of claims 1 to 12 in which the protein is a fusion protein comprising a MAGE antigen and a fusion partner.
14. A process according to claim 13 in which the fusion partner is protein D or fragment thereof from Haemophilus influenzae B comprising first 1/3 of protein D, NS1 protein from influenza or a fragment thereof comprising the N terminal 81 amino acids of NS1, or LytA from Streptococcus pneumoniae or fragment thereof comprising residues 188-305 of LytA.
15. A process as claimed in claim 14 in which the fusion partner is the lapidated form of protein D.
16. A process according to any one of claims 8 to 15 in which the protein comprises LytA or a fragment thereof comprising residues 188-305, and in which the protein is purified by affinity chromatography to choline or choline analogues such as DEAE.
17. A process according to any one of claims 1 to 16 in which the MAGE antigen is MAGE A1, MAGE A2, MAGE A3, MAGE A4, MAGE A5, MAGE A6, MAGE A7, MAGE A8, MAGE A9, MAGE A10, MAGE A11, MAGE A12, MAGE B1, MAGE B2, MAGE B3, MAGE B4, MAGE C1 or MAGE C2.
18. A process for the production of a vaccine, comprising the steps of producing or purifying a MAGE protein by the process of any one of claims 1 to 17 and formulating the resulting protein as a vaccine.

Figure 1 : LPD-MAGE-3-His

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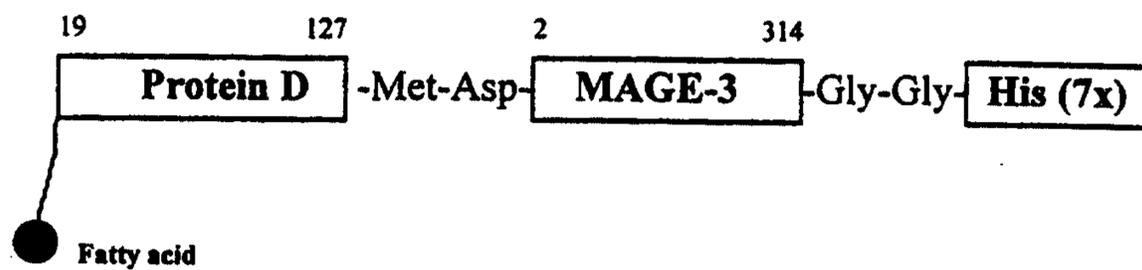


FIGURE 2 : Construction of the expression vector pRIT 14586

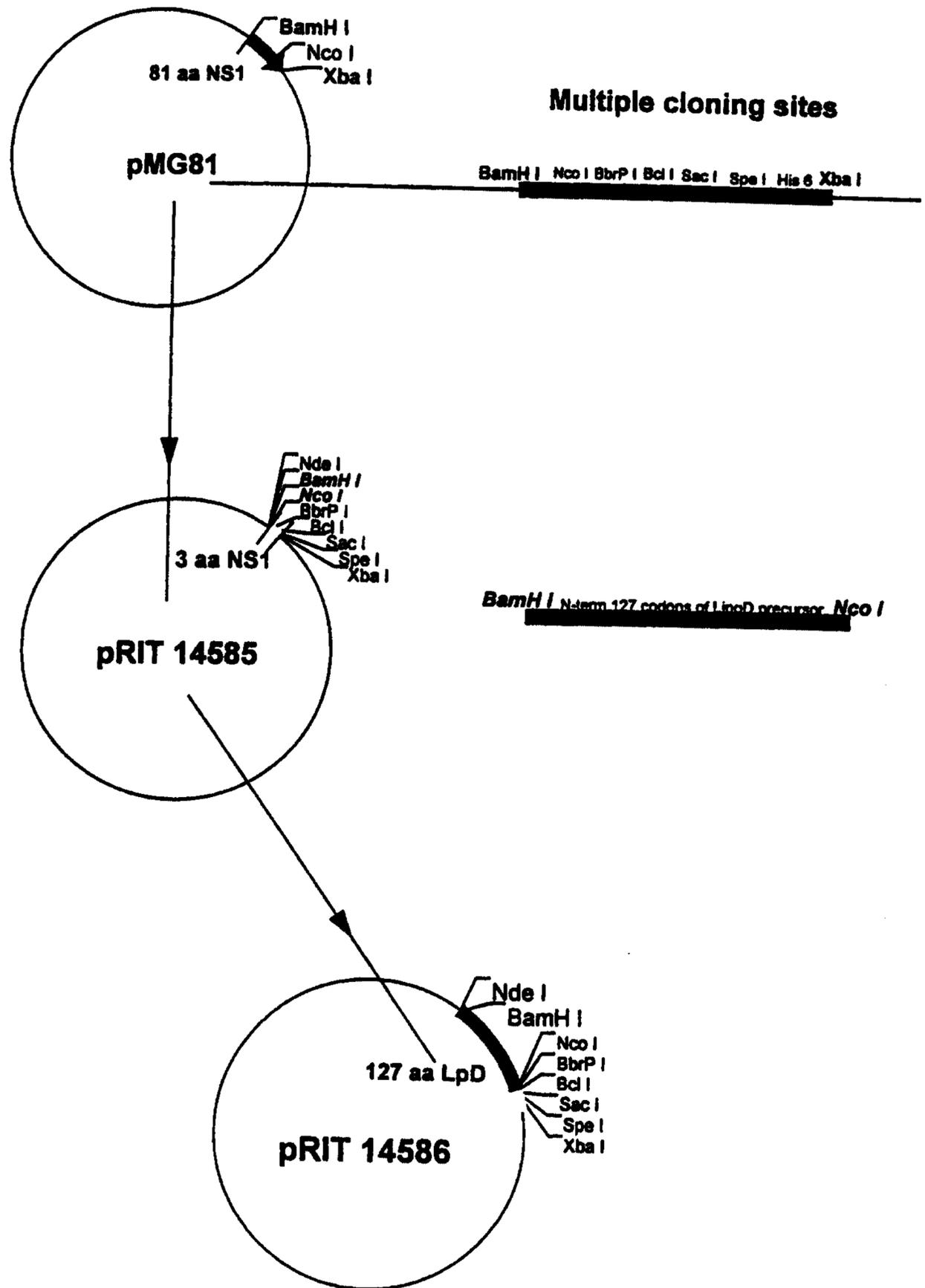


FIGURE 3 : Construction of plasmid pRIT 14477 expressing the fusion protein Prot. D 1/3-MAGE-3-His tail

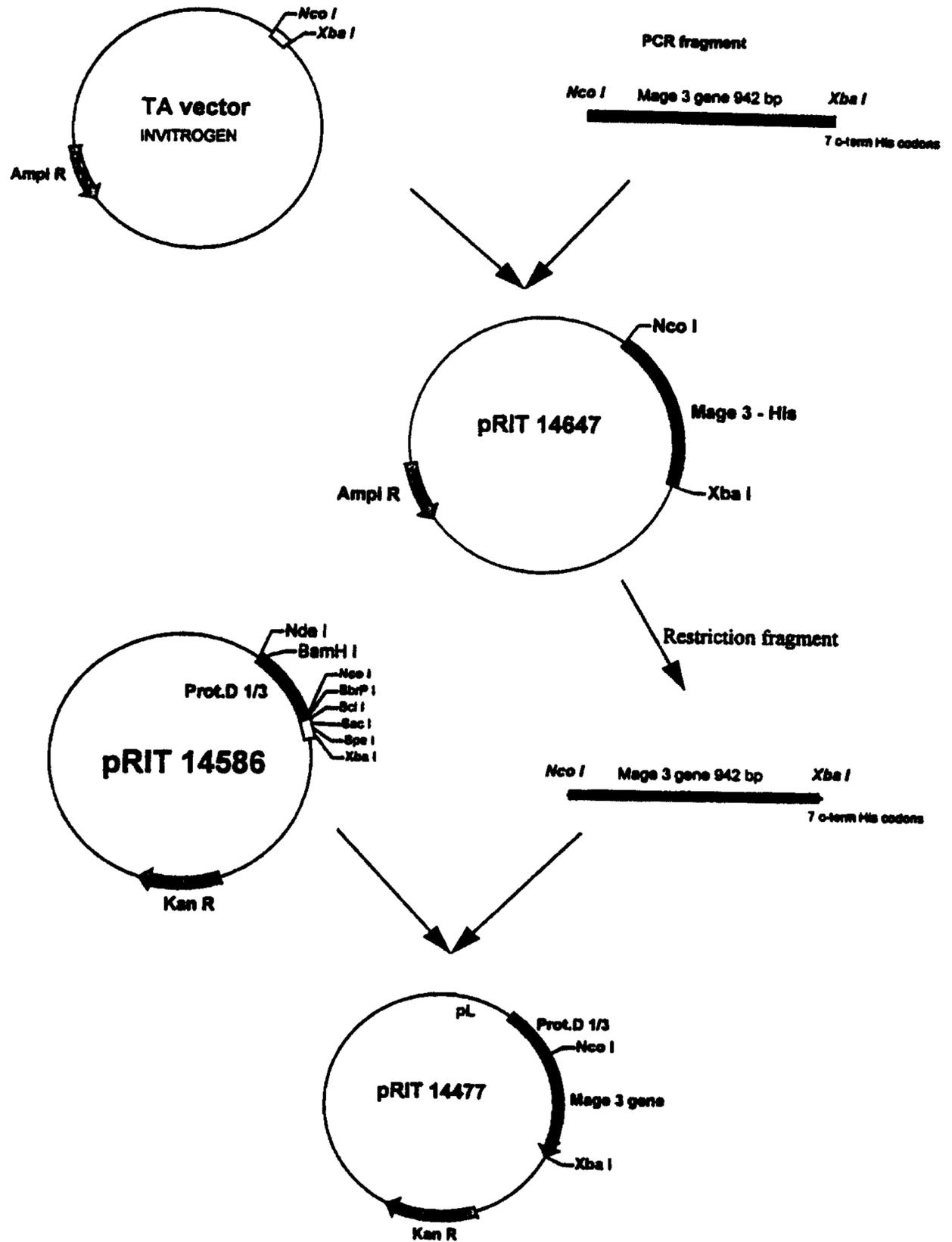


Figure 12

5

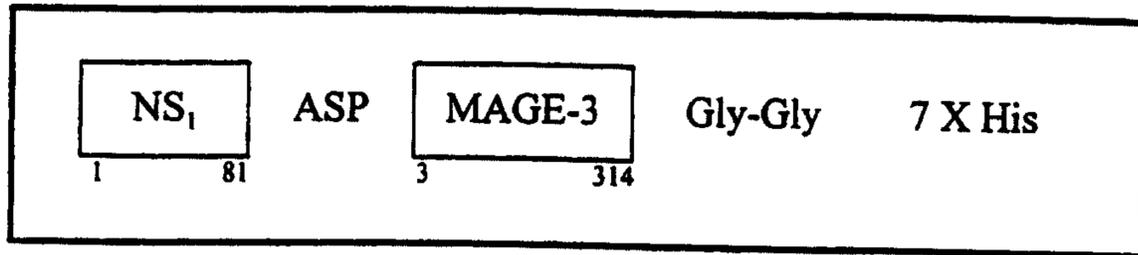


Figure 13

Construction of plasmid pRIT14426

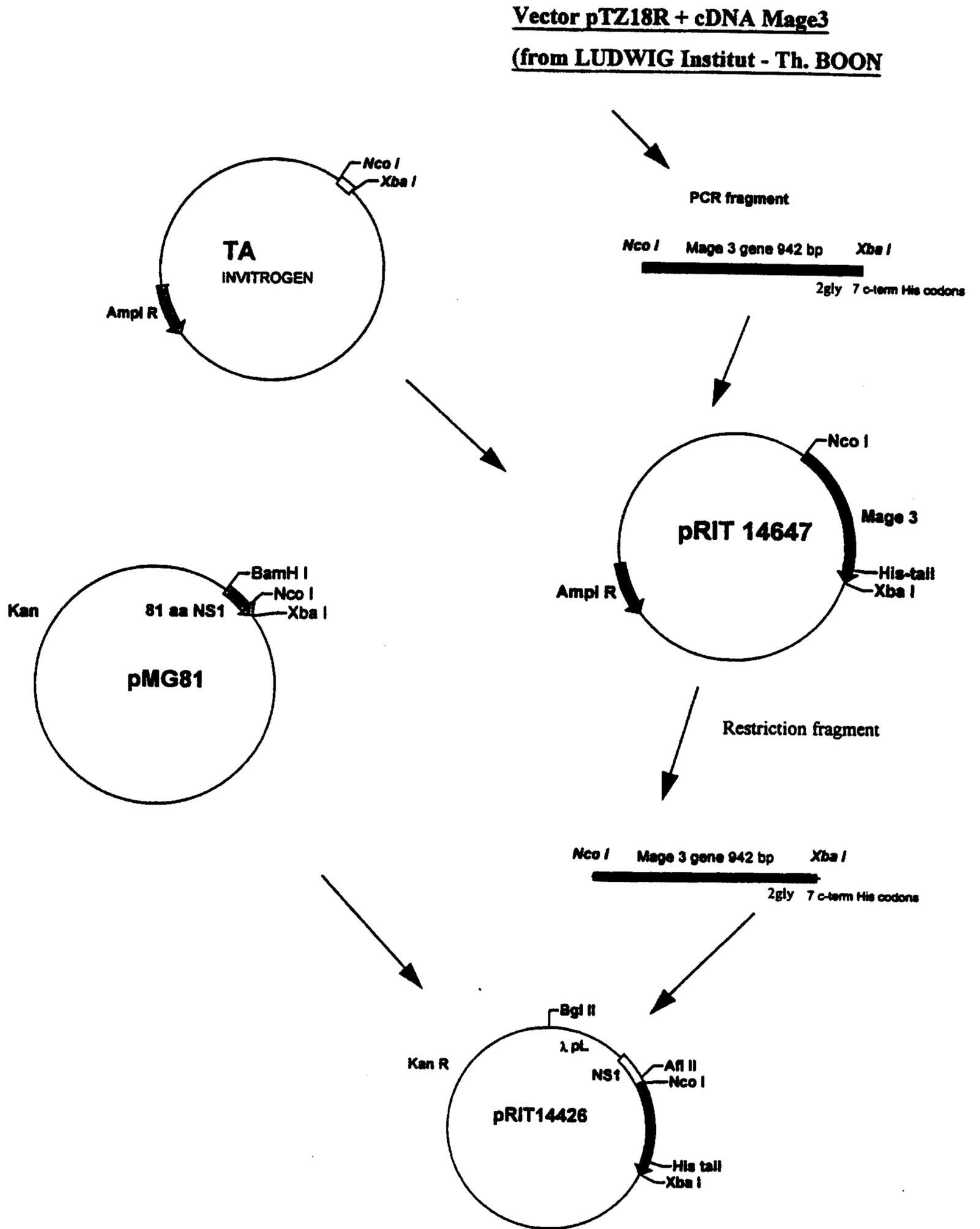
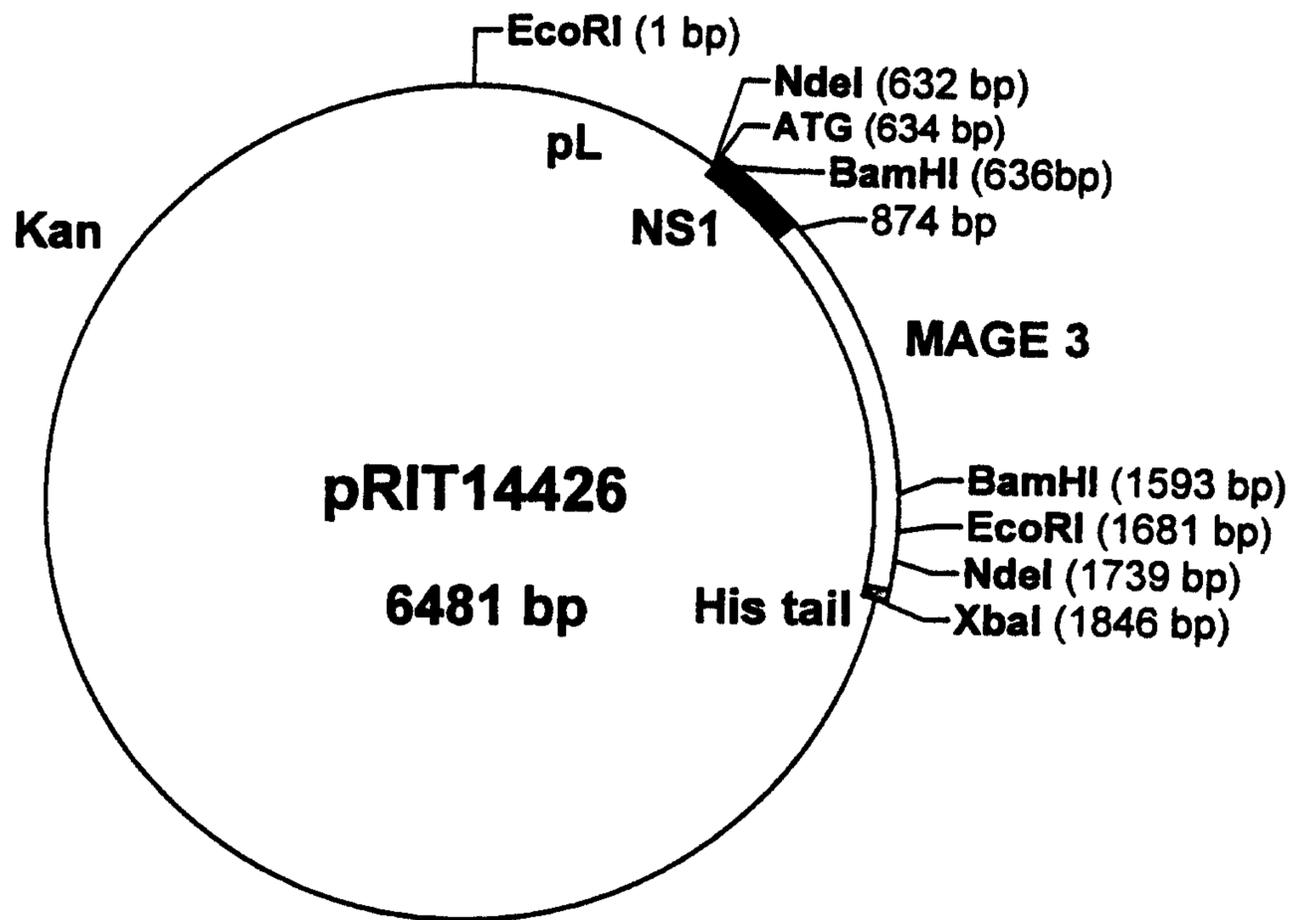


Figure 14:

Plasmid map of pRIT14426



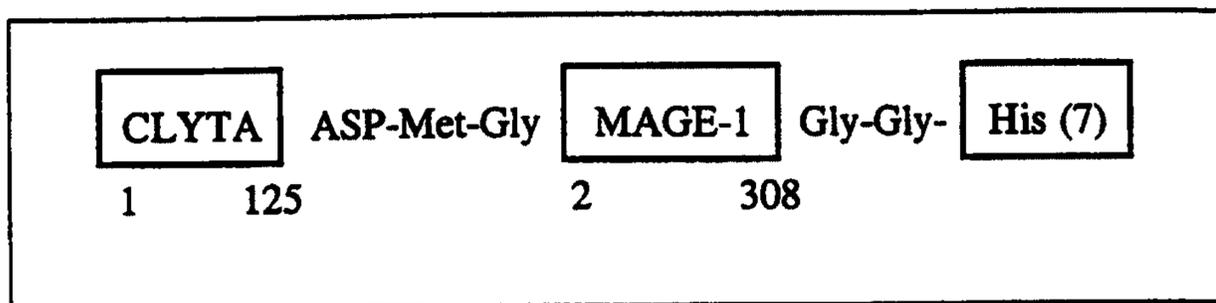


Figure 16 : construction of plasmid pRIT 14613.

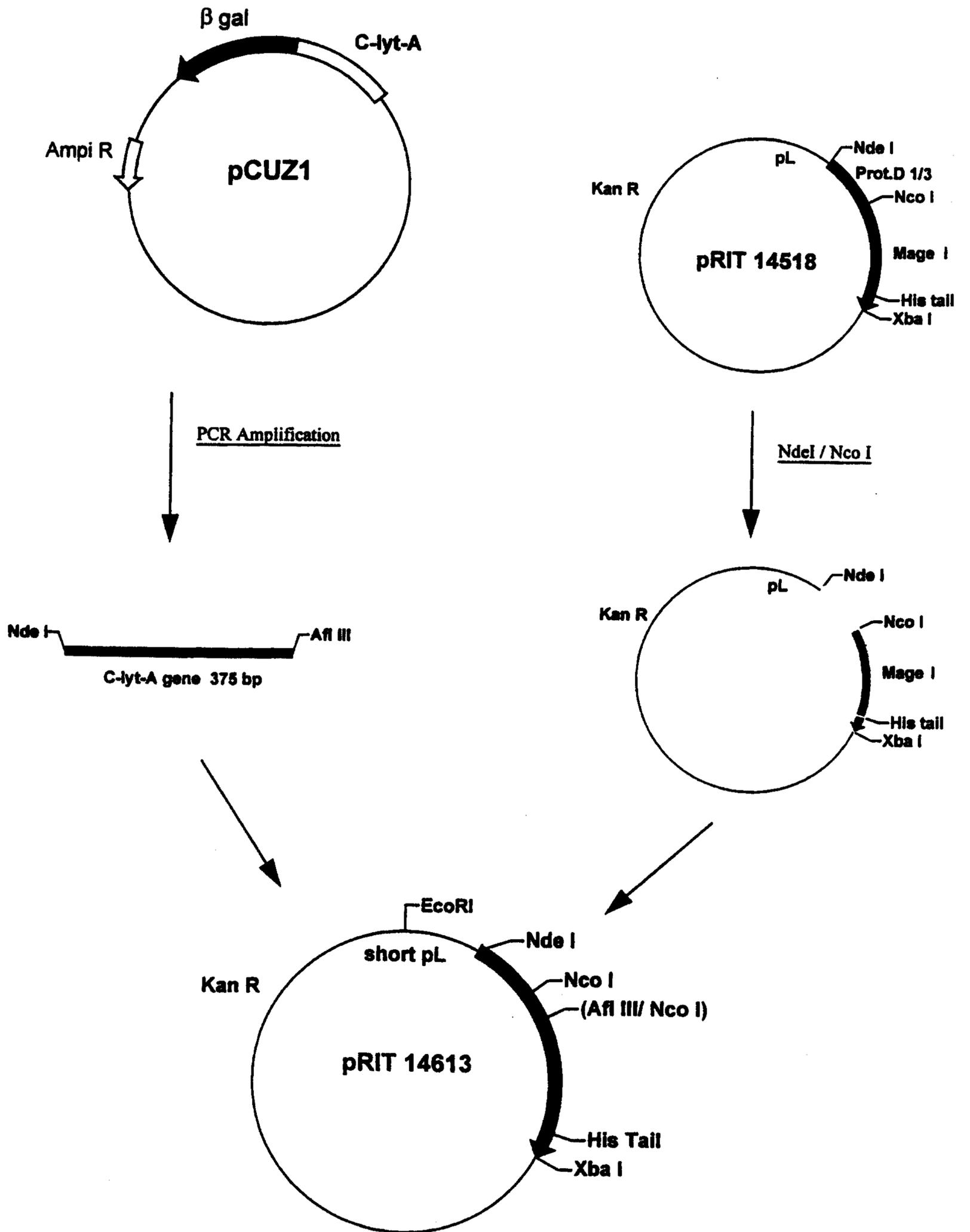


Figure 17 construction of plasmid pRIT 14614

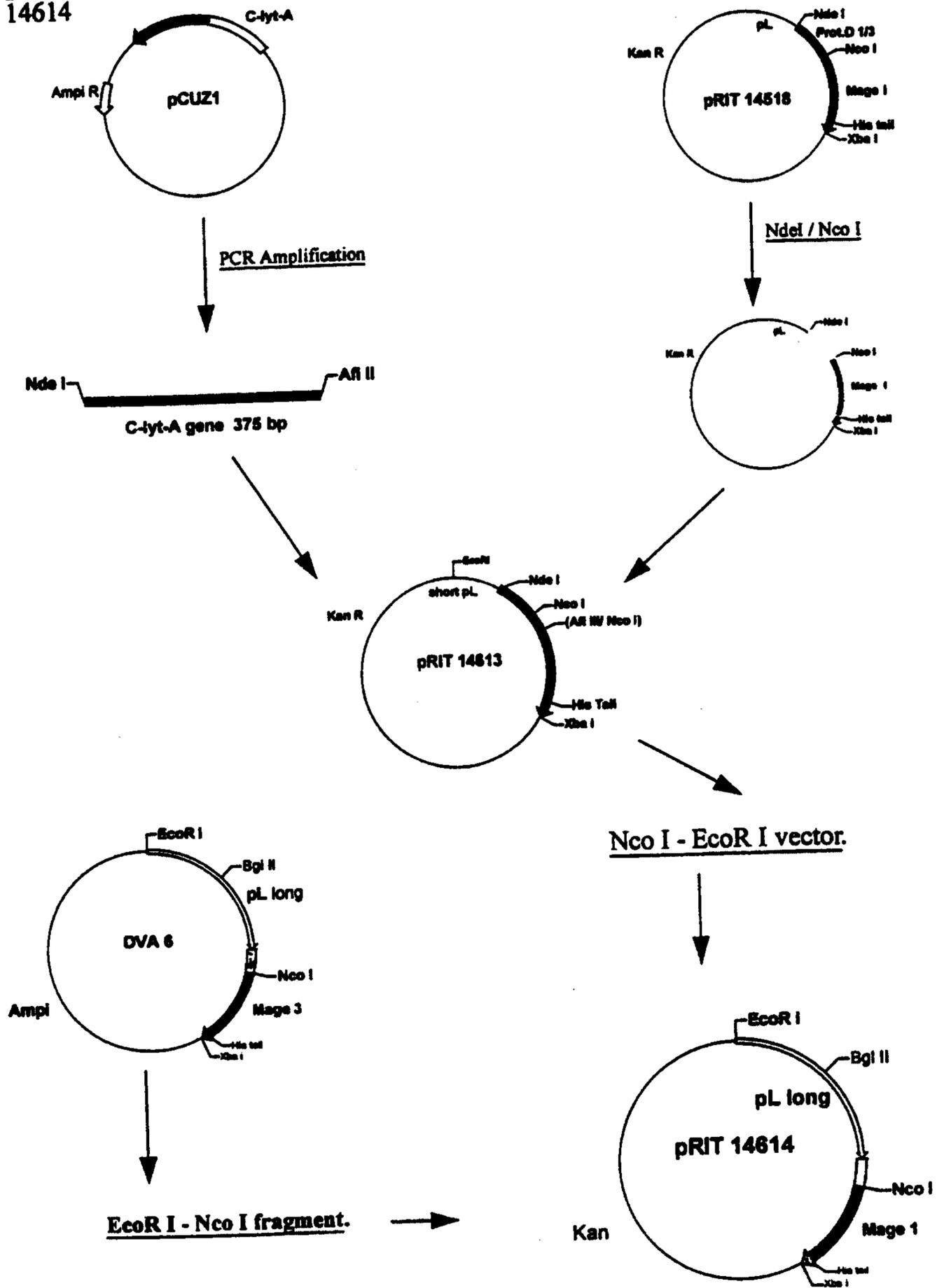


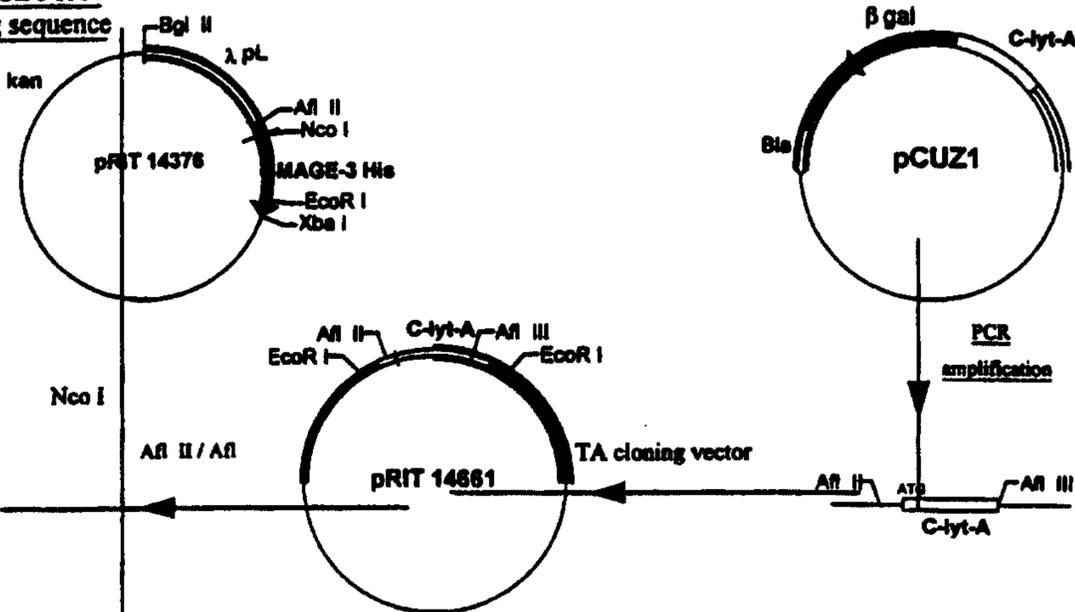
Figure-18

CLYTA Ala-Ser-Met-Leu-Asp **MAGE-3** Gly-Gly- **HIS (7)**

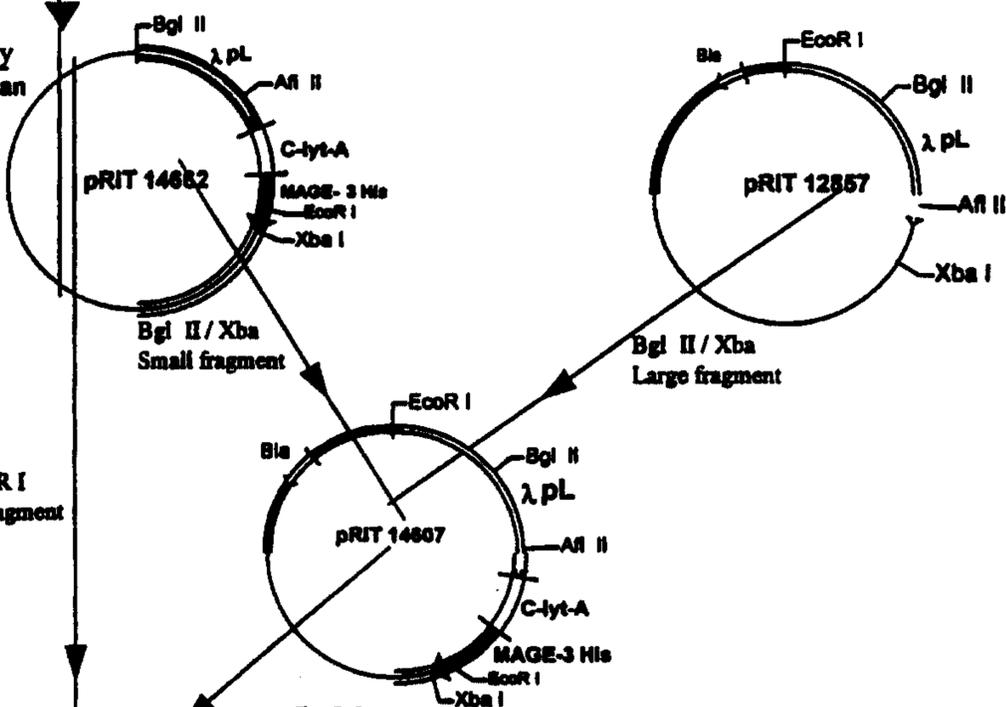
Figure 19

FIGURE 19 : Construction of plasmid pRIT 14646

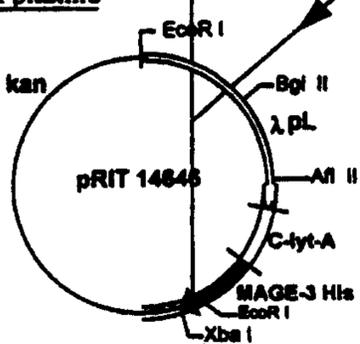
I. Preparation of the CLYTA - Mage - 3 His coding sequence module.



II. Reconstitution of the expression unit composed by the long pL promoter kan and the CLYTA - Mage - 3 coding sequence



III. Preparation of plasmid pRIT 14646.



UNSCANNABLE ITEM

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(ITEM ON THE 10TH FLOOR ZONE 5 IN THE FILE PREPARATION SECTION)

DOCUMENT REÇU AVEC CETTE DEMANDE

NE POUVANT ÊTRE BALAYÉ

(DOCUMENT AU 10 IÈME ÉTAGE AIRE 5 DANS LA SECTION DE LA
PRÉPARATION DES DOSSIERS)