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(54) Title: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING HELICASE ACTIVITY AND METHOD THEREFOR		
(57) Abstract <p>The present invention relates to a method for isolating cloned papillomavirus E1 protein from a eukaryotic expression system having demonstrable and reproducible viral helicase activity and preparation containing essentially pure E1 protein. The invention further relates to the use of this E1 protein preparation in a screening assay for identifying antiviral agents. More particularly a high throughput assay to screen for agents capable of inhibiting HPV DNA replication. The assay is based on measuring the effect of antiviral agents on the activity of the E1 protein and more specifically on its helicase activity.</p>		

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PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING HELICASE
ACTIVITY AND METHOD THEREFOR

FIELD OF THE INVENTION

The present invention relates to a method for isolating
5 and purifying cloned papillomavirus (PV) E1 protein from a
eukaryotic expression system, having demonstrable and
reproducible viral helicase activity and devoid of
contaminating activities. The invention further relates to the
use of this novel protein extraction method to isolate
10 substantially purified, preferably essentially pure, E1
protein having helicase activity to establish a screening
assay for antiviral agents. More particularly the invention
relates to E1 protein to establish a high throughput assay to
screen for agents capable of inhibiting PV DNA replication.
15 The assay is based on measuring the inhibition of the
antiviral agents on the activity of the E1 protein and more
specifically on its helicase activity.

BACKGROUND OF THE INVENTION

Papillomaviruses (PV) are non-enveloped DNA viruses that
20 induce hyperproliferative lesions of the epithelia. The
papillomaviruses are widespread in nature and have been
recognized in higher vertebrates. Viruses have been
characterized, amongst others, from humans, cattle, rabbits,
horses, and dogs. The first papillomavirus was described in
25 1933 as cottontail rabbit papillomavirus (CRPV). Since then,
the cottontail rabbit as well as bovine papillomavirus type 1
(BPV-1) have served as experimental prototypes for studies on
papillomaviruses. Most animal papillomaviruses are associated
with purely epithelial proliferative lesions, and most lesions
30 in animals are cutaneous. In the human there are more than 75
types of papillomavirus (HPV) that have been identified and
they have been catalogued by site of infection: cutaneous
epithelium and mucosal epithelium (oral and genital mucosa).

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The cutaneous-related diseases include flat warts, plantar warts, etc. The mucosal-related diseases include laryngeal papillomas and anogenital diseases comprising cervical carcinomas (Fields, 1996, Virology, 3rd ed. Lippincott - Raven
5 Pub., Philadelphia, N.Y.).

There are more than 25 HPV types that are implicated in anogenital diseases, these are grouped into "low risk" and "high risk" types. The low risk types include HPV type 6, type 11 and type 13 and induce mostly benign lesions such as
10 condyloma acuminata (genital warts) and low grade squamous intraepithelial lesions (SIL). In the United States there are 5 million people with genital warts of which 90% is attributed to HPV-6 and HPV-11. About 90% of SIL is also caused by low risk types 6 and 11. The other 10% of SIL is caused by high
15 risk HPVs.

The high risk types are associated with high grade SIL and cervical cancer and include most frequently HPV types 16, 18, 31, 33, 35, 45, 52, and 58. The progression from low-grade SIL to high-grade SIL is much more frequent for lesions
20 that contain high risk HPV-16 and 18 as compared to those that contain low risk HPV types. In addition, only four HPV types are detected frequently in cervical cancer (types 16, 18, 31 and 45). About 500,000 new cases of invasive cancer of the cervix are diagnosed annually worldwide (Fields, 1996, supra).

25 Treatments for genital warts include physical removal such as cryotherapy, CO₂ laser, electrosurgery, or surgical excision. Cytotoxic agents may also be used such as trichloroacetic acid (TCA), podophyllin or podofilox. Immunomodulatory agents are also available such as Interferon
30 or Imiquimod. These treatments are not completely effective in eliminating all viral particles and there is either a high cost incurred or uncomfortable side effects related thereto.

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In fact, there are currently no effective antiviral treatments for HPV infection since with all current therapies recurrent warts are common (Beutner & Ferenczy, 1997, *Amer. J. Med.*, 102(5A), 28-37).

5 The ineffectiveness of the current methods to treat HPV infections has demonstrated the need to identify new means to control or eliminate such infections. In recent years, efforts have been directed towards finding antiviral compounds, and especially compounds capable of interfering with viral
10 replication at the onset of infection (Hughes, 1993, *Nucleic Acids Res.* 21:5817-5823). To that end, it has therefore become important to study the genetics of HPVs in order to identify potential chemotherapeutic targets to contain and possibly eliminate any diseases caused by HPV infections at the onset
15 of infection. It is equally important to identify a measurable viral activity that demonstrates specificity and reliability to be used as an indicator in assessing the effectiveness of the potential chemotherapeutic agents against PVs.

 The life cycle of PV is closely coupled to keratinocyte
20 differentiation. Infection is believed to occur at a site of tissue disruption in the basal epithelium. As the infected cells undergo progressive differentiation the cellular machinery is maintained allowing viral gene expression to increase, with eventual late gene expression and virion
25 assembly in terminally differentiated keratinocytes and the release of viral particles (Fields, *supra*).

 The coding strands for each of the papillomavirus contains approximately ten designated translational open reading frames (ORFs) that have been classified as either
30 early ORFs or late ORFs based on their location in the genome.

 E1 to E8 are expressed early in the viral replication cycle, and two late genes (L1 and L2) represent the major and minor

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capside proteins respectively. The E1 and E2 gene products function in viral DNA replication, whereas E5, E6 and E7 are expressed in connection with host cell proliferation. The L1 and L2 are involved in virion structure. The functions of E3, 5 E4 and E8 gene products is uncertain at present.

Studies of HPV have shown that proteins E1 and E2 are both essential and sufficient for viral DNA replication *in vitro* (Kuo et al., 1994, J. Biol. Chem. 30: 24058-24065). This requirement is similar to that of bovine papillomavirus 10 type 1 (BPV-1). Indeed, there is a high degree of similarity between E1 and E2 proteins and the ori-sequences of all papillomaviruses (PV) regardless of the viral species and type (Kuo et al., 1994, supra). Of note, E1 is the most highly conserved protein in PV and its enzymatic activity is presumed 15 to be similar for all PV types (Jenkins, 1996, J. Gen. Virol., 77:1805-1809).

Evidence emanating from studies of BPV-1 have shown that E1 possesses ATPase and helicase activities that are required in the initiation of viral DNA replication (Seo et al., 1993a, 20 Proc. Natl. Acad. Sci. USA 90:702-706; Yang et al., 1993, Proc. Natl. Acad. Sci. 90:5086-5090; and MacPherson et al., 1994, 204:403-408).

The E2 protein is a transcriptional activator that binds to E1 protein and forms a complex that binds specifically to 25 the ori sequence (see FIGURE 1) (Mohr et al., 1990, Science 250:1694-1699). It is believed that E2 enhances binding of E1 to the BPV origin of replication (Seo et al., 1993b, Proc. Natl. Acad. Sci., 90:2865-2869). In HPV, Lui et al. suggested that E2 stabilizes E1 binding to the ori (1995, J. Biol. 30 Chem., 270(45):27283-27291).

The helicase activity of the E1 proteins of papillomavirus therefore constitute a good molecular target to

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design chemical entities capable of inhibiting viral replication. Such objective requires that the E1 protein be extracted and purified to an extent where its helicase activity can be measured reliably and reproducibly. Such
5 isolation of E1 helicase has however remained elusive or at best unreliable, especially on a scale sufficient to establish an assay to screen for such inhibitors.

Seo et al. (1993a, supra) disclose the extraction and purification of BPV-E1 from a baculovirus expression system
10 with the step consisting of the use of PEG and 1M NaCl in the nuclear extraction buffer. They obtained BPV-E1 preparation about 90% pure. However, we have not found it possible to obtain pure HPV-11 E1 by this procedure, and in any case the procedure is not suitable to the large scale required to
15 purify E1 for high-throughput screening.

The two BPV-1 genes encoding E1 and E2 proteins have been cloned into a Baculovirus expression system and the proteins substantially purified (US patent 5,464,936). US patent '936 discloses a purification process for E1 consisting
20 of a nuclear extraction in a hypertonic buffer (containing 300 mM NaCl) followed by 3 sequential chromatographic separations. The disclosure, however, does not demonstrate the purity and specific activity of the resulting E1 helicase. The absence of affinity chromatography purification step leads to the
25 presence of contaminating nucleases that prevent accurate measurement of the E1 helicase activity. In addition, even if such a process would in fact yield E1 helicase of sufficient purity to assess the helicase activity, it is believed that it would be inapplicable to a high-yield, large-scale process for
30 HTS purposes.

An extraction process wherein nuclei were suspended in lysis buffer containing 300 mM NaCl followed by further

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purification has been described (Bream *et al.*, 1993, J. Virol., 2655). However, the authors were unable to detect helicase activity from these crude preparations of E1. Further attempts to isolate HPVs E1 protein cloned into
5 different expression systems, having demonstrable and specific helicase activity, have failed (Jenkins *et al.*, 1996, *supra*).

Kuo *et al.*, 1994, *supra* discloses a purification procedure (using 420 mM salt during the nuclear extraction) but does not discuss the scale on which the procedure was
10 carried out or the total yield of protein.

It has been hypothesized that the conformation of the E1 protein and its hydrophobicity cause the protein to be "sticky" and to form aggregates thus making it difficult to extract and purify. In addition, difficulties in establishing
15 enzymatic activities that are specific and free of cellular contaminants have generally been encountered. For example, viral helicase and/or ATPase activity may not be distinguishable from cellular helicase and/or ATPase
contaminants present in the host cell used to express the E1
20 gene. In addition, very low levels of nucleases will destroy the substrate rendering any assessment impossible.

One common denominator in the various purification processes outlined above lies in the presence of high concentrations of salt (hypertonic conditions) during the
25 nuclear extraction step. Indeed, according to conventional wisdom, it is believed that nucleic acid-binding proteins may be solubilized in high concentrations of salt and thereby separated from nucleic acids. At present, the prior art has not revealed satisfactory processes for the purification of
30 E1.

There thus remains a need to isolate a demonstrable and reproducible viral helicase activity that can be used as an

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indicator of the inhibitory effect of antiviral chemotherapeutic agents. More particularly, there remains a need to provide a method of preparing a PV E1 preparation displaying a high helicase activity.

- 5 There also remains a need to obtain a preparation of human papillomavirus E1 protein which displays a helicase activity sufficient for the purposes of a screening assay, particularly, a high throughput screening assay.

 Since E1 structure/function is highly conserved amongst
10 different papillomaviruses and amongst subtypes, it is assumed that the BPV and CRPV E1 proteins can be extracted and purified by the procedure of the invention. Therefore, there remains a need for a method for the isolation/purification of E1 protein from several species of papillomavirus, including,
15 but not limited to bovine papillomavirus (BPV), cottontail rabbit papillomavirus (CRPV) and human papillomavirus (HPV). There also remains a need to isolate and purify the E1 protein from different subtypes of HPV, including but not limited to, HPV-6, 11, 16, 18, 31, 33, 35, 45, 52, and 58.

- 20 Before the present invention, E1 protein preparations, including human E1 preparations, did not demonstrate reproducible helicase activity. The deficiency in the prior art created a road block in being able to screen a large collection of antiviral agents capable of inhibiting papilloma
25 viral DNA replication. This deficiency is overcome by the present invention which is capable of providing the means to design a HTS for the screening for such agents. The Applicant has now found a reliable and reproducible purification process for the preparation of E1 having helicase activity. The
30 resulting E1 preparation is free from degradation products and amenable to large scale production of E1.

 The present description refers to a number of documents,

the content of which is herein incorporated by reference.

SUMMARY OF THE INVENTION

Therefore, in accordance with a first embodiment of the present invention, there is provided, a means for the
5 isolation and purification of E1 protein having demonstrable, reliable and reproducible helicase activity.

Thus, the invention mostly concerns the isolation and purification of E1 protein from papillomavirus or a functional derivative thereof, having detectable helicase activity above
10 background levels. The E1 preparation according to the present invention is significantly free of contaminating cellular helicase, ATPase and nuclease activities. The E1 preparation according to the present invention displays reproducible viral helicase activity.

15 In accordance with this first embodiment, there is provided a method for the isolation of the expressed E1 protein from the cloned E1 gene. There is therefore provided a method for extracting from a nuclear extract the papillomavirus E1 protein or a functional derivative thereof
20 having viral helicase activity comprising the steps of:

- a) producing an E1 recombinant protein in a eukaryotic expression system and isolating a nuclei preparation thereof;
- b) extracting E1 protein from said nuclei preparation in a buffer comprising salt at a concentration lower than 300 mM.

25 This novel method for extracting E1 protein having helicase activity from a eukaryotic cell nuclei preparation, comprises the use of salt concentrations lower than those taught in the prior art.

There is further provided a method for isolating said E1
30 protein further comprising the step of:

- c) purifying E1 protein from said nuclear extract by affinity

chromatography.

The applicant was the first to design a method for the isolation of human papillomavirus E1 protein capable of demonstrating reproducible viral helicase activity, thus
5 providing the essential element for the design of an assay for identifying potential antiviral agents capable of inhibiting E1 helicase activity and thereby preventing viral DNA replication. This method can also be applied for the isolation and purification of BPV and CRPV E1 helicases.

10 In accordance with a further aspect of the present invention, there is provided a preparation of recombinant papillomavirus E1 protein from a eukaryotic expression system, said E1 having viral helicase activity, wherein the E1 protein is extracted from a nuclei preparation in the presence of salt
15 at a concentration less than 300 mM, and optionally purified by affinity chromatography.

In accordance with a further embodiment of the present invention, there is therefore provided the means to use the isolated E1 protein preparation in screening for the level of
20 inhibition of candidate antiviral agents on E1 helicase activity.

There is therefore provided a method for assaying the specific viral helicase activity of papillomavirus E1 protein, said method comprising the steps of:

- 25 -incubating a mixture of said E1 protein preparation as defined above, and a suitable substrate for said viral helicase enzymatic activity; and
- measuring the amount of specific helicase activity of said E1 protein.

30 There is further provided a method for identifying agents capable of modulating said helicase activity, said

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method comprising the steps of:

- a) assaying the activity of said E1 helicase in the absence of said agent by the method as defined above;
- b) assaying the activity of said helicase in the presence of
5 said agent by the method as defined above, wherein said agent is added to said helicase and substrate mixture during said incubation; and
- c) comparing the result of step a) with the result of step b).

In accordance with a further embodiment, the isolated E1
10 protein has detectable and specific helicase activity, and, in the presence of E2 protein is capable of binding DNA to form a complex at the origin of replication, and contribute to viral DNA replication. Therefore, an alternative way to measure inhibition of E1 helicase activity is to measure the
15 inhibition of viral DNA replication.

There is therefore provided a method for assaying papillomavirus DNA replication, said method comprising the steps of:

- incubating a candidate agent with a mixture of E1 protein
20 preparation as defined above, with E2 protein and a suitable DNA origin of replication; and
- measuring the amount of DNA unwinding.

There is also provided a method for identifying an agent capable of modulating papillomavirus DNA replication, said
25 method comprising the steps of:

- a) assaying said DNA replication activity in the absence of said agent by the method as defined above;
- b) assaying said DNA replication activity in the presence of said agent by the method as defined above, wherein said agent
30 is added to said mixture during said incubation; and

c) comparing the result of step a) with the result of step b).

Other aspects of the present invention will become more apparent upon reading of the following non-restrictive description of preferred embodiments with reference to the accompanying drawing which is exemplary and should not be
5 interpreted as limiting the scope of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Having thus generally described the invention, reference will now be made to the accompanying drawings, showing by way
10 of illustration a preferred embodiment thereof, and in which:

FIGURE 1 shows a pictorial representation of the E1 and E2 interaction at the origin of replication of the papillomavirus. Briefly, the E1 protein is recruited at the origin of replication by the E2 protein and then forms a
15 complex activating the helicase activity of the E1 to unwind DNA. The E1-E2 complex later recruits cellular replication proteins to eventually initiate DNA replication.

FIGURE 2 shows the alignment of the amino acid sequences of the E1 helicases of several papillomaviruses and shows
20 their % identity compared to the sequence of the E1 helicase of HPV-11;

FIGURE 3A shows a Coomassie blue-stained gel of different conditions for the nuclear extraction of the E1 protein according to the present invention (the legend of
25 which is presented in Example 2);

FIGURE 3B shows a Western immunoblot of the gel of Figure 3A, stained with an anti-E1 K72 polyclonal antibody and developed with a chemiluminescent reagent;

FIGURE 4A shows a schematic representation of the
30 purification process according to the invention;

FIGURE 4B shows a Coomassie blue-stained gel of the

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different fractions recovered from the affinity-chromatography purification (the legend of which is presented in Example 4);

Figure 5A shows the results of the E1/E2/ori binding assay described in Example 8;

5 **FIGURE 5B** shows three experiments with purified wild-type and mutants HPV-11 E1 proteins. The top panel shows the results of a helicase gel-based assay by detecting unwinding activity of the enzyme; the middle panel shows the results of an ATPase assay; and the bottom figure shows the results of a
10 helicase assay, as detected by SPA. These experiments are described in Example 9;

FIGURE 6 shows a schematic representation of the high throughput screening assay for the E1 helicase as described in Example 11;

15 **FIGURE 7** shows the IC_{50} curve for inhibition of the E1 helicase activity by the M13 plasmid as described in Example 12;

20 **FIGURE 8** shows the IC_{50} curve of inhibition of the E1 helicase activity by ethidium bromide as described in Example 12;

FIGURE 9A shows a Coomassie blue-stained gel of the loaded material and the different fractions recovered from the affinity-chromatography purification (the legend of which is presented in Example 14);

25 **FIGURE 9B** shows a Western immunoblot of the gel of the different fractions recovered from the affinity-chromatography purification (the legend of which is presented in Example 15);

30 **FIGURE 10A** shows a Coomassie blue-stained gel of different conditions for the nuclear extraction of the E1 protein (the legend of which is presented in Example 15) and also the no-salt extraction of HPV-6 E1 protein;

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FIGURE 10B shows a Western immunoblot of the gel of Figure 9A. The blot was incubated with an anti-E1 polyclonal antibody and horseradish peroxidase (HRP)-conjugated second antibody. Bands were visualized using a chemiluminescent reagent;

FIGURE 11 represents the amino acid sequence of HPV-11 E1 protein as isolated by the method of the invention. The amino acids in bold indicate the modifications observed compared to the published sequence of Figure 2; and

FIGURE 12 represents the amino acid sequence of HPV-6a E1 protein as isolated by the method of the invention. The amino acid in bold indicates the modification observed compared to the published sequence of Figure 2.

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

Definitions

Unless defined otherwise, the scientific and technological terms and nomenclature used herein have the same meaning as commonly understood by a person of ordinary skill to which this invention pertains. Generally, the procedures for cell culture, infection, molecular biology methods and the like are common methods used in the art. Such standard techniques can be found in reference manuals such as for example Sambrook et al. (1989, Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratories) and Ausubel et al. (1994, Current Protocols in Molecular Biology, Wiley, New York).

Nucleotide sequences are presented herein by single strand, in the 5' to 3' direction, from left to right, using the one letter nucleotide symbols as commonly used in the art and in accordance with the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission (Biochemistry, 1972, 11:1726-1732).

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The present description refers to a number of routinely used recombinant DNA (rDNA) technology terms. Nevertheless, definitions of selected examples of such rDNA terms are provided for clarity and consistency.

- 5 The term "recombinant DNA" or "recombinant plasmid" as known in the art refers to a DNA molecule resulting from the joining of DNA segments. This is often referred to as genetic engineering.

- 10 The term "DNA segment", is used herein, to refer to a DNA molecule comprising a linear stretch or sequence of nucleotides. This sequence when read in accordance with the genetic code, can encode a linear stretch or sequence of amino acids which can be referred to as a polypeptide, protein, protein fragment and the like.

- 15 The term "oligonucleotide" or "DNA" molecule or sequence refers to a molecule comprised of the deoxyribonucleotides adenine (A), guanine (G), thymine (T) and/or cytosine (C). The term "oligonucleotide" or "DNA" can be found in linear DNA molecules or fragments, viruses, plasmids, vectors,
20 chromosomes or synthetically derived DNA. As used herein, DNA sequences are described according to the normal convention of giving only the sequence in the 5' to 3' direction.

- 25 As used herein, the term "gene" is well known in the art and relates to a nucleic acid sequence defining a single protein or polypeptide. A "structural gene" defines a DNA sequence which is transcribed into RNA and translated into a protein having a specific amino acid sequence thereby giving rise to a specific polypeptide or protein.

- 30 The term "fusion protein" as defined herein refers to two polypeptidic segments that are not joined together in nature.

Non-limiting examples of such "fusion proteins" according to the present invention include the E1 protein fused to the

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polypeptide of an "affinity label". In some embodiments it may be beneficial to introduce a cleavage site between the two polypeptide sequences which have been fused. Such protease cleavage sites between two heterologously fused protein are
5 well known in the art.

The terms "vectors" or "DNA construct" are commonly known in the art and refer to any genetic element, including, but not limited to, plasmid DNA, phage DNA, viral DNA and the like which can incorporate the oligonucleotide sequences, or
10 sequences of the present invention and serve as DNA vehicle into which DNA of the present invention can be cloned. Numerous types of vectors exist and are well known in the art.

The term "expression" defines the process by which a structural gene is transcribed into mRNA (transcription), the
15 mRNA is then being translated (translation) into one polypeptide (or protein) or more.

The terminology "expression vector" defines a vector or vehicle as described above but designed to enable the expression of an inserted sequence following transformation
20 into a host. The cloned gene (inserted sequence) is usually placed under the control of control element sequences such as promoter sequences. Such expression control sequences will vary depending on whether the vector is designed to express the operably linked gene in a prokaryotic or eukaryotic host
25 or both (shuttle vectors) and can additionally contain transcriptional elements such as enhancer elements, termination sequences, tissue-specificity elements, and/or translational initiation and termination sites.

By "eukaryotic expression system" is meant the
30 combination of an appropriate expression vector and a eukaryotic cell line which can be used to express a protein of interest. In some systems the gene for the protein may be

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inserted into the genome of a virus which can infect the cell type being used. Plasmid vectors containing the desired gene may also be used. In all cases, the vector will contain appropriate control elements (promoter) to express protein in the cell type of interest. Additional components, for example a vector or viral genome coding for T7 polymerase, may also be necessary in certain expression systems. Eukaryotic cell types typically used are yeast (e.g. *Saccharomyces cerevisiae*, *Pischia pastoris*) transfected with a plasmid vector; insect cells (e.g. SF9, SF21) infected with baculovirus (*Autographa californica* or *Bombyx mori*) (Luckow, Curr. Op. Biotech., 1993, 4:564-572; Griffiths and Page, 1994, Methods in Molec. Biol. 75:427-440; and Merrington et al., 1997, Molec. Biotech. 8(3):283-297); mammalian cells infected with adenovirus, vaccinia virus, Sindbis virus, or semliki forest virus; and mammalian cells transfected with DNA vectors for transient or constitutive expression. Particularly preferred here is the insect cell/baculovirus system.

A host cell or indicator cell has been "transfected" by exogenous or heterologous DNA (e.g. a DNA construct) when such DNA has been introduced inside the cell. The transfecting DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transfecting DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transfected cell is one in which the transfecting DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transfecting DNA. Transfection methods are well known in the art (Sambrook et al., 1989,

supra; Ausubel et al., 1994, *supra*).

The term "affinity label" or "affinity tag" as used herein refers to a label which is specifically trapped by a complementary ligand. Examples of pairs of affinity
5 marker/affinity ligand include but are not limited to: Maltose-Binding Protein (MBP)/maltose; Glutathione S Transferase (GST)/ glutathione; histidine (His)/ metal. The metal used as affinity ligand may be selected from the group consisting of: cobalt, zinc, copper, iron, and nickel (Wong et
10 al. (1991), Separation and Purification Methods, 20(1), 49-106). Preferably, the metal selected is nickel. The affinity ligand can be set up in columns to facilitate separation by affinity chromatography.

The affinity label may be positioned on the N- or C-
15 terminal end of the protein, but preferably on the N-terminus of the protein.

For certainty, the nucleotide sequences and polypeptides useful to practice the invention includes "functional derivatives". The term "functional derivatives" is intended
20 to include "fragments", "segments", "variants", "analogs" or "chemical derivatives" of the subject matter of the present invention. The functional derivatives of the present invention can be synthesized chemically or produced through recombinant DNA technology. All these methods are well known
25 in the art.

Thus, the term "variant" refers herein to a protein or nucleic acid molecule which is substantially similar in structure and biological activity to the protein or nucleic acid of the present invention.

30 As used herein, "chemical derivatives" is meant to cover additional chemical moieties not normally part of the subject matter of the invention. Such moieties could affect the

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physico-chemical characteristic of the derivative (i.e. solubility, absorption, half life and the like, decrease of toxicity). Such moieties are exemplified in Remington's Pharmaceutical Sciences (1980). Methods of coupling these
5 chemical-physical moieties to a polypeptide are well known in the art.

As exemplified herein below, the nucleotide sequences and polypeptides used in the present invention can be modified, for example by *in vitro* mutagenesis, to dissect the
10 catalytic and structure-function relationship thereof and permit a better design and identification of the resulting proteins. As used herein, the designation "functional derivative" denotes, in the context of a functional derivative of a sequence whether a nucleic acid or amino acid sequence, a
15 molecule that retains a biological activity (either function or structural) that is substantially similar to that of the original sequence. This functional derivative or equivalent may be a natural derivatives or may be prepared synthetically. Such derivatives include amino acid sequences having
20 substitutions, deletions, or additions of one or more amino acids, provided that the biological activity of the protein is conserved. The same applies to derivatives of nucleic acid sequences which can have substitutions, deletions, or additions of one or more nucleotides, provided that the
25 biological activity of the sequence is generally maintained. When relating to a protein sequence, the substituting amino acid has chemico-physical properties which usually, but not necessarily, are similar to that of the substituted amino acid. The similar chemico-physical properties include,
30 similarities in charge, bulkiness, hydrophobicity, hydrophilicity and the like. Some of the most commonly known conservative amino acid substitutions include, but are not limited to:

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Leu or Val or Ile; Gly or Ala; Asp or Glu;
Asp or Asn or His; Glu or Gln; Lys or Arg;
Phe or Trp or Tyr; Val or Ala; Cys or Ser;
Thr or Ser; and Met or Leu.

5 As used herein, the term "purified" refers to a molecule having been separated from other cellular or viral components. Thus, for example, a "purified protein" has been purified to a level not found in nature.

The term "substantially purified" refers to a protein
10 that is pure to about 60% or higher.

The term "substantially pure" refers to a protein that is pure to about 80% or higher.

The term "essentially pure" refers to a protein that is pure to about 90% or higher.

15 **Preferred embodiments**

In a particularly preferred embodiment, the method of purification of E1 protein comprises an incubation of a nuclei extract from eukaryotic expression system at a salt concentration lower than 300 mM, preferably from 0-100 mM,
20 more preferably from 0-50 mM and most preferably in the absence of salt.

Preferably, the salt refers to NaCl although other salts well known in the art (such as LiCl or KCl) may be used for nuclear extractions.

25 In accordance with a further embodiment of the invention, there is provided a method as described above wherein the E1 protein is the E1 helicase from bovine papillomavirus (BPV), cottontail rabbit papillomavirus (CRPV) or human papillomavirus (HPV). In a preferred embodiment, the
30 E1 protein is from HPV low risk or high risk types.

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Preferably, when the E1 protein is a low risk type, it is selected from type 6, type 11 and type 13, and especially HPV type 11 and type 6. Alternatively, when the E1 protein is a high risk type, it is selected from the group consisting of
5 types 16, 18, 31, 33, 35, 45, 52, or 58, preferably type 16.

A further aspect of the present invention provides the method as described above wherein the eukaryotic expression system is selected from the group consisting of: baculovirus in insect cells; Vaccinia, Sindbis, and Semliki forest
10 viruses, or Adenovirus in mammalian cells (such as COS or Vero cells); and plasmid in yeast expression systems, preferably a baculovirus in insect cells expression system.

A further aspect of the present invention provides the method as described above wherein said E1 protein comprises an
15 affinity label selected from the group consisting of: histidine tag, glutathione-S-transferase, and maltose-binding-protein and the complementary affinity ligand is selected from the group consisting of: antibody, nickel, maltose and glutathione columns.

20 Preferably, the antibody column comprises monoclonal or polyclonal antibodies, more preferably monoclonal antibodies.

Most preferably, the E1 protein is labeled with a histidine-tag and the His-labeled protein is separated on a nickel affinity ligand column.

25 Preferably, the affinity label is positioned at one terminus of the E1 protein, more preferably at the N-terminus thereof.

Still, a further aspect of the present invention provides a HPV E1 preparation prepared from low salt
30 concentration, preferably extracted from a nuclei preparation in the presence of 0-100 mM NaCl, more preferably 0-50 mM

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NaCl, most preferably in the absence of NaCl, and further purified with affinity chromatography.

Preferably, the E1 preparation as described above is "substantially purified" at least about 60% purity and above, more preferably "substantially pure" at least about 80% purity and above, especially "essentially pure" at least about 90% purity.

Preferably, the E1 preparation as described above is the E1 helicase from bovine papillomavirus (BPV), cottontail rabbit papillomavirus (CRPV) or human papillomavirus (HPV), preferably from HPV low risk or high risk type. Preferably, when the E1 protein is a low risk type, it is selected from type 6, type 11 and type 13, and especially HPV type 11 and type 6. Alternatively, when the E1 protein is a high risk type, it is selected from the group consisting of types 16, 18, 31, 33, 35, 45, 52, or 58, preferably, type 16.

Methodology

The recombinant DNA constructs in accordance with the present invention can be constructed using conventional molecular biology, microbiology, and recombinant DNA techniques well known to those of skilled in the art (i.e. Sambrook et al, 1989, *supra*). With a suitable DNA construct transfected into a host cell, the present invention provides a method for the expression of a gene of interest.

Alternatively, the DNA construct comprises a sequence coding for a affinity label, such as nucleotides coding for histidine (His). Transfection of the DNA construct into a host cell provides a convenient means for expressing a fusion protein comprised of the polypeptide of interest and the affinity label, thus allowing the isolation of the expressed fusion product by an affinity ligand column complementary to the affinity label.

Construction and Expression

We have used a particular version of the system from Gibco Lifesciences, in which the gene of interest is subcloned into a transfer vector which is then transformed into an *E.*
5 *coli* strain containing a baculovirus genome. Specific sites on the vector then allow transposition which inserts the gene into the baculovirus genome (bacmid). This recombinant bacmid can then be isolated and transfected into SF9 or SF21 insect cells, which then produce the protein of interest, as well as
10 infectious virus which can be used in the future to produce the protein of interest.

In other baculovirus systems, the gene of interest may be recombined into the baculovirus genome within the insect cell. This is done by transfecting insect cells with a vector
15 containing the gene of interest and at the same time infecting them with baculovirus. In a certain percentage of the cases, the gene of interest is transferred to the viral genome by homologous recombination. Various methods well known in the art may be used to select for recombinant genomes carrying the
20 gene of interest.

Extraction and Purification

The E1 protein of the invention can be purified using a specific protocol enabling it to be separated quickly and in a limited number of steps from the bulk of eukaryotic cellular
25 and nuclear proteins and other viral contaminating components.

Contrary to conventional wisdom suggesting that nucleic acid binding proteins are more soluble in high salt concentrations, it has been established by the Applicant that the E1 protein is quickly and efficiently separated from the
30 bulk of nuclear proteins and DNA by a low salt extraction protocol. Without wishing to be bound by theory, it is hypothesized that, when suspended in a hypotonic salt

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solution, the E1 protein leaches out selectively from the nucleus preparation. That is why the critical step of the invention comprises the low salt extraction of the E1 protein from nuclear extracts of HPV-infected baculovirus cell
5 culture.

One of the peculiar aspect of the extraction protocol relies in the incubation time in which the nuclear extraction is carried out in the low salt solution (30-40 min as opposed to 5-10 min for the cell lysis). Indeed, in a preferred
10 embodiment of the invention, the cell lysis buffer may also be hypotonic, however in this case it is important not to leave the lysed cells in the cell lysis buffer before the nuclei are centrifuged and separated to avoid E1 leaching in the lysis buffer prior to extraction.

15 Although our experiments allowed us to extract E1 at a salt concentration up to 500 mM, it was shown that some contaminants are observed at that concentration. It is therefore preferred to use salt concentrations that are below 300 mM, and preferably salt concentrations equal or below
20 isotonic salt concentrations (150 mM) such as 100 mM, more preferably 50 mM, and most preferably, the extraction is carried out in the absence of salt.

Following the nuclear extraction, the E1 protein is preferably further purified via affinity chromatography. For
25 such purposes the protein can be expressed as a fusion protein comprising an affinity label which is specifically trapped by a complementary affinity ligand optionally bound to chromatographic column media. The affinity label is preferably localized on the N-terminus of the protein

30 Examples of pairs of affinity label/affinity ligand column include but are not limited to: Maltose-Binding Protein (MBP)/maltose column; Glutathione S Transferase (GST)/

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glutathione column; histidine (His)/ Ni column.

In a preferred embodiment, the E1 is expressed as a His-E1 fusion protein and is purified through Ni column affinity chromatography according to methods well known in the art.

5 Alternatively, the protein can also be trapped by polyclonal or monoclonal antibodies, in which case it does not need to be modified with a affinity label. For that purpose, an antiserum must be prepared.

In general, techniques for preparing antibodies
10 (including monoclonal antibodies and hybridomas) and for detecting antigens using antibodies are well known in the art (Campbell, 1984, In "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", Elsevier Science Publisher, Amsterdam, The Netherlands) and in
15 Harlow et al., 1988 (in: Antibody - A Laboratory Manual, CSH Laboratories).

In accordance with an additional aspect of the present invention, there is provided the means for detecting antiviral agents using assays for screening their level of inhibition
20 against HPV. The effectiveness of the candidate agents can be assessed by their ability to inhibit the viral helicase activity. This can be accomplished directly, by measuring the level of inhibition on the viral helicase activity or indirectly, by assessing the disruption on the interaction
25 between the E1/E2/ori complex by measuring the inhibition on the viral DNA replication process.

Methods for detecting such antiviral agents include, without limitations, the use of colorimetric, fluorescent or radioactive reagents. Such detection methods can be applied
30 in several types of assays such as culture plate assays or gel-based assays including for example Enzyme-Linked Immunosorbent Assay (ELISA), or Scintillation Proximity Assay

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(SPA) or any other assay well known in the art.

In one particular embodiment, there is provided an assay for screening and identifying candidate agents which modulate the helicase activity of E1, and more particularly the E1
5 helicase activity of HPV type 11 and type 6.

A preferred embodiment of such assay relies in a high throughput screening (HTS) assay for candidate agents capable of inhibiting E1 helicase activity and to identify such agents. Such high throughput screening assay is preferably
10 selected from a fluorescence assay or a scintillation proximity assay, more preferably the latter.

In this assay, the duplex DNA substrate consists of M13 single-stranded DNA (about 8000 bases) to which is annealed a 19 base oligodeoxynucleotide (see Figure 6). This partial
15 duplex is extended to 24 bases with the incorporation of [³³P]-labeled dATP by a reaction with the Klenow fragment of DNA polymerase I. Helicase activity results in the separation of this radiolabeled oligo from the M13 DNA. In the absence of a functional helicase, the double-stranded DNA substrate is
20 stable for several hours at the assay temperature.

To detect activity, a second 24-base deoxyoligonucleotide, complementary to the substrate oligo, is added to the reaction mixture in a second step. This oligo anneals to any free radiolabeled oligo, but cannot interact
25 with oligo still annealed to M13 DNA. A biotin is covalently attached to the 5'-terminus of the second oligo.

In the third step, streptavidin-coated SPA beads (Amersham Life Science, code TRKQ7030) are added to the mixture. The biotinylated oligo and any associated
30 radiolabeled oligo then bind to these beads. SPA beads are impregnated with a scintillant, which allows detection of radiolabel in close proximity to the beads. Thus radiolabeled

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oligo annealed to the biotinylated oligo will be detected, whereas unreacted substrate still hybridized to M13 is not in close proximity to the beads and will not be detected.

In the presence of an inhibitor, less substrate is unwound, so a lower signal is detected. Positive controls used for the validation of this assay may be, among others cold substrate (such as the M13 single-stranded DNA) or DNA intercalators (such as ethidium bromide). The M13 DNA competes with the labeled M13 substrate and inhibits the signal detected. Ethidium bromide is a recognized DNA intercalator and stabilizes the M13-oligo substrate, thereby preventing helicase activity.

EXAMPLES

The present invention is illustrated in further detail by the following non-limiting examples.

EXAMPLE 1: E1 EXPRESSIONConstruction of recombinant plasmid

Recombinant baculovirus construct (Bac-to-Bac™ Baculovirus Expression Systems) (Gibco BRL):

The E1 gene from HPV type 11 was pcr-amplified using recombinant plasmid pCR3-E1 as DNA template according to Lu et al. (1993, J. Virology 67:7131-7138). The forward primer was 5'-CGC GGA TCC AGG ATG CAT CAC CAT CAC CAT CAC GCG GAC GAT TCA CGT ACA GAA AAT GAG-3' (SEQ ID NO. 1) and the reverse was GG CTG AAT TCA TAA AGT TCT AAC AAC T (SEQ ID NO. 2). Purified pcr products were then restricted with EcoRI and BamHI and ligated with donor plasmid pFASTBAC1™ (Gibco, BRL) which had been linearized with the same enzymes.

HPV-11 E1 protein expression

His-E1-pFASTBAC was then transformed into *E. coli* strain DH10Bac™ for transposition following the manufacturer's

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instructions (Gibco-BRL). White colonies were selected and transposition confirmed by analytical pcr using primers flanking the bacmid (baculovirus circular DNA) insertion site.

Mini-preparation of recombinant bacmids was carried out and the purified bacmid DNA transfected into SF9 cells. Baculovirus-containing supernatants were collected 72 h post-transfection, and infected cells resuspended in 2X Leammli buffer for expression analysis by Western using anti-E1 K72 polyclonal antibody (see description of E2-dependent E1-DNA binding assay, Example 8). Recombinant baculovirus, confirmed to express His-E1 protein was reamplified and further used to infect SF21 insect cells for large scale production.

EXAMPLE 2: HPV-11 His-E1 extraction using different concentrations of salt

E1 extraction. SF21 insect cells infected with E1-pFASTBAC recombinant baculovirus were harvested from 425 ml culture in SF-900 II SFM medium to give a cell pellet of 5 ml which has been frozen rapidly in dry ice. Frozen pellet was then thawed rapidly and cells resuspended in 5 ml of cell lysis buffer A (20 mM tris, pH 8.0, 1 mM DTT, 1 mM EDTA, 5 mM KCl, 1mM MgCl₂ - antipain, leupeptin and pepstatin each at 1 µg/ml - 1 mM Pefabloc™). Following 15 min incubation on ice, cells were broken with a Dounce homogenizer (≈5 min, pestle B) and then centrifuged at 2500 g, 20 min, 4°. Pelleted nuclei were resuspended to 7 ml with resuspension buffer (20 mM Tris, pH 8.0, 1 mM DTT, 1 mM EDTA, antipain, leupeptin and pepstatin each at 2 µg/ml, 2 mM Pefabloc™) and distributed in 0,5 ml aliquots in 14 tubes. 0,5 ml of 13 different 2X extraction buffers (at varying concentrations of salt and detergents) were then mixed separately to 13 aliquots of nuclei, by pipetting up and down to give the final conditions listed below. Samples were incubated at 4° with rocking for 30 min

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and centrifuged in a microcentrifuge at maximal speed for 30 min. Supernatants were finally recovered and 4 µl of each run in 10% SDS-PAGE. 1 gel was stained with Coomassie Blue (Figure 3A) and another one transferred for the membrane to be
5 hybridized with anti-E1 K72 polyclonal antibody and detected with "western blot chemiluminescent reagent" (DuPont NEN, Boston, MA) and the emitted light was captured on autoradiography film (Figure 3B).

Figures 3A and 3B Legend:

- 10 Lane 0: 10 mM Tris, pH 8,0; 0,5 mM DTT; 0,5 mM EDTA
Lane 1: 20 mM tris, pH 8,0 ; 1 mM DTT; 0,5 mM EDTA
Lane 2: #1 + 100 mM NaCl
Lane 3: #1 + 450 mM NaCl
Lane 4: #1 + 0,01% Triton X-100
15 Lane 5: #1 + 0,01% Triton + 100 mM NaCl
Lane 6: #1 + 0,01% Triton + 450 mM NaCl
Lane 7: #1 + 0,1% Triton
Lane 8: #1 + 0,1% Triton+ 100 mM NaCl
Lane 9: #1 + 0,1% Triton+ 450 mM NaCl
20 Lane 10: #1 + 10% glycerol
Lane 11: #1 + 10% glycerol + 100 mM NaCl
Lane 12: #1 + 10% glycerol + 450 mM NaCl

Lanes indicated 50, 100, and 200 µg were samples of E1 fragment from *E. coli* that were used as positive control for
25 the K72 antibody immunoblot.

Figures 3A and 3B show that the extraction of E1 from the nuclei preparation is not greatly improved by the use of detergent (lanes 4 to 12). As salt concentrations increase, more contaminants leach out of the nuclei. In absence of
30 salt, almost all of the E1 protein is already extracted, and 100 mM does not show more E1 extracted. At 450 mM salt, the gel shows more contaminants and some degradation of the E1 protein.

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EXAMPLE 3: HPV-11 His-E1 extraction

Cells infected with recombinant baculovirus were harvested and frozen rapidly in liquid nitrogen before being stored at -80°. For nuclear extraction, frozen cell pellets
5 were thawed and resuspended in 1 volume (relative to the volume of cell pellet) of cell lysis buffer B containing protease-inhibitors (20 mM Tris pH 8, 5 mM β -mercaptoethanol, 5 mM KCl, 1 mM MgCl₂, 1 mM Pefabloc™, 1 μ g/ml pepstatin, 1 μ g/ml leupeptin, and 1 μ g/ml antipain) and left on ice for 15
10 min. Cells were then broken on ice with a Dounce homogenizer (\approx 5 min, pestle B) followed by centrifugation at 2500g, 4° for 20 min. Supernatant (cytosol) was discarded and nuclei resuspended to 1.4 volume with extraction buffer A (20 mM Tris pH 8, 5 mM β -mercaptoethanol, 2 mM Pefabloc™, 2 μ g/ml
15 pepstatin, 2 μ g/ml leupeptin, and 2 μ g/ml antipain). Finally, 1.4 volume of extraction buffer B (20 mM Tris pH 8, 5 mM β -mercaptoethanol, and 0.02% Triton X-100) was added and the nuclei incubated at 4° with rocking for 30 min before ultracentrifugation at 148,000g, 4° for 45 min. Glycerol was
20 added to the supernatant to 10% final concentration and the extract was frozen rapidly on dry ice and stored at -80°.

EXAMPLE 4: HPV-11 His-E1 purification

Nuclear extracts were thawed rapidly and the NaCl concentration adjusted to 500 mM before the preparation was
25 loaded on 5 ml Hi-Trap™ chelating column previously charged with NiSO₄ according to the Manufacturer's instructions (Pharmacia, Biotech). The column was then pre-equilibrated in equilibration buffer (20 mM Tris pH 8, 5 mM β -mercaptoethanol, 500 mM NaCl, 10 mM imidazole, and 10% glycerol) and the flow-
30 through collected for analysis. The column was washed first with 10 volumes of equilibration buffer and then with 10 volumes of washing buffer (equilibration buffer but with 50 mM

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imidazole) before His-E1 (or mutant proteins) was eluted (1 mL fractions 1 to 10) with elution buffer (equilibration buffer but with 180 mM imidazole). E1 proteins were then dialyzed in dialysis buffer (20 mM MES pH 7.0, 500 mM NaCl, 1 mM DTT, 0.05 mM EDTA, and 10 % glycerol) before being frozen on dry ice and stored at -80°.

As an example of the yields obtained from this preparation, one 10 L preparation gave a 10 mL solution of purified E1 at 30 µg/mL (3 mg protein total).

10 Legend of Figure 4B:

A: total load of the column;

B: flow-through;

C: equilibration with 10 mM imidazole;

D: washing with 50 mM imidazole;

15 Lanes 1 to 10 represent 1 mL fractions eluted with the elution buffer (180 mM imidazole).

Figure 4B shows a Coomassie blue-stained gel where fractions 2, 3, and 4 contain most of the essentially pure E1 protein.

20 **EXAMPLE 5: Mutation analysis of HPV-11 E1 helicase**

Mutant E1 proteins were made by disabling the helicase active site to validate that the helicase activity observed was due to the E1 protein and not to contaminants co-purified with E1.

25 Mutant plasmids encoding the K484A, K484H, K484I and, K484R mutations were constructed using the QuickChange™ site-directed mutagenesis kit from Stratagene using the protocol supplied by the manufacturer.

The template for mutagenesis was the E1 DNA sequence carrying the K484E mutation. This mutant DNA template was used instead of wild type E1 because the K484E mutation

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creates a restriction site. This allowed us to identify quickly clones which carried the K484A, -H, -I, and -R mutations by simply screening for loss of the restriction site. The K484E mutation differed from the wild type E1 DNA sequence in the following way:

WT E1 5'-CCTGACACTGGGAAGTCGTGCTTTTGC-3'

(SEQ ID NO. 3)

K484E 5'-CCTGACACTGGGGAGTCGTGCTTTTGC-3'

(SEQ ID NO. 4)

10 (GAGTC is a site cut by the Ple 1 enzyme)

Pairs of complementary primers used for mutagenesis were:

K484A

MUT-TOP 5'-CCTGACACTGGGGCGTCGTGCTTTTGC-3'

15 (SEQ ID NO 5)

MUT-BOT 5'-GCAAAAGCACGACGCCCCAGTGTTCAGG-3'

(SEQ ID NO. 22)

K484H

20 MUT-TOP 5'-CCTGACACTGGGCACTCGTGCTTTTGC-3'

(SEQ ID NO. 6)

MUT-BOT 5'-GCAAAAGCACGAGTGCCCAGTGTTCAGG-3'

(SEQ ID NO. 23)

25 K484I

MUT-TOP 5'-CCTGACACTGGGATCTCGTGCTTTTGC-3'

(SEQ ID NO. 7)

MUT-BOT 5'-GCAAAAGCACGAGATCCCAGTGTTCAGG-3'

(SEQ ID NO. 24)

30

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K484R

MUT-TOP 5'-CCTGACACTGGGCGGTCGTGCTTTTGC-3'
(SEQ ID NO 8)

5 MUT-BOT 5'-GCAAAAGCACGACCGCCAGTGTCTCAGG-3'
(SEQ ID NO 25)

The subcloning of these mutant alleles in baculovirus was amplified by pcr using the same primers as described above.

10 All His-E1-K484A, -H, -I, and -R constructs were cloned into the same pFASTBac™ vector, transformed into *E. coli* DH10Bac™ plasmids according to Example 1. The resulting bacmids were transfected in SF9 cells, and the recombinant viruses infected in SF21 cells also according to Example 1.

15 **EXAMPLE 6: HPV-11 E2 protein expression**

HPV-11 E2 was obtained by expression in baculovirus-infected insect cells. A baculovirus encoding the gene for HPV-11 E2 was obtained from R. Rose (U. Rochester, N.Y.) and used to infect SF21 insect cells. Infected cells were
20 resuspended in cell lysis buffer C (30 mM HEPES pH 7.6, 1 mM EDTA, 2 mM DTT, 1% NP-40, and protease inhibitors: 1 mM Pefabloc™, 1 mM PMSF, and 2.5 µg/mL each antipain, leupeptin, and pepstatin). Lysis occurred on stirring the cells, and nuclei were recovered by centrifugation. Nuclei were
25 resuspended in nuclear extraction buffer C (30 mM HEPES pH 7.6, 10% glycerol, 250 mM NaCl, 5 mM EDTA, 2 mM DTT, 0.5% NP-40, and the same protease inhibitors as above). The suspension was stirred for 45 min, then sonicated. E2 was recovered in the supernatant following centrifugation.

30 **EXAMPLE 7: Purification of HPV-11 E2**

E2 was purified from the nuclear extract using a DNA affinity chromatography by a procedure based on that of Seo et

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al. (PNAS 90(93) 2865). To prepare the affinity ligand column, duplex DNA containing three E2 binding sites was prepared by annealing two oligos (5'-biotin-AGT GAC CGA AAA CGG TCG GGA CCG AAA ACG GTG TAG ACC GAA AAC GGT GTA-3' (SEQ ID NO. 9) and
5 5'-CTA CAC CGT TTT CGG TCT ACA CCG TTT TCG GTC CCG ACC GTT TTC GGT CAC T-3' (SEQ ID NO. 10)). The duplex was bound to streptavidin agarose by virtue of the biotin incorporated into the first oligo. Chromatography was carried out using elution buffer D (nuclear extraction buffer C without protease
10 inhibitors) and elution buffer E (elution buffer D plus 1M NaCl). A typical column consisted of 10 mL of the above resin. The nuclear extract was centrifuged at 50,000 g for 20 min. to remove any precipitated material, then applied to the column, washed with elution buffer D until the absorbance of the
15 eluent at 280 nm reached baseline, then eluted with a linear gradient of elution buffers D and E, 60 mL of each. Fractions containing pure E2 (by SDS-PAGE) were pooled and concentrated to approximately 150 µg/mL using a Millipore centrifugal filter device (Ultrafree-15™), then stored at -80°.

20 **EXAMPLE 8: E2-dependent E1 DNA binding assay**

This assay was modeled on a similar assay for SV40 T Antigen described by McKay (J. Mol. Biol., 1981,145:471). A 400bp radiolabeled DNA probe, containing the HPV-11 origin of replication (Chiang et al., 1992, Proc. Natl. Acad. Sci. USA
25 89:5799) was produced by pcr, using plasmid pBluescript™ SK encoding the origin (nucleotides 7886-61 of the HPV-11 genome in unique BAMH1 site) as template and primers flanking the origin. Radiolabel was incorporated as [³³P]dCTP. Binding assay buffer consisted of: 20 mM Tris pH 7.6, 100 mM NaCl, 1 mM DTT,
30 1 mM EDTA.

Other reagents used were protein A-SPA beads (type II, Amersham) and K72 rabbit polyclonal antiserum, raised against

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a peptide corresponding to the C-terminal 14 amino acids of HPV-11 E1. Following the protocol from Amersham, one bottle of beads was mixed with 25 mL of binding assay buffer. For the assay, a saturating amount of K72 antiserum was added to
5 the beads and the mixture was incubated for 1 h, washed with one volume of binding assay buffer, and then resuspended in the same volume of fresh binding assay buffer. Binding reactions contained 8 ng of E2, approximately 100-200 ng of purified E1, and 0.4 ng of radiolabeled probe in a total of 80
10 μ L of binding assay buffer. After 1 h at room temperature, 25 μ L of K72 antibody-SPA bead suspension was added to with the binding reaction and mixed. After an additional hour of incubation at room temperature, the reactions were centrifuged briefly to pellet the beads and the extent of complex
15 formation was determined by scintillation counting on a Packard TopCount™. Typically, the signal for reactions containing E1 and E2 was 20-30 fold higher than the background observed when either E1, E2, or both was omitted.

Figure 5A shows the DNA binding activity of the E1/E2
20 complex of the wild type (wt) E1 helicase and the four mutants produced in Example 5. There was no significant difference in the E1/E2/ori binding between any of the proteins indicating that the mutant proteins were folding in a normal fashion.

EXAMPLE 9: HELICASE/ ATPase ASSAYS25 Helicase/ATPase assays

The substrate for the analytical helicase assay consisted of a 24-base oligonucleotide (GTA AAA CGA CCA GTG CCA AGC) (SEQ ID NO. 11) end-labeled using [³³P]ATP and polynucleotide kinase, annealed to M13mp18. Combined
30 helicase/ATPase reactions contained 800 or 1600 ng of E1, 2 mM MgCl₂, 1 mM ATP, and 1 μ M helicase substrate (concentration in nucleotides) in a total volume of 80 μ L of helicase assay

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buffer (20mM MES, pH 7.0, 1mM DTT, 0.05mM EDTA, 10% glycerol). Reactions were incubated for 2 h at 37° and then placed on ice.

Helicase gel-based detection:

5 25 µL of each reaction was mixed with 5x helicase stop/loading solution (12.5% Ficoll 4000, 0.5% SDS, 50 mM EDTA, and 0.125% each bromophenol blue and xylene cyanol); 20 µL of the mixture was electrophoresed for 1 h at 125 V through a 20% polyacrylamide/1x TBE gel. Blank reactions containing
10 no enzyme were run in parallel. The gel was dried and scanned on a Molecular Dynamics PhosphorImager™. The substrate and reaction product separated by size, with the substrate remaining at the top of the gel and the unwound radiolabeled oligonucleotide migrating approximately half-way down. In
15 some cases degradation products due to nuclease activity are apparent further down the gel.

Figure 5B top panel shows the gel migration of the helicase substrate and product after incubation with the wild-type (wt) and the mutants E1 proteins. Lane 13 is a boiled
20 sample, lane 12 is a blank, whereas lane 11 is a blank which has been incubated for 2 h at 37°.

As apparent from Figure 5B, none of the mutants show any significant helicase activity compared to the wild-type E1 protein.

25 The intensity of the unwound oligonucleotide band may be quantitated using the PhosphorImager™, and the amount of activity may be expressed relative to 100% unwinding as described below for the SPA.

ATPase assay

30 An additional 15 µL of each reaction was used to detect ATPase activity by the procedure of Lanzetta et al. (Anal.

Biochem., 1979, 100, 95).

Figure 5B middle panel shows that the ATPase activity follows the helicase activity as demonstrated by the gel assay.

5 Helicase Scintillation Proximity Detection (SPA)

An additional 30 μ L was transferred to another 96-well plate containing 30 μ L of SPA stop hybridization buffer, which is identical to the "stop" buffer in Example 11, except that the biotinylated capture oligonucleotide is complementary to
10 the substrate sequence above.

Helicase activity was quantitated as follows:

A separate reaction mixture, containing no enzyme was heated to 95° for 10 min., and the resulting free substrate oligonucleotide (completely denatured) was detected as
15 described for reaction mixtures. The level of signal generated in this experiment represents 100% unwinding. Similar samples, which were not heated, serve as blanks, representing background signal. Quantitation of unwinding is calculated relative to the boiled sample with background
20 subtracted.

Figure 5B bottom panel shows that the percent of unwinding is negligible with the mutant proteins as compared to the wild-type (wt) control. These results are in accordance with the ones obtained from the gel-based assay.

EXAMPLE 10: ENZYMATIC ACTIVITY

His-E1 helicase specific activityEnzymatic Activities of HPV-11 E1
-Comparison to Literature

TABLE 1

Helicase Activity	V (% unwinding/ μ M protein/ min)	Reference
HPV-11 E1	2.5	this work
HPV-6a E1	2.3	this work
SV-40 TAg	5.0	this work
BPV E1	2.9	Yang, PNAS (1993)

Table 1 compares the enzymatic activity of the helicase from HPV-11 and -6 as purified according to the present invention, to another helicase reported in the literature. This represents the first instance where the human papillomavirus helicase E1 is purified to an extent where its unwinding activity can be quantified.

In all cases the enzyme concentration was greater than the substrate concentration and the substrate was partial duplex DNA. All experiments were done at 37° except for the BPV-E1 which was assayed at 32°. The SV-40 TAg was also assessed in the literature and V of 50 and 80 % unwinding/ μ M protein/min were obtained from these groups respectively (Goetz, JBC (1988); Stahl, EMBO (1986)). The extent of the difference with our results stem from the fact that our assay conditions were optimized for E1 activity and may not be optimal for TAg activity (lower pH, etc..).

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EXAMPLE 11: High-throughput screening assay

SPA references:

N. Bosworth, P. Towers, "Scintillation proximity assay"
Nature 341, 167-168 (1989).

- 5 N.D. Cook, "Scintillation proximity assay- a versatile
high throughput screening technology" *Drug Discovery Today*, 1,
287-294 (1996).

"Determination of DNA helicase activity using a [³H]
scintillation proximity assay (SPA) system" *Proximity News*,
10 July 1996.

This assay is similar to that in Example 9. The
radiolabeled DNA substrate for this assay consists of a 19-
base oligonucleotide (TTC CCA GTC ACG ACG TTG T) (SEQ ID NO
12) annealed to single-stranded M13mp18 plasmid. The Klenow
15 fragment is used to extend the partial duplex to 24 bases,
using four [³³P]dATP and one unlabeled dCTP. Helicase
reactions are run by mixing 10 µL each of the following
components:

- 1) a substrate cocktail comprising radiolabeled DNA substrate,
20 ATP, and magnesium acetate;
- 2) inhibitors dissolved in buffer plus 18% DMSO;
- 3) HPV-11 E1 purified as in Example 4.

Assay buffer, used for all dilutions, consisted of 20 mM
MES, pH 7.0, 10% glycerol, 1.0 mM DTT, and 0.05 mM EDTA.
25 Final concentrations in the assay are 0.8 µM (concentration in
nucleotides), 1.0 mM ATP, 1.0 mM magnesium acetate, 6% DMSO.
Sufficient E1 is used to give approximately 20% unwinding (as
determined in Example 9). Reaction mixtures are incubated at
37° for 2 h in Microfluor® 96-well plates (Dynex). 30 µL of a
30 "stop" buffer is then added, which consists of 100 mM HEPES,
pH 7.5, 300 mM NaCl, 20 mM EDTA, 1% SDS, and a biotinylated

oligonucleotide (complementary to the substrate
oligonucleotide) at 20 nM. After 1.5 h at room temperature,
50 μ L of a suspension of streptavidin-coated polyvinyl toluene
SPA beads (1.25 mg/mL in 50 mM HEPES, pH 7.5, 0.02% NaN₃) is
5 added, followed by a further 0.5 h incubation at room
temperature. Assay plates are then centrifuged briefly to
pellet the SPA beads and the amount of reaction product is
detected by scintillation counting using a Packard Topcount™.

EXAMPLE 12: Inhibition of E1 helicase activity (IC₅₀ curves)

10 To determine the potency of potential inhibitors, E1
helicase SPA reactions (Example 11) were run in the presence
of serially diluted inhibitors. The concentrations of both
M13 and ethidium bromide ranged from 0.04 to 20 μ M.

Reaction controls with no inhibitor, and blanks with no
15 inhibitor and no enzyme, were run simultaneously. Unwinding
was detected as described above and results were fit to a
logistic using the SAS software package. [SAS is a registered
trademark of the SAS Institute, Inc. of Cary, North Carolina]

For both Figures 7 and 8, data points are graphed as the
20 percent inhibition at each inhibitor concentration.
Concentration is expressed in μ M on a log scale. Percent
inhibition at each inhibitor concentration ([I]) is determined
from the following formula:

$$100 - 100 \times \frac{(\text{activity at [I]} - \text{blank})}{(\text{control activity} - \text{blank})}$$

25

The solid line shows the best fit to the data determined
by SAS. Some data points are out of range and are not shown
in the figures.

From Figures 7 and 8, it can be approximated that the
30 IC₅₀ are 3 and 4 μ M respectively for M13 and ethidium bromide.

40

EXAMPLE 13: HPV-6 E1 EXPRESSIONConstruction of recombinant plasmid

Recombinant baculovirus construct (Bac-to-Bac system):
E1 gene from HPV type 6a was PCR-amplified using recombinant
5 plasmid pCR3.1-E1(6a) as DNA template previously constructed
in our lab from DNA isolated from a clinical sample. The
forward primer was 5'-CGC GGA TCC AGG ATG CAT CAC CAT CAC CAT
CACGCG GAC GAT TCA CGT ACA GAA AAT GAG 3' (SEQ ID NO.1) and
the reverse one was GG CTG AAT TCA TAA AGT TCT AAC AAC T (SEQ
10 ID NO.2). The resulting PCR fragment was then purified and
restricted with EcoRI and BamHI and ligated with donor plasmid
pFASTBAC1 linearized with the same enzymes.

HPV-6 E1 protein expression

HIS-E1-pFASTBAC was then transformed in E. coli DH10Bac®
15 strain for transposition following the manufacturer's
instructions (Gibco-BRL). White colonies were first selected
and transposition confirmed by analytical PCR using primers
flanking the insertion site in bacmid (baculovirus circular
DNA).

20 Mini-preparation of recombinant bacmids was conducted
and then transfected in SF9 cell. 72 h post-transfection,
baculovirus-containing supernatants were collected and
infected cells resuspended in 2X Leammli buffer for expression
analysis by Western using K72 polyclonal antibody.
25 Recombinant baculovirus confirmed to express E1HIS was
reamplified and further used to infect SF21 cells for large
scale production.

**EXAMPLE 14: HPV-11 and HPV-6a His-E1 extraction using
different concentrations of salt**

30 **E1 extraction.** SF21 insect cells infected with E1-pFASTBAC
recombinant baculovirus were harvested from 5 L culture in SF-
900 II SFM medium to give a cell pellet of 65 ml which has

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been frozen rapidly in dry ice. Frozen pellet was then thawed rapidly and cells resuspended in 65 ml of cell lysis buffer A (20 mM tris, pH 8.0, 1 mM DTT, 1 mM EDTA, 5 mM KCl, 1mM MgCl₂, - antipain, leupeptin and pepstatin each at 1 µg/ml - 1 mM Pefabloc™). Following 15 min incubation on ice, cells were broken with a Dounce homogenizer (≈5 min, pestle B) and then centrifuged at 2500 g, 20 min, 4°. Supernatant was re-centrifuged at 148 000 g, 4° for 45 min and this second supernatant was kept as "cytosol". Glycerol was added to this supernatant to 10% final concentration and this sample was frozen rapidly on dry ice and stored at -80°. Pelleted nuclei were resuspended to 90 ml with extraction buffer A (20 mM Tris pH 8, 5 mM β-mercaptoethanol, 2 mM Pefabloc™, 2 µg/ml pepstatin, 2 µg/ml leupeptin, and 2 µg/ml antipain) and distributed in 18 ml aliquots in 5 tubes. 18 ml of extraction buffer B (20 mM Tris pH 8, 5 mM β-mercaptoethanol, and 0.02% Triton X-100) was added and NaCl concentration was adjusted with a 5M solution to the conditions listed below. Samples were incubated at 4° with rocking for 30 min and centrifuged at 148000 g, 4° for 45 min. Supernatants were finally recovered and glycerol was added to the supernatant to 10% final concentration and the extract was frozen rapidly on dry ice and stored at -80°.

Example 15: HPV-11 and HPV-6a His-E1 purification.

Nuclear extracts were thawed rapidly and the NaCl concentration adjusted to 500 mM before the preparation was loaded on 1 ml Hi-Trap™ chelating column previously charged with NiSO₄ according to the Manufacturer's instructions (Pharmacia, Biotech). The column was then pre-equilibrated in equilibration buffer (20 mM Tris pH 8, 5 mM β-mercaptoethanol, 500 mM NaCl, 10 mM imidazole, and 10% glycerol) and the flow-through collected for analysis. The column was washed first

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with 5-6 volumes of equilibration buffer and then with 5-6 volumes of washing buffer (equilibration buffer but with 50 mM imidazole) before His-E1 was eluted (1 mL fractions 1 to 10) with elution buffer (equilibration buffer but with 180 mM imidazole). E1 proteins were then dialyzed in dialysis buffer (20 mM MES pH 7.0, 500 mM NaCl, 1 mM DTT, 0.05 mM EDTA, and 10 % glycerol) before being frozen on dry ice and stored at -80°.

For load and flow-through samples, 4 µl of each fractions were run on 10% SDS-PAGE). For each comparison experiment, 1 gel was stained with Coomassie Blue (Figure 9A) and another one transferred for the membrane to be hybridized with anti-E1 K72 polyclonal antibody and detected with "western blot chemiluminescent reagent" (DuPont NEN, Boston, MA) and the emitted light was captured on autoradiography film (Figure 9B).

Legends of Figures 9A (Coomassie) and 9B (Western blot):

A: load on Hi-Trap column (Crude Extract)

B: Flow through from Hi-Trap column

Lane 1: HPV-11 E1 extracted in absence of NaCl

20 Lane 2: HPV-11 E1 extracted with 50mM NaCl

Lane 3: HPV-11 E1 extracted with 100mM NaCl

Lane 4: HPV-11 E1 extracted with 250mM NaCl

Lane 5: HPV-11 E1 extracted with 500mM NaCl

Lane 6: HPV-11 E1 extracted from cytosol

25 Figure 9A shows a Coomassie blue-stained gel of crude E1 extract obtained from the protocol of Example 14. Lanes 4 and 5 reveal that there is a lot more material extracted at 250 and 500 mM salt but most of that material is not retained on the column, indicating that the majority of the material
30 extracted at these salt concentrations is not E1.

Figure 9B allowed us to see that most of the E1 bound to the column. Once again the results of this experiment are in

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agreement with example 4.

Bradford protein assay was performed on elution fractions and SDS-PAGE and western blot of purified E1 were done with a content amount of total protein (1 μ g for SDS-PAGE;
5 0.2 μ g for western) (Figures 10A, 10B).

Figures 10A Legend:

SDS-PAGE purified E1

- Lane 1: HPV-11 E1 extracted in absence of NaCl
Lane 2: HPV-11 E1 extracted with 50mM NaCl
10 Lane 3: HPV-11 E1 extracted with 100mM NaCl
Lane 4: HPV-11 E1 extracted with 250mM NaCl
Lane 5: HPV-11 E1 extracted with 500mM NaCl
Lane 6: HPV-11 E1 extracted from cytosol
Lane 7: HPV-6a E1 extracted in absence of NaCl

15 Figures 10B Legend:

Western Blot of purified E1

- Lane 1: HPV-11 E1 extracted in absence of NaCl
Lane 2: HPV-11 E1 extracted with 50mM NaCl
Lane 3: HPV-11 E1 extracted with 100mM NaCl
20 Lane 4: HPV-11 E1 extracted with 250mM NaCl
Lane 5: HPV-11 E1 extracted with 500mM NaCl
Lane 6: HPV-11 E1 extracted from cytosol
Lane 7: HPV-6a E1 extracted in absence of NaCl

Figures 10A and 10B reproduce and extend the results of
25 example 3 where, as salt concentrations increase, the nuclear preparation is less pure and the preparation from the column is also less pure. In absence of salt and at 50 mM almost all of the E1 protein is already extracted. Concentrations of 100 mM and over do not improve the extraction of E1. Lane 6 also
30 shows clearly that the extraction and purification of HPV-6 E1 is as effective in the absence of salt.

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It was therefore established that the conditions for routine extraction would be performed at a salt concentration equal or lower than 300 mM for optimal results, preferably in hypotonic conditions equal or lower than 100 mM, more
5 preferably equal or lower than 50 mM, and most preferably in the absence thereof.

The E1 proteins from HPV-11 and HPV-6a were sequenced and showed minor amino acid changes from the published literature. Our sequences are presented in Figure 11 (as SEQ
10 ID NO.26) for HPV-11, and in Figure 12 (SEQ ID NO.27) for HPV-6a.

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CLAIMS

1. A method for isolating the papillomavirus E1 protein or a functional derivative thereof having viral helicase activity comprising the steps of:
 - producing an E1 recombinant protein in a eukaryotic expression system and isolating a nuclei preparation thereof; and
 - extracting E1 protein from said nuclei preparation in a buffer comprising salt at a concentration lower than 300 mM.
2. The method of claim 1, further comprising the step of:
 - purifying E1 protein from said nuclear extract by affinity chromatography.
3. The method of claim 1, wherein said HPV E1 is purified from a nuclei preparation in the presence of 0-100 mM salt.
4. The method of claim 1, wherein said HPV E1 is purified from a nuclei preparation in the presence of 0-50 mM salt.
5. The method of claim 1, wherein said HPV E1 is purified from a nuclei preparation in the absence of salt.
6. The method according to claim 1, wherein said salt is NaCl.
7. The method of claim 1, wherein said E1 protein is the E1 helicase from cottontail rabbit papillomavirus (CRPV), bovine papillomavirus (BPV) or human papillomavirus (HPV).
8. The method of claim 7, wherein said E1 protein is from HPV low risk or high risk types.

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9. The method of claim 7, wherein said recombinant HPV E1 protein is from a low risk type HPV selected from the group consisting of: type 6, type 11 and type 13.
10. The method of claim 7, wherein said low risk HPV is type 11 or type 6.
11. The method of claim 8, wherein said recombinant HPV E1 protein is from a high risk type HPV selected from the group consisting of types 16, 18, 31, 33, 35, 45, 52, or 58.
12. The method of claim 11, wherein said high risk HPV is type 16.
13. The method of claim 1, wherein said eukaryotic expression system is selected from the group consisting of: baculovirus in insect cells; Vaccinia, Sindbis, Semliki forest viruses, or Adenovirus in mammalian cells; and plasmid in yeast expression systems.
14. The method of claim 13, wherein said eukaryotic expression system is insect cells infected with a baculovirus.
15. The method of claim 1, wherein said E1 protein comprises an affinity label.
16. The method of claim 15, wherein said affinity label is selected from the group consisting of: histidine tag, glutathione-S-transferase, and maltose-binding-protein.
17. The method of claim 16, wherein said affinity label is recognized by an affinity ligand selected from the group consisting of: antibody, metal, maltose and glutathione.

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18. The method of claim 17, wherein said affinity label is positioned at the N-terminus of said E1 protein.
19. The method of claim 17, wherein said antibody is a monoclonal or a polyclonal antibody.
20. The method of claim 17, wherein said E1 protein is labeled with a histidine-tag and said metal affinity ligand is a nickel column.
21. A preparation of recombinant papillomavirus E1 protein from a eukaryotic expression system, said E1 having viral helicase activity, wherein the E1 protein is extracted from a nuclei preparation in the presence of salt at a concentration less than 300 mM, and purified by affinity chromatography.
22. The HPV E1 preparation of claim 21, wherein said HPV E1 is purified from a nuclei preparation in the presence of 0-100 mM salt.
23. The HPV E1 preparation of claim 22, wherein said HPV E1 is purified from a nuclei preparation in the presence of 0-50 mM salt.
24. The HPV E1 preparation of claim 23, wherein said HPV E1 is purified from a nuclei preparation in the absence of salt.
25. The E1 preparation of claim 20, wherein said E1 protein is substantially purified.
26. The E1 preparation of claim 20, wherein said E1 protein is substantially pure.
27. The E1 preparation of claim 20, wherein said E1 protein is essentially pure.

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28. The E1 preparation of claim 20, wherein said E1 protein is the E1 helicase from cottontail rabbit papillomavirus (CRPV), bovine papillomavirus (BPV) or human papillomavirus (HPV).
29. The E1 preparation of claim 28, wherein said E1 protein is from HPV low risk or high risk type.
30. The HPV E1 preparation of claim 29, wherein said recombinant HPV E1 protein is from a low risk type HPV selected from the group consisting of: type 6, type 11 and type 13.
31. The HPV E1 preparation of claim 30, wherein said low risk HPV is type 11 and type 6.
32. The HPV E1 preparation of claim 29, wherein said recombinant HPV E1 protein is from a high risk type HPV selected from the group consisting of: of types 16, 18, 31, 33, 35, 45, 52, or 58.
33. The HPV E1 preparation of claim 32, wherein said high risk HPV is type 16.
34. The HPV E1 preparation of claim 21, wherein said E1 protein is selected from the group consisting of: SEQ ID NO. 13; SEQ ID NO. 14; SEQ ID NO. 15; SEQ ID NO. 16; SEQ ID NO. 17; SEQ ID NO. 18; SEQ ID NO. 19; SEQ ID NO. 20; SEQ ID NO. 26; and SEQ ID NO. 27.
35. A method for assaying the specific viral helicase activity of papillomavirus E1 protein, said method comprising the steps of:
- incubating a mixture of said E1 protein preparation according to claim 1, and a suitable substrate for said

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viral helicase enzymatic activity; and

- measuring the amount of specific helicase activity of said E1 protein.

36. The assay according to claim 35, wherein said papillomavirus is HPV-11 or HPV-6.

37. The assay of claim 35, wherein said E1 protein is selected from the group consisting of: SEQ ID NO. 13; SEQ ID NO. 14; SEQ ID NO. 15; SEQ ID NO. 16; SEQ ID NO. 17; SEQ ID NO. 18; SEQ ID NO. 19; SEQ ID NO. 20; SEQ ID NO. 26; and SEQ ID NO. 27.

38. A method for identifying agents capable of modulating said helicase activity, said method comprising the steps of:

a) assaying the activity of said E1 helicase in the absence of said agent by the method according to claim 35;

b) assaying the activity of said helicase in the presence of said agent by the method of claim 35, wherein said agent is added to said helicase and substrate mixture during said incubation; and

c) comparing the result of step a) with the result of step b).

39. The assay according to claim 38, wherein said papillomavirus is HPV-11 or HPV-6.

40. The assay of claim 38, wherein said E1 protein is selected from the group consisting of: SEQ ID NO. 13; SEQ ID NO. 14; SEQ ID NO. 15; SEQ ID NO. 16; SEQ ID NO. 17; SEQ ID NO. 18; SEQ ID NO. 19; SEQ ID NO. 20; SEQ ID NO. 26; and SEQ ID NO. 27.

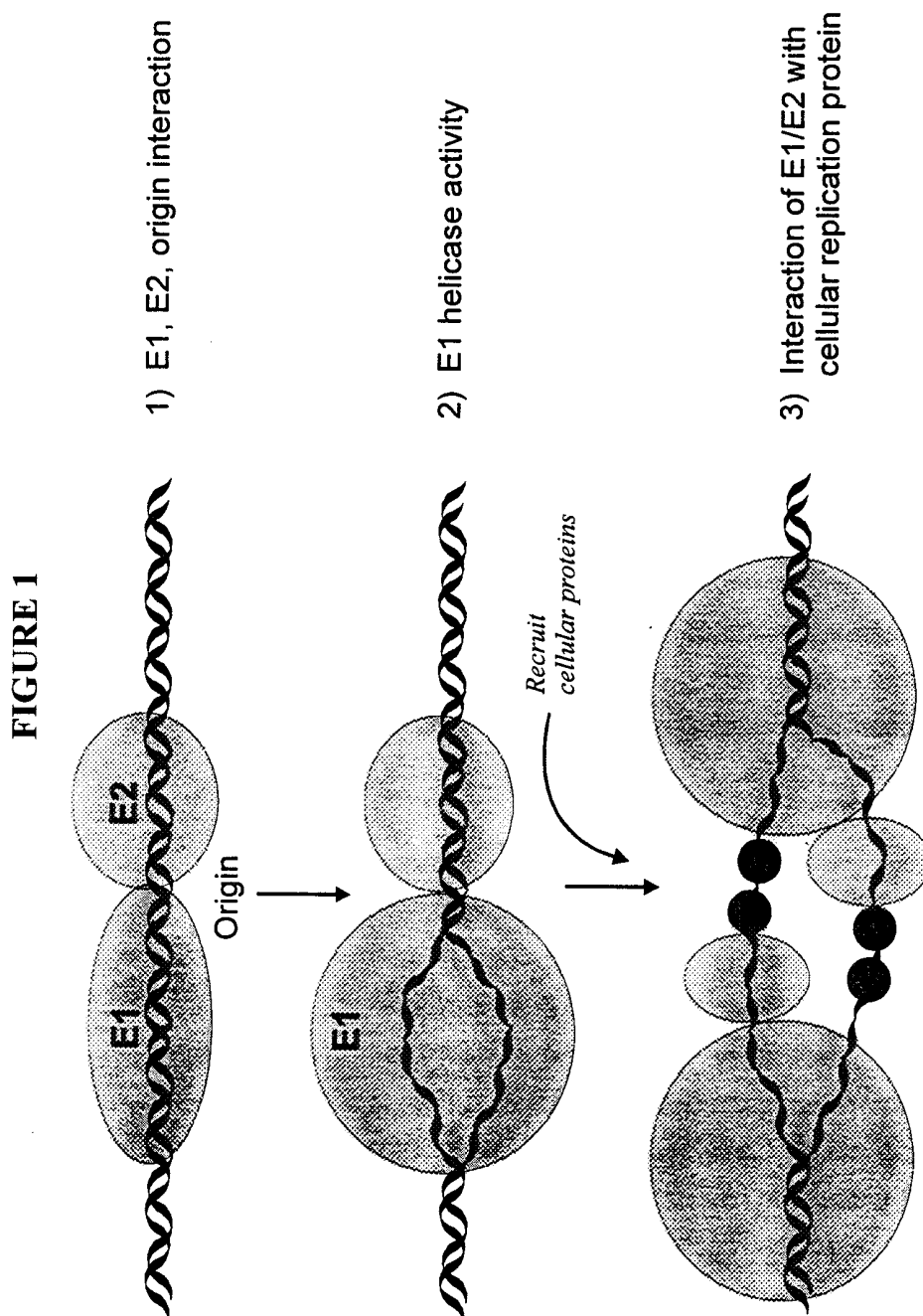
50

41. A method for assaying papillomavirus DNA replication, said method comprising the steps of:
- incubating a candidate agent with a mixture of E1 protein preparation according to claim 1, with E2 protein and a suitable DNA origin of replication; and
 - measuring the amount of DNA unwinding.
42. The assay according to claim 41, wherein said papillomavirus is HPV-11 or HPV-6.
43. The assay of claim 41, wherein said E1 protein is selected from the group consisting of: SEQ ID NO. 13; SEQ ID NO. 14; SEQ ID NO. 15; SEQ ID NO. 16; SEQ ID NO. 17; SEQ ID NO. 18; SEQ ID NO. 19; SEQ ID NO. 20; SEQ ID NO. 26; and SEQ ID NO. 27.
44. A method for identifying an agent capable of modulating papillomavirus DNA replication, said method comprising the steps of:
- a) assaying said DNA replication activity in the absence of said agent by the method according to claim 41;
 - b) assaying said DNA replication activity in the presence of said agent by the method of claim 41, wherein said agent is added to said mixture during said incubation; and
 - c) comparing the result of step a) with the result of step b).
45. The assay according to claim 44, wherein said papillomavirus is HPV-11 or HPV-6.

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46. The assay of claim 44, wherein said E1 protein is selected from the group consisting of: SEQ ID NO. 13; SEQ ID NO. 14; SEQ ID NO. 15; SEQ ID NO. 16; SEQ ID NO. 17; SEQ ID NO. 18; SEQ ID NO. 19; SEQ ID NO. 20; SEQ ID NO. 26; and SEQ ID NO. 27.

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FIGURE 2

		% identity with	
		type 11	
Low risk:			
W1wl11	E1 protein - HPV (type 11)	649aa	
W1wl13	E1 protein - HPV (type 13)	646aa	
W1wl6	E1 protein - HPV (type 6b)	649aa;	89%
High risk:			
W1wl18	E1 protein - HPV (type 18)	657aa;	51%
W1wl39	E1 protein - HPV (type 39)	647aa	
W1wl33	E1 protein - HPV (type 33)	644aa	
W1wl31	E1 protein - HPV (type 31)	629aa;	55%
W1wl35	E1 protein - HPV (type 35)	630aa	
W1wlhs	E1 protein - HPV (type 16)	506aa;	51%
W1wleb	E1 protein - BPV (type 1)	605aa;	40%
		1	33
(SEQ ID NO.13)	W1wl11	MADDSGTE.NE GSGCTGWFMV	EAIVEHTTGT QIS
(SEQ ID NO.14)	W1wl13	MAEDTGTN.NE GTGCSGWFLV	EAVVERTTGQ QIS
(SEQ ID NO.15)	W1wl 6	MADDSGTE.NE GSGCTGWFMV	EAIVQHPTGT QIS
(SEQ ID NO.16)	W1wl18	MADPEGTD.GE GTGCNGWFYV	QAIVDKKTGD VIS
(SEQ ID NO.17)	W1wl39	MANREGTD.GD GSGCNGWFLV	QAIVDKQTGD TVS
(SEQ ID NO.18)	W1wl33	MADPEGTN.GA GMGCTGWFEV	EAVIERRTGD NIS
(SEQ ID NO.19)	W1wl31	MADPAGTD.GE GTGCNGWFYV	EAVIDRQTGD NIS
(SEQ ID NO.20)	W1wl35	MADPAGTDEGE GTGCNGWFFV	EAVVSRRTGS SV.
(SEQ ID NO.21)	W1wlhs
34		77	
W1wl11	EDEEEEV	EDSGYDMVDF IDDRHI..TQNS	.VEAQALFNRQ EADAHYA
W1wl13	DDEDETV	EDSGLDMVDF IDDRPI..THNS	.VEAQALLNEQ EADAHYA
W1wl 6	DDEDEEV	EDSGYDMVDF IDDSNI..THNS	.LEAQALFNRQ EADTHYA
W1wl18	DDEDENA	TDTGSDMVDF IDTQGTFCQAE	LETAQALFHAQ EVHNDQAQ
W1wl39	EDEDENA	TDTGSDLADF IDDESTICVQAE	RETAQVLLHMQ EAQRDAQ
W1wl33	EDEDETA	DDSGTDLLEF IDDSMENSIQAD	TEAARALFNIQ EGEDDLN
W1wl31	EDENEDS	SDTGEDMVDF IDNCNVYNNQAE	AETAQALFHAQ EAEHAE

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W1wl35 EDENEDD CDRGEDMVDF INDTDILNIQAE TETAQALFHAQ EEQTHKE
 W1wlhs

78

127

W1wl11 TVQ DLKRKYLGGSP YVSPISNVAN AVESEISPRL DAIKLTTQPK KVKRRLF
 W1wl13 AVQ DLKRKYLGGSP YVSPLGHVEQ SVDCDISPRL DAIKLSRNSK KVKRRLF
 W1wl 6 TVQ DLKRKYLGGSP YVSPINTIAE AVESEISPRL DAIKLTRQPK KVKRRLF
 W1wl18 VLH VLKRKFAGGS TENSPLGERL EVDTELSPLRL QEISLNSGQK KAKRRLF
 W1wl39 AVR ALKRKYTDSS GDTRPYGKKV GRNT..RGTL QEISLNVSS TATQTVY
 W1wl33 AVC ALKRKFAGGS..CSQSAAED VVDRAANPCR TSINKNKECT YRKRKID
 W1wl31 AVQ VLKRKYVG..SPLSDISS CVDYNISPRL KAICIENNSK TAKRRLF
 W1wl35 AVQ VLKRKYAS..SPLSSVSL CVNNNISPRL KAICIENKNT AAKRRLF
 W1wlhs

128

172

W1wl11 ETR ELTDSGYGYS EVEA..ATQVEK HGDPE...NGGDG QERDTGRDIE GE
 W1wl13 QSR EITDSGYGYS ..EVEAETQVER NGEPE...NDCGG GGH..GRDKE GE
 W1wl 6 QTR ELTDSGYGYS EVEAGTGTQVEK HGVPE...NGGDG QEKDTGRDIE GE
 W1wl18 ... TISDSGYGCS EVEATQIQVTTN GEHGGNVCSGGST EAIDNGGTEG NN
 W1wl39 ... SVPDSGYGNM EVETAEEVEVTV ATNT....NGDA EGEHGGSVRE EC
 W1wl33 ... ELEDSDGYGNT EVETQOMVQVE SONGDTNLNDLES SGVGDDSEVS CE
 W1wl31 ... ELPDSGYGNT EVETQOMVQVEE QQ.....T TLSCNGSDG. TH
 W1wl35 ... ELPDSGYGNS EVEIHEIQQVEG HD.....TV EQCSMGSGDS IT
 W1wlhs ... MLQVEGRHET ETPCSQYSGGSG GG.....C SQYSSGSGGE GV

173

221

W1wl11 GVEHREAE AVD.DSTREHA DTSGILELLK CKDIRSTLHG KFKDCFGLSF V
 W1wl13 GQVHTEVH TGS.Q.IEEHT GTTRVLELLK CKDVTRATLYG KFKDCYGLSF T
 W1wl 6 ..EHTEAE APT.NSVREHA GTAGILELLK CKDLRAALLG KFKECFGLSF I
 W1wl18 SSVDTGSD NSNIENVNPQC TIAQLKDLLK VNNKQGAMLA VFKDTYGLSF T
 W1wl39 SSVDSAID S...ENQDPKS PTAQIKLLLQ SNNKKAAMLT QFKETYGLSF T
 W1wl33 TNVDSCEN V.....TLQEISNVLH SSNTKANILY KFKEAYGISF M
 W1wl31 SEREN..E T.....PTRNILQVLK TSNGKAAMLG KFKELYGVSF M
 W1wl35 SSSDERHD E.....T PTRDIIQILK CSNANAAMLA KFKELFGISF T
 W1wlhs SERHTICQ T.....PLTNILNLVK TSNKAAMLA KFKELYGVSF S

4/20

222 270

W1w111 DLIRPFKSD RTTCADWVVA GFGIHHSIAD AFQKLIEPLS LYAHIQWLTN
W1w113 DLIRPFKSD KTTCDWVVA AFGIHHSVSE AFEKLMQPLT TYMHQWLTN
W1w1 6 DLIRPFKSD KTTCLDWVVA GFGIHHSISE AFQKLIEPLS LYAHIQWLTN
W1w118 DLVRNFKSD KTTCTDWVTA IFGVNPTIAE GFKTLIQPFI LYAHIQCLDC
W1w139 DLVRTFKSD KTTCTDWVAA IFGVHPTIAE GFKTLINKYA LYTHIQSLDT
W1w133 ELVRPFKSD KTSCTDWCIT GYGISPSVAE SLKVLIKQHS LYTHLQCLTC
W1w131 ELIRPFQSN KSTCTDWCVA AFGVTGTVAE GFKTLLQPYC LYCHLQSLAC
W1w135 ELIRPFKSD KSTCTDWCVA AFGIAPSVANFKHIT YVYIYNVYRV
W1wlhs ELVRPFKSN KSTCCDWCIA AFGLTPSIAD SIKTLLQQYC LYLHIQSLAC

271 319

W1w111 AWGMVLLVLI RFKVNKSRCR VARTLGTLN IPENHMLIEP PKIQSGVRA
W1w113 AWGMVLLVLI RFKVNKSRCR VARTLATFLN IPEDHMLIEP PKIQSSVAA
W1w1 6 AWGMVLLVLL RFKVNKSRSR VARTLATLLN IPENQMLIEP PKIQSGVAA
W1w118 KWGVLLILALL RYKCGKSRLT VAKGLSTLLH VPETCMLIQP PKLRSSVAA
W1w139 KQGVLLILMLI RYTCGKNRVT VGKGLSTLLH VPESCMLLEP PKLRSPVAA
W1w133 DRGIIILLI RFRC SKNRLT VAKLMSNLLS IPETCMVIEP PKLRSTQCA
W1w131 SWGMVMLMLV RFKCAKNRIT IEKLLKLLC ISTNCMLIQP PKLRSTAAA
W1w135 HGAMVILALL RFKVEKREQQ LKTIDAKLLC ISAASMLIQP PKLRSTPAA
W1wlhs SWGMVLLLLV RYKCGKNRET IEKLLSKLLC VSPMCMMLIEP PKLRSTAAA

320 368

W1w111 L YWFRTGISNA STVIGEAPEW ITRQTVIEHS LADSQFKLTE MVQWAYDN
W1w113 L YWFRTGISNA SIVTGETPEW IKRQTIVEHG LADNQFKLTE MVQWAYDN
W1w1 6 L YWFRTGISNA STVIGEAPEW ITRQTVIEHG LADSQFKLTE MVQWAYDN
W1w118 L YWYRTGISNI SEVMGDTPEW IQRLTIIQHG IDDSNFDLSE MVQWAFDN
W1w139 L YWYRTGISNI SVVTGDTPEW IQRLTVIQHG IDDSVFDLSD MVQWAFDN
W1w133 L YWFRTAMSNI SDVQGTTPPEW IDRLTVLQHS FNDNIFDLSE MVQWAYDN
W1w131 L YWYRTGMSNI SDVYGETPEW IERQTVLQHS FNDTTFDLSD MVQWAYDN
W1w135 L YWFKTAMSNI SEVDGETPEW IQRQTVLQHS FNDADFDLSE MVQWAYDN
W1wlhs L YWYKTGISNI SEVYGDTPPEW IQRQTVLQHS FNDCTFELSQ MVQWAYDN

369 418

W1w111 DI CESEIAFEY AQRGDFDSNA RAFLNSNMQA KYVKDCAIMC RHYKHAEM
W1w113 DF CDESEIAFEY AQRGDFDSNA RAFLNSNCQA KYVKDCATMC KHYKNAEM

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W1w1 6 DI CEESEIAFEY AQRGDFDSNA RAFLNSNMQA KYVKDCATMC RHYKHAEM
 W1w118 EL TDESMAFEY ALLADSNSNA AAFLKSNCQA KYLKDCATMC KHYRRAQK
 W1w139 EY TDESIAFNY AMLADCNSNA AAFLKSNCQA KYVKDCATMC KHYKRAQK
 W1w133 EL TDDSDIAYYY AQLADSNSNA AAFLKSNSQA KIVKDCGIMC RHYKKA EK
 W1w131 DV MDDSEIAYKY AQLADSDSNA CAFLKSNSQA KIVKDCGTMC RHYKRAEK
 W1w135 DF IDSDIAYKY AQLAETNSNA CAFLKSNSQA KIVKDCATMC RHYKRAEK
 W1w1hs DI VDDSEIAYKY AQLADTNSNA SAFLKSNSQA KIVKDCATMC RHYKRAEK

419

466

W1w111 KK MSIKQWIKYR GTKVDSVGNW KPIVQFLRHQ NIEFIPFLSK LKLWLH
 W1w113 KK MSMKQWITYR SKKIEEAGNW KPIVQFLRHQ NIEFIPFLSK LKLWLH
 W1w1 6 RK MSIKQWIKHR GSKIEGTGNW KPIVQFLRHQ NIEFIPFLTK FKLWLH
 W1w118 RQ MNMSQWIRFR CSKIDEGGDW RPIVQFLRYQ QIEFITFLGA LKSFLK
 W1w139 RQ MSMSQWIKFR CSKCDEGGDW RPIVQFLRYQ GIEFISFLCA LKEFLK
 W1w133 RK MSIGQWIOSR CEKTNDGGNW RPIVQLLRYQ NIEFTAFLGA FKKFLK
 W1w131 RQ MSMGQWIKSR CDKVSDEGDW RDIVKFLRYQ QIEFVSFLSA LKLFLK
 W1w135 RE MTMSQWIKRR CAQVDDGDW RDIVRFLRYQ QVDFVAFLSA LKNFLH
 W1w1hs KQ MSMSQWIKYR CDRVDDGGDW KQIVMFLRYQ GVEFMSFLTA LKRFLQ

467

516

W1w111 GTPK KNCIAIVGPP DTGKSCFCMS LIKFLGGTVI SYVNCSHFW LQPLTD
 W1w113 GTPK KNCIAIVGPP DTGKSCFCMS LIKFLGGTVI SYVNSSSHFW LQPLCN
 W1w1 6 GTPK KNCIAIVGPP DTGKSYFCMS LISFLGGTVI SHVNSSSHFW LQPLVD
 W1w118 GTPK KNCLVFCGPA NTGKSYFGMS FIHFIQGAVI SFVNSTSHFW LEPLTD
 W1w139 GTPK KNCIVIYGPA NTGKSHFCMS LMHFLQGTVI SYVNSTSHFW LEPLAD
 W1w133 GIPK KSCMLICGPA NTGKSYFGMS LIQFLKGCVI SCVNSKSHFW LQPLSD
 W1w131 GVPK KNCILIHGAP NTGKSYFGMS LISFLQGCII SYANSKSHFW LQPLAD
 W1w135 GVPK KNCILIIYGAP NTGKSLFGMS LMHFLQGAI SYVNSKSHFW LQPLYD
 W1w1hs GIPK KNCILLYGAA NTGKSLFGMS LMKFLQGSVI CFVNSKSHFW LQPLAD

517

566

W1w111 AKVA LLDDATQPCW TYMDTYMRNL LDGNPMSIDR KHRALTLIK PPLLVT
 W1w113 AKVA LLDDATQSCW VYMDTYMRNL LDGNPMSIDR KHKSLALIK PPLLVT
 W1w1 6 AKVA LLDDATQPCW IYMDTYMRNL LDGNPMSIDR KHKALTLIK PPLLVT
 W1w118 TKVA MLDDATTTWC TYFDTYMRNA LDGNPISIDR KHKPLIQLKC PPILLT
 W1w139 AKLA MLDDATGTCW SYFDNYMRNA LDGYAISLDR KYKSLQMKC PPLLIT

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W1wl33 AKIG MIDDVTPISW TYIDDYMRNA LDGNEISIDV KHRALVQLKC PPLLLT
 W1wl31 AKIG MLDDATTPCW HYIDNYLRNA LDGNPVSIDV KHKALMQLKC PPLLIT
 W1wl35 AKIA MLDDATSPCG IYRPIFKKCT RWKSYISFRC KALSIVHIM. PTFTYY
 W1wlhs AKIG MLDDATVPCW NYIDDNLRNA LDGNLVSMDV KHRPLVQLKC PPLLIT

567

616

W1wl11 SNID ISKEEKYKYL HSRVTTFTFP NPFPFDRNGN AVYELSDANW KCFFER
 W1wl13 SNVD ITKDDKYKYL YSRVTTLTFP NPFPFDRNGN AVYELSDANW KCFFTR
 W1wl 6 SNID ITKEDKYKYL HTRVTTFTFP NPFPFDRNGN AVYELSNTNW KCFFER
 W1wl18 TNIH PAKDNRWPYL ESRITVFEFP NAFPPDKNGN PVYEINDKNW KCFFER
 W1wl39 SNTN PVEDDRWPYL RSRLTVFKFP NAFPPDQNRN PVYTINDKNW KCFFEK
 W1wl33 SNTN AGTDSRWPYL HSRLTVFEFK NPFPFDENG N PVYAINDENW KSFFSR
 W1wl31 SNIN AGKDDRWPYL HSRLVVFTFP NPFPFDKNGN PVYELSDKNW KSFFSR
 W1wl35 ININ AGKDDRWPYL HSRVVVFTFH NEFPFDKNGN PEYGLNDKNW KSFFSR
 W1wlhs SNIN AGTDSRWPYL HNRLVVFTFP NEFPFDENG N PVYELNDKNW KSFFSR

617

649

W1wl11 LSSS LDIEDSEDE.E D.GSNSQAFRC VPGSVVRTL.. (SEQ ID NO. 13)
 W1wl13 LSAS LDIQDSEDE.D D.GDNSQAFRC VPGTVVRTV.. (SEQ ID NO. 14)
 W1wl 6 LSSS LDIQDSEDE.E D.GSNSQAFRC VPGTVVRTL.. (SEQ ID NO. 15)
 W1wl18 TWSR LDLHEEEEDAD TEGNPFGTFKL RAGQNRPL.. (SEQ ID NO. 16)
 W1wl39 TWCR LDLQQDEDEGD NDENTFTTFKC VTGQNTLIL.. (SEQ ID NO. 17)
 W1wl33 TWCK LDLIEEEDK.E NHGGNISTFKC SAGENTRSLRS (SEQ ID NO. 18)
 W1wl31 TWCR LNLHEEEDK.E NDGDSFSTFKC VSGQNIRTL.. (SEQ ID NO. 19)
 W1wl35 TWCR LNLHEEEVK.E NDGDAFPAFKC VSGQNTRTLRLD (SEQ ID NO. 20)
 W1wlhs TWSR LSLHEDEDK.E NDGDSLPTFKC VSGQNTNTL.. (SEQ ID NO. 21)

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FIGURE 3A

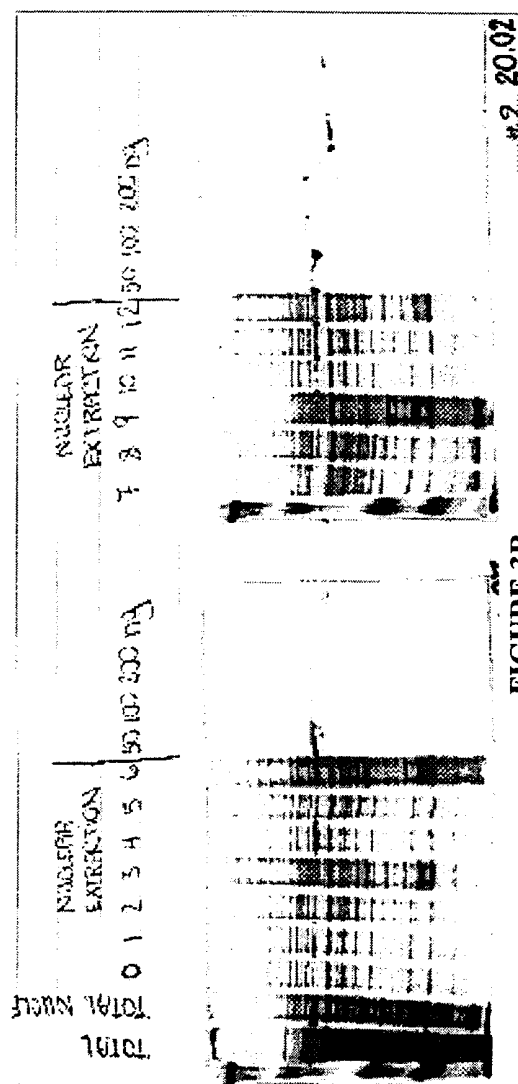
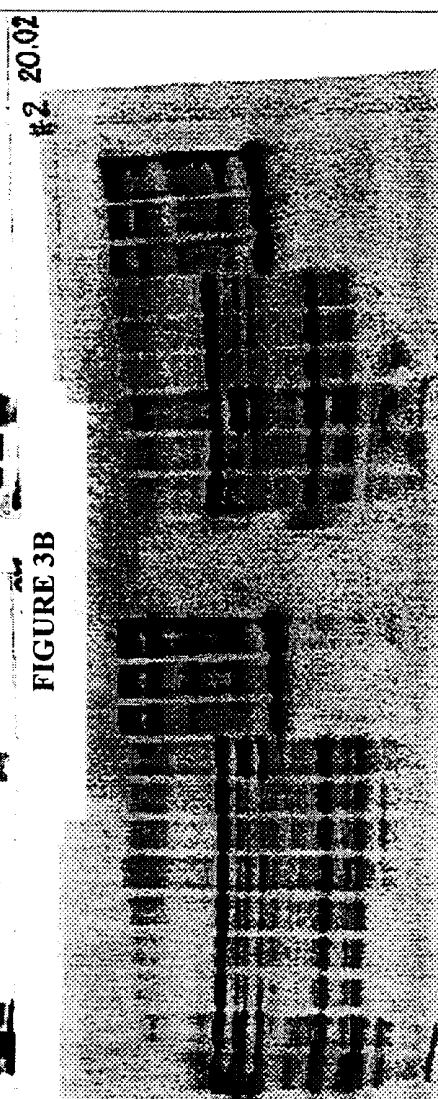
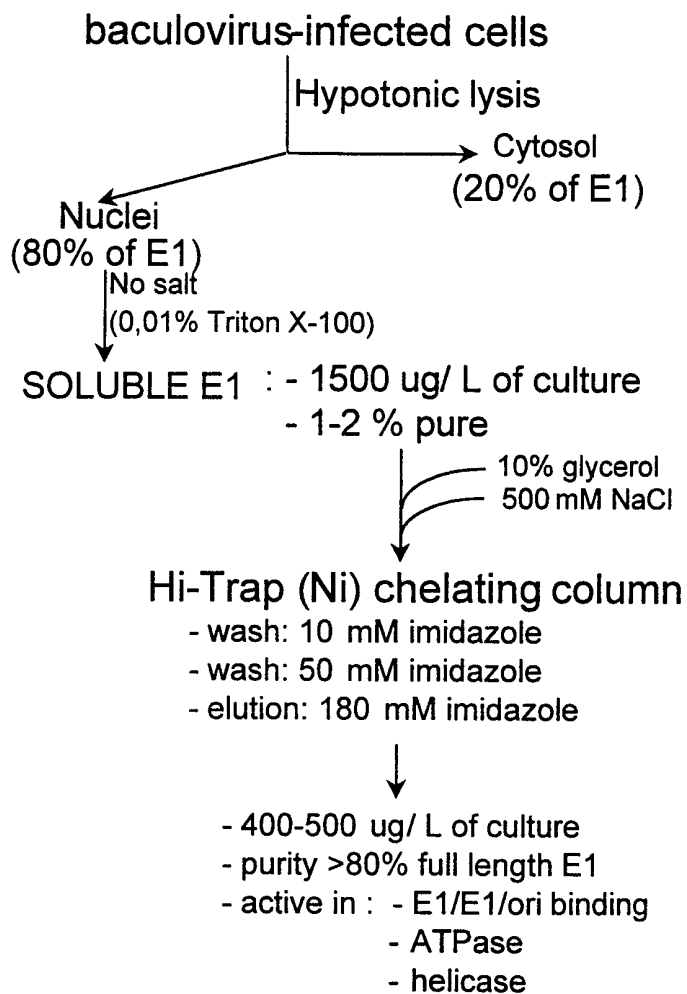


FIGURE 3B



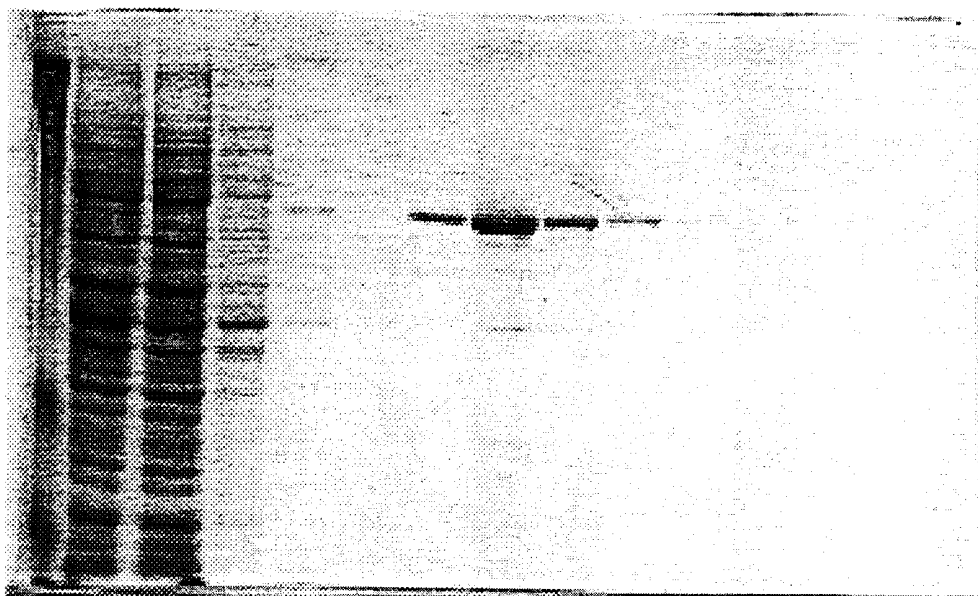
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FIGURE 4A**PURIFICATION PROCEDURE**

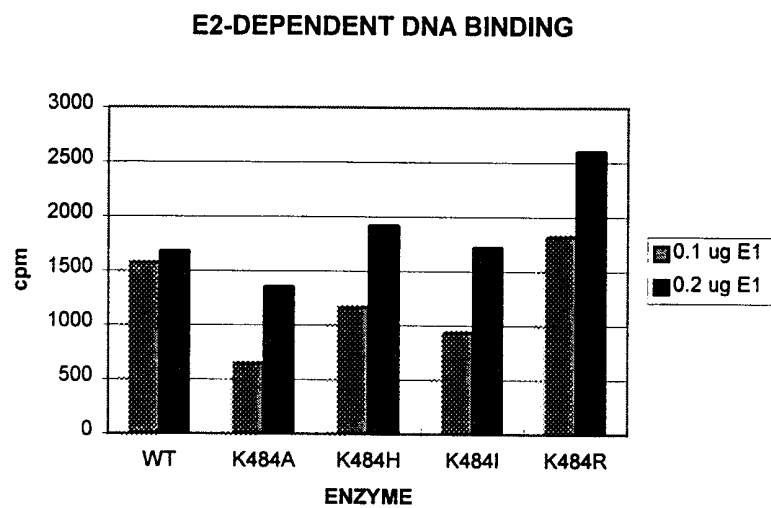
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FIGURE 4B

ctl LD F.T. A B 1 2 3 4 5 6 7 8 9 10



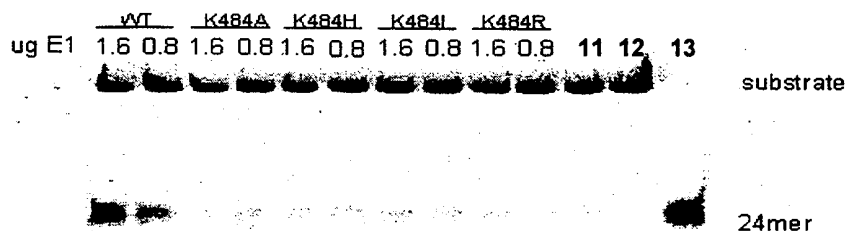
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FIGURE 5A

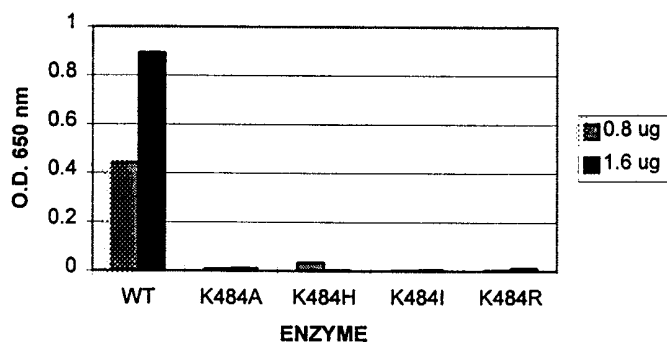
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FIGURE 5B

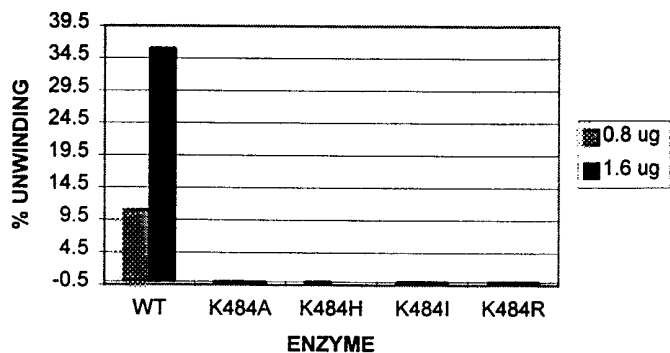
VALIDATION OF E1 HELICASE ACTIVITY - GEL ASSAY



ATPase ACTIVITY

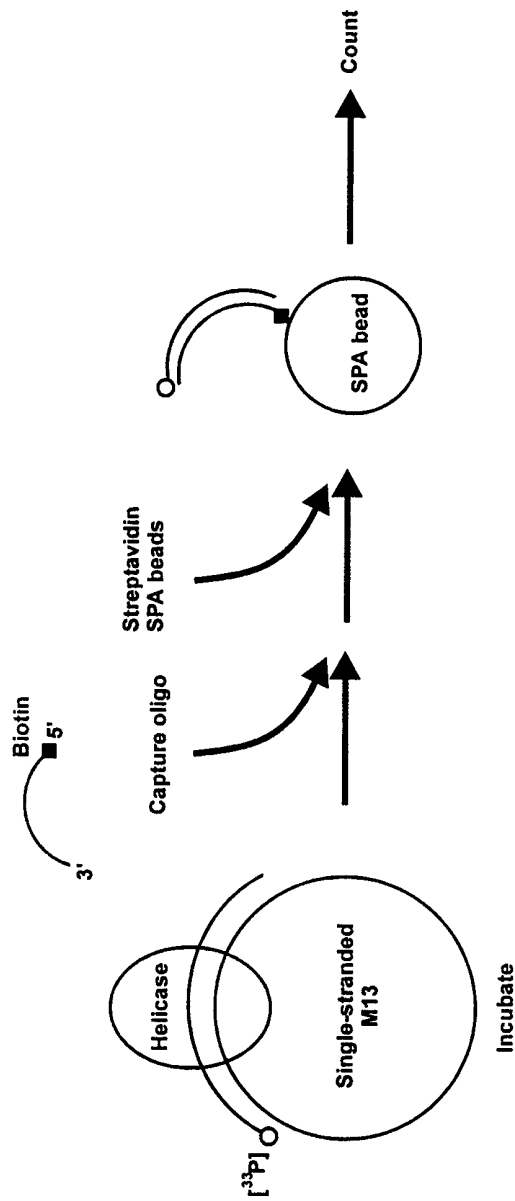


UNWINDING ACTIVITY



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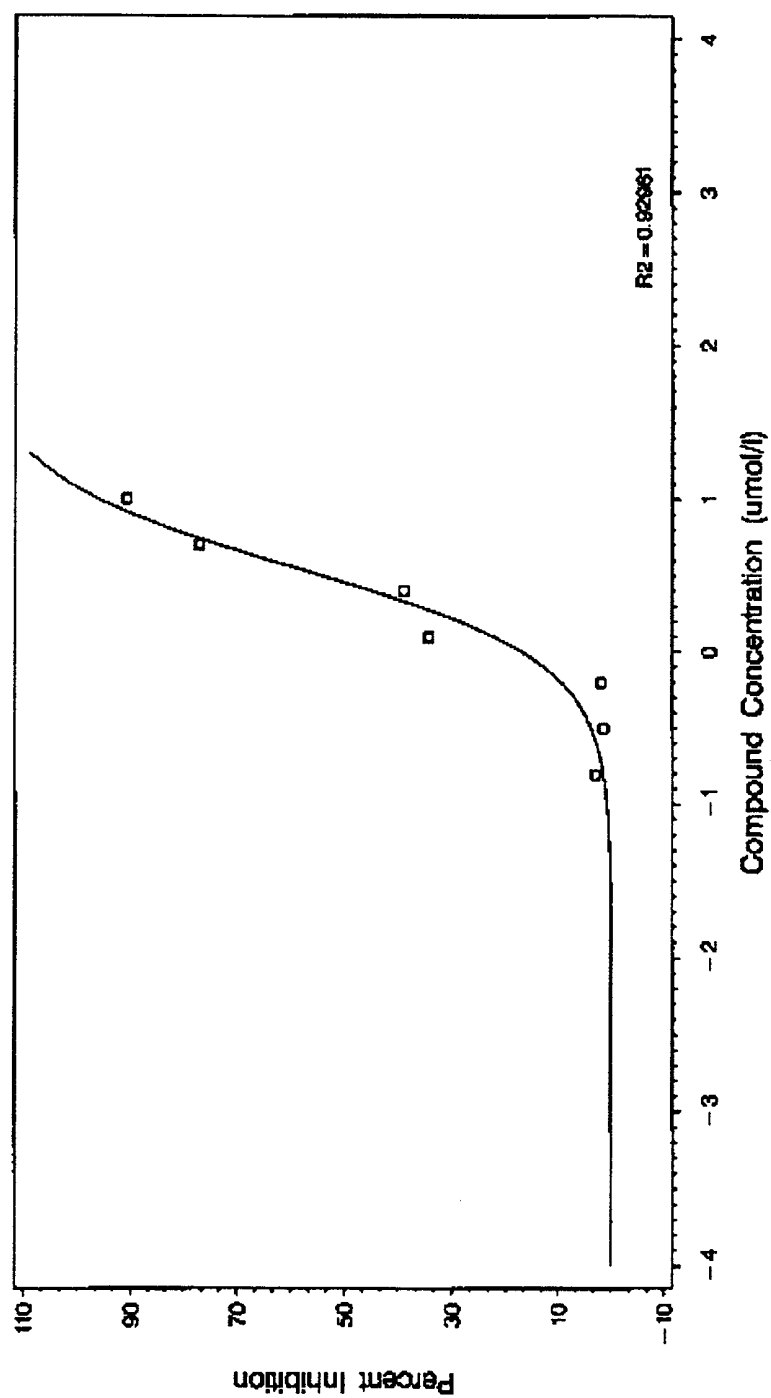
FIGURE 6
SCINTILLATION PROXIMITY ASSAY FOR E1 HELICASE



Reaction conditions:	Hybridization conditions
30 μ L, 120 min., pH 7.0 MES, 37°C	60 μ L, 90 min., pH 7.5 HEPES, r.t.
10% glycerol, 6% DMSO,	150 mM NaCl, 0.5% SDS
1 mM DTT, 0.05 mM EDTA	10 Nm biotinylated oligo
1 mM ATP/Mg(OAc) ₂	Then
~ 600 ng E1 (250 nM)	0.063 mg streptavidin SPA beads, 30 min.
0.1 nM M13/oligo substrate	

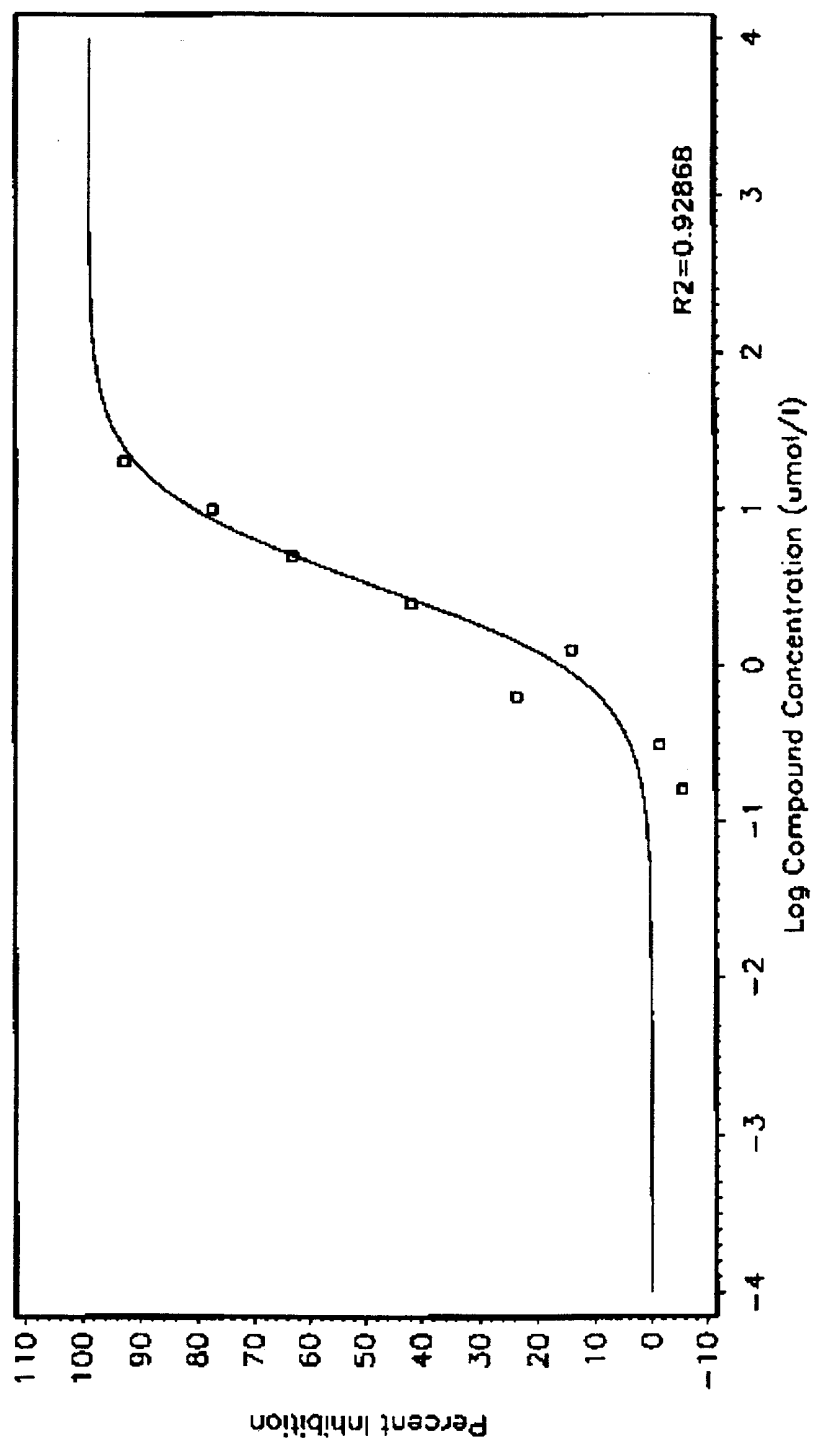
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FIGURE 7
M13

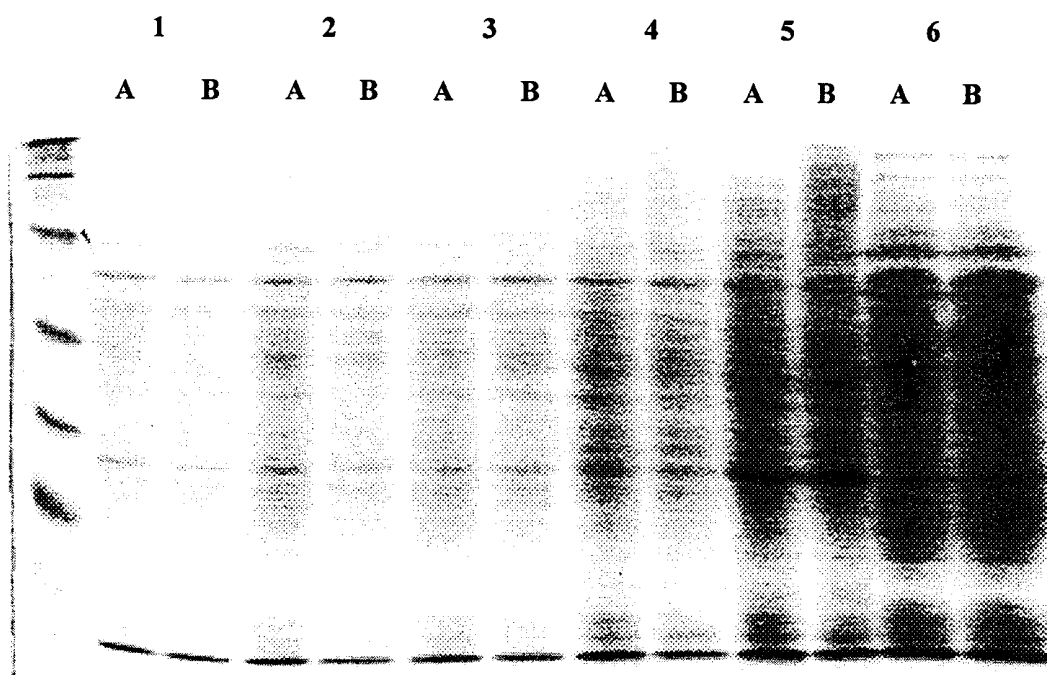


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FIGURE 8
ETHIDIUM BROMIDE



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FIGURE 9A

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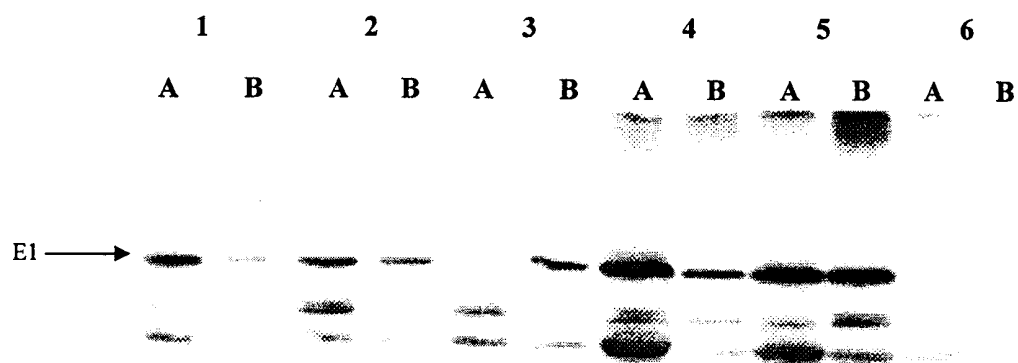
FIGURE 9B

FIGURE 10A

1 2 3 4 5 6 7

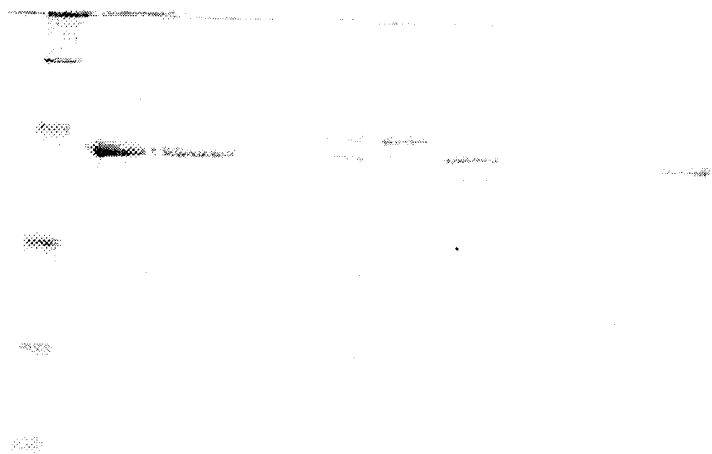
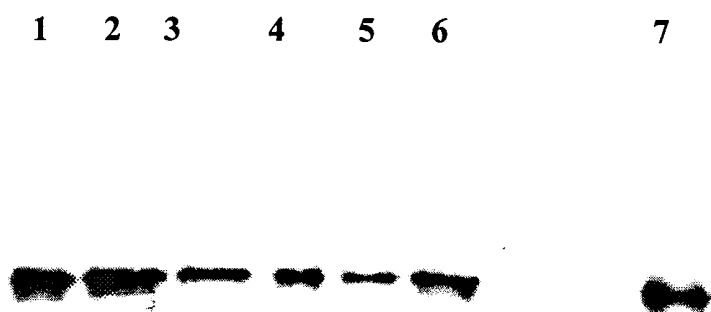


FIGURE 10B



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FIGURE 11

HPV-11 E1 (SEQ ID NO. 26)

Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
 Trp Phe Met Val Glu Ala Ile Val Glu His Thr Thr Gly Thr Gln Ile
 Ser Glu Asp Glu Glu Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
 Asp Phe Ile Asp Asp Arg His Ile Thr Gln Asn Ser Val Glu Ala Gln
 Ala Leu Phe Asn Arg Gln Glu Ala Asp Ala His Tyr Ala Thr Val Gln
 Asp Leu Lys Arg Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Ser
 Asn Val Ala Asn Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
 Ile Lys Leu Thr Thr Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Glu
 Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
 Ala Thr Gln Val Glu Lys His Gly Asp Pro Glu Asn Gly Gly Asp Gly
 Glu Glu Arg Asp Thr Gly Arg Asp Ile Glu Gly Glu Gly Val Glu His
 Arg Glu Ala Glu Ala Val Asp Asp Ser Thr Arg Glu His Ala Asp Thr
 Ser Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Ile Arg Ser Thr Leu
 His Gly Lys Phe Lys Asp Cys Phe Gly Leu Ser Phe Val Asp Leu Ile
 Arg Pro Phe Lys Ser Asp Arg Thr Thr Cys Ala Asp Trp Val Val Ala
 Gly Phe Gly Ile His His Ser Ile Ala Asp Ala Phe Gln Lys Leu Ile
 Glu Pro Leu Ser Leu Tyr Ala His Ile Gln Trp Leu Thr Asn Ala Trp
 Gly Met Val Leu Leu Val Leu Ile Arg Phe Lys Val Asn Lys Ser Arg
 Cys Thr Val Ala Arg Thr Leu Gly Thr Leu Leu Asn Ile Pro Glu Asn
 His Met Leu Ile Glu Pro Pro Lys Ile Gln Ser Gly Val Ala Ala Leu
 Tyr Trp Phe Arg Thr Gly Ile Ser Asn Ala Ser Thr Val Ile Gly Glu
 Ala Pro Glu Trp Ile Thr Arg Gln Thr Val Ile Glu His Ser Leu Ala
 Asp Ser Gln Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn
 Asp Ile Cys Glu Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly
 Asp Phe Asp Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Met Gln Ala
 Lys Tyr Val Lys Asp Cys Ala Ile Met Cys Arg His Tyr Lys His Ala
 Glu Met Lys Lys Met Ser Ile Lys Gln Trp Ile Lys Tyr Arg Gly Thr
 Lys Val Asp Ser Val Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg
 His Gln Asn Ile Glu Phe Ile Pro Phe Leu Ser Lys Leu Lys Leu Trp
 Leu His Gly Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro
 Asp Thr Gly Lys Ser Cys Phe Cys Met Ser Leu Ile Lys Phe Leu Gly
 Gly Thr Val Ile Ser Tyr Val Asn Ser Cys Ser His Phe Trp Leu Gln
 Pro Leu Thr Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro
 Cys Trp Thr Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 Pro Met Ser Ile Asp Arg Lys His Arg Ala Leu Thr Leu Ile Lys Cys
 Pro Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Ser Lys Glu Glu Lys
 Tyr Lys Tyr Leu His Ser Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asp Ala
 Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Glu
 Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 Val Pro Gly Ser Val Val Arg Thr Leu

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FIGURE 12

HPV-6a E1 (SEQ ID NO. 27)

Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
 Trp Phe Met Val Glu Ala Ile Val Gln His Pro Thr Gly Thr Gln Ile
 Ser Asp Asp Glu Asp Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
 Asp Phe Ile Asp Asp Ser Asn Ile Thr His Asn Ser Leu Glu Ala Gln
 Ala Leu Phe Asn Arg Gln Glu Ala Asp Thr His Tyr Ala Thr Val Gln
 Asp Leu Lys Arg Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Asn
 Thr Ile Ala Glu Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
 Ile Lys Leu Thr Arg Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Gln
 Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
 Gly Thr Gly Thr Gln Val Glu Lys His Gly Val Pro Glu Asn Gly Gly
 Asp Gly Gln Glu Lys Asp Thr Gly Arg Asp Ile Glu Gly Glu Glu His
 Thr Glu Ala Glu Ala Pro Thr Asn Ser Val Arg Glu His Ala Gly Thr
 Ala Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Leu Arg Ala Ala Leu
 Leu Gly Lys Phe Lys Glu Cys Phe Gly Leu Ser Phe Ile Asp Leu Ile
 Arg Pro Phe Lys Ser Asp Lys Thr Thr Cys Leu Asp Trp Val Val Ala
Arg Phe Gly Ile His His Ser Ile Ser Glu Ala Phe Gln Lys Leu Ile
 Glu Pro Leu Ser Leu Tyr Ala His Ile Gln Trp Leu Thr Asn Ala Trp
 Gly Met Val Leu Leu Val Leu Leu Arg Phe Lys Val Asn Lys Ser Arg
 Ser Thr Val Ala Arg Thr Leu Ala Thr Leu Leu Asn Ile Pro Glu Asn
 Gln Met Leu Ile Glu Pro Pro Lys Ile Gln Ser Gly Val Ala Ala Leu
 Tyr Trp Phe Arg Thr Gly Ile Ser Asn Ala Ser Thr Val Ile Gly Glu
 Ala Pro Glu Trp Ile Thr Arg Gln Thr Val Ile Glu His Gly Leu Ala
 Asp Ser Gln Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn
 Asp Ile Cys Glu Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly
 Asp Phe Asp Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Met Gln Ala
 Lys Tyr Val Lys Asp Cys Ala Thr Met Cys Arg His Tyr Lys His Ala
 Glu Met Arg Lys Met Ser Ile Lys Gln Trp Ile Lys His Arg Gly Ser
 Lys Ile Glu Gly Thr Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg
 His Gln Asn Ile Glu Phe Ile Pro Phe Leu Thr Lys Phe Lys Leu Trp
 Leu His Gly Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro
 Asp Thr Gly Lys Ser Tyr Phe Cys Met Ser Leu Ile Ser Phe Leu Gly
 Gly Thr Val Ile Ser His Val Asn Ser Ser Ser His Phe Trp Leu Gln
 Pro Leu Val Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro
 Cys Trp Ile Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 Pro Met Ser Ile Asp Arg Lys His Lys Ala Leu Thr Leu Ile Lys Cys
 Pro Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Thr Lys Glu Asp Lys
 Tyr Lys Tyr Leu His Thr Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asn Thr
 Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Gln
 Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 Val Pro Gly Thr Val Val Arg Thr Leu

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1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Boehringer Ingelheim (Canada) Ltd.
- (B) STREET: 2100 Cunard Street
- (C) CITY: Laval
- (D) STATE: Quebec
- (E) COUNTRY: Canada
- (F) POSTAL CODE (ZIP): H7S 2G5
- (G) TELEPHONE: (450) 682-4640
- (H) TELEFAX: (450) 682-8434

- (ii) TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS E1
HAVING HELICASE ACTIVITY AND METHOD THEREFOR

- (iii) NUMBER OF SEQUENCES: 27

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/083,942
- (B) FILING DATE: 01-MAY-1998

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CGCGGATCCA GGATGCATCA CCATCACCAT CACGCGGACG ATTACGTAC AGAAAATGAG

60

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

GGCTGAATTC ATAAAGTTCT AACAACT

27

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CCTGACACTG GGAAGTCGTG CTTTTC

27

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CCTGACACTG GGGAGTCGTG CTTTTC

27

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

3

CCTGACACTG GGGCGTCGTG CTTTTC

27

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CCTGACACTG GGCACCTCGTG CTTTTC

27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CCTGACACTG GGATCTCGTG CTTTTC

27

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CCTGACACTG GGCAGTCGTG CTTTTC

27

4

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

AGTGACCGAA AACGGTCGGG ACCGAAAACG GTGTAGACCG AAAACGGTGT A

51

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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

CTACACCGTT TTCGGTCTAC ACCGTTTTCG GTCCCGACCG TTTTCGGTCA CT

52

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTAAAACGAC CAGTGCCAAG C

21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TTCCCAGTCA CGACGTTGT

19

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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

6

145		150		155		160
Gln Glu Arg Asp Thr Gly Arg Asp Ile Glu Gly Glu Gly Val Glu His						
	165		170		175	
Arg Glu Ala Glu Ala Val Asp Asp Ser Thr Arg Glu His Ala Asp Thr						
	180		185		190	
Ser Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Ile Arg Ser Thr Leu						
	195		200		205	
His Gly Lys Phe Lys Asp Cys Phe Gly Leu Ser Phe Val Asp Leu Ile						
	210		215		220	
Arg Pro Phe Lys Ser Asp Arg Thr Thr Cys Ala Asp Trp Val Val Ala						
225		230		235		240
Gly Phe Gly Ile His His Ser Ile Ala Asp Ala Phe Gln Lys Leu Ile						
	245		250			255
Glu Pro Leu Ser Leu Tyr Ala His Ile Gln Trp Leu Thr Asn Ala Trp						
	260		265		270	
Gly Met Val Leu Leu Val Leu Ile Arg Phe Lys Val Asn Lys Ser Arg						
	275		280		285	
Cys Thr Val Ala Arg Thr Leu Gly Thr Leu Leu Asn Ile Pro Glu Asn						
	290		295		300	
His Met Leu Ile Glu Pro Pro Lys Ile Gln Ser Gly Val Arg Ala Leu						
305		310		315		320
Tyr Trp Phe Arg Thr Gly Ile Ser Asn Ala Ser Thr Val Ile Gly Glu						
	325		330			335
Ala Pro Glu Trp Ile Thr Arg Gln Thr Val Ile Glu His Ser Leu Ala						
	340		345		350	
Asp Ser Gln Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn						
	355		360		365	
Asp Ile Cys Glu Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly						
	370		375		380	
Asp Phe Asp Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Met Gln Ala						
385		390		395		400
Lys Tyr Val Lys Asp Cys Ala Ile Met Cys Arg His Tyr Lys His Ala						
	405		410		415	
Glu Met Lys Lys Met Ser Ile Lys Gln Trp Ile Lys Tyr Arg Gly Thr						
	420		425		430	

7

Lys Val Asp Ser Val Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg
 435 440 445
 His Gln Asn Ile Glu Phe Ile Pro Phe Leu Ser Lys Leu Lys Leu Trp
 450 455 460
 Leu His Gly Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro
 465 470 475 480
 Asp Thr Gly Lys Ser Cys Phe Cys Met Ser Leu Ile Lys Phe Leu Gly
 485 490 495
 Gly Thr Val Ile Ser Tyr Val Asn Ser Cys Ser His Phe Trp Leu Gln
 500 505 510
 Pro Leu Thr Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro
 515 520 525
 Cys Trp Thr Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 530 535 540
 Pro Met Ser Ile Asp Arg Lys His Arg Ala Leu Thr Leu Ile Lys Cys
 545 550 555 560
 Pro Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Ser Lys Glu Glu Lys
 565 570 575
 Tyr Lys Tyr Leu His Ser Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 580 585 590
 Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asp Ala
 595 600 605
 Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Glu
 610 615 620
 Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 625 630 635 640
 Val Pro Gly Ser Val Val Arg Thr Leu
 645

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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

9

Leu Leu Val Leu Ile Arg Phe Lys Val Asn Lys Ser Arg Cys Thr Val
 275 280 285
 Ala Arg Thr Leu Ala Thr Phe Leu Asn Ile Pro Glu Asp His Met Leu
 290 295 300
 Ile Glu Pro Pro Lys Ile Gln Ser Ser Val Ala Ala Leu Tyr Trp Phe
 305 310 315 320
 Arg Thr Gly Ile Ser Asn Ala Ser Ile Val Thr Gly Glu Thr Pro Glu
 325 330 335
 Trp Ile Lys Arg Gln Thr Ile Val Glu His Gly Leu Ala Asp Asn Gln
 340 345 350
 Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn Asp Phe Cys
 355 360 365
 Asp Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly Asp Phe Asp
 370 375 380
 Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Cys Gln Ala Lys Tyr Val
 385 390 395 400
 Lys Asp Cys Ala Thr Met Cys Lys His Tyr Lys Asn Ala Glu Met Lys
 405 410 415
 Lys Met Ser Met Lys Gln Trp Ile Thr Tyr Arg Ser Lys Lys Ile Glu
 420 425 430
 Glu Ala Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg His Gln Asn
 435 440 445
 Ile Glu Phe Ile Pro Phe Leu Ser Lys Leu Lys Leu Trp Leu His Gly
 450 455 460
 Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro Asp Thr Gly
 465 470 475 480
 Lys Ser Cys Phe Cys Met Ser Leu Ile Lys Phe Leu Gly Gly Thr Val
 485 490 495
 Ile Ser Tyr Val Asn Ser Ser Ser His Phe Trp Leu Gln Pro Leu Cys
 500 505 510
 Asn Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Ser Cys Trp Val
 515 520 525
 Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn Pro Met Ser
 530 535 540

10

Ile Asp Arg Lys His Lys Ser Leu Ala Leu Ile Lys Cys Pro Pro Leu
 545 550 555 560
 Leu Val Thr Ser Asn Val Asp Ile Thr Lys Asp Asp Lys Tyr Lys Tyr
 565 570 575
 Leu Tyr Ser Arg Val Thr Thr Leu Thr Phe Pro Asn Pro Phe Pro Phe
 580 585 590
 Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asp Ala Asn Trp Lys
 595 600 605
 Cys Phe Phe Thr Arg Leu Ser Ala Ser Leu Asp Ile Gln Asp Ser Glu
 610 615 620
 Asp Glu Asp Asp Gly Asp Asn Ser Gln Ala Phe Arg Cys Val Pro Gly
 625 630 635 640
 Thr Val Val Arg Thr Val
 645

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
 1 5 10 15
 Trp Phe Met Val Glu Ala Ile Val Gln His Pro Thr Gly Thr Gln Ile
 20 25 30
 Ser Asp Asp Glu Asp Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
 35 40 45
 Asp Phe Ile Asp Asp Ser Asn Ile Thr His Asn Ser Leu Glu Ala Gln
 50 55 60
 Ala Leu Phe Asn Arg Gln Glu Ala Asp Thr His Tyr Ala Thr Val Gln
 65 70 75 80
 Asp Leu Lys Arg Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Asn
 85 90 95

11

Thr Ile Ala Glu Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
 100 105 110
 Ile Lys Leu Thr Arg Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Gln
 115 120 125
 Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
 130 135 140
 Gly Thr Gly Thr Gln Val Glu Lys His Gly Val Pro Glu Asn Gly Gly
 145 150 155 160
 Asp Gly Gln Glu Lys Asp Thr Gly Arg Asp Ile Glu Gly Glu Glu His
 165 170 175
 Thr Glu Ala Glu Ala Pro Thr Asn Ser Val Arg Glu His Ala Gly Thr
 180 185 190
 Ala Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Leu Arg Ala Ala Leu
 195 200 205
 Leu Gly Lys Phe Lys Glu Cys Phe Gly Leu Ser Phe Ile Asp Leu Ile
 210 215 220
 Arg Pro Phe Lys Ser Asp Lys Thr Thr Cys Leu Asp Trp Val Val Ala
 225 230 235 240
 Gly Phe Gly Ile His His Ser Ile Ser Glu Ala Phe Gln Lys Leu Ile
 245 250 255
 Glu Pro Leu Ser Leu Tyr Ala His Ile Gln Trp Leu Thr Asn Ala Trp
 260 265 270
 Gly Met Val Leu Leu Val Leu Leu Arg Phe Lys Val Asn Lys Ser Arg
 275 280 285
 Ser Thr Val Ala Arg Thr Leu Ala Thr Leu Leu Asn Ile Pro Glu Asn
 290 295 300
 Gln Met Leu Ile Glu Pro Pro Lys Ile Gln Ser Gly Val Ala Ala Leu
 305 310 315 320
 Tyr Trp Phe Arg Thr Gly Ile Ser Asn Ala Ser Thr Val Ile Gly Glu
 325 330 335
 Ala Pro Glu Trp Ile Thr Arg Gln Thr Val Ile Glu His Gly Leu Ala
 340 345 350
 Asp Ser Gln Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn
 355 360 365
 Asp Ile Cys Glu Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly
 370 375 380

12

Asp Phe Asp Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Met Gln Ala
 385 390 395 400
 Lys Tyr Val Lys Asp Cys Ala Thr Met Cys Arg His Tyr Lys His Ala
 405 410 415
 Glu Met Arg Lys Met Ser Ile Lys Gln Trp Ile Lys His Arg Gly Ser
 420 425 430
 Lys Ile Glu Gly Thr Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg
 435 440 445
 His Gln Asn Ile Glu Phe Ile Pro Phe Leu Thr Lys Phe Lys Leu Trp
 450 455 460
 Leu His Gly Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro
 465 470 475 480
 Asp Thr Gly Lys Ser Tyr Phe Cys Met Ser Leu Ile Ser Phe Leu Gly
 485 490 495
 Gly Thr Val Ile Ser His Val Asn Ser Ser Ser His Phe Trp Leu Gln
 500 505 510
 Pro Leu Val Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro
 515 520 525
 Cys Trp Ile Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 530 535 540
 Pro Met Ser Ile Asp Arg Lys His Lys Ala Leu Thr Leu Ile Lys Cys
 545 550 555 560
 Pro Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Thr Lys Glu Asp Lys
 565 570 575
 Tyr Lys Tyr Leu His Thr Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 580 585 590
 Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asn Thr
 595 600 605
 Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Gln
 610 615 620
 Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 625 630 635 640
 Val Pro Gly Thr Val Val Arg Thr Leu
 645

13

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

Met Ala Asp Pro Glu Gly Thr Asp Gly Glu Gly Thr Gly Cys Asn Gly
1           5           10           15

Trp Phe Tyr Val Gln Ala Ile Val Asp Lys Lys Thr Gly Asp Val Ile
          20           25           30

Ser Asp Asp Glu Asp Glu Asn Ala Thr Asp Thr Gly Ser Asp Met Val
          35           40           45

Asp Phe Ile Asp Thr Gln Gly Thr Phe Cys Glu Gln Ala Glu Leu Glu
50           55           60

Thr Ala Gln Ala Leu Phe His Ala Gln Glu Val His Asn Asp Ala Gln
65           70           75           80

Val Leu His Val Leu Lys Arg Lys Phe Ala Gly Gly Ser Thr Glu Asn
          85           90           95

Ser Pro Leu Gly Glu Arg Leu Glu Val Asp Thr Glu Leu Ser Pro Arg
          100          105          110

Leu Gln Glu Ile Ser Leu Asn Ser Gly Gln Lys Lys Ala Lys Arg Arg
          115          120          125

Leu Phe Thr Ile Ser Asp Ser Gly Tyr Gly Cys Ser Glu Val Glu Ala
          130          135          140

Thr Gln Ile Gln Val Thr Thr Asn Gly Glu His Gly Gly Asn Val Cys
          145          150          155          160

Ser Gly Gly Ser Thr Glu Ala Ile Asp Asn Gly Gly Thr Glu Gly Asn
          165          170          175

Asn Ser Ser Val Asp Gly Thr Ser Asp Asn Ser Asn Ile Glu Asn Val
          180          185          190

Asn Pro Gln Cys Thr Ile Ala Gln Leu Lys Asp Leu Leu Lys Val Asn
          195          200          205

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14

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

15

Phe Ile His Phe Ile Gln Gly Ala Val Ile Ser Phe Val Asn Ser Thr
 500 505 510
 Ser His Phe Trp Leu Glu Pro Leu Thr Asp Thr Lys Val Ala Met Leu
 515 520 525
 Asp Asp Ala Thr Thr Thr Cys Trp Thr Tyr Phe Asp Thr Tyr Met Arg
 530 535 540
 Asn Ala Leu Asp Gly Asn Pro Ile Ser Ile Asp Arg Lys His Lys Pro
 545 550 555 560
 Leu Ile Gln Leu Lys Cys Pro Pro Ile Leu Leu Thr Thr Asn Ile His
 565 570 575
 Pro Ala Lys Asp Asn Arg Trp Pro Tyr Leu Glu Ser Arg Ile Thr Val
 580 585 590
 Phe Glu Phe Pro Asn Ala Phe Pro Phe Asp Lys Asn Gly Asn Pro Val
 595 600 605
 Tyr Glu Ile Asn Asp Lys Asn Trp Lys Cys Phe Phe Glu Arg Thr Trp
 610 615 620
 Ser Arg Leu Asp Leu His Glu Glu Glu Glu Asp Ala Asp Thr Glu Gly
 625 630 635 640
 Asn Pro Phe Gly Thr Phe Lys Leu Arg Ala Gly Gln Asn His Arg Pro
 645 650 655
 Leu

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 647 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Ala Asn Arg Glu Gly Thr Asp Gly Asp Gly Ser Gly Cys Asn Gly
 1 5 10 15
 Trp Phe Leu Val Gln Ala Ile Val Asp Lys Gln Thr Gly Asp Thr Val
 20 25 30

16

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

17

305		310		315		320
Thr Gly Ile Ser Asn Ile Ser Val Val Thr Gly Asp Thr Pro Glu Trp						
	325			330		335
Ile Gln Arg Leu Thr Val Ile Gln His Gly Ile Asp Asp Ser Val Phe						
	340		345			350
Asp Leu Ser Asp Met Val Gln Trp Ala Phe Asp Asn Glu Tyr Thr Asp						
	355		360			365
Glu Ser Asp Ile Ala Phe Asn Tyr Ala Met Leu Ala Asp Cys Asn Ser						
	370		375			380
Asn Ala Ala Ala Phe Leu Lys Ser Asn Cys Gln Ala Lys Tyr Val Lys						
	385		390		395	400
Asp Cys Ala Thr Met Cys Lys His Tyr Lys Arg Ala Gln Lys Arg Gln						
	405			410		415
Met Ser Met Ser Gln Trp Ile Lys Phe Arg Cys Ser Lys Cys Asp Glu						
	420			425		430
Gly Gly Asp Trp Arg Pro Ile Val Gln Phe Leu Arg Tyr Gln Gly Ile						
	435		440			445
Glu Phe Ile Ser Phe Leu Cys Ala Leu Lys Glu Phe Leu Lys Gly Thr						
	450		455			460
Pro Lys Lys Asn Cys Ile Val Ile Tyr Gly Pro Ala Asn Thr Gly Lys						
	465		470		475	480
Ser His Phe Cys Met Ser Leu Met His Phe Leu Gln Gly Thr Val Ile						
	485			490		495
Ser Tyr Val Asn Ser Thr Ser His Phe Trp Leu Glu Pro Leu Ala Asp						
	500			505		510
Ala Lys Leu Ala Met Leu Asp Asp Ala Thr Gly Thr Cys Trp Ser Tyr						
	515			520		525
Phe Asp Asn Tyr Met Arg Asn Ala Leu Asp Gly Tyr Ala Ile Ser Leu						
	530		535			540
Asp Arg Lys Tyr Lys Ser Leu Leu Gln Met Lys Cys Pro Pro Leu Leu						
	545		550		555	560
Ile Thr Ser Asn Thr Asn Pro Val Glu Asp Asp Arg Trp Pro Tyr Leu						
	565			570		575
Arg Ser Arg Leu Thr Val Phe Lys Phe Pro Asn Ala Phe Pro Phe Asp						
	580			585		590

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Ala	Asp	Pro	Glu	Gly	Thr	Asn	Gly	Ala	Gly	Met	Gly	Cys	Thr	Gly
1				5					10					15	
Trp	Phe	Glu	Val	Glu	Ala	Val	Ile	Glu	Arg	Arg	Thr	Gly	Asp	Asn	Ile
			20					25					30		
Ser	Glu	Asp	Glu	Asp	Glu	Thr	Ala	Asp	Asp	Ser	Gly	Thr	Asp	Leu	Leu
		35					40					45			
Glu	Phe	Ile	Asp	Asp	Ser	Met	Glu	Asn	Ser	Ile	Gln	Ala	Asp	Thr	Glu
	50					55					60				
Ala	Ala	Arg	Ala	Leu	Phe	Asn	Ile	Gln	Glu	Gly	Glu	Asp	Asp	Leu	Asn
65					70					75					80
Ala	Val	Cys	Ala	Leu	Lys	Arg	Lys	Phe	Ala	Ala	Cys	Ser	Gln	Ser	Ala
				85					90					95	
Ala	Glu	Asp	Val	Val	Asp	Arg	Ala	Ala	Asn	Pro	Cys	Arg	Thr	Ser	Ile
			100					105					110		
Asn	Lys	Asn	Lys	Glu	Cys	Thr	Tyr	Arg	Lys	Arg	Lys	Ile	Asp	Glu	Leu
		115					120					125			

19

Glu Asp Ser Gly Tyr Gly Asn Thr Glu Val Glu Thr Gln Gln Met Val
 130 135 140
 Gln Gln Val Glu Ser Gln Asn Gly Asp Thr Asn Leu Asn Asp Leu Glu
 145 150 155 160
 Ser Ser Gly Val Gly Asp Asp Ser Glu Val Ser Cys Glu Thr Asn Val
 165 170 175
 Asp Ser Cys Glu Asn Val Thr Leu Gln Glu Ile Ser Asn Val Leu His
 180 185 190
 Ser Ser Asn Thr Lys Ala Asn Ile Leu Tyr Lys Phe Lys Glu Ala Tyr
 195 200 205
 Gly Ile Ser Phe Met Glu Leu Val Arg Pro Phe Lys Ser Asp Lys Thr
 210 215 220
 Ser Cys Thr Asp Trp Cys Ile Thr Gly Tyr Gly Ile Ser Pro Ser Val
 225 230 235 240
 Ala Glu Ser Leu Lys Val Leu Ile Lys Gln His Ser Leu Tyr Thr His
 245 250 255
 Leu Gln Cys Leu Thr Cys Asp Arg Gly Ile Ile Ile Leu Leu Leu Ile
 260 265 270
 Arg Phe Arg Cys Ser Lys Asn Arg Leu Thr Val Ala Lys Leu Met Ser
 275 280 285
 Asn Leu Leu Ser Ile Pro Glu Thr Cys Met Val Ile Glu Pro Pro Lys
 290 295 300
 Leu Arg Ser Gln Thr Cys Ala Leu Tyr Trp Phe Arg Thr Ala Met Ser
 305 310 315 320
 Asn Ile Ser Asp Val Gln Gly Thr Thr Pro Glu Trp Ile Asp Arg Leu
 325 330 335
 Thr Val Leu Gln His Ser Phe Asn Asp Asn Ile Phe Asp Leu Ser Glu
 340 345 350
 Met Val Gln Trp Ala Tyr Asp Asn Glu Leu Thr Asp Asp Ser Asp Ile
 355 360 365
 Ala Tyr Tyr Tyr Ala Gln Leu Ala Asp Ser Asn Ser Asn Ala Ala Ala
 370 375 380
 Phe Leu Lys Ser Asn Ser Gln Ala Lys Ile Val Lys Asp Cys Gly Ile
 385 390 395 400
 Met Cys Arg His Tyr Lys Lys Ala Glu Lys Arg Lys Met Ser Ile Gly

20

	405		410		415
Gln Trp Ile Gln Ser Arg Cys Glu Lys Thr Asn Asp Gly Gly Asn Trp	420		425		430
Arg Pro Ile Val Gln Leu Leu Arg Tyr Gln Asn Ile Glu Phe Thr Ala	435		440		445
Phe Leu Gly Ala Phe Lys Lys Phe Leu Lys Gly Ile Pro Lys Lys Ser	450		455		460
Cys Met Leu Ile Cys Gly Pro Ala Asn Thr Gly Lys Ser Tyr Phe Gly	465		470		475
					480
Met Ser Leu Ile Gln Phe Leu Lys Gly Cys Val Ile Ser Cys Val Asn	485		490		495
Ser Lys Ser His Phe Trp Leu Gln Pro Leu Ser Asp Ala Lys Ile Gly	500		505		510
Met Ile Asp Asp Val Thr Pro Ile Ser Trp Thr Tyr Ile Asp Asp Tyr	515		520		525
Met Arg Asn Ala Leu Asp Gly Asn Glu Ile Ser Ile Asp Val Lys His	530		535		540
Arg Ala Leu Val Gln Leu Lys Cys Pro Pro Leu Leu Leu Thr Ser Asn	545		550		555
					560
Thr Asn Ala Gly Thr Asp Ser Arg Trp Pro Tyr Leu His Ser Arg Leu	565		570		575
Thr Val Phe Glu Phe Lys Asn Pro Phe Pro Phe Asp Glu Asn Gly Asn	580		585		590
Pro Val Tyr Ala Ile Asn Asp Glu Asn Trp Lys Ser Phe Phe Ser Arg	595		600		605
Thr Trp Cys Lys Leu Asp Leu Ile Glu Glu Glu Asp Lys Glu Asn His	610		615		620
Gly Gly Asn Ile Ser Thr Phe Lys Cys Ser Ala Gly Glu Asn Thr Arg	625		630		635
					640
Ser Leu Arg Ser					

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

21

- (A) LENGTH: 629 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

Met Ala Asp Pro Ala Gly Thr Asp Gly Glu Gly Thr Gly Cys Asn Gly
1           5           10           15

Trp Phe Tyr Val Glu Ala Val Ile Asp Arg Gln Thr Gly Asp Asn Ile
          20           25           30

Ser Glu Asp Glu Asn Glu Asp Ser Ser Asp Thr Gly Glu Asp Met Val
          35           40           45

Asp Phe Ile Asp Asn Cys Asn Val Tyr Asn Asn Gln Ala Glu Ala Glu
          50           55           60

Thr Ala Gln Ala Leu Phe His Ala Gln Glu Ala Glu Glu His Ala Glu
65           70           75           80

Ala Val Gln Val Leu Lys Arg Lys Tyr Val Gly Ser Pro Leu Ser Asp
          85           90           95

Ile Ser Ser Cys Val Asp Tyr Asn Ile Ser Pro Arg Leu Lys Ala Ile
          100          105          110

Cys Ile Glu Asn Asn Ser Lys Thr Ala Lys Arg Arg Leu Phe Glu Leu
          115          120          125

Pro Asp Ser Gly Tyr Gly Asn Thr Glu Val Glu Thr Gln Gln Met Val
          130          135          140

Gln Val Glu Glu Gln Gln Thr Thr Leu Ser Cys Asn Gly Ser Asp Gly
          145          150          155          160

Thr His Ser Glu Arg Glu Asn Glu Thr Pro Thr Arg Asn Ile Leu Gln
          165          170          175

Val Leu Lys Thr Ser Asn Gly Lys Ala Ala Met Leu Gly Lys Phe Lys
          180          185          190

Glu Leu Tyr Gly Val Ser Phe Met Glu Leu Ile Arg Pro Phe Gln Ser
          195          200          205

Asn Lys Ser Thr Cys Thr Asp Trp Cys Val Ala Ala Phe Gly Val Thr
          210          215          220

Gly Thr Val Ala Glu Gly Phe Lys Thr Leu Leu Gln Pro Tyr Cys Leu
          225          230          235          240

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22

Tyr Cys His Leu Gln Ser Leu Ala Cys Ser Trp Gly Met Val Met Leu
 245 250 255
 Met Leu Val Arg Phe Lys Cys Ala Lys Asn Arg Ile Thr Ile Glu Lys
 260 265 270
 Leu Leu Glu Lys Leu Leu Cys Ile Ser Thr Asn Cys Met Leu Ile Gln
 275 280 285
 Pro Pro Lys Leu Arg Ser Thr Ala Ala Ala Leu Tyr Trp Tyr Arg Thr
 290 295 300
 Gly Met Ser Asn Ile Ser Asp Val Tyr Gly Glu Thr Pro Glu Trp Ile
 305 310 315 320
 Glu Arg Gln Thr Val Leu Gln His Ser Phe Asn Asp Thr Thr Phe Asp
 325 330 335
 Leu Ser Gln Met Val Gln Trp Ala Tyr Asp Asn Asp Val Met Asp Asp
 340 345 350
 Ser Glu Ile Ala Tyr Lys Tyr Ala Gln Leu Ala Asp Ser Asp Ser Asn
 355 360 365
 Ala Cys Ala Phe Leu Lys Ser Asn Ser Gln Ala Lys Ile Val Lys Asp
 370 375 380
 Cys Gly Thr Met Cys Arg His Tyr Lys Arg Ala Glu Lys Arg Gln Met
 385 390 395 400
 Ser Met Gly Gln Trp Ile Lys Ser Arg Cys Asp Lys Val Ser Asp Glu
 405 410 415
 Gly Asp Trp Arg Asp Ile Val Lys Phe Leu Arg Tyr Gln Gln Ile Glu
 420 425 430
 Phe Val Ser Phe Leu Ser Ala Leu Lys Leu Phe Leu Lys Gly Val Pro
 435 440 445
 Lys Lys Asn Cys Ile Leu Ile His Gly Ala Pro Asn Thr Gly Lys Ser
 450 455 460
 Tyr Phe Gly Met Ser Leu Ile Ser Phe Leu Gln Gly Cys Ile Ile Ser
 465 470 475 480
 Tyr Ala Asn Ser Lys Ser His Phe Trp Leu Gln Pro Leu Ala Asp Ala
 485 490 495
 Lys Ile Gly Met Leu Asp Asp Ala Thr Thr Pro Cys Trp His Tyr Ile
 500 505 510
 Asp Asn Tyr Leu Arg Asn Ala Leu Asp Gly Asn Pro Val Ser Ile Asp

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[illegible]

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met	Ala	Asp	Pro	Ala	Gly	Thr	Asp	Glu	Gly	Glu	Gly	Thr	Gly	Cys	Asn
1				5					10					15	
Gly	Trp	Phe	Phe	Val	Glu	Ala	Val	Val	Ser	Arg	Arg	Thr	Gly	Ser	Ser
			20					25					30		
Val	Glu	Asp	Glu	Asn	Glu	Asp	Asp	Cys	Asp	Arg	Gly	Glu	Asp	Met	Val
		35					40					45			
Asp	Phe	Ile	Asn	Asp	Thr	Asp	Ile	Leu	Asn	Ile	Gln	Ala	Glu	Thr	Glu
	50					55					60				
Thr	Ala	Gln	Ala	Leu	Phe	His	Ala	Gln	Glu	Glu	Gln	Thr	His	Lys	Glu
65					70					75					80
Ala	Val	Gln	Val	Leu	Lys	Arg	Lys	Tyr	Ala	Ser	Ser	Pro	Leu	Ser	Ser

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				85					90				95				
Val	Ser	Leu	Cys	Val	Asn	Asn	Asn	Ile	Ser	Pro	Arg	Leu	Lys	Ala	Ile		
			100					105					110				
Cys	Ile	Glu	Asn	Lys	Asn	Thr	Ala	Ala	Lys	Arg	Arg	Leu	Phe	Glu	Leu		
		115					120					125					
Pro	Asp	Ser	Gly	Tyr	Gly	Asn	Ser	Glu	Val	Glu	Ile	His	Glu	Ile	Gln		
	130					135						140					
Gln	Val	Glu	Gly	His	Asp	Thr	Val	Glu	Gln	Cys	Ser	Met	Gly	Ser	Gly		
145					150					155					160		
Asp	Ser	Ile	Thr	Ser	Ser	Ser	Asp	Glu	Arg	His	Asp	Glu	Thr	Pro	Thr		
				165					170					175			
Arg	Asp	Ile	Ile	Gln	Ile	Leu	Lys	Cys	Ser	Asn	Ala	Asn	Ala	Ala	Met		
			180					185					190				
Leu	Ala	Lys	Phe	Lys	Glu	Leu	Phe	Gly	Ile	Ser	Phe	Thr	Glu	Leu	Ile		
		195					200					205					
Arg	Pro	Phe	Lys	Ser	Asp	Lys	Ser	Thr	Cys	Thr	Asp	Trp	Cys	Val	Ala		
	210					215					220						
Ala	Phe	Gly	Ile	Ala	Pro	Ser	Val	Ala	Asn	Phe	Lys	His	Ile	Thr	Tyr		
225					230					235					240		
Val	Tyr	Ile	Tyr	Asn	Val	Tyr	Arg	Val	His	Gly	Ala	Met	Val	Ile	Leu		
				245					250					255			
Ala	Leu	Leu	Arg	Phe	Lys	Val	Glu	Lys	Arg	Glu	Gln	Gln	Leu	Lys	Thr		
			260					265					270				
Ile	Asp	Ala	Lys	Leu	Leu	Cys	Ile	Ser	Ala	Ala	Ser	Met	Leu	Ile	Gln		
	275						280					285					
Pro	Pro	Lys	Leu	Arg	Ser	Thr	Pro	Ala	Ala	Leu	Tyr	Trp	Phe	Lys	Thr		
	290					295					300						
Ala	Met	Ser	Asn	Ile	Ser	Glu	Val	Asp	Gly	Glu	Thr	Pro	Glu	Trp	Ile		
305					310					315					320		
Gln	Arg	Gln	Thr	Val	Leu	Gln	His	Ser	Phe	Asn	Asp	Ala	Ile	Phe	Asp		
				325					330					335			
Leu	Ser	Glu	Met	Val	Gln	Trp	Ala	Tyr	Asp	Asn	Asp	Phe	Ile	Asp	Asp		
			340					345					350				
Ser	Asp	Ile	Ala	Tyr	Lys	Tyr	Ala	Gln	Leu	Ala	Glu	Thr	Asn	Ser	Asn		
	355						360					365					

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Ala Cys Ala Phe Leu Lys Ser Asn Ser Gln Ala Lys Ile Val Lys Asp
 370 375 380

Cys Ala Thr Met Cys Arg His Tyr Lys Arg Ala Glu Lys Arg Glu Met
 385 390 395 400

Thr Met Ser Gln Trp Ile Lys Arg Arg Cys Ala Gln Val Asp Asp Asp
 405 410 415

Gly Asp Trp Arg Asp Ile Val Arg Phe Leu Arg Tyr Gln Gln Val Asp
 420 425 430

Phe Val Ala Phe Leu Ser Ala Leu Lys Asn Phe Leu His Gly Val Pro
 435 440 445

Lys Lys Asn Cys Ile Leu Ile Tyr Gly Ala Pro Asn Thr Gly Lys Ser
 450 455 460

Leu Phe Gly Met Ser Leu Met His Phe Leu Gln Gly Ala Ile Ile Ser
 465 470 475 480

Tyr Val Asn Ser Lys Ser His Phe Trp Leu Gln Pro Leu Tyr Asp Ala
 485 490 495

Lys Ile Ala Met Leu Asp Asp Ala Thr Ser Pro Cys Gly Ile Tyr Arg
 500 505 510

Pro Ile Phe Lys Lys Cys Thr Arg Trp Lys Ser Tyr Ile Ser Phe Arg
 515 520 525

Cys Lys Ala Leu Ser Ile Val His Ile Met Pro Thr Phe Thr Tyr Tyr
 530 535 540

Ile Asn Ile Asn Ala Gly Lys Asp Asp Arg Trp Pro Tyr Leu His Ser
 545 550 555 560

Arg Val Val Val Phe Thr Phe His Asn Glu Phe Pro Phe Asp Lys Asn
 565 570 575

Gly Asn Pro Glu Tyr Gly Leu Asn Asp Lys Asn Trp Lys Ser Phe Phe
 580 585 590

Ser Arg Thr Trp Cys Arg Leu Asn Leu His Glu Glu Glu Val Lys Glu
 595 600 605

Asn Asp Gly Asp Ala Phe Pro Ala Phe Lys Cys Val Ser Gly Gln Asn
 610 615 620

Thr Arg Thr Leu Arg Asp
 625 630

26

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

Met Leu Gln Val Glu Gly Arg His Glu Thr Glu Thr Pro Cys Ser Gln
 1              5              10              15

Tyr Ser Gly Gly Ser Gly Gly Gly Cys Ser Gln Tyr Ser Ser Gly Ser
      20              25              30

Gly Gly Glu Gly Val Ser Glu Arg His Thr Ile Cys Gln Thr Pro Leu
      35              40              45

Thr Asn Ile Leu Asn Val Leu Lys Thr Ser Asn Ala Lys Ala Ala Met
      50              55              60

Leu Ala Lys Phe Lys Glu Leu Tyr Gly Val Ser Phe Ser Glu Leu Val
      65              70              75              80

Arg Pro Phe Lys Ser Asn Lys Ser Thr Cys Cys Asp Trp Cys Ile Ala
      85              90              95

Ala Phe Gly Leu Thr Pro Ser Ile Ala Asp Ser Ile Lys Thr Leu Leu
      100              105              110

Gln Gln Tyr Cys Leu Tyr Leu His Ile Gln Ser Leu Ala Cys Ser Trp
      115              120              125

Gly Met Val Val Leu Leu Leu Val Arg Tyr Lys Cys Gly Lys Asn Arg
      130              135              140

Glu Thr Ile Glu Lys Leu Leu Ser Lys Leu Leu Cys Val Ser Pro Met
      145              150              155              160

Cys Met Met Ile Glu Pro Pro Lys Leu Arg Ser Thr Ala Ala Ala Leu
      165              170              175

Tyr Trp Tyr Lys Thr Gly Ile Ser Asn Ile Ser Glu Val Tyr Gly Asp
      180              185              190

Thr Pro Glu Trp Ile Gln Arg Gln Thr Val Leu Gln His Ser Phe Asn
      195              200              205

Asp Cys Thr Phe Glu Leu Ser Gln Met Val Gln Trp Ala Tyr Asp Asn

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

28

Cys Val Ser Gly Gln Asn Thr Asn Thr Leu
500 505

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GCAAAAGCAC GACGCCCCAG TGTCAGG

27

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GCAAAAGCAC GAGTGCCCAG TGTCAGG

27

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCAAAAGCAC GAGATCCCAG TGTCAGG

27

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCAAAAGCAC GACCGCCCAG TGTCAGG

27

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
1 5 10 15

Trp Phe Met Val Glu Ala Ile Val Glu His Thr Thr Gly Thr Gln Ile
20 25 30

Ser Glu Asp Glu Glu Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
35 40 45

Asp Phe Ile Asp Asp Arg His Ile Thr Gln Asn Ser Val Glu Ala Gln
50 55 60

Ala Leu Phe Asn Arg Gln Glu Ala Asp Ala His Tyr Ala Thr Val Gln
65 70 75 80

Asp Leu Lys Arg Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Ser
85 90 95

Asn Val Ala Asn Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
100 105 110

Ile Lys Leu Thr Thr Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Glu
115 120 125

30

Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
 130 135 140
 Ala Thr Gln Val Glu Lys His Gly Asp Pro Glu Asn Gly Gly Asp Gly
 145 150 155 160
 Glu Glu Arg Asp Thr Gly Arg Asp Ile Glu Gly Glu Gly Val Glu His
 165 170 175
 Arg Glu Ala Glu Ala Val Asp Asp Ser Thr Arg Glu His Ala Asp Thr
 180 185 190
 Ser Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Ile Arg Ser Thr Leu
 195 200 205
 His Gly Lys Phe Lys Asp Cys Phe Gly Leu Ser Phe Val Asp Leu Ile
 210 215 220
 Arg Pro Phe Lys Ser Asp Arg Thr Thr Cys Ala Asp Trp Val Val Ala
 225 230 235 240
 Gly Phe Gly Ile His His Ser Ile Ala Asp Ala Phe Gln Lys Leu Ile
 245 250 255
 Glu Pro Leu Ser Leu Tyr Ala His Ile Gln Trp Leu Thr Asn Ala Trp
 260 265 270
 Gly Met Val Leu Leu Val Leu Ile Arg Phe Lys Val Asn Lys Ser Arg
 275 280 285
 Cys Thr Val Ala Arg Thr Leu Gly Thr Leu Leu Asn Ile Pro Glu Asn
 290 295 300
 His Met Leu Ile Glu Pro Pro Lys Ile Gln Ser Gly Val Ala Ala Leu
 305 310 315 320
 Tyr Trp Phe Arg Thr Gly Ile Ser Asn Ala Ser Thr Val Ile Gly Glu
 325 330 335
 Ala Pro Glu Trp Ile Thr Arg Gln Thr Val Ile Glu His Ser Leu Ala
 340 345 350
 Asp Ser Gln Phe Lys Leu Thr Glu Met Val Gln Trp Ala Tyr Asp Asn
 355 360 365
 Asp Ile Cys Glu Glu Ser Glu Ile Ala Phe Glu Tyr Ala Gln Arg Gly
 370 375 380
 Asp Phe Asp Ser Asn Ala Arg Ala Phe Leu Asn Ser Asn Met Gln Ala
 385 390 395 400
 Lys Tyr Val Lys Asp Cys Ala Ile Met Cys Arg His Tyr Lys His Ala
 405 410 415

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Glu Met Lys Lys Met Ser Ile Lys Gln Trp Ile Lys Tyr Arg Gly Thr
 420 425 430
 Lys Val Asp Ser Val Gly Asn Trp Lys Pro Ile Val Gln Phe Leu Arg
 435 440 445
 His Gln Asn Ile Glu Phe Ile Pro Phe Leu Ser Lys Leu Lys Leu Trp
 450 455 460
 Leu His Gly Thr Pro Lys Lys Asn Cys Ile Ala Ile Val Gly Pro Pro
 465 470 475 480
 Asp Thr Gly Lys Ser Cys Phe Cys Met Ser Leu Ile Lys Phe Leu Gly
 485 490 495
 Gly Thr Val Ile Ser Tyr Val Asn Ser Cys Ser His Phe Trp Leu Gln
 500 505 510
 Pro Leu Thr Asp Ala Lys Val Ala Leu Leu Asp Asp Ala Thr Gln Pro
 515 520 525
 Cys Trp Thr Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 530 535 540
 Pro Met Ser Ile Asp Arg Lys His Arg Ala Leu Thr Leu Ile Lys Cys
 545 550 555 560
 Pro Pro Leu Leu Val Thr Ser Asn Ile Asp Ile Ser Lys Glu Glu Lys
 565 570 575
 Tyr Lys Tyr Leu His Ser Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 580 585 590
 Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asp Ala
 595 600 605
 Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Glu
 610 615 620
 Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 625 630 635 640
 Val Pro Gly Ser Val Val Arg Thr Leu
 645

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 amino acids
 (B) TYPE: amino acid

32

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Ala Asp Asp Ser Gly Thr Glu Asn Glu Gly Ser Gly Cys Thr Gly
1           5           10           15

Trp Phe Met Val Glu Ala Ile Val Gln His Pro Thr Gly Thr Gln Ile
          20           25           30

Ser Asp Asp Glu Asp Glu Glu Val Glu Asp Ser Gly Tyr Asp Met Val
          35           40           45

Asp Phe Ile Asp Asp Ser Asn Ile Thr His Asn Ser Leu Glu Ala Gln
          50           55           60

Ala Leu Phe Asn Arg Gln Glu Ala Asp Thr His Tyr Ala Thr Val Gln
65           70           75           80

Asp Leu Lys Arg Lys Tyr Leu Gly Ser Pro Tyr Val Ser Pro Ile Asn
          85           90           95

Thr Ile Ala Glu Ala Val Glu Ser Glu Ile Ser Pro Arg Leu Asp Ala
          100          105          110

Ile Lys Leu Thr Arg Gln Pro Lys Lys Val Lys Arg Arg Leu Phe Gln
          115          120          125

Thr Arg Glu Leu Thr Asp Ser Gly Tyr Gly Tyr Ser Glu Val Glu Ala
          130          135          140

Gly Thr Gly Thr Gln Val Glu Lys His Gly Val Pro Glu Asn Gly Gly
145          150          155          160

Asp Gly Gln Glu Lys Asp Thr Gly Arg Asp Ile Glu Gly Glu Glu His
          165          170          175

Thr Glu Ala Glu Ala Pro Thr Asn Ser Val Arg Glu His Ala Gly Thr
          180          185          190

Ala Gly Ile Leu Glu Leu Leu Lys Cys Lys Asp Leu Arg Ala Ala Leu
          195          200          205

Leu Gly Lys Phe Lys Glu Cys Phe Gly Leu Ser Phe Ile Asp Leu Ile
          210          215          220

Arg Pro Phe Lys Ser Asp Lys Thr Thr Cys Leu Asp Trp Val Val Ala
225          230          235          240

Arg Phe Gly Ile His His Ser Ile Ser Glu Ala Phe Gln Lys Leu Ile

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

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Cys Trp Ile Tyr Met Asp Thr Tyr Met Arg Asn Leu Leu Asp Gly Asn
 530 535 540

Pro Met Ser Ile Asp Arg Lys His Lys Ala Leu Thr Leu Ile Lys Cys
 545 550 555 560

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

Tyr Lys Tyr Leu His Thr Arg Val Thr Thr Phe Thr Phe Pro Asn Pro
 580 585 590

Phe Pro Phe Asp Arg Asn Gly Asn Ala Val Tyr Glu Leu Ser Asn Thr
 595 600 605

Asn Trp Lys Cys Phe Phe Glu Arg Leu Ser Ser Ser Leu Asp Ile Gln
 610 615 620

Asp Ser Glu Asp Glu Glu Asp Gly Ser Asn Ser Gln Ala Phe Arg Cys
 625 630 635 640

Val Pro Gly Thr Val Val Arg Thr Leu
 645

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/00389

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/37 C07K14/025 C07K19/00 C12Q1/70

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	YANG L ET AL: "The E1 protein of bovine papilloma virus 1 is an ATP-dependent DNA helicase." PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1993 JUN 1) 90 (11) 5086-90. , XP002112364	21-28, 35,38, 41,44
Y	abstract page 5086, right-hand column, paragraph 3 -page 5088, right-hand column, paragraph 1 page 5089, left-hand column, paragraph 2 -page 5090, right-hand column, paragraph 2 --- -/--	1,2, 6-10, 13-18, 29,31

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

28 September 1999

Date of mailing of the international search report

12/10/1999

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Montero Lopez, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/00389

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	IAN J. MOHR ET AL.: "Targeting the E1 replication protein to the papillomavirus origin of replication by complex formation with the E2 transactivator" SCIENCE, vol. 250, 21 December 1990 (1990-12-21), pages 1694-1699, XP002112365 DC	41,44
Y	page 1695, left-hand column, last line -page 1697, right-hand column, paragraph 2 page 1699, left-hand column, reference 45. ----	1,6,7, 13,14
X	WO 92 11290 A (CETUS CORPORATION) 9 July 1992 (1992-07-09)	21, 25-28, 41,44
Y	page 6, line 3 -page 15, line 2 page 17, line 10 - line 15 & US 5 464 936 A cited in the application ----	29,31
X	HUGHES F J ET AL: "E1 protein of human papillomavirus is a DNA helicase /ATPase." NUCLEIC ACIDS RESEARCH, (1993 DEC 25) 21 (25) 5817-23. , XP002112366	21-31, 35,36, 38,39
Y	page 5818, left-hand column, paragraph 2 -right-hand column, paragraph 5 page 5819, left-hand column, paragraph 5 page 5819, left-hand column, last paragraph -page 5821, left-hand column, paragraph 3 page 5822, left-hand column, paragraph 2 page 5822, right-hand column, paragraph 2 page 5823, left-hand column, paragraph 3 ----	15-18
X	OWEN JENKIS ET AL.: "Characterization of the helicase and ATPase activity of human papillomavirus type 6b E1 protein." JOURNAL OF GENERAL VIROLOGY, vol. 77, 1996, pages 1805-1809, XP002112367 cited in the application page 1806, left-hand column, paragraph 2 -page 1808, left-hand column, paragraph 2 ----	21-31, 35,36, 41,42
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 99/00389

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>SHU-RU KUO ET AL. : "Cell-free replication of the human Papillomavirus DNA with homologous viral E1 and E2 proteins and human cell extracts" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 269, no. 39, 30 September 1994 (1994-09-30), pages 24058-24065, XP002112368 MD US</p> <p>cited in the application page 24058, right-hand column, last paragraph -page 24059, left-hand column, paragraph 1 page 24059, left-hand column, last paragraph -right-hand column, paragraph 2 page 24059, right-hand column, paragraph 4 page 24060, left-hand column, paragraph 2 -right-hand column, paragraph 1</p> <p>-----</p>	<p>2,8-10, 15,29,31</p>

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/CA 99/00389

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9211290 A	09-07-1992	US 5464936 A	07-11-1995
		AU 9173191 A	22-07-1992
		CA 2098926 A	22-06-1992
		EP 0563307 A	06-10-1993
		JP 7503230 T	06-04-1995
		US 5925516 A	20-07-1999
