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(54) Titre : PROCEDES DE CONSERVATION D'ORGANES ET DE TISSUS
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(57) Abrégé/Abstract:
The invention relates to a method for preserving an organ or tissue comprising contacting the organ or tissue with an effective amount of a kallikrein inhibitor and solutions useful for such a method. Also provided is a method for reducing reperfusion injury of an organ during surgery and/or following removal of the organ from a subject comprising placing the organ in an organ storage and preservative solution, wherein the solution comprises a kallikrein inhibitor.

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(54) **Title:** METHODS FOR PRESERVING ORGANS AND TISSUES

(57) **Abstract:** The invention relates to a method for preserving an organ or tissue comprising contacting the organ or tissue with an effective amount of a kallikrein inhibitor and solutions useful for such a method. Also provided is a method for reducing reperfusion injury of an organ during surgery and/or following removal of the organ from a subject comprising placing the organ in an organ storage and preservative solution, wherein the solution comprises a kallikrein inhibitor.

METHODS FOR PRESERVING ORGANS AND TISSUES

BACKGROUND OF THE INVENTION

Preservation of the viability of donor organs is an important goal for organ transplantation. Typically the organ to be transplanted must be stored and shipped to the prospective recipient. The ability to prolong the cellular viability of the organ during storage and transportation is very important to the success of the transplant operation. Preservative solutions play an important role in the longevity of the organ. Solutions for organ preservation include those described by Berdyaev *et al.*, U.S. Pat. No. 5,432,053; Belzer *et al.*, U.S. Pat. Nos. 4,798,824, 4,879,283, and 4,873,230; Taylor, U.S. Pat. No. 5,405,742; Dohi *et al.*, U.S. Pat. No. 5,565,317; Stern *et al.*, U.S. Pat. Nos. 5,370,989 and 5,552,267. However, a need exists for improved methods and solutions for organ preservation.

Proteases are involved in a broad range of biological pathways. In particular, serine proteases such as kallikrein, plasmin, elastase, urokinase plasminogen activator, thrombin, human lipoprotein-associated coagulation inhibitor, and coagulation factors such as factors VIIa, IXa, Xa, XIa, and XIIa have been implicated in pathways affecting blood flow, *e.g.*, general and focal ischemia, tumor invasion, fibrinolysis, perioperative blood loss, and inflammation. Inhibitors of specific serine proteases, therefore, have received attention as potential drug targets for various ischemic maladies.

One such inhibitor, aprotinin (also called bovine pancreatic trypsin inhibitor or BPTI), obtained from bovine lung, has been approved in the United States for prophylactic use in reducing perioperative blood loss and the need for transfusion in patients undergoing CPB, *e.g.*, in the course of a coronary artery bypass grafting procedure. Aprotinin is commercially available under the trade name TRASYLOL® (Bayer Corporation Pharmaceutical Division, West Haven, Connecticut) and was previously approved for use to treat pancreatitis. The effectiveness of aprotinin is associated with its relatively non-specific abilities to inhibit a variety of serine proteases, including plasma kallikrein, and plasmin. These proteases are important in a number of pathways of the contact activation system (CAS).

CAS is initially activated when whole blood contacts the surface of foreign substrates (*e.g.*, kaolin, glass, dextran sulfate, or damaged bone surfaces). Kallikrein, a serine protease, is a plasma enzyme that initiates the CAS cascade leading to activation of neutrophils, plasmin, coagulation, and various kinins. Kallikrein is secreted as a zymogen (pre-kallikrein) that circulates as an inactive molecule until activated by a proteolytic event early in the contact activation cascade.

However, the use of specific kallikrein inhibitors for organ preservation has not been successfully demonstrated.

SUMMARY OF THE INVENTION

This invention is based on the discovery of peptides that inhibit serine proteases, such as, for example, kallikrein, which can successfully be employed to preserve an organ pending transplant. More specifically, the invention provides methods of using kallikrein inhibitors in a method for preserving an organ or tissue and compositions for such use. The invention also relates to methods for reducing, inhibiting or preventing reperfusion injury or damage in an organ or tissue that has been removed from its host and compositions for such use. Preferred kallikrein peptides include those described in United States Patent Nos. 6,333,402 and 6,057,287 to Markland *et al.*

In a particularly preferred embodiment, the invention is directed to compositions comprising a polypeptide comprising the amino acid sequence:

Xaa1 Xaa2 Xaa3 Xaa4 Cys Xaa6 Xaa7 Xaa8 Xaa9 Xaa10 Xaa11 Gly Xaa13 Cys Xaa15 Xaa16 Xaa17 Xaa18 Xaa19 Xaa20 Xaa21 Xaa22 Xaa23 Xaa24 Xaa25 Xaa26 Xaa27 Xaa28 Xaa29 Cys Xaa31 Xaa32 Phe Xaa34 Xaa35 Gly Gly Cys Xaa39 Xaa40 Xaa41 Xaa42 Xaa43 Xaa44 Xaa45 Xaa46 Xaa47 Xaa48 Xaa49 Xaa50 Cys Xaa52 Xaa53 Xaa54 Cys Xaa56 Xaa57 Xaa58 (SEQ ID NO:1),

wherein Xaa1, Xaa2, Xaa3, Xaa4, Xaa56, Xaa57 or Xaa58 are each individually an amino acid or absent; Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid; Xaa10 is an amino acid selected from the group consisting of: Asp and Glu; Xaa11 is an amino acid selected from the group consisting of: Asp, Gly, Ser, Val, Asn, Ile, Ala and Thr; Xaa13 is an amino acid selected from the group consisting of: Arg, His, Pro, Asn, Ser, Thr, Ala, Gly, Lys and Gln; Xaa15 is an amino acid selected from the group consisting of: Arg, Lys, Ala, Ser, Gly, Met, Asn and Gln; Xaa16 is an amino acid selected from the group consisting of: Ala, Gly, Ser, Asp and Asn; Xaa17 is an amino acid selected from the group consisting of: Ala, Asn, Ser, Ile, Gly, Val, Gln and Thr; Xaa18 is an amino acid selected from the group consisting of: His, Leu, Gln and Ala; Xaa19 is an amino acid selected from the group consisting of: Pro, Gln, Leu, Asn and Ile; Xaa21 is an amino acid selected from the group consisting of: Trp, Phe, Tyr, His and Ile; Xaa22 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa23 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa31 is an amino acid selected from the group consisting of: Glu, Asp, Gln, Asn, Ser, Ala, Val, Leu, Ile and Thr; Xaa32 is an amino acid selected from the group consisting of: Glu, Gln, Asp Asn, Pro, Thr, Leu, Ser, Ala, Gly and Val; Xaa34 is an amino acid selected from the group consisting of: Thr, Ile, Ser, Val, Ala, Asn, Gly and Leu; Xaa35 is an amino acid selected from the group consisting of: Tyr, Trp and Phe; Xaa39 is an amino acid selected from the group consisting of: Glu, Gly, Ala, Ser and

Asp; Xaa40 is an amino acid selected from the group consisting of: Gly and Ala; Xaa43 is an amino acid selected from the group consisting of: Asn and Gly; Xaa45 is an amino acid selected from the group consisting of: Phe and Tyr; and wherein said polypeptide inhibits kallikrein, and methods of using such compositions.

In a particular embodiment, specific amino acid positions can be the following: Xaa6 can be Ala, Xaa7 can be Phe, Xaa8 can be Lys, Xaa9 can be Ala, Xaa10 can be Asp, Xaa11 can be Asp, Xaa13 can be Pro, Xaa15 can be Arg, Xaa16 can be Ala, Xaa17 can be Ala, Xaa18 can be His, Xaa19 can be Pro, Xaa20 can be Arg, Xaa24 can be Asn, Xaa25 can be Ile, Xaa26 can be Phe, Xaa27 can be Thr, Xaa28 can be Arg, Xaa29 can be Gln, Xaa31 can be Glu, Xaa32 can be Glu, Xaa34 can be Ile, Xaa35 can be Tyr, Xaa39 can be Glu, Xaa41 can be Asn, Xaa42 can be Arg, Xaa44 can be Arg, Xaa46 can be Glu, Xaa47 can be Ser, Xaa48 can be Leu, Xaa49 can be Glu, and/or Xaa50 can be Glu; any of these specific amino acids at these positions can occur individually or in combination with one or more of the amino acids at one or more position otherwise described.

In a particular embodiment, the present invention is directed to a composition comprising a polypeptide as described in SEQ ID NO:1, such that two or more of the following amino acid positions are defined as follows: Xaa10 can be Asp; Xaa11 can be Asp; Xaa13 can be Pro; Xaa15 can be Arg; Xaa16 can be Ala; Xaa17 can be Ala; Xaa18 can be His; Xaa19 can be Pro; Xaa21 can be Trp; Xaa22 can be Phe; Xaa23 can be Phe; Xaa31 can be Glu; Xaa32 can be Glu; Xaa34 can be Ile; Xaa35 can be Tyr; Xaa39 can be Glu; Xaa40 can be Gly; Xaa43 can be Asn; and Xaa45 can be Phe, and methods of using such compositions. In another embodiment, five or more of the following of the following amino acid positions are defined as follows: Xaa10 can be Asp; Xaa11 can be Asp; Xaa13 can be Pro; Xaa15 can be Arg; Xaa16 can be Ala; Xaa17 can be Ala; Xaa18 can be His; Xaa19 can be Pro; Xaa21 can be Trp; Xaa22 can be Phe; Xaa23 can be Phe; Xaa31 can be Glu; Xaa32 can be Glu; Xaa34 can be Ile; Xaa35 can be Tyr; Xaa39 can be Glu; Xaa40 can be Gly; Xaa43 can be Asn; and Xaa45 can be Phe. In another embodiment, 10 or more of the amino acids are defined as follows: Xaa10 can be Asp; Xaa11 can be

Asp; Xaa13 can be Pro; Xaa15 can be Arg; Xaa16 can be Ala; Xaa17 can be Ala; Xaa18 can be His; Xaa19 can be Pro; Xaa21 can be Trp; Xaa22 can be Phe; Xaa23 can be Phe; Xaa31 can be Glu; Xaa32 can be Glu; Xaa34 can be Ile; Xaa35 can be Tyr; Xaa39 can be Glu; Xaa40 can be Gly; Xaa43 can be Asn; and Xaa45 can be Phe. In yet another embodiment, 15 or more of the amino acids are defined as follows: Xaa10 can be Asp; Xaa11 can be Asp; Xaa13 can be Pro; Xaa15 can be Arg; Xaa16 can be Ala; Xaa17 can be Ala; Xaa18 can be His; Xaa19 can be Pro; Xaa21 can be Trp; Xaa22 can be Phe; Xaa23 can be Phe; Xaa31 can be Glu; Xaa32 can be Glu; Xaa34 can be Ile; Xaa35 can be Tyr; Xaa39 can be Glu; Xaa40 can be Gly; Xaa43 can be Asn; and Xaa45 can be Phe.

In a particular embodiment, the invention is directed to a composition comprising a polypeptide as defined by SEQ ID NO:1, such that, if present, Xaa3 is Ser, Xaa2 is His, Xaa1 is Met, Xaa56 is Thr, Xaa57 is Arg, and/or Xaa58 is Asp, and methods of using such compositions.

In another embodiment, the invention is directed to a composition comprising a polypeptide comprising the amino acid sequence:

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:2), and methods of using such compositions.

In a particular embodiment, the present invention is directed to a composition comprising a kallikrein binding polypeptide of 53-60 amino acids comprising a Kunitz domain, wherein the Kunitz domain comprises the potential for disulfide bonds between cysteines at positions 5 and 55; 14 and 38; and 30 and 51 (according to amino acid positions corresponding to bovine pancreatic trypsin inhibitor (BPTI)), and further comprising:

amino acid number 13 selected from His and Pro;
amino acid number 16 selected from Ala and Gly;
amino acid number 17 selected from Ala, Asn, and Ser;
amino acid number 18 selected from His and Leu; and
amino acid number 19 selected from Gln, Leu, and Pro (SEQ ID NO:23).

In a particular embodiment, the present invention is directed to a composition comprising a kallikrein binding polypeptide of 53-60 amino acids comprising a Kunitz domain, wherein the Kunitz domain comprises the potential for disulfide bonds between cysteines at positions 5 and 55; 14 and 38; and 30 and 51 (according to amino acid positions corresponding to bovine pancreatic trypsin inhibitor (BPTI)), and further comprising:

amino acid number 13 selected from His and Pro;
amino acid number 15 selected from Lys and Arg;
amino acid number 16 selected from Ala and Gly;
amino acid number 17 selected from Ala, Asn, and Ser;
amino acid number 18 selected from His and Leu; and
amino acid number 19 selected from Gln, Leu, and Pro,
amino acid number 31 is Glu;
amino acid number 32 selected from Glu and Gln;
amino acid number 34 selected from Ser, Thr, and Ile; and
amino acid number 39 selected from Gly, Glu, and Ala (SEQ ID NO:24).

In a particular embodiment, the present invention is directed to a composition comprising a kallikrein binding polypeptide of 53-60 amino acids comprising a Kunitz domain, wherein the Kunitz domain comprises a cysteine at each of positions 5 and 55; 14 and 38; and 30 and 51 (according to amino acid positions corresponding to bovine pancreatic trypsin inhibitor (BPTI)), and further comprising:

amino acid number 13 selected from His and Pro;
amino acid number 15 selected from Lys and Arg;
amino acid number 16 selected from Ala and Gly;
amino acid number 17 selected from Ala, Asn, and Ser;
amino acid number 18 selected from His and Leu; and
amino acid number 19 selected from Gln, Leu, and Pro,
amino acid number 31 is Glu;
amino acid number 32 selected from Glu and Gln;
amino acid number 34 selected from Ser, Thr, and Ile; and
amino acid number 39 selected from Gly, Glu, and Ala (SEQ ID NO:24).

In a particular embodiment, the Kunitz domain is selected from the group consisting of:

KKII/3 #1 (SEQ ID NO:24)
KKII/3 #2 (SEQ ID NO:25)
KKII/3 #3 (SEQ ID NO:26)
KKII/3 #4 (SEQ ID NO:27)
KKII/3 #5 (SEQ ID NO:28)
KKII/3 #6 (SEQ ID NO:29)
KKII/3 #7 (SEQ ID NO:30)
KKII/3 #8 (SEQ ID NO:31)
KKII/3 #9 (SEQ ID NO:32) and
KKII/3 #10 (SEQ ID NO:33)

as described in Table 1.

Each of the compositions described herein can be used in the methods of the invention. Further, the compounds described herein can be used in the manufacture of a medicament or composition for the indications or methods described herein.

According to another embodiment, the invention is directed to use of a kallikrein inhibitor for preservation of an organ or tissue, the kallikrein inhibitor comprising a polypeptide of SEQ ID NO:l, wherein Xaal, Xaa2, Xaa3, Xaa4, Xaa56, Xaa57 or Xaa58 are each individually an amino acid or absent; Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid; Xaal0 is Asp; Xaal1 is Asp; Xaal3 is Pro; Xaal5 is Arg; Xaal6 is Ala; Xaal7 is Ala; Xaal8 is His; Xaal9 is Pro; Xaa21 is Trp; Xaa22 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa23 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa31 is Glu; Xaa32 is Glu; Xaa34 is Ile; Xaa35 is Tyr; Xaa39 is Glu; Xaa40 is an amino acid selected from the group consisting of: Gly and Ala; Xaa43 is an amino acid selected from the group consisting of: Asn and Gly; Xaa45 is an amino acid selected from the group consisting of: Phe and Tyr; and wherein said polypeptide inhibits kallikrein.

According to another embodiment, the invention is directed to use of an organ storage and preservative solution for reducing reperfusion injury of an organ during surgery and/or following removal of the organ from a subject, wherein the solution comprises a kallikrein inhibitor, wherein the kallikrein inhibitor is a polypeptide comprising SEQ ID NO:l, wherein Xaal, Xaa2, Xaa3, Xaa4, Xaa56, Xaa57 or Xaa58 are each individually an amino acid or absent; Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid; Xaa 10 is Asp; Xaal1 is Asp; Xaal3 is Pro; Xaal5 is Arg; Xaal6 is Ala; Xaal7 is Ala; Xaal8 is His; Xaal9 is Pro; Xaa21 is Trp; Xaa22 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa23 is an amino acid selected from the group consisting of: Tyr and Phe; Xaa31 is Glu; Xaa32 is Glu; Xaa34 is Ile; Xaa35 is Tyr; Xaa39 is Glu; Xaa40 is an amino acid selected from the group consisting of: Gly and Ala; Xaa43 is an amino acid selected from the group consisting of: Asn and Gly; Xaa45 is an amino acid selected from the group consisting of: Phe and Tyr.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a simplified diagram of major multiple pathways and related events involved in the contact activation system and systemic inflammatory response (SIR) that may arise in a patient subjected to soft and bone tissue trauma such as that associated with a coronary artery bypass grafting (CABG) procedure, especially when the CABG procedure involves extra-corporeal blood circulation, such as cardiopulmonary bypass (CPB; Bypass Apparatus). Arrows indicate activation from one component or event to another component or event in the cascade. Arrows in both directions indicate activating effects of components or events in both directions. Broken arrows indicate likely participation of one component or event in the activation of another component or event. Abbreviations are as follows: "tPA" = tissue plasminogen activator; "C5a" = a protein component of the complement system; "fXIIa" = activator protein of pre-kallikrein to form active kallikrein; "Extrinsic" = extrinsic coagulation system; "Intrinsic" = intrinsic coagulation system.

FIG. 2 shows a portion of a DNA and corresponding deduced amino acid for a kallikrein inhibitor ("KI") polypeptide of the invention in plasmid pPIC-K503. The inserted DNA encodes the mata prepro signal peptide of *Saccharomyces cerevisiae* (underlined) fused in frame to the amino terminus of the PEP-1 KI polypeptide having the amino acid sequence enclosed by the boxed area. The amino acid sequence of the PEP-1 KI polypeptide shown in the boxed region is SEQ ID NO:2, and the corresponding nucleotide coding sequence of the KI polypeptide is SEQ ID NO:3. The dashed arrows indicate the location and direction of two PCR primer sequences in AOX regions that were used to produce sequencing templates. DNA sequence for the entire nucleotide sequence of the figure comprises the structural coding sequence for the fusion protein and is designated SEQ ID NO:35. The double underlined portion of the sequence indicates a diagnostic probe sequence. *Bst*BI and *Eco*RI indicate locations of their respective palindromic, hexameric, restriction endonuclease sites in the sequence. Asterisks denote translational stop codons.

FIG. 3 shows an alignment of amino acid sequences of the preferred embodiments of the invention.

DETAILED DESCRIPTION OF THE INVENTION

A description of preferred embodiments of the invention follows.

The invention is based on the discovery of kallikrein inhibitor (KI) polypeptides that inhibit plasma kallikrein with a specificity that permits their use in improved methods of preserving organs and tissues, such as pending a transplantation, and and to corresponding methods. The invention also relates to reducing, inhibiting or preventing reperfusion injury or damage in an organ or tissue that has been removed from its host and compositions therefor.

Polypeptides Useful in the Invention

KI polypeptides useful in the invention comprise Kunitz domain polypeptides. In one embodiment these Kunitz domains are variant forms comprising the looped structure of Kunitz domain 1 of human lipoprotein-associated coagulation inhibitor (LACI) protein. LACI contains three internal, well-defined, peptide loop structures that are paradigm Kunitz domains (Girard, T. *et al.*, 1989. *Nature*, 338:518-520). The three Kunitz domains of LACI confer the ability to bind and inhibit kallikrein, although not with exceptional affinity. Variants of Kunitz domain 1 of LACI described herein have been screened, isolated and bind kallikrein with enhanced affinity and specificity (see, for example, U.S. Patent Nos. 5,795,865 and 6,057,287). An example of a preferred polypeptide useful in the invention has the amino acid sequence defined by amino acids 3-60 of SEQ ID NO:2.

Kallikrein binding polypeptides can be used to target therapeutic or diagnostic molecules to kallikrein in, for example, organ tissue, cells, or whole organisms. Such methods of targeted delivery for therapeutic or diagnostic purposes would be known to one of skill in the art. For example, targeted kallikrein binding polypeptides could be used by one of skill in the art to identify an organ that has been damaged by the effects of kallikrien, or kallikrein can be targeted for the effects of a particular therapeutic agent using kallikrein binding polypeptides of the invention.

Every polypeptide useful in the invention binds kallikrein. In preferred embodiments, the polypeptides are kallikrein inhibitors (KI) as determined using kallikrein binding and inhibition assays known in the art. The enhanced affinity and specificity for kallikrein of the variant Kunitz domain polypeptides described herein provides the basis for their use in CPB and especially CABG surgical procedures to prevent or reduce perioperative blood loss and/or SIR in patients undergoing such procedures. The KI polypeptides used in the invention can have or comprise the amino acid sequence of a variant Kunitz domain polypeptide originally isolated by screening phage display libraries for the ability to bind kallikrein.

KI polypeptides useful in the methods and compositions of the invention comprise a Kunitz domain polypeptide comprising the amino acid sequence:

Xaa1 Xaa2 Xaa3 Xaa4 Cys Xaa6 Xaa7 Xaa8 Xaa9 Xaa10 Xaa11 Gly Xaa13 Cys Xaa15 Xaa16 Xaa17 Xaa18 Xaa19 Xaa20 Xaa21 Xaa22 Xaa23 Xaa24 Xaa25 Xaa26 Xaa27 Xaa28 Xaa29 Cys Xaa31 Xaa32 Phe Xaa34 Xaa35 Gly Gly Cys Xaa39 Xaa40 Xaa41 Xaa42 Xaa43 Xaa44 Xaa45 Xaa46 Xaa47 Xaa48 Xaa49 Xaa50 Cys Xaa52 Xaa53 Xaa54 Cys Xaa56 Xaa57 Xaa58 (SEQ ID NO:1)

"Xaa" refers to a position in a peptide chain that can be any of a number of different amino acids. For example, for the KI peptides described herein, Xaa10 can be Asp or Glu; Xaa11 can be Asp, Gly, Ser, Val, Asn, Ile, Ala or Thr; Xaa13 can be Pro, Arg, His, Asn, Ser, Thr, Ala, Gly, Lys or Gln; Xaa15 can be Arg, Lys, Ala, Ser, Gly, Met, Asn or Gln; Xaa16 can be Ala, Gly, Ser, Asp or Asn; Xaa17 can be Ala, Asn, Ser, Ile, Gly, Val, Gln or Thr; Xaa18 can be His, Leu, Gln or Ala; Xaa19 can be Pro, Gln, Leu, Asn or Ile; Xaa21 can be Trp, Phe, Tyr, His or Ile; Xaa31 can be Glu, Asp, Gln, Asn, Ser, Ala, Val, Leu, Ile or Thr; Xaa32 can be Glu, Gln, Asp Asn, Pro, Thr, Leu, Ser, Ala, Gly or Val; Xaa34 can be Ile, Thr, Ser, Val, Ala, Asn, Gly or Leu; Xaa35 can be Tyr, Trp or Phe; Xaa39 can be Glu, Gly, Ala, Ser or Asp. Amino acids Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid. Additionally, each of the first four and at last three amino acids of SEQ ID NO:1 can optionally be present or absent and can be any amino acid, if present.

Peptides defined according to SEQ ID NO:1 form a set of polypeptides that bind to and inhibit kallikrein. The diversity of the KI's is increased as the number of variable positions in the peptide sequence is increased or as the number of amino acids possible at a variable position increases. For example, in a preferred embodiment of the invention, a KI polypeptide useful in the methods and compositions of the invention has the following variable positions: Xaa11 can be Asp, Gly, Ser or Val; Xaa13 can be Pro, Arg, His or Asn; Xaa15 can be Arg or Lys; Xaa16 can be Ala or Gly; Xaa17 can be Ala, Asn, Ser or Ile; Xaa18 can be His, Leu or Gln; Xaa19 can be Pro, Gln or Leu; Xaa21 can be Trp or Phe; Xaa31 is Glu; Xaa32 can be Glu or Gln; Xaa34 can be Ile, Thr or Ser; Xaa35 is Tyr; and Xaa39 can be Glu, Gly or Ala.

A more specific embodiment of the claimed invention is defined by the following amino acids at variable positions: Xaa10 is Asp; Xaa11 is Asp; Xaa13 can be Pro or Arg; Xaa15 is Arg; Xaa16 can be Ala or Gly; Xaa17 is Ala; Xaa18 is His; Xaa19 is Pro; Xaa21 is Trp; Xaa31 is Glu; Xaa32 is Glu; Xaa34 can be Ile or Ser; Xaa35 is Tyr; and Xaa39 is Gly.

Also encompassed within the scope of the invention are peptides that comprise portions of the polypeptides described herein. For example, polypeptides could comprise binding domains for specific kallikrein epitopes. Such fragments of the polypeptides described herein would also be encompassed.

KI polypeptides useful in the methods and compositions described herein comprise a Kunitz domain. A subset of the sequences encompassed by SEQ ID NO:1 are described by the following (where not indicated, "Xaa" refers to the same set of amino acids that are allowed for SEQ ID NO:1):

Met His Ser Phe Cys Ala Phe Lys Ala Xaa10 Xaa11 Gly Xaa13 Cys Xaa15 Xaa16 Xaa17 Xaa18 Xaa19 Arg Xaa21 Phe Phe Asn Ile Phe Thr Arg Gln Cys Xaa31 Xaa32 Phe Xaa34 Xaa35 Gly Gly Cys Xaa39 Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:36).

Specific and particular examples of KI peptides useful in the invention described herein are as follows:

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (amino acids 3-60 of SEQ ID NO:2),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys Ala Asn His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:4),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Thr Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:5),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Gln Phe Thr Tyr Gly Gly Cys Ala Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:6), Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Ser Leu Pro Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:7),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:8),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Gly Ala His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:9),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Arg Cys Lys Gly Ala His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:10),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Gly Gly Arg Cys Arg Gly Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:11),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:12), Met His Ser Phe Cys Ala Phe Lys Ala Asp Val Gly Arg Cys Arg Gly Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:13),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Val Gly Arg Cys Arg Gly Ala Gln Pro Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:14),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Ser Cys Arg Ala Ala His Leu Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:15),

Met His Ser Phe Cys Ala Phe Lys Ala Glu Gly Gly Ser Cys Arg Ala Ala His Gln Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:16),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Arg Gly Ala His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:17),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Arg Gly Ala Leu Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:18), Met His Ser Phe Cys Ala Phe Lys Ala Asp Ser Gly Asn Cys Arg Gly Asn Leu Pro Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:19),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Ser Gly Arg Cys Arg Gly Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:20),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Gly Gly Arg Cys Arg Ala Ile Gln Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:21),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Arg Cys Arg Gly Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:22).

FIG. 3 provides an amino acid sequence alignment of these sequences.

Other KI polypeptides useful in the present invention include:

Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Lys Ala Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala Glu Asp Cys Met Arg Thr Cys Gly Gly Ala (SEQ ID NO:23),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Ser Leu Pro Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:24), Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys Ala Asn His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:25),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Thr Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:26),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Gln Phe Thr Tyr Gly Gly Cys Ala Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:27),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Ser Leu Pro Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:28),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:29),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:30), Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:31),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Ala Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:32),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly His Cys Lys Gly Ala His Leu Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:33),

Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:34).

These sequences are summarized in the following Table 1.

TABLE 1: Amino acid sequences of LACI(K1) variants selected for binding to human plasma kallikrein.

	13	16	17	18	19	31	32	34	39(a)
KKII/3#1 (SEQ ID NO:24)	H	A	S	L	P	E	E	I	E
KKII/3#2 (SEQ ID NO:25)	P	A	N	H	L	E	E	S	G
KKII/3#3 (SEQ ID NO:26)	H	A	N	H	Q	E	E	T	G
KKII/3#4 (SEQ ID NO:27)	H	A	N	H	Q	E	Q	T	A
KKII/3#5 (SEQ ID NO:28)	H	A	S	L	P	E	E	I	G
KKII/3#6 (SEQ ID NO:29)	H	A	N	H	Q	E	E	S	G
KKII/3#7 (SEQ ID NO:30)	H	A	N	H	Q	E	E	S	G
KKII/3#8 (SEQ ID NO:31)	H	A	N	H	Q	E	E	S	G
KKII/3#9 (SEQ ID NO:32)	H	A	N	H	Q	E	E	S	G
KKII/3#10 (SEQ ID NO:33)	H	G	A	H	L	E	E	I	E
Consensus	H	A	N	H	Q	E	E	S/T	G

(a) Amino acid numbers of variegated residues. LACI(K1) (LACI residues 50-107 (SEQ ID NO:32)) is 58 amino acids long with the P1 position being residue number 15 and fixed as lysine in this instance.

The polypeptides useful in the methods and compositions described herein may be made synthetically using any standard polypeptide synthesis protocol and equipment. For example, the stepwise synthesis of a KI polypeptide described herein may be carried out by the removal of an amino (N) terminal-protecting group from an initial (*i.e.*, carboxy-terminal) amino acid, and coupling thereto of the carboxyl end of the next amino acid in the sequence of the polypeptide. This amino acid is also suitably protected. The carboxyl group of the incoming amino acid can

be activated to react with the N-terminus of the bound amino acid by formation into a reactive group such as formation into a carbodiimide, a symmetric acid anhydride, or an "active ester" group such as hydroxybenzotriazole or pentafluorophenyl esters. Preferred solid-phase peptide synthesis methods include the BOC method, which utilizes tert-butyloxycarbonyl as the a-amino protecting group, and the FMOC method, which utilizes 9-fluorenylmethloxycarbonyl to protect the a-amino of the amino acid residues. Both methods are well known to those of skill in the art (Stewart, J. and Young, J., *Solid-Phase Peptide Synthesis* (W. H. Freeman Co., San Francisco 1989); Merrifield, J., 1963. *Am. Chem. Soc.*, 85:2149-2154; Bodanszky, M. and Bodanszky, A., *The Practice of Peptide Synthesis* (Springer-Verlag, New York 1984).
If desired, additional amino- and/or carboxy-
terminal amino acids may be designed into the amino acid sequence and added during polypeptide synthesis.

Alternatively, Kunitz domain polypeptides and KI polypeptides useful in the compositions and methods of the invention may be produced by recombinant methods using any of a number of cells and corresponding expression vectors, including but not limited to bacterial expression vectors, yeast expression vectors, baculovirus expression vectors, mammalian viral expression vectors, and the like. Kunitz domain polypeptides and KI polypeptides useful in the compositions and methods of the invention may also be produced transgenically using nucleic acid molecules comprising a coding sequence for a Kunitz domain or KI polypeptide described herein, wherein the nucleic acid molecule can be integrated into and expressed from the genome of a host animal using transgenic methods available in the art. In some cases, it may be necessary or advantageous to fuse the coding sequence for a Kunitz domain polypeptide or a KI polypeptide comprising the Kunitz domain to another coding sequence in an expression vector to form a fusion polypeptide that is readily expressed in a host cell. Preferably, the host cell that expresses such a fusion polypeptide also processes the fusion polypeptide to yield a Kunitz domain or KI polypeptide useful in the invention that contains only the desired amino acid sequence. Obviously, if any other amino acid(s) remain attached to the expressed Kunitz domain or KI polypeptide, such additional amino acid(s) should not diminish the kallikrein binding and/or kallikrein inhibitory activity of the Kunitz domain or KI polypeptide so as to preclude use of the polypeptide in the methods or compositions of the invention.

A preferred recombinant expression system for producing KI polypeptides useful in the methods and compositions described herein is a yeast expression vector, which permits a nucleic acid sequence encoding the amino acid sequence for a KI polypeptide or Kunitz domain polypeptide to be linked in the same reading frame with a nucleotide sequence encoding the mata prepro leader peptide sequence of *Saccharomyces cerevisiae*, which in turn is under the control of an operable yeast promoter. The resulting recombinant yeast expression plasmid may then be transformed by standard methods into the cells of an appropriate, compatible yeast host, which cells are able to express the recombinant protein from the recombinant yeast expression vector. Preferably, a host yeast cell transformed with such a recombinant expression vector is also able to process the fusion protein to provide an active KI polypeptide useful in the methods and compositions of the invention. A preferred yeast host for producing recombinant Kunitz domain polypeptides and KI polypeptides comprising such Kunitz domains is *Pichia pastoris*.

As noted above, KI polypeptides that are useful in the methods and compositions described herein may comprise a Kunitz domain polypeptide described herein. Some KI polypeptides may have an additional flanking sequence, preferably of one to six amino acids in length, at the amino and/or carboxy-terminal end, provided such additional amino acids do not significantly diminish kallikrein binding affinity or kallikrein inhibition activity so as to preclude use in the methods and compositions described herein. Such additional amino acids may be deliberately added to express a KI polypeptide in a particular recombinant host cell or may be added to provide an additional function, *e.g.*, to provide a peptide to link the KI polypeptide to another molecule or to provide an affinity moiety that facilitates purification of the polypeptide. Preferably, the additional amino acid(s) do not include cysteine, which could interfere with the disulfide bonds of the Kunitz domain. Native examples of Kunitz domains exhibit disulfide bonds, *e.g.*, BPTI contains disulfide bonds between cysteine residues at amino acid positions 5 and 55; 14 and 38; and 30 and 51

An example of a preferred Kunitz domain polypeptide useful in the methods and compositions of the invention has the amino acid sequence of residues 3-60 of SEQ ID NO:2. When expressed and processed in a yeast fusion protein expression system (*e.g.*, based on the integrating expression plasmid pHIL-D2), such a Kunitz domain polypeptide retains an additional amino terminal Glu-Ala dipeptide from the fusion with the mata prepro leader peptide sequence of *S. cerevisiae*. When secreted from the yeast host cell, most of the leader peptide is processed from the fusion protein to yield a functional KI polypeptide (also referred to as "PEP-1" or "DX88") having the amino acid sequence of SEQ ID NO:2 (see boxed region in FIG. 2).

Particularly preferred KI polypeptides useful in the methods and compositions described herein have a binding affinity for kallikrein that is on the order of 1000 times higher than that of aprotinin, which is currently approved for use in CABG procedures to reduce blood loss. The surprisingly high binding affinities of such KI polypeptides described herein indicate that such KI polypeptides exhibit a high degree of specificity for kallikrein to the exclusion of other molecular targets (see Table 1, below). Thus, use of such polypeptides according to the invention reduces much of the speculation as to the possible therapeutic targets. The lower degree of specificity exhibited by, for example, aprotinin, leads to possible pleiotropic side effects and ambiguity as to its therapeutic mechanism.

The polypeptides defined by, for example, SEQ ID NO:1 contain invariant positions, *e.g.*, positions 5, 14, 30, 51 and 55 can be Cys only. Other positions such as, for example, positions 6, 7, 8, 9, 20, 24, 25, 26, 27, 28, 29, 41, 42, 44, 46, 47, 48, 49, 50, 52, 53 and 54 can be any amino acid (including non-naturally occurring amino acids). In a particularly preferred embodiment, one or more amino acids correspond to that of a native sequence (*e.g.*, LACI (SEQ ID NOS:32-34)). In a preferred embodiment, at least one variable position is different from that of the native sequence. In yet another preferred embodiment, the amino acids can each be individually or collectively substituted by a conservative or non-conservative amino acid substitution. Conservative amino acid substitutions replace an amino acid with another amino acid of similar chemical structure and may have no affect on protein function. Non-conservative amino acid substitutions replace an amino acid with another amino acid of dissimilar chemical structure. Examples of conserved amino acid substitutions include, for example, Asn->Asp, Arg->Lys and Ser->Thr. In a preferred embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 and/or 21 of these amino acids can be independently or collectively, in any combination, selected to correspond to the corresponding position of SEQ ID NO:2.

Other positions, for example, positions 10, 11, 13, 15, 16, 17, 18, 19, 21, 22, 23, 31, 32, 34, 35, 39, 40, 43 and 45, can be any of a selected set of amino acids. Thus SEQ ID NO:1 defines a set of possible sequences. Each member of this set contains, for example, a cysteine at positions 5, 14, 30, 51 and 55, and any one of a specific set of amino acids at positions 10, 11, 13, 15, 16, 17, 18, 19, 221, 22, 23, 31, 32, 34, 35, 39, 40, 43 and 45. In a preferred embodiment, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 and/or 19 of these amino acids can be independently or collectively, in any combination, selected to correspond to the corresponding position of SEQ ID NO:2. The peptide preferably has at least 80%, at least 85%, at least 90% or at least 95% identity to SEQ ID NO:2.

Methods and Compositions

The present invention is directed to methods for preserving organs and tissues comprising contacting the organ or tissue with a preservative solution comprising a kallikrein inhibitor, such as those described herein. The invention also relates to reducing, inhibiting or preventing reperfusion injury or damage in an organ or tissue that has been removed from its host comprising contacting the organ or tissue with a kallikrein inhibitor. The preservative solutions of the invention can be used to preserve and/or protect organ tissue, or whole organs, when said organs or tissue are brought into contact with the solution. A specific embodiment of the invention is for the preservation of a human heart, or human myocardial tissue. Another embodiment of the invention is for the preservation of a human lung or human lung tissue. Other organs, or parts thereof, that can be preserved according to the invention include kidney, liver, endothelial tissue, intestinal tissue, vascular tissue (*e.g.*, an aorta graft), skin, and pancreas. The invention contemplates the use of the solutions to preserve mammalian tissue, organs or portion thereof. In addition, the solutions can be used to facilitate transplantation of organs, *e.g.*, by perfusion of the organ or tissue during the transplantation procedure. The solution can also be used as a cardioplegia solution in cardiac surgery. Preferably, the organ or portion thereof, is maintained in the appropriate solution at all times, particularly, prior to the transplant procedure.

The solutions of the invention can be used to maintain viability of the organ or tissue during storage, transplantation or other surgery. The invention includes a method of storing tissue or organs comprising contacting said tissue, organ or part thereof, with the solution of the invention, such that the *in vivo* and/or *in vitro* viability is prolonged. The solutions permit maintenance of viability of heart or lung tissue for up to 24 hours or more. Use of the solutions of the invention results in improved organ viability.

Alternatively or in addition, once removed from the donor, the organ or living tissue may be placed in a preservation solution containing the inhibitor. In addition, the kallikrein inhibitor is also preferably administered to the transplant recipient just prior to, or concommitant with, transplantation. In all cases, the inhibitor alsocan be administered directly to the tissue at risk, as by injection to the tissue, or it may be provided systemically, either by oral or parenteral administration, using any of the methods and formulations described herein and/or known in the art.

In one embodiment, any commercially available preservation solution may be used to advantage. Examples of such solutions include the Belzer UW solution sold under the trademark VIASPAN, described in U.S. Patent Nos. 4,798,824, 4,873,230, 4,879,283.

The preservation solution and perfusate composition described in the aforementioned patents includes, but is not limited to, the following:

TABLE 2

Substance	Amount in 1 Liter
K^+ - lactobionate	100 mmol
KH_2 PO_4	25 mmol
$MgSO_4$	5 mmol
Raffinose	30 mmol
Adenosine	5 mmol
Glutathione	3 mmol
Insulin	100 U
Bactrim	0.5 mL
Dexamethasone	8 mg
Allopurinol	1 mM
Hydroxyethyl starch having a molecular weight of about 200,000 to about 300,000 daltons and a degree of substitution of from about 0.4 to 0.7	50 g

The solution is brought to pH 7.4 at room temperature with NaOH. The final concentrations are Na=30.±.5 mM, $K^+ = 120 \pm 5$ mM, mOsm/liter=320 ± 5. Bactrim = trimethoprim (16 mg/mL) and sulfamethoxazole (80 mg/mL). The hydroxyethyl starch can be present in the range of from about 3 to about 8%.

This solution typically provides for a 72 hour preservation of the pancreas, 48 hour preservation for the kidney and at least 24 hour preservation for the liver. U.S. Patent 5,145,771, incorporated herein by reference, described the organ preservation solution known as the "Carolina Solution," which is also useful in the present invention. The rinse or preservation solution composition described in the aforementioned patent includes, but is not limited to, the components in about the concentration ranges set forth in Table 3 below.

TABLE 3

Concentration Ranges in 1 Liter 10% modified hydroxyethyl starch 30 g/L to 100 g/L			
NaCl	85 mM	to	145 mM
KCl	3 mM	to	6 mM
$CaCl_2$	1.0 mM	to	1.6 mM
KH_2PO_4	0.7 mM	to	1.3 mM
$MgSO_4$	0.9 mM	to	1.5 mM
Allopurinol	0.05 mM	to	5.0 mM
Desferrioxamine	0.02 mM	to	2.0 mM
Glutathione	0.5 mM	to	10.0 mM
Nicardipene	0.1 .mu.M	to	5.0 .mu.M
Adenosine	0.1 mM	to	5.0 mM
Fructose	1.0 mM	to	50.0 mM
Glucose	1.0 mM	to	50.0 mM
Insulin	5 U/L	to	250 U/L
Mops	2 mM		40 mM

One specific embodiment is prepared with the components in the amounts set forth in Table 4 below in accordance with the instructions set forth below.

TABLE 4: Components of 1 Liter Rinse Solution

500 mL	Distilled Deionized Water	
50 g/L	10% modified hydroxyethyl starch	
115 mM	NaC1	6.7 g
5 mM	KCl	0.37 g
1.30 mM	$CaCl_2$	0.19 g
1 mM	$KH_2 PO_4$	0.14 g
1.2 mM	$MgSO_4$	0.15 g
1 mM	Allopurinol	0.14 g
1 mM	Desferrioxamine	0.65 g
3 mM	Glutathione	0.92 g
2 .mu.M	Nicardipene	0.80 mg
1 mM	Adenosine	0.32 g
10 mM	Fructose	1.8 g
10 mM	Glucose	1.8 g
100 U/L	Insulin	100 units
20 mM	Mops	4.2 g

In one embodiment this solution can be prepared as follows: using a 500 mL volumetric flask, measure 500 mL of 10% (weight/volume) hydroxyethyl starch solution and pour into a 1 L beaker. Add 400 mL of double distilled water and stir vigorously using a magnetic stir bar. Add the rest of the components one at a time. After all components are added, adjust the pH to 6.5 with 1-2 mL 5N NaOH. The solution should be stirred for at least thirty minutes. Transfer the solution to a 1 L volumetric flask and bring to 1 L final volume. Filter to remove any undissolved particles.

Still another embodiment is exemplified by Table 5 below.

TABLE 5: Concentration Ranges in 1 Liter

NaCl	85 mM	to	145 mM
KCl	3 mM	to	6 mM
$CaCl_2$	1.0 mM	to	1.6 mM
KH_2PO_4	0.7 mM	to	1.3 mM
$MgSO_4$	0.9 mM	to	1.5 mM
Adenosine	0.12 mM	to	1.2 mM

A composition according to Table 5 above may optionally include one, several, or all of the further ingredients specified in Table 3 above. Preferably, the composition includes at least one antioxidant. Thus, one specific embodiment of a composition is set forth in Table 6 below:

TABLE 6: Components of 1 Liter Rinse Solution

500 mL	Distilled Deionized Water	
115 mM	NaCl	6.7 g
5 mM	KCl	0.37 g
1.30 mM	$CaCl_2$	0.19 g
1 mM	KH_2PO_4	0.14 g
1.2 mM	$MgSO_4$	0.15 g
1 mM	Allopurinol	0.14 g
1 mM	Desferrioxamine	0.65 g
3 mM	Glutathione	0.92 g
.12 mM	Adenosine	0.038g

Preferred compositions may further comprise one or more pharmaceutically acceptable buffers, carriers, antioxidants, protease inhibitors, or other anti-ischemia agents.

Compositions useful in the methods of the invention comprise any of the Kunitz domain polypeptides or KI polypeptides comprising such Kunitz domain polypeptides described herein. Particularly preferred are KI polypeptides comprising a Kunitz domain polypeptide having a 58-amino acid sequence of amino acids 3-60 of SEQ ID NO:2. An example of such a particularly preferred KI polypeptide useful in the methods and compositions of the invention is the PEP-1 KI polypeptide having the 60-amino acid sequence of SEQ ID NO:2. A nucleotide sequence encoding the amino acid sequence of SEQ ID NO:2 is provided in SEQ ID NO:3 (see, *e.g.*, nucleotides 309-488 in FIG. 2). It is understood that based on the known genetic code, the invention also provides degenerate forms of the nucleotide sequence of SEQ ID NO:3 by simply substituting one or more of the known degenerate codons for each amino acid encoded by the nucleotide sequence. Nucleotides 7-180 of SEQ ID NO:3, and degenerate forms thereof, encode the non-naturally occurring Kunitz domain polypeptide having the 58-amino acid sequence of amino acids 3-60 of SEQ ID NO:2.

Concentration Considerations for KI polypeptides

Several considerations regarding dosing with a KI polypeptide in methods of the invention may be illustrated by way of example with the representative PEP-1 KI polypeptide of the invention having the amino sequence of SEQ ID NO:2 (molecular weight of 7,054 Daltons).

Table 7, below, provides a comparison of the affinity ($K_{i,app}$) of the PEP-1 KI polypeptide for kallikrein and eleven other known plasma proteases.

TABLE 7

Protease Substrate	PEP-1 $K_{i,app}$ (pM)	Aprotinin $K_{i,app}$ (pM)
human plasma kallikrein	44	3.0×10^4
human urine kallikrein	$>1 \times 10^8$	4.0×10^3
porcine pancreatic kallikrein	2.7×10^7	550
human C1r, activated	$>2.0 \times 10^8$	1.0×10^7
human C1s, activated	$>2.0 \times 10^7$	$>1.0 \times 10^8$
human plasma factor XIa	1.0×10^4	ND
human plasma factor XIIa	$>2.0 \times 10^7$	$>1.0 \times 10^8$
human plasmin	1.4×10^5	894
human pancreatic trypsin	$>2 \times 10^7$	ND
human pancreatic chymotrypsin	$>2.0 \times 10^7$	7.3×10^5
human neutrophil elastase	$>2.0 \times 10^7$	1.7×10^6
human plasma thrombin	$>2.0 \times 10^7$	$>1.0 \times 10^8$

ND = not determined

Clearly, the PEP-1 KI polypeptide is highly specific for human plasma kallikrein. Furthermore, the affinity ($K_{i,app}$) of PEP-1 for kallikrein is 1000 times higher than the affinity of aprotinin for kallikrein: the $K_{i,app}$ of PEP-1 for kallikrein is about 44 pM (Table 1), whereas the $K_{i,app}$ of aprotinin for kallikrein is 30,000 pM. Thus, a dose of PEP-1 could be approximately 1000 times lower than that used for aprotinin on a per mole basis. However, consideration of several other factors may provide a more accurate estimation of the dose of PEP-1 required in practice. Such factors include the amount of kallikrein activated upon organ removal from a particular patient, and will be recognized by the skilled artisan.

The invention will be further described with reference to the following non-limiting examples.

EXEMPLIFICATION

Example 1: A representative KI polypeptide.

A KI polypeptide (PEP-1) useful in the compositions and methods of the invention was identified as a kallikrein binding polypeptide displayed on a recombinant phage from a phage display library. PEP-1 has the following amino acid sequence: Glu Ala Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp (SEQ ID NO:2). The molecular weight of PEP-1 is 7,054 Daltons.

The nucleotide sequence (SEQ ID NO:3) of the recombinant phage DNA encoding the PEP-1 amino acid sequence (amino acids 3-60 of SEQ ID NO:2) was isolated and sequenced by standard methods determined from the recombinant phage DNA. PEP-1 was produced in amounts useful for further characterization as a recombinant protein in *His4*$^-$ phenotype host cells of yeast strain *Pichia pastoris*.

Example 2: Construction of a recombinant plasmid to express KI polypeptides.

The initial plasmid, pHIL-D2, is ampicillin resistant and contains a wild-type allele of *His4* from *P. pastoris*. The final DNA sequence comprising the coding sequence for the mata Prepro-PEP-1 fusion protein in the recombinant expression plasmid pPIC-K503 is shown in FIG. 2. The DNA sequence of pHIL-D2 was modified to produce pPIC-K503, as follows:

1. The *Bst*BI site in the 3' AOX1 region of pHIL-D2, located downstream of the *His4* gene, was removed by partial restriction digestion, fill-in, and ligation, altering the sequence from TTCGAA (SEQ ID NO:23) to TTCGCGAA (SEQ ID NO:24). This modification was made to facilitate and direct the cloning of the expression cassette into the plasmid.

2. The *Aat*II site bearing the *bla* gene located downstream of *His4* was removed by restriction digestion, fill-in, and ligation modifying the sequence from GACGTC (SEQ ID NO:25) to GACGTACGTC (SEQ ID NO:26). This modification was made to facilitate the cloning of expression cassettes having *Aat*II sites into the plasmid. The DNA encoding PEP-1 was synthesized based on the nucleotide sequence from the original kallikrein-binding display phage and consisted of 450 base pairs (bp). The final DNA sequence of the insert in the pHIL-D2 plasmid is flanked by a 5' AOX1 sequence and a 3' AOX1 sequence (portions of which are shown in FIG. 2) and encode a fusion protein comprising the mata prepro signal peptide of *S. cerevisiae* fused to the structural coding sequence for the PEP-1 KI polypeptide. The signal peptide was added to facilitate the secretion of PEP-1 from the yeast host cells. The oligonucleotides to form the insert were synthesized and obtained commercially (Genesis Labs, The Woodlands, TX), and the insert was generated by polymerase chain reaction (PCR). The linked synthetic DNA encoding the mata prepro/PEP-1 fusion protein was then incorporated by ligation into the modified pHIL-D2 plasmid between the *Bst*BI and *Eco*RI sites.

The ligation products were used to transform *Escherichia coli* strain XL1 Blue. A PCR assay was used to screen *E. coli* transformants for the desired plasmid construct. DNA from cell extracts was amplified by PCR using primers containing the 5' AOX1 and 3' AOX1 sequences (see above and FIG. 2). PCR products of the correct number of base pairs were sequenced. In addition, approximately 20-50 bp on either side of the cloning sites were sequenced, and the predicted sequence was obtained. The final DNA sequence of the insert in the pHIL-D2 plasmid (to yield plasmid pPIC-K503) is shown in FIG. 2 along with portions of flanking 5' and 3' AOX1 sequences and corresponding amino acid sequence of the fusion protein comprising the mata prepro signal peptide of *S. cerevisiae* fused to the structural coding sequence for the PEP-1 KI polypeptide. A transformant with the desired expression plasmid construct, plasmid pPIC-K503, was selected for preparing yeast cell lines for routine production of PEP-1.

Example 3: Manufacture of PEP-1 from recombinant yeast cell line.

Spheroplasts of *P. pastoris* GS115 having the *His4*$^-$ phenotype were transformed with the expression plasmid pPIC-K503 (above) following linearization of the plasmid at the *Sac*I site and homologous recombination of the plasmid DNA into the host 5' AOX1 locus. The phenotype of the production strain is *His4*$^+$. The entire plasmid was inserted into the 5' AOX1 genomic sequence of the yeast.

Isolates from the transformation were screened for growth in the absence of exogenous histidine with methanol as the sole carbon source. Greater than 95% of the transformants retained the wild-type ability to grow with methanol as the sole carbon source, thereby demonstrating that the plasmid had been inserted into the host genome by homologous recombination rather than transplacement. These transformants did not require exogenous histidine for growth, thereby demonstrating that the plasmid had integrated into the host genome. Selected colonies were cloned. Small culture expression studies were performed to identify clones secreting the highest levels of active PEP-1 into the culture medium. PEP-1 secretion levels in clarified culture supernatant solutions were quantified for PEP-1 levels by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and evaluated for kallikrein inhibition. A yeast clone was selected for PEP-1 production based on its high level of PEP-1 expression among cultures sampled.

Master and working cell banks of *P. pastoris* producing PEP-1 were prepared commercially (MDS Pharma Services, Bothell, Washington). A standard production of PEP-1 in yeast comprised three steps as follows: (1) preparation of the seed culture, (2) fermentation, and (3) recovery of the culture.

The seed culture step consisted of the inoculation of six flasks (300 mL each) containing sterile inoculum broth (yeast nitrogen base, potassium phosphate, and glycerol, pH = 5) with the contents of a single vial of a working cell bank of *P. pastoris* producing PEP-1. Flasks were inoculated in an orbital shaker (300 rpm) for approximately 13 hours at 30°C ± 2°C.

Fermentations were performed in a closed 100 liter Braun fermenter filled with sterile broth. Each fermentation was initiated with the transfer of the contents of the six seed culture flasks to the fermenter. After approximately 24 hours, the glycerol in the fermenter became exhausted and additional glycerol was added for approximately 8 additional hours.

A mixed feed phase, which lasted approximately 83 hours, was then initiated by the addition of a glycerol and methanol feed. At the end of this time, the fermentation was terminated, and the fermenter contents were diluted with purified water. The purification and processing of PEP-1 consisted of five steps as follows: (1) expanded bed chromatography, (2) cation exchange chromatography, (3) hydrophobic interaction chromatography (HIC), (4) ultrafiltration and diafiltration, and (5) final filtration and packaging.

The initial purification step consisted of expanded bed chromatography. The diluted fermenter culture was applied to the equilibrated column packed with Streamline SP resin (Amersham Pharmacia Streamline 200 chromatography column, Amersham Pharmacia, Piscataway, New Jersey). The column was then washed (50 mM acetic acid, pH = 3.0 - 3.5) in an up-flow mode to flush the yeast cells from the expanded bed. The top adaptor was raised above the expanded bed enhance washing. The flow was stopped and the bed was allowed to settle. The adaptor was moved down so that it was slightly above the settled bed. The direction of the flow was reversed. The effluent was collected. Washing was continued in a downward mode using 50 mM sodium acetate, pH 4.0. The effluent was collected. PEP-1 was eluted from the column using 50 mM sodium acetate, pH 6.0. The eluate was collected in a 50 liter container. The eluate was then filtered through a 0.22 m filter into a clean container located in the purification site. Additional samples were collected for the determination of PEP-1 concentration. A cation exchange chromatography step was then performed using the filtered eluate from the expanded bed column. PEP-1 was eluted from the column using 15 mM trisodium citrate, pH 6.2.

Additional proteins were removed from the PEP-1 preparation by hydrophobic interaction chromatography (HIC). Prior to HIC, the eluate from the cation exchange column was diluted with ammonium sulfate. The eluate was applied to the column, and the PEP-1 was eluted using ammonium sulfate (0.572 M) in potassium phosphate (100 mM), pH 7.0. The eluate was collected in fractions based on A280 values. All fractions were collected into sterile, pre-weighed PETG bottles.

Selected fractions were pooled into a clean container. The pool was concentrated by ultrafiltration. The concentrated PEP-1 preparation was immediately diafiltered against ten volumes of PBS, pH 7.0.

A final filtration step was performed prior to packaging in order to minimize the bioburden in the bulk PEP-1. The bulk solution was filtered through a 0.22 m filter and collected into a sterile, pre-weighed PETG bottle. A sample was removed for lot release testing. The remainder of the bulk was dispensed aseptically into sterile PETG bottles and stored at -20°C.

Example 4: Kallikrein Inhibition Assay.

A kinetic test was used to measure inhibitory activity of KI polypeptides, such as PEP-1. The kinetic assay measures fluorescence following kallikrein-mediated cleavage of a substrate, prolylphenylalanylarginyl amino methyl coumarin. A known amount of kallikrein was incubated with a serially diluted KI polypeptide reference standard or serially diluted KI polypeptide test samples, in a suitable reaction buffer on a microtiter plate. Each sample was run in triplicate. The substrate solution was added, and the plate read immediately using an excitation wavelength of 360 nm and an emission wavelength of 460 nm. At least two each of the reference standard and sample curves were required to have an R-squared value of 0.95 to be considered valid.

Example 5: Organ Preservation

HUVEC at confluence were washed in PBS and further incubated at 4 degrees for 24-48 hours in a serum free medium (SFM). After cold storage, cells were washed several times with PBS, and kallikrein (0.125 U) and the specific kallikrein substrate S2302 were added to the cells. Changes in optical density were recorded. For light microscopy evaluation of cell-bound PEP-1, after cold storage, HUVEC were treated with PEP-1, formalin fixed and treated with rabbit anti-PEP-1 and peroxidase conjugated anti-rabbit IgG. The ability of HUVEC to produce kallikrein was also evaluated on cell surface and in the supernatants of cells maintained at 37°C. Kallikrein activity was 380 ± 19 A.U. in supernatants of HUVEC maintained at 37°C; no activity was measurable on the surface of the same cells. At light microscopy evaluation there was significant binding of PEP-1 to the surface of HUVEC cold treated for 24 hours. The maximum of the binding was obtained by incubating cells in presence of PEP-1 (5 mg/ml). Cell-bound PEP-1 retained the ability to inhibit exogenous kallikrein. These results indicate that PEP-1 binds to endothelial cells, maintaining its kallikrein inhibitory activity. Therefore it can be used to detect and modulate kinin-mediated damage on the vascular surface.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

SEQUENCE LISTING

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Bergamaschini, Luigi

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Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu
20 25 30
Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu
35 40 45
Glu Glu Cys Lys Lys Met Cys Thr Arg Asp
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20 25 30
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35 40 45
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20 25 30
Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu
35 40 45
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Asn His Gln Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu
20 25 30
Phe Ser Tyr Gly Gly Cys Gly Gly Asn Gln Asn Arg Phe Glu Ser Leu
35 40 45
Glu Glu Cys Lys Lys Met Cys Thr Arg Asp
50 55

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Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu
35 40 45
Glu Glu Cys Lys Lys Met Cys Thr Arg Asp
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Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu
35 40 45
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Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser Ala
5 10 15

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Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
20 25 30

cct gct gag gct gtc atc ggt tac tct gac ttg gaa ggt gac ttc gac 200
Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
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gtc gct gtt ttg cca ttc tct aac tct act aac aac ggt ttg ttg ttc 248
Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
50 55 60 65

atc aac act acc atc gct tct atc gct gct aag gag gaa ggt gtt tcc 296
Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
70 75 80

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Leu Glu Lys Arg Glu Ala Met His Ser Phe Cys Ala Phe Lys Ala Asp
            85                  90                  95

gac ggt ccg tgc aga gct gct cac cca aga tgg ttc ttc aac atc ttc   392
Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile Phe
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acg cgt caa tgc gag gag ttc atc tac ggt ggt tgt gag ggt aac caa   440
Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln
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aac aga ttc gag tct cta gag gag tgt aag aag atg tgt act aga gac   488
Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp
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            20                  25                  30
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35 40 45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80
Ser Leu Glu Lys Arg Glu Ala Met His Ser Phe Cys Ala Phe Lys Ala
85 90 95
Asp Asp Gly Pro Cys Arg Ala Ala His Pro Arg Trp Phe Phe Asn Ile
100 105 110
Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn
115 120 125
Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg
130 135 140
Asp
145

CLAIMS:

1. Use of a kallikrein inhibitor for preservation of an organ or tissue, the kallikrein inhibitor comprising a polypeptide of SEQ ID NO:1, wherein

Xaa1, Xaa2, Xaa3, Xaa4, Xaa56, Xaa57 or Xaa58 are each individually an amino acid or absent;

Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid;

Xaa10 is Asp;

Xaa11 is Asp;

Xaa13 is Pro;

Xaa15 is Arg;

Xaa16 is Ala;

Xaa17 is Ala;

Xaa18 is His;

Xaa19 is Pro;

Xaa21 is Trp;

Xaa22 is an amino acid selected from the group consisting of: Tyr and Phe;

Xaa23 is an amino acid selected from the group consisting of: Tyr and Phe;

Xaa31 is Glu;

Xaa32 is Glu;

Xaa34 is Ile;

Xaa35 is Tyr;

Xaa39 is Glu;

Xaa40 is an amino acid selected from the group consisting of: Gly and Ala;

Xaa43 is an amino acid selected from the group consisting of: Asn and Gly;

Xaa45 is an amino acid selected from the group consisting of: Phe and Tyr; and

wherein said polypeptide inhibits kallikrein.

2. The use according to Claim 1, wherein the kallikrein inhibitor is a polypeptide comprising SEQ ID NO:2.

3. The use according to Claim 1, wherein the kallikrein inhibitor is a polypeptide comprising amino acids 3-60 of SEQ ID NO:2.

4. The use of Claim 1, wherein the organ or tissue is heart, lung, kidney, pancreas, liver, intestine, endothelial tissue, vascular tissue or skin.

5. The use of Claim 1, wherein Xaa6 is Ala.

6. The use of Claim 1, wherein Xaa7 is Phe.

7. The use of Claim 1, wherein Xaa8 is Lys.

8. The use of Claim 1, wherein Xaa9 is Ala.

9. The use of Claim 1, wherein Xaa20 is Arg.

10. The use of Claim 1, wherein Xaa24 is Asn.

11. The use of Claim 1, wherein Xaa25 is Ile.

12. The use of Claim 1, wherein Xaa26 is Phe.

13. The use of Claim 1, wherein Xaa27 is Thr.

14. The use of Claim 1, wherein Xaa28 is Arg.

15. The use of Claim 1, wherein Xaa29 is Gln.

16. The use of Claim 1, wherein Xaa41 is Asn.

17. The use of Claim 1, wherein Xaa42 is Arg.

18. The use of Claim 1, wherein Xaa44 is Arg.

19. The use of Claim 1, wherein Xaa46 is Glu.

20. The use of Claim 1, wherein Xaa47 is Ser.

21. The use of Claim 1, wherein Xaa48 is Leu.

22. The use of Claim 1, wherein Xaa49 is Glu.

23. The use of Claim 1, wherein Xaa50 is Glu.

24. The use of Claim 1, wherein the polypeptide comprises two or more amino acids selected from the group consisting of: Phe at Xaa22; Phe at Xaa23; Gly at Xaa40; Asn at Xaa43; and Phe at Xaa45.

25. The use of Claim 1, wherein Xaa3 is Ser.

26. The use of Claim 1, wherein Xaa2 is His.

27. The use of Claim 1, wherein Xaa1 is Met.

28. The use of Claim 1, wherein Xaa56 is Thr.

29. The use of Claim 1, wherein Xaa57 is Arg.

30. The use of Claim 1, wherein Xaa58 is Asp.

31. The use of any one of Claims 1-30, wherein the organ or tissue is heart, lung, kidney, pancreas, liver, intestine, endothelial tissue, vascular tissue or skin.

32. Use of an organ storage and preservative solution for reducing reperfusion injury of an organ during surgery and/or following removal of the organ from a subject, wherein the solution comprises a kallikrein inhibitor,

wherein the kallikrein inhibitor is a polypeptide comprising SEQ ID NO:1, wherein

Xaa1, Xaa2, Xaa3, Xaa4, Xaa56, Xaa57 or Xaa58 are each individually an amino acid or absent;

Xaa6, Xaa7, Xaa8, Xaa9, Xaa20, Xaa24, Xaa25, Xaa26, Xaa27, Xaa28, Xaa29, Xaa41, Xaa42, Xaa44, Xaa46, Xaa47, Xaa48, Xaa49, Xaa50, Xaa52, Xaa53 and Xaa54 can be any amino acid;

Xaa10 is Asp;

Xaa11 is Asp;

Xaa13 is Pro;

Xaa15 is Arg;

Xaa16 is Ala;

Xaa17 is Ala;

Xaa18 is His;

Xaa19 is Pro;

Xaa21 is Trp;

Xaa22 is an amino acid selected from the group consisting of: Tyr and Phe;

Xaa23 is an amino acid selected from the group consisting of: Tyr and Phe;

Xaa31 is Glu;

Xaa32 is Glu;

Xaa34 is Ile;

Xaa35 is Tyr;

Xaa39 is Glu;

Xaa40 is an amino acid selected from the group consisting of: Gly and Ala;

Xaa43 is an amino acid selected from the group consisting of: Asn and Gly;

Xaa45 is an amino acid selected from the group consisting of: Phe and Tyr.

33. The use according to Claim 32, wherein the kallikrein inhibitor is a polypeptide comprising amino acids 3-60 of SEQ ID NO:2.

34. The use according to Claim 32, wherein the kallikrein inhibitor is a polypeptide comprising SEQ ID NO:2.

35. The use of any one of Claims 32-34, wherein the organ or tissue is heart, lung, kidney, pancreas, liver, intestine, endothelial tissue, vascular tissue or skin.

Figure 1

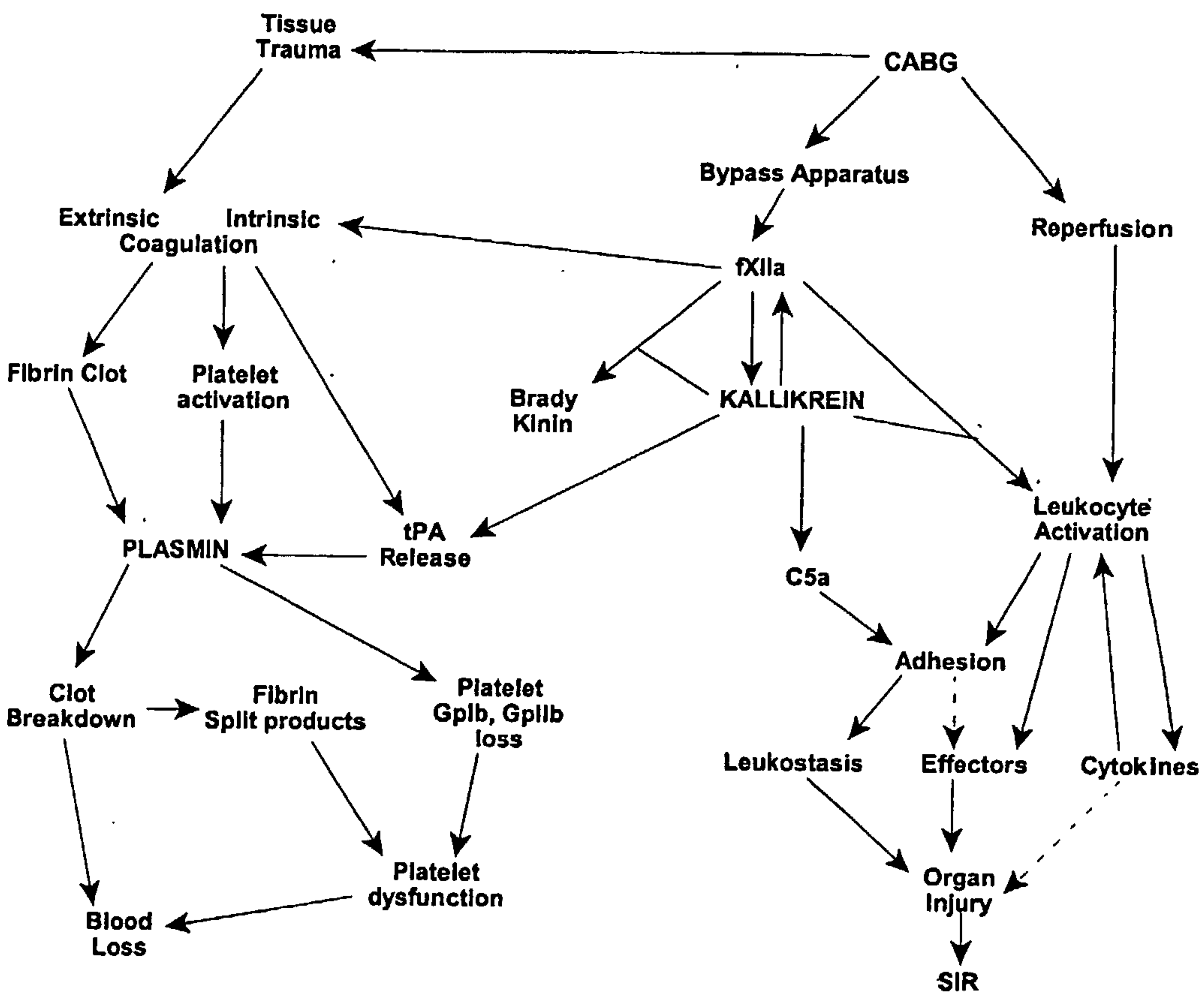
Tissue Trauma
CABG
Bypass Apparatus
Reperfusion
Extrinsic Intrinsic Coagulation
fXIIa
Fibrin Clot
Platelet activation
Brady Kinin
KALLIKREIN
Leukocyte Activation
PLASMIN
tPA Release
C5a
Adhesion
Clot Breakdown
Fibrin Split products
Platelet GpIb, GpIIb loss
Leukostasis
Effectors
Cytokines
Platelet dysfunction
Organ Injury
Blood Loss
SIR

Figure 2

5'AOX1 BstB I

CG ACT TTT AAC GAC AAC TTG AGA AGA TCA AAA AAC AAC TAA TTA TTC GAA

ACG ATG AGA TTC CCA TCT ATC TTC ACT GCT GTT TTG TTC GCT GCT
M R F P S I F T A V L F A A

TCC TCT GCT TTG GCT GCT CCA GTT AAC ACC ACT ACT GAA GAC GAG ACT
S S A L A A P V N T T T E D E T

GCT CAA ATT CCT GCT GAG GCT GTC ATC GGT TAC TCT GAC TTG GAA GGT
A Q I P A E A V I G Y S D L E G

GAC TTC GAC GTC GCT GTT TTG CCA TTC TCT AAC TCT ACT AAC AAC GGT
D F D V A V L P F S N S T N N G

TTG TTG TTC ATC AAC ACT ACC ATC GCT TCT ATC GCT GCT AAG GAG GAA
L L F I N T T I A S I A A K E E

GGT GTT TCC CTC GAG AAG AGA GAG GCT ATG CAC TCT TTC TGT GCT TTC
G V S L E K R E A M H S F C A F

AAG GCT GAC GAC GGT CCG TGC AGA GCT GCT CAC CCA AGA TGG TTC TTC
K A D D G P C R A A H P R W F F

AAC ATC TTC ACG CGT CAA TGC GAG GAG TTC ATC TAC GGT GGT TGT GAG
N I F T R Q C E E F I Y G G C E

GGT AAC CAA AAC AGA TTC GAG TCT CTA GAG GAG TGT AAG AAG ATG TGT
G N Q N R F E S L E E C K K M C

EcoR I

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T R D * *

3'AOX1

AAG TTG GGC ACT TAC GAG AAG

3'AOX1

FIGURE 3

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SEQ ID 5:	----MHSFCAFKA-DDGHCKANHQRFFFNIFTRQCEEFTYGG
SEQ ID 6:	----MHSFCAFKA-DDGHCKANHQRFFFNIFTRQCEQFTYGG
SEQ ID 7:	----MHSFCAFKA-DDGHCKASLPRFFFNIFTRQCEEFIYGG
SEQ ID 8:	----MHSFCAFKA-DDGHCKANHQRFFFNIFTRQCEEFSYGG
SEQ ID 9:	----MHSFCAFKA-DDGHCKGAHLRFFFNIFTRQCEEFIYGG
SEQ ID 10:	----MHSFCAFKA-DDGRCKGAHLRFFFNIFTRQCEEFIYGG
SEQ ID 11:	----MHSFCAFKA-DGGRCRGAHPRWFFNIFTRQCEEFSYGG
SEQ ID 12:	----MHSFCAFKA-DDGPCRAAHPRWFFNIFTRQCEEFSYGG
SEQ ID 13:	----MHSFCAFKA-DVGRCRGAHPRWFFNIFTRQCEEFSYGG
SEQ ID 14:	----MHSFCAFKA-DVGRCRGAQPRFFFNIFTRQCEEFSYGG
SEQ ID 15:	----MHSFCAFKA-DDGSCRAAHLRWFFNIFTRQCEEFSYGG
SEQ ID 16:	----MHSFCAFKA-EGGSCRAAHQRWFFNIFTRQCEEFSYGG
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SEQ ID 18:	----MHSFCAFKA-DDGHCRGALPRWFFNIFTRQCEEFSYGG
SEQ ID 19:	----MHSFCAFKA-DSGNCRGNLPRFFFNIFTRQCEEFSYGG
SEQ ID 20:	----MHSFCAFKA-DSGRCRGNHQRFFFNIFTRQCEEFSYGG
SEQ ID 21:	----MHSFCAFKA-DGGRCRAIQPRWFFNIFTRQCEEFSYGG
SEQ ID 22:	----MHSFCAFKA-DDGRCRGAHPRWFFNIFTRQCEEFSYGG

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SEQ ID 4: (con't.)	CGGNQ--NRFESLEECKKMCTRD
SEQ ID 5: (con't.)	CGGNQ--NRFESLEECKKMCTRD
SEQ ID 6: (con't.)	CAGNQ--NRFESLEECKKMCTRD
SEQ ID 7: (con't.)	CGGNQ--NRFESLEECKKMCTRD
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SEQ ID 15:(con't)	CGGNQ--NRFESLEECKKMCTRD
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