SOLUBILIZED APYRASES, METHODS AND USE

TECHNICAL FIELD

The present invention relates to design and therapeutic use of solubilized apyrase polypeptides, pharmaceuticals compositions, and methods useful for preventing and treating tissue damage.

BACKGROUND OF THE DISCLOSURE

Apyrase (ATP-diphosphatase, adenosine diphosphatase, ADPase, or ATP diphosphohydrolase) is a plasma membrane-bound enzyme group of enzymes active against both di- and triphosphate nucleotides (NDPs and NTPs) and hydrolyze NTPs to nucleotide monophosphates (NMPs) in two distinct successive phosphate-releasing steps, with NDPs as intermediates. Most of the ecto-ATPases that occur on the cell surface and hydrolyze extracellular nucleotides belong to this enzyme family. They differ from ATPases, which specifically hydrolyze ATP, by hydrolyzing both ATP and ADP.

The first known human apyrase, ectonucleoside triphosphate diphosphohydrolase-1 (gene: ENTPD1, protein: NTPDase1), also known as cluster of differentiation 39 (CD39, UniProt P49961, or SEQ ID NO: 1) is a cell surface-located enzymes with an extracellularly facing catalytic site.

Among the known human CD39 family, the member CD39L3 is known as an ecto-apyrase (ecto-ATPDase) with biochemical activity between CD39 and CD39L1 (ecto-ATPase). Specifically human CD39L3 has been solubilized and purified for therapeutic purposes, e.g. as disclosed in US7247300B1 (incorporated herein by reference) or included herein as SEQ ID NO: 3.

SUMMARY OF THE DISCLOSURE

The present disclosure is *inter alia* based on the unexpected finding that certain modifications of solubilized human apyrase, such as human CD39 lead to a surprisingly active protein, which is still safe and easy to manufacture.

According to a first aspect of the invention, a solubilized human apyrase with at least two modifications selected from the list consisting of: N terminal deletion, C terminal deletion and central modification is provided.

In one embodiment the solubilized human apyrase comprises a N terminal deletion, a C terminal deletion and a modification deletion.

In one embodiment, the central modification comprises a deletion of one or more amino acids. In another embodiment, the central modification comprises a point mutation of one or more amino acids, such as a substitution mutation. In yet another embodiment,

the central modification is a combination of a deletion of one or more amino acids and a point mutation, such as a substitution mutation, of one or more amino acids.

The N terminal deletion may be between 30 and 50 amino acids deleted from the N terminus of the wild type CD39 sequence according to SEQ ID NO: 1, such as a deletion of 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 amino acids. In a preferred embodiment, the N terminal deletion is 34, 37, 38 or 45 amino acids.

The C terminal deletion may be between 20 and 40 amino acids deleted from the C terminus of the wild type CD39 sequence according to SEQ ID NO: 1, such as a deletion of 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 amino acids. In a preferred embodiment, the C terminal deletion is 22, 29 of 37 amino acids.

The central deletion may be between 10 and 15 consecutive amino acids, deleted from the wild type CD39 sequence according to SEQ ID NO: 1, such as a deletion of 10, 11, 12, 13, 14 or 15 amino acids. In a preferred embodiment, the central deletion is 12 amino acids, such as amino acids number 193 to 204 in relation to the wild type CD39 sequence according to SEQ ID NO: 1.

In one embodiment, the solubilized human apyrase comprises one, two, three, four, or five point mutation(s) in relation to the wild type CD39 sequence according to SEQ ID NO: 1, selected from the group consisting of K71E, N73Q, V95A, G102D, Y104S, T106S, R113M, L149M, V151A, E173D, T229A, L254M, K258R, W263R, E276D, N292Q, R304G, I319T, N327Q, A362N, F365S, N371Q, K405N, Y412F, L424Q, H436D, I437N, F439S, G441D, N457Q, P463S, and S469R.

In one embodiment the solubilized human apyrase comprises a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 32, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 70, SEQ ID NO: 76, and SEQ ID NO: 78.

In one embodiment, the solubilized human apyrase comprises a sequence selected from the group consisting of SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139 and SEQ ID NO: 141.

In one specific embodiment, the solubilized human apyrase comprises of a sequence selected from the group consisting of SEQ ID NO: 213, SEQ ID NO: 227, SEQ ID NO: 219, SEQ ID NO: 227, SEQ ID NO: 217, SEQ ID NO: 209, SEQ ID NO: 221, SEQ ID NO: 72, SEQ ID NO: 215, SEQ ID NO: 223, SEQ ID NO: 211, SEQ ID NO: 58 and SEQ ID NO: 229.

In one specific embodiment, the solubilized human apyrase consists of a sequence selected from the group consisting of SEQ ID NO: 213, SEQ ID NO: 227, SEQ ID NO: 219, SEQ ID NO: 227, SEQ ID NO: 217, SEQ ID NO: 209, SEQ ID NO: 221,

SEQ ID NO: 72, SEQ ID NO: 215, SEQ ID NO: 223, SEQ ID NO: 211, SEQ ID NO: 58 and SEQ ID NO: 229.

In a preferred embodiment, the solubilized human apyrase comprises a sequence selected from the group consisting of SEQ ID NO: 58, SEQ ID NO: 72 and SEQ ID NO: 229.

In one embodiment, the solubilized human apyrase comprises SEQ ID NO: 58. In one embodiment, the solubilized human apyrase comprises SEQ ID NO: 72. In one embodiment, the solubilized human apyrase comprises SEQ ID NO: 229.

In a preferred embodiment, the solubilized human apyrase consists of a sequence selected from the group consisting of SEQ ID NO: 58, SEQ ID NO: 72 and SEQ ID NO: 229.

In one embodiment, the solubilized human apyrase consists SEQ ID NO: 58. In one embodiment, the solubilized human apyrase consists SEQ ID NO: 72. In one embodiment, the solubilized human apyrase consists SEQ ID NO: 229.

According to a second aspect of the invention, the invention relates to a pharmaceutical composition comprising a therapeutically effective dose of the apyrase according to the first aspect of the invention, and one or more pharmaceutically acceptable carriers is provided.

In one embodiment, the pharmaceutical composition further comprises one or more additional active ingredients.

According to a third aspect of the invention, an isolated apyrase according to the first aspect for use as a medicament is provided.

According to a fourth aspect of the invention, an isolated apyrase according to the first aspect for use in the treatment of tissue damage is provided.

The tissue damage may be acute brain injury (stroke); acute multi-organ failure; delayed graft function after transplantation of kidney or other solid organs; burn damage; radiation damage; acute damage due to trauma and/or hypoxia, such as acute respiratory distress syndrome (ARDS) or lung injury; acute kidney injury, such as acute kidney injury secondary to thoracic surgery (e.g. aortic valve replacement, coronary artery bypass surgery) or sepsis or rhabdomyolysis or toxic effects of antibiotics or other medication; acute myocardial injury.

In another embodiment, the fourth aspect of the disclosure relates to an isolated apyrase according to the first aspect of the invention for use in the treatment of cardiac surgery associated acute kidney injury.

In another embodiment, the fourth aspect of the disclosure relates to an isolated apyrase according to the first aspect of the invention for use in the treatment of delayed graft function (DGF), acute respiratory distress syndrome (ARDS), acute myocardial

infarction (AMI), traumatic brain injury (TBI) / acute ischemic stroke (AIS), ischemia-reperfusion injury (IRI), or combinations thereof often referred to as multi-organ failures (MOF).

In one embodiment, the solubilized human apyrase used for the treatment of cardiac surgery associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 58.

In one embodiment, the solubilized human apyrase used for the treatment of cardiac surgery associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 72. In one embodiment, the solubilized human apyrase used for the treatment of cardiac surgery associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 229.

In an additional preferred embodiment the disclosure relates to the use of an isolated apyrase according to the first aspect of the invention for the treatment of sepsis associated acute kidney injury.

In one embodiment of the fourth aspect, the solubilized human apyrase for use in the treatment of sepsis associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 58.

In one embodiment of the fourth aspect, the solubilized human apyrase for use in the treatment of sepsis associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 72.

In one embodiment of the fourth aspect, the solubilized human apyrase for use in the treatment of sepsis associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 229.

According to a fifth aspect of the invention, a method of treating tissue damage in a human subject is provided, comprising administering a therapeutically effective dose of solubilized human apyrase according to the first aspect to said subject. One embodiment of the fifth aspect of the invention relates to a method of treating cardiac surgery associated acute kidney injury comprising administering a therapeutically effective dose of an isolated apyrase according to the first aspect of the invention to a subject in need of such treatment.

Another embodiment of the fifth aspect of the invention relates to a method of treating delayed graft function (DGF), acute respiratory distress syndrome (ARDS), acute myocardial infarction (AMI), traumatic brain injury (TBI) / acute ischemic stroke (AIS) ischemia-reperfusion injury (IRI), or combinations thereof often referred to as multi-organ failures (MOF) comprising administering a therapeutically effective dose of an isolated apyrase according to the first aspect of the invention to a subject in need of such treatment.

In one embodiment of the fifth aspect, the solubilized human apyrase used in the method of treating cardiac surgery associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 58, SEQ ID NO: 72 or SEQ ID NO: 229.

One embodiment of the fifth aspect of the invention relates to a method of treating sepsis associated acute kidney injury comprising administering a therapeutically effective dose of an isolated apyrase according to the first aspect of the invention to a subject in need of such treatment.

In one embodiment of the fifth aspect, the solubilized human apyrase used in the method of treating sepsis associated acute kidney injury comprises an amino acid sequence of SEQ ID NO: 58, SEQ ID NO: 72 or SEQ ID NO: 229.The tissue damage may be acute brain injury (stroke); acute multi-organ failure; delayed graft function after transplantation of kidney or other solid organs; burn damage; radiation damage; acute damage due to trauma and/or hypoxia, such as acute respiratory distress syndrome (ARDS) or lung injury; acute kidney injury, such as acute kidney injury secondary to thoracic surgery (e.g. aortic valve replacement, coronary artery bypass surgery) or sepsis or rhabdomyolysis or toxic effects of antibiotics or other medication; acute myocardial injury.

According to a sixth aspect of the invention, an isolated nucleic acid molecule encoding any apyrase according to the first aspect is provided.

According to a seventh aspect of the invention, a cloning or expression vector comprising one or more nucleic acid sequences according to the sixth aspect is provided, wherein the vector is suitable for the recombinant production of isolated apyrase according to the first aspect.

According to an eight aspect of the invention, a host cell is provided comprising one or more cloning or expression vectors according the seventh aspect.

According to a ninth aspect of the invention, a process for the production of an apyrase according to the first aspect is provided, comprising culturing a host cell according to the eight aspect, purifying and recovering said apyrase.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a sequence alignment;

Figure 2A is a representation of an expression level of supernatant containing human CD39 by anti-APP Western Blot according to an embodiment;

Figure 2B is a representation of expression level of supernatant containing cysteine bridge deletion human CD39 variants by anti-APP Western Blot according to an embodiment;

Figure 3 is a graph showing solid-phase ATPase assay results of CD39 variants;

Figure 4 is a graph showing solid-phase ATP cleavage on HEK293 cells transformed with human CD39 variants according to an embodiment;

Figure 5 is a schematic overview of a vector according to an embodiment;

Figure 6 is an enzymatic model based on steady state approximation;

Figure 7 is an overview of kinetic data and model fit for a protein according to an embodiment;

Figure 8 is an overview of kinetic data and model fit for a protein according to an embodiment;

Figure 9 is an overview of kinetic data and model fit for a protein according to an embodiment;

Figure 10 is a schematic representation of experimental conditions;

Figure 11 is a graph showing AMP levels for proteins according to embodiments; and

Figure 12 are graphs showing in vivo results for proteins according to embodiments.

DETAILED DESCRIPTION OF THE DISCLOSURE

The present disclosure is *inter alia* based on the unexpected finding that certain modifications of solubilized CD39 lead to a surprisingly active protein, which is safe and easy to manufacture.

As will be shown in the specific examples below, a preferred embodiment is a solubilized human apyrase with at least two modifications selected from the list consisting of: N terminal deletion, C terminal deletion and central deletion, such as a solubilized human apyrase comprising a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 32, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 70, SEQ ID NO: 76, and SEQ ID NO: 78.

The inventors tried several different sequence modification strategies to achieve solubilized human apyrase with both retained activity and ability to be expressed, while still not introducing too many modifications because of the risk of increased immunogenicity and thus increased safety risk. Surprisingly, one sequence modification which was found to both increase efficiency and ability to express human apyrase was a deletion of a central section, the so called delta MIL (ΔMIL) modification, at the same time as not adding too much immunogenicity risk.

To increase the expression of the solubilized human apyrase according to embodiments of the invention, N terminal expression tags were tested. Various N

terminal expression tags are known in the art, but surprisingly not all tags worked. The inventors found that a few tags worked, which could not have been foreseen.

These N terminal tags were SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139 or SEQ ID NO: 141. As is shown herein, particularly preferred tags are SEQ ID NO: 133, SEQ ID NO: 135 or SEQ ID NO: 137.

Specific details are set forth in Examples 9 to 13 below. However, in order to illustrate the unpredictable nature of these Examples, a comparative summary is presented in **Table 1**.

Table 1. Summary of preferred embodiments.

Construct	Modifications		Activity compared to parental EP28		Titer (g/L)
	No of N-terminal aa from SEQ ID NO: 131	Number of point mutations	In vitro	In vivo	
EP1xEP17	6	2	1.5x		0.6
EP17xEP19	6	2	1.5x		0.26
EP1xEP17xEP19	6	3	1.5x		0.46
EP17xEP19	3	2	1.5x		0.40
EP1xEP17xEP19	3	3	1.5x		0.58
EP1	3	1	1x		0.29
EP1xEP14	3	2	4x		0.50
EP28	16	0	1x	1x	0.08
EP1xEP17_K405N	15	3	1.5x	1x	1.4
EP1xEP14	6	2	4x		0.3
EP1xEP17	3	2	1.5x		0.68
EP28	3	0	1x		0.10
EP14	3	1	4x	4x	0.27

1. Definitions

To facilitate for a person skilled in the art to practice the invention, the following terms are used throughout the description.

The terms “CD39” and “hCD39” are used synonymously throughout the disclosure and unless stated otherwise means human cluster of differentiation 39 (CD39) according to UniProt P49961 or SEQ ID NO: 1.

The term “apyrase” refers to human apyrase unless stated otherwise. A “solubilized apyrase” as used herein means that that the apyrase, which as a wild type protein exist bound to a cell membrane, has been modified so that it is no longer bound to the cell membrane but exists in a soluble state i.e. no longer anchored to the cell membrane.

The abbreviation “MIL” refers to membrane interaction loop, which is a central part of the wild type (human) CD39 protein which interacts with the cell membrane, in addition to the N terminal and C terminal parts which are physically anchored through the cell membrane. The term “delta MIL”, or “ΔMIL”, refers to the deletion of the MIL sequence from wild type (human) CD39.

The term “about” in relation to a numerical value x means, for example, +/-10%. When used in front of a numerical range or list of numbers, the term “about” applies to each number in the series, e.g., the phrase “about 1-5” should be interpreted as “about 1 – about 5”, or, e.g., the phrase “about 1, 2, 3, 4” should be interpreted as “about 1, about 2, about 3, about 4, etc.”

The word “substantially” does not exclude “completely,” e.g., a composition which is “substantially free” from Y may be completely free from Y. Where necessary, the word “substantially” may be omitted from the definition of the disclosure.

The term “comprising” encompasses “including” as well as “consisting,” e.g., a composition “comprising” X may consist exclusively of X or may include something additional, e.g., X + Y.

”Identity” with respect to a native polypeptide and its functional derivative is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues of a corresponding native polypeptide, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent identity, and not considering any conservative substitutions as part of the sequence identity. Neither N- or C-terminal extensions nor insertions shall be construed as reducing identity. Methods and computer programs for the alignment are well known. The percent identity can be determined by standard alignment algorithms, for example, the Basic Local Alignment Search Tool (BLAST) described by Altshul et al. ((1990) J. Mol. Biol., 215: 403 410); the algorithm of Needleman et al. ((1970) J. Mol. Biol., 48: 444 453); or the algorithm of Meyers et al. ((1988) Comput. Appl. Biosci., 4: 11 17). A set of parameters may be the Blosum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5. The percent identity between two amino

acid or nucleotide sequences can also be determined using the algorithm of E. Meyers and W. Miller ((1989) CABIOS, 4:11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

"Amino acid(s)" refer to all naturally occurring L-α-amino acids, e.g., and include D-amino acids. The phrase "amino acid sequence variant" refers to molecules with some differences in their amino acid sequences as compared to the sequences according to the present disclosure. Amino acid sequence variants of a protein according to the present disclosure, e.g., of a specified sequence, still have apyrase activity. Amino acid sequence variants include substitutional variants (those that have at least one amino acid residue removed and a different amino acid inserted in its place at the same position in a polypeptide according to the present disclosure), insertional variants (those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in a polypeptide according to the present disclosure) and deletional variants (those with one or more amino acids removed in a polypeptide according to the present disclosure).

The term "treatment" or “treat” is herein defined as the application or administration of apyrase according to the invention to a subject, or application or administration a pharmaceutical composition comprising said apyrase to a subject, or an isolated tissue or cell line from a subject, where the subject has tissue damage, a symptom associated with tissue damage, where the purpose is to alleviate, ameliorate, or improve the tissue damage or any associated symptoms of the tissue damage *inter alia* by reducing levels of extracellular ATP.

By "treatment" is also intended the application or administration of a pharmaceutical composition comprising an apyrase to a subject, or application or administration of a pharmaceutical composition comprising apyrase of the invention to an isolated tissue or cell line from a subject, where the subject has an tissue damage or a symptom associated with tissue damage, where the purpose is to alleviate, ameliorate, or improve the tissue damage or any associated symptoms of the tissue damage.

The term “prevent” or “preventing” refer to prophylactic or preventative treatment; it is concerned about delaying the onset of, or preventing the onset of the disease, disorders and/or symptoms associated thereto.

As used herein, a subject is “in need of” a treatment if such subject would benefit biologically, medically or in quality of life from such treatment.

The term “pharmaceutically acceptable” means a nontoxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s).

As used herein, the term "administration" or "administering" of the subject compound means providing a compound of the invention and prodrugs thereof to a subject in need of treatment. Administration “in combination with” one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order, and in any route of administration.

As used herein, a “therapeutically effective dose” refers to a dose (an amount) of an apyrase that is effective, upon single or multiple dose administration to a patient (such as a human) for treating, preventing, preventing the onset of, curing, delaying, reducing the severity of, ameliorating at least one symptom of a disorder or recurring disorder, or prolonging the survival of the patient beyond that expected in the absence of such treatment. When applied to an individual active ingredient (e.g., apyrase) administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined doses or amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

The phrase “dosage regimen” means the regimen used to treat an illness, e.g., the dosing protocol used during the treatment of tissue damage.

The phrase “means for administering” is used to indicate any available implement for systemically administering a drug to a patient, including, but not limited to, a pre-filled syringe, a vial and syringe, an injection pen, an autoinjector, an intraveneous (i.v.) drip and bag, a pump, a patch pump, etc. With such items, a patient may self-administer the drug (i.e., administer the drug on their own behalf) or a physician may administer the drug.

2. Example 1: Membrane free CD39

Wild type human apyrase CD39 (hCD39, UniProt P49961, or SEQ ID NO: 1) is naturally anchored in the cell membrane by a transmembrane domain at the N-terminus (putative aa 17-37), a central putative membrane interaction loop (MIL putative aa 193-204) and a C-terminal transmembrane domain (putative aa 479-499). To enable expression of a soluble variant of CD39 using a mammalian host cell, several elements of the CD39 sequence have been modified to obtain a membrane free, or solubilized, protein. The natural leader sequence and N-terminal transmembrane region were substituted by a secretion leader and a purification tag (SEQ ID NO: 133). The boundaries of the extracellular domain of CD39 have been varied to optimize expression, purification and activity parameters (amino acids no. 38-476 of SEQ ID NO: 1, amino acids no. 39-469 of SEQ ID NO: 1, amino acids 46-461 of SEQ ID NO: 1, and amino acids 46-476 of SEQ ID NO: 1, respectively). The impact of the cysteines and disulfide bridges on aggregation propensity and enzymatic activity was systematically assessed

by substituting the cysteines by alanine or by shortening the loop made up by the disulfide bridge (SEQ ID 107, 109, 111, 113, and 115). A stretch of hydrophobic amino acid was described in the structural work of the rat-CD39 (Zebisch et al, J.Mol. Biol. (2012), 415, 288-306, wild type rat CD39, Uniprot P97687, set forth in SEQ ID NO: 2) and it is thought that this loop may be interacting with the cell membrane (MIL). We translated the findings to the human CD39 sequence by sequence alignment and generated CD39 variants having a loop deletion (CD39ΔMIL or EP28, as set forth in SEQ ID NO: 4). The impact of the deletion (or delta/Δ) of the MIL on expression level of functional CD39 and thermal stability was assessed.

As can be seen from Figure 1, showing a sequence alignment of SEQ ID NO: 1 and SEQ ID NO: 4, N terminal amino acids 1 to 27, C terminal amino acids 477 to 510, and the central membrane interaction loop (MIL) amino acids 193 to 204, were deleted from wtCD39 (SEQ ID NO: 1) to form CD39ΔMIL (SEQ ID NO: 4).

The impact of the different sequences modifications on thermal stability was studied. In addition, impact of the different sequences modifications on CHO cell expression yields and monomeric content was studied.

(1) Methods

(a) Generation of expression plasmids

DNA sequences coding for different hCD39 boundary variants and membrane interaction loop (MIL) deletion were ordered at GeneArt (Life Technologies Inc. Regensburg, Germany) including codon optimization for Homo sapiens. Sequences coding for hCD39 variants were sub cloned by standard molecular biology techniques from the GeneArt derived vectors or internally generated variants thereof into an expression vector suitable for secretion in mammalian cells. Cysteine to alanine mutations present in the cysteine bridge deleted variants were targeted by modified oligonucleotides and after a subsequent assembly PCR step the generated fragments were sub cloned into the same expression vector mentioned previously. Elements of the expression vector include a promoter (Cytomegalovirus (CMV) enhancer-promoter), a signal sequence to facilitate secretion, a polyadenylation signal and transcription terminator (Bovine Growth Hormone (BGH) gene), an element allowing episomal replication and replication in prokaryotes (e.g. SV40 origin and ColE1 or others known in the art) and elements to allow selection (ampicillin resistance gene and zeocin marker). A list of truncated, solubilized human CD39 versions is illustrated in **Table 2**, with amino acid modifications numbered with reference to SEQ ID NO: 1.

Table 2. Truncated, solubilized human CD39 versions.

Reference	Amino acid sequence ID	Modification(s)
CD39(aa39-469)	SEQ ID NO: 99	N and C terminal truncations
CD39(aa46-476)	SEQ ID NO: 101	N and C terminal truncations
CD39(aa46-461)	SEQ ID NO: 103	N and C terminal truncations
CD39(aa46-461)_dMIL(193-204)	SEQ ID NO: 105	N and C terminal truncations, and central deletion
CD39(aa46-461)_delta cys1	SEQ ID NO: 107	N and C terminal truncations, and cysteine deletion
CD39(aa46-461)_delta cys2	SEQ ID NO: 109	N and C terminal truncations, and cysteine deletion
CD39(aa46-461)_delta cys3	SEQ ID NO: 111	N and C terminal truncations, and cysteine deletion
CD39(aa46-461)_delta cys4	SEQ ID NO: 113	N and C terminal truncations, and cysteine deletion
CD39(aa46-461)_delta cys5	SEQ ID NO: 115	N and C terminal truncations, and cysteine deletion
CD39(aa46-461)_dMIL(193-204)_delta cys1	SEQ ID NO: 117	N and C terminal truncations, central deletion and cysteine deletion
CD39(aa46-461)_dMIL(193-204)_delta cys2	SEQ ID NO: 119	N and C terminal truncations, central deletion and cysteine deletion
CD39(aa46-461)_dMIL(193-204)_delta cys3	SEQ ID NO: 121	N and C terminal truncations, central deletion and cysteine deletion
CD39(aa46-461)_dMIL(193-204)_delta cys4	SEQ ID NO: 123	N and C terminal truncations, central deletion and cysteine deletion
CD39(aa46-461)_dMIL(193-204)_delta cys5	SEQ ID NO: 125	N and C terminal truncations, central deletion and cysteine deletion
CD39(aa38-476)_delta337-344	SEQ ID NO: 127	N and C terminal truncations, and cysteine deletion

CD39(aa38-476)_C338A_C343A	SEQ ID NO: 129	N and C terminal truncations, and cysteine point mutations

(b) Micro-scale expression of hCD39 variants

293-6E cells (as disclosed in WO2006096989A2, incorporated herein by reference) were chosen for micro-scale experiment as one of the preferred host cell lines for transient expression of proteins in absence of serum. Transfection was performed using FuGene HD (Roche Applied Science, Cat. No. 04709705001) as transfection reagent. 293-6E cells were cultivated in suspension culture using V3 serum-free culture medium (Bioconcept, Cat. No. V3-K) for transfection and propagation of the cells. Cells were grown in Corning shake flasks (Corning, Tewksbury, MA) on an orbital shaker (100-120 rpm) in a humidified incubator at 5% CO_2 (seed flasks). Cells in the seed cultures should be maintained in the exponential growth phase (cell densities between $5x10^5$ and $3x10^6$/mL) and display a viability of >90% for transfection. Cell densities outside of this range will result in either a lag phase after dilution or reduced transfection efficiency.

For micro-scale (0.5ml) transfections, an aliquot of cells was taken out of the seed cultures and adjusted to $0.5x10^6$ cells/mL in V3 serum-free culture medium. The DNA solution (called Solution 1) was prepared by diluting 0.5µg of hCD39 expression plasmids in 14µl of V3 serum-free culture medium, then 2.3µl of FuGene HD solution was also diluted in 14µl of V3 serum-free culture medium (Solution 2). Both solutions were incubated for 5-10 min at room temperature (RT). Thereafter solution 2 was added to solution 1 with gentle mixing and incubated for another 5-15 minutes at room temperature. The transfection mix was then added to 0.5ml of cells at $0.5x10^6$ cells/mL seeded in a 48-well tissue culture plate (Corning, Tewksbury, MA) and plate placed on an orbital shaker (300 rpm) in a humidified incubator at 5% CO_2. The culture was harvested 3 days post transfection by centrifugation at 4000 rpm for 10 minutes at 4°C (Heraeus, Multifuge 3 S-R, Thermo Scientific, Rockford, IL). The recovered cell supernatant was stored at 4°C until further processing.

(c) Western-blot analysis on micro-scale expression supernatant

Western-Blot analysis was performed on micro-scale expression supernatant in order to check expression and correct formation of recombinant hCD39 variants. 8µl of supernatant was diluted in E-PAGE™ Loading Buffer (4x, Invitrogen, #EPBNF-01) and loaded on E-Page 48, 8% gel (Invitrogen, #EP04808) in non-reducing conditions. Gel was run on E-base mother device (Invitrogen) for 23 min and proteins were transferred to

Nitrocellulose membrane (Invitrogen IB301001) using the iBlot system (Invitrogen) according to manufacturer's instructions (7min run). After 3 times washing in TBS/0.05 Tween20 (TBST), membrane was incubated for 1h with 5% Milk/TBST in gentle agitation followed by 1hr incubation with 4µg/ml solution of anti-APP mouse antibody (Novartis internally antibody raised against a peptide stretch of amyloid precursor protein (APP) used for protein tagging) diluted in 2% Milk/TBST. After an additional 3 washing steps, membrane was incubated with 1:1000 dilution of Anti-Mouse IgG-Alkaline Phosphatase (Sigma-Aldrich, A5153-1ML) diluted in 2% Milk/TBST and washed again 3 times in TBST followed by a rinsing step in TBS. Signal was developed for 1-5 minutes using SIGMAFAST™ BCIP®/NBT (Sigma-Aldrich, #B5655-25TAB) according to manufacturer's instructions and signal stopped by rinsing the membrane with water.

(d) Solid-phase AxPase assay

ATPase, ADPase and AMPase activities were determined using Pi ColorLock Gold phosphate detection system (Innova Biosciences, cat n. 303-0030) on plate-captured hCD39 variants from micro-scale expression supernatant (Solid-phase Axpase assay). This method was found to be less sensitive compared to solution based assay (Liquid-phase Axpase assay) recommended by manufacturer, but would have the advantage to reduce AxPase activity mediated by host cell enzymes potentially present in the micro-scale expression supernatant. 20µl of anti-APP mouse antibody 10µg/ml solution antibody (Novartis internally antibody raised against a peptide stretch of amyloid precursor protein (APP) used for protein tagging) diluted in PBS was added to each well of a maxisorp 384 well clear plate (Nunc) and incubated over-night at 4°C. After three washing with TBST, wells were blocked for 1h using 100µl of 5% Milk/TBST at room temperature in gentle agitation. After an additional three washing steps, 20µl of serially diluted micro-scale expression supernatant in 2% Milk/TBST was added in triplicate to the wells and incubated for 2hrs at room temperature with gentle agitation. Wells were then washed again four times with 100µl of TBST and twice with 80µl of 50mM Tris-Cl / 5mM $MgCl_2$ pH 7.5. 30µl of 80µM Adenosine Phosphate solutions diluted in 50mM Tris-Cl / 5mM $MgCl_2$ pH 7.5 (ATP: SIGMA A2383, ADP: SIGMA A2754) was added to each triplicate and incubated for 24hrs at 37°C. Signal was developed using 7.5µl of Gold reagent mix prepared according to manufacturer's instructions for 10 minutes and reaction stopped using 3µl of Stabilizer. Absorbance at 620nm read using TECAN Genios Pro instrument.

(2) Results

(a) Effect of Boundaries, Membrane Interaction Loop (MIL) Deletion and Cysteine Bridge Deletion on hCD39 Expression Level

In order to evaluate expression level of different hCD39 variants, corresponding expression plasmids were transfected in duplicate in 0.5ml of 293-6E cells and Western Blot (anti-APP detection Ab) performed on supernatant collected 3 days post transfection. Results are illustrated in Figure 2A and Figure 2B.

Results indicate a higher expression level of hCD39 starting at aa38 compared to aa46. N-terminal boundaries as well as MIL deletion seem to have no major impact on expression level. Higher expression level of hCD39 having the first or fourth cysteine-bridge deleted in the context of hCD39 (aa46-461) was also observed. Higher expression level of first cysteine bridge deletion was confirmed also using hCD39 (aa46-461) ΔMIL backbone.

(b) Effect of Boundaries, Membrane Interaction Loop (MIL) Deletion and Cysteine Bridge Deletion on hCD39 Activity

CD39 enzymatic activity was measured by solid-phase AxPase assay on the above described supernatant samples. Results are illustrated in Figure 3 and Figure 4, as well as **Table 3**.

Table 3. Solid-phase ATP assay on CD39 variants

Sample	Sequence	Average signal			
		Dilution 1/2	Dilution 1/6	Dilution 1/18	Dilution 1/54
Figure 3					
hCD39 (aa46-461)_Delta Cys1	SEQ ID NO: 107	0.12755	0.12905	0.13155	0.13545
hCD39 (aa46-461)_Delta Cys2	SEQ ID NO: 109	0.1287	0.13615	0.12915	0.1375
hCD39 (aa46-461)_Delta Cys3	SEQ ID NO: 111	0.12265	0.1336	0.13485	0.1365
hCD39 (aa46-461)_Delta Cys4	SEQ ID NO: 113	0.14	0.1302	0.13535	0.1322

hCD39 (aa46-461)_Delta Cys5	SEQ ID NO: 115	0.1226	0.13865	0.13375	0.13225
hCD39 (aa46-461)_Delta MIL_Delta Cys1	SEQ ID NO: 117	0.17695	0.16	0.15755	0.1551
hCD39 (aa46-461)_Delta MIL_Delta Cys2	SEQ ID NO: 119	0.1318	0.1419	0.13065	0.1299
hCD39 (aa46-461)_Delta MIL_Delta Cys3	SEQ ID NO: 121	0.13505	0.1376	0.1347	0.13775
hCD39 (aa46-461)_Delta MIL_Delta Cys4	SEQ ID NO: 123	0.21195	0.18745	0.16915	0.14975
hCD39 (aa46-461)_Delta MIL_Delta Cys5	SEQ ID NO: 125	0.1343	0.1486	0.13135	0.10465
hCD39 (aa46-461)	SEQ ID NO: 103	0.30345	0.2433	0.1879	0.1851
hCD39 (aa46-461)_Delta MIL	SEQ ID NO: 105	0.5037	0.3779	0.32345	0.2567
hCD39 (aa38-476)	Sequence not shown	0.30745	0.23855	0.18315	0.17295
hCD39 (aa46-476)	SEQ ID NO: 101	0.34815	0.254	0.1975	0.1817
untransfected		0.1459	0.14155	0.13855	0.13675
Figure 4					
hCD39 (aa38-476)	Sequence not shown	0.45775	0.4007	0.1997	0.14215
hCD39 (aa46-461)_Delta MIL	SEQ ID NO: 105	0.8983	0.9294	0.6561	0.35405
hCD39 (aa46-476)	SEQ ID NO: 101	0.5756	0.4855	0.27525	0.153
hCD39 (aa46-461)	SEQ ID NO: 103	0.562	0.52455	0.28625	0.15175

hCD39 (aa38-476)_Delta MIL (EP28)	SEQ ID NO: 4	1.0224	0.9696	0.6263	0.4354
untransfected		0.1483	0.1494	0.158	0.1502

Deletion of MIL seems to increase the fraction of functionally expressed CD39 recombinant proteins. Different boundaries do not show any major impact on active hCD39 activity. Results indicate strongly reduced or completely abolished ATPase activity of all the cysteine-bridge deleted variants. Similar results were obtained using Solid-Phase ADPase assay. Thus, surprisingly, the sequence modification which both increase efficiency and ability to express CD39 is the delta MIL (ΔMIL) modification.

3. Example 2: Expression tags

In order to improve the expression properties of the candidates, different expression tags were tested.

Different expression tags based on the N-terminal portion of IL-2 (SEQ ID NO: 131) were tested, as set forth in Table 4. Expression tag 1-16 aa, according to SEQ ID NO: 131, was synthesized by Geneart.

Table 4. IL-2 expression tag variant overview

Reference	Amino acid sequence ID	Forward primer sequence ID	Reverse primer sequence ID
Expression tag aa1-16	SEQ ID NO: 131	n/a	n/a
Expression tag aa1-15	SEQ ID NO: 133	SEQ ID NO: 157	SEQ ID NO: 158
Expression tag aa1-6	SEQ ID NO: 135	SEQ ID NO: 159	SEQ ID NO: 158
Expression tag aa1-3	SEQ ID NO: 137	SEQ ID NO: 161	SEQ ID NO: 158
Expression tag aa1-9	SEQ ID NO: 139	SEQ ID NO: 162	SEQ ID NO: 158
Expression tag aa1-12	SEQ ID NO: 141	SEQ ID NO: 163	SEQ ID NO: 158
Expression tag aa4-12	SEQ ID NO: 143	SEQ ID NO: 164	SEQ ID NO: 158

All expression tags were tested in relation to CD39ΔMIL, as set forth in SEQ ID NO: 4. All the constructs included an APP tag and a His tag.

The vector pRS5a, as set forth in Figure 5, was used for the expression. Primer pairs were as set forth in **Table 4**.

Annealing temperature was 64°C in all cases.

PCR solution was prepared by mixing 1 µl Template DNA stock, 25 µl Kapa Hifi Hotstart polymerase (from kappa Biosystems/KK2602). 1.5 µl forward Primer, 1.5 µl reverse primer, and adjusting the final volume to 50 µl with H_2O.

The PCR reaction was run according to schedule in **Table 5**.

Table 5. PCR schedule

	Temperature (C°)	Time (min)	Cycles
Denaturation	94	5	1
Denaturation	94	0.5	35
Annealing	64	1.5	
Polymerization	72	0.5	
Final Polymerization	72	5	

After completion of PCR reaction, DNA extraction was performed using Wizard® SV Gel and PCR Clean-Up Kit, Promega, No. 9282, 1 column, elution in 30µl according to the instructions of the manufacturer.

Inserts and vector were cut with enzyme supplied by New England Biolabs (NEB), NruI-HF (NEB #R3192) and NotI-HF (NEB #R3189), in CutSmart(R) buffer. Reaction time was 3 h at 37°C.

Ligation has been performed over night with dephosphorylated Vector with Rapid DNA Dephosphorylation and Ligation Kit, Fa. Roche, No. 04898117001 according to the valid protocol of the producer.

Next day, single colonies were picked for DNA-Miniprep and sequence analysis with forward Primer P270 (SEQ ID NO: 165) and reverse Primer P271 (SEQ ID NO: 166).

In addition, the a few protein sequences known in the art to increase expression were tested, according to **Table 6**.

Table 6. Prior art tags

Reference	Sequence identifier
Ubiquitin	SEQ ID NO: 167
CKappa	SEQ ID NO: 168
HSA Domain I	SEQ ID NO: 169
HSA Domain II	SEQ ID NO: 170

The resulting combinations tested are set forth in Table 7.

Table 7. Tested constructs

Plasmid Name	Resulting amino acid sequence
pRS5a_IL2 leader -APP6-Flag- hCD39 (aa38-476)_delta MIL (aa193-204)_8M opt	SEQ ID NO: 145
pRS5a_IL2 leader-hsUbiquitin- hCD39 (aa38-476)_delta MIL (aa193-204)_APP_His	SEQ ID NO: 149
pRS5a_IL2 leader-hsCKappa- hCD39 (aa38-476)_delta MIL (aa193-204)_APP_His	SEQ ID NO: 147
pRS5a_IL2 leader-HSA-Dom.I- hCD39 (aa38-476)_delta MIL (aa193-204)_APP_His	SEQ ID NO: 151
pRS5a_IL2 leader-HSA-Dom.II- hCD39 (aa38-476)_delta MIL (aa193-204)_APP_His	SEQ ID NO: 153

None of the prior art tags from **Table 6** gave expression of protein (data not shown). This was unexpected, since prior art teaches that these sequences should increase expression.

4. Example 3: Further mutations

In order to improve the characteristics of soluble CD39, and make it suitable for pharmaceutical development, further modifications were introduced in the CD39ΔMIL, EP28, set forth in SEQ ID NO: 4. The different mutations and mutated variants are seen in **Table 8** and are numbered according to the amino acid positions of the wild type CD39 as set forth in SEQ ID NO: 1.

Table 8. Point mutations

Short name	No. Mutations	Mutation Pos. 1	Mutation Pos. 2	Mutation Pos. 3	Mutation Pos. 4	Mutation Pos. 5	Amino acid sequence ID
EP1	1	113: R->M					SEQ ID NO: 6
EP2	2	113: R->M	149: L->M				SEQ ID NO: 8

EP3	3	113: R->M	304: R->G	469: S->R			SEQ ID NO: 10
EP4	3	95: V->A	113: R->M	469: S->R			SEQ ID NO: 12
EP5	2	149: L->M	441: G->D				SEQ ID NO: 14
EP6	3	104: Y->S	149: L->M	263: W->R			SEQ ID NO: 16
EP7	4	71: K->E	106: T->S	151: V->A	319: I->T		SEQ ID NO: 18
EP8	1	151: V->A					SEQ ID NO: 20
EP9	1	263: W->R					SEQ ID NO: 22
EP10	1	319: I->T					SEQ ID NO: 24
EP11	2	113: R->M	319: I->T				SEQ ID NO: 26
EP12	2	276: E->D	319: I->T				SEQ ID NO: 28
EP13	2	365: F->S	424: L->P				SEQ ID NO: 30
EP14	1	365: F->S					SEQ ID NO: 32
EP15	4	292: N->K	365: F->S	424: L->P	463: P->S		SEQ ID NO: 34
EP17.1	1	412: Y->F					SEQ ID NO: 38
EP17	2	405: K->N	412: Y->F				SEQ ID No. 36
EP18	2	102: G->D	424: L->Q				SEQ ID No. 40
EP19	2	424: L->Q	436: H->D				SEQ ID No. 42
EP20	2	276: E->G	439: F->S				SEQ ID No. 44
EP21	2	113: R->M	469: S->R				SEQ ID No. 46
EP22	2	276: E->G	469: S->G				SEQ ID No. 48
EP23	4		254: L->M	263: W->R	439: F->S	469: S->R	SEQ ID No. 50
EP24	3	113: R->K	424: L->Q	437: I->N			SEQ ID No. 52
EP28_8M	8	173: E->D	258: K->R	362: A->N	365: F->Y	404-411: VKEKYLSE->-	SEQ ID No. 145

						QERWL RD	

Two mutations in active site lead to higher activity (365 and 412).

5. Example 4: Glycosylation site removal

Based on the EP14 variant above, the effect of glycosylation sites was checked by introducing point mutations according to Table 9, numbered according to the amino acid positions of the wild type CD39 as set forth in SEQ ID NO: 1.

Table 9. Glycosylation site mutations

Mutation position	Glycosylation site	Primer
N73Q	NDT	P928/P929
T229A	NQT	P930/P931
N292Q	NVS	P932/P933
N327Q	NTS	P934/P935
N371Q	NLT	P936/P937
N457Q	NLT	P938/P939

(a) Materials and methods

The expression vector pRS5a (Figure 5) was used for the cloning. Primers were used as set forth in Table 10.

Table 10. Primer sequences

Primers	Sequence	Description
P928	SEQ ID NO: 171	Forward primer for removal of Glycosylation site N73Q
P929	SEQ ID NO: 172	Reverse primer for removal of Glycosylation site N73Q
P930	SEQ ID NO: 173	Forward primer for removal of Glycosylation site T229A
P931	SEQ ID NO: 174	Reverse primer for removal of Glycosylation site T229A
P932	SEQ ID NO: 175	Forward primer for removal of Glycosylation site N292Q
P933	SEQ ID NO: 176	Reverse primer for removal of Glycosylation site N292Q

P934	SEQ ID NO: 177	Forward primer for removal of Glycosylation site N327Q
P935	SEQ ID NO: 178	Reverse primer for removal of Glycosylation site N327Q
P936	SEQ ID NO: 179	Forward primer for removal of Glycosylation site N371Q
P937	SEQ ID NO: 180	Reverse primer for removal of Glycosylation site N371Q
P938	SEQ ID NO: 181	Forward primer for removal of Glycosylation site N457Q
P939	SEQ ID NO: 182	Reverse primer for removal of Glycosylation site N457Q

The QuikChange Lightning Site-directed Mutagenesis Kit (Agilent, No. 210519-5) was used for the PCR, according to the manufacturer's instructions.

Next day, single colonies were picked for DNA-Miniprep and sequence analysis was performed with forward Primer P270 (SEQ ID NO: 165) and reverse Primer P271 (SEQ ID NO: 166).

To ensure the correctness of the vector backbone as well (because of mutagenesis), the sequenced insert fragment was cloned into a new vector backbone of pRS5a (Figure 5) using the following method.

The vector was prepared using the vector backbone of SEQ ID NO: 36 with expression tag SEQ ID NO: 135, containing an APP_HIS-Tag, stock conc. 3.3µg/µl.

Vector was digested by mixing 10µg vector-DNA, 0.4 µl HindIII (100U/µl, NEB), 2 µl EcoRI (20U/µl, NEB), 5 µl Cutsmart buffer 10x conc. (NEB), H_2O to final volume of 50µl. Digestion was run for 3h at 37°C.

Dephosphorylation was performed with Alkaline Phosphatase, Calf intestinal (CIP, NEB, No. M0290L), 10U/µl. Directly after digestion, 3µl of CIP was added to digested vector and incubated for 30 min. at 37°C. Digested and dephosphorylated Vector was loaded on preparative 0.8% TAE Agarose gel, correct band size of vector with ~6100bp had been cut out. Cleanup was done with Wizard® SV Gel and PCR Clean-Up Kit, Promega, No. 9282, 1 column, elution in 100ul. OD260nm showed a concentration of 64ng/µl.

Digestion of mutated Insert fragments was done by mixing 42.5µl DNA (~3-5ug for each DNA), 5 µl Cutsmart buffer, 10x conc., NEB no B7204S, 0.4 µl HindIII-HF, 100 U/µl, NEB no. R3104S, 2 µl EcoRI-HF, 20 U/µl, NEB no. R3103L, and adjust volume to 50µl with H_2O. Digestion was carried out for 3h at 37°C in PCR-machine. Digested inserts were loaded on preparative 0.8% TAE Agarose gel, correct band size of vector with ~1400bp had been cut out. Cleanup was done with Wizard® SV Gel and PCR Clean-Up Kit, Promega, No. 9282, 1 column, elution in 30µl. OD260nm showed a concentration of 1-25 ng/µl.

Ligation was done using (vector:insert ratio ~1:10), with Rapid DNA Ligation Kit, No. K1423, Fa. Thermo Scientific. 4 µl 5x Ligation Buffer was mixed with 1 µl Ligase, 2 µl vector fragment, HindIII/EcoRI-digested, stock conc. 64ng/µl, 13 µl insert fragment, HindIII/EcoRI-digested, stock conc. 1-25ng/µl. Ligation was run for 10 minutes at RT.

Transformation was done by incubation of 10µl of ligation with 80 µl chemical competent XL1Blue cells (Novartis, FS/RL) for 30 min on ice. Heat shock for 45 sec at 42°C on Eppendorf incubator, followed by incubation for 2 min on ice. After that, 1ml 2YT media was added, followed by incubation for 1.5h at 37°C on Eppendorf shaker (800rpm). Cells were centrifuged for 3min at 7000rpm and colonies plating on LB/Carb/Gluc. Plates, followed by incubation overnight at 37°C.

Next day, single colonies were picked for DNA-Miniprep and sequence analysis was performed with forward Primer P270 (SEQ ID NO: 165) and reverse Primer P271 (SEQ ID NO: 166).

Correct sequences were transfected into HEK293 cells according to 7 days of expression, 200ml scale.

The following material was used:

Human Embryonic Kidney cells constitutively expressing the SV40 large T antigen (HEK293-T), e.g. ATCC11268

Polyethylenimine "MAX" MW 40.000 (PEI) (Polysciences, Cat. 24765), dissolved in H20 at RT, adjusted with NaOH to pH7.05.

M11V3 serum-free culture medium (Bioconcept, CH, Cat: V3-K)

DNA: prepared with Qiagen DNA Kit, Midiprep-Kit (No. 12943) according to protocol recommended by supplier

All cell culture work for the transient transfections is carried out using suspension adapted HEK293-Tcells growing in serum-free M11V3 medium.

Cells are grown in Corning shake flasks (Corning, USA) on an orbital shaker (115 rpm) in a humidified CO_2-incubator with 5% CO_2 (seed flasks).

Used Cells have been in exponential growth phase (cell density between $5x10^5$ and $3x10^6$/ml) and had a viability of >90%.

Transfection was performed in small scale (here 20/50 or 100ml), using cells that have been counted and corresponding amount of cells has been adjusted to $1.4x10^6$ cells/ml with M11V3-media. 36% cell suspension of the final transfection volume is used.

The DNA solution (solution 1) is prepared by diluting 1mg/L final volume DNA in 7% final volume M11V3 and gentle mixing. To prevent contamination of the cultures because of the not steril filtrated DNA, Penc./Strep has been added to the transfection after the feeding. Then 3mg/L final volume PEI solution is diluted in 7% final volume M11V3 and mixed gently (solution 2). Both solutions are incubated for 5-10 min at room

temperature (RT). Thereafter solution 2 is added to solution 1 with gentle mixing and incubated another 5-15 minutes at RT After the incubation the transfection mix is added to the cells and the culture is cultivated for four hours (115rpm, 37°C, 5% CO2).

Supernatant was harvested after 7 days of expression.

Centrifugation 4500rpm., 15min., 4°C (Heraeus, Multifuge 3 S-R)

Clarification through a sterile filter, 0.22µm (Stericup filter, Thermo Scientific, Cat.567-0020))

Deliver supernatant to purification for further steps. 1ml sample of supernatant are used for IPC on Open Access APP-column

Sample vials were glass crimp vials, 2ml Agilent, catalog number 5182-0543 and caps: crimp 11mm, catalog number 5040-4667.

Protein was purified using immobilized metal affinity chromatography (IMAC) on Aekta Pure or Aekta Avant (GE Healthcare), according to the following protocol, using a 5ml Histrap HP column (GE Life Sciences, Order No. 17-5248-02). The specifications are set forth in Table 11.

Table 11. IMAC protocol

	CV	Flow (ml/min)	Buffer
Equilibration	5	5	IMAC A
Sample load		3	Cell supernatant
Column Wash	10	3	IMAC A
Elution	10	3	Gradient 0-20% IMAC B
	10	3	100% IMAC B
Fractionation			2 ml fractions

The buffers used were composed according to Table 12 and Table 13.

Table 12. IMAC A, equilibration- and wash buffer

Concentration	Chemical
10 mM	Na_2HPO_4
10 mM	NaH_2PO_4
500 mM	NaCl
20 mM	Imidazol (Merck)

Table 13. IMAC B, elution buffer

Concentration	Chemical
10 mM	Na_2HPO_4
10 mM	NaH_2PO_4
500 mM	NaCl
500 mM	Imidazol (Merck)

The resulting protein, according to Table 14, was stored.

Table 14. Constructs

Construct	Mutation positions
C1140	N73A/F365S
C1141	T229A/F365S
C1142	N292Q/F365S
C1143	N334Q/F365S
C1144	F365S/N371Q
C1145	F365S/N457Q
C1058	F365S

(b) Results and interpretation

There was no improvement of mutants concerning yield and monomeric peak of analytical SEC. The parental protein (EP14) with expression tag according to SEQ ID NO: 137 gave best yield and highest monomeric peak in analytical. Lowest yield and as well worst monomeric peak achieved with mutant N371Q.

6. Example 5: Combinations

In order to try and further improve properties, some of the mutations introduced in Example 3 above were combined according to **Table 15**, below. Mutations are numbered according to the amino acid positions of the wild type CD39 as set forth in SEQ ID NO: 1.

Table 15. Combination of constructs

Construct	Mutation 1	Mutation 2	Mutation 3	Without	Primers	SEQ ID

EP14xEP19	365: F->S	424: L->Q		436: H->D	P878/P879	SEQ ID NO: 64
EP17xEP19	424: L->Q	436: H->D	412: Y->F	405: K->N	P880/P881	SEQ ID NO: 70
EP14xEP17	365: F->S	412: Y->F		405: K->N	P880/P881	SEQ ID NO: 60
EP10xEP19_H436D	424: L->Q	436: H->D	319: I->T		P882/P883	SEQ ID NO: 62
EP19 w/o H436D	424: L->Q			436: H->D	P884/P885	Sequence not included

(a) Materials and methods

The primers according to **Table 16** were used.

Table 16. Primers

Primer	Sequence
P878	SEQ ID NO: 183
P879	SEQ ID NO: 184
P880	SEQ ID NO: 185
P881	SEQ ID NO: 186
P882	SEQ ID NO: 187
P883	SEQ ID NO: 188
P884	SEQ ID NO: 189
P885	SEQ ID NO: 190

A PCR reaction was set up using the following pipetting scheme:

5 µl of 10x reaction buffer,

1 µl ds-DNA-template (stock conc. 100 ng/µl),

1.5 µl primer 1,

1.5 µl primer 2,

1 µl dNTP mix

1.5 µl QuickSolution reagent,

35.5 µl H_2O (for final volume of 50 µl), and

1 µl QuickChange Lightning Enzyme.

The PCR cycling parameters according to Table 17 were used.

Table 17. PCR cycling parameters

	No. of cycles	Temp	Time
1	1	96ºC	2 min
2	18	96ºC	20 sec
		60ºC	10 sec
		68ºC	3 min (30 sec/kb)
3	1	68ºC	6 min

Directly after reaction, 2 µl DpnI-Enzyme was added to each reaction, mixed and incubated for 5 min at 37ºC.

Transformation into XL10-gold ultra-competent cells was performed as follows. Cells were thawed on ice. 45 µl/transformation was used, and 2 µl B-ME was added to each vial. Then, 3 µl DpnI-digested PCR product was added, and incubated for 30 min on ice in 15 ml BD tubes. Thereafter, the samples were heat shocked for 40 seconds and incubated on ice for 2 min. Next, 950 µl SOC media was added, followed by incubation for 1.5 h at 37ºC in a shaking incubator. Finally, cells were plated on LB-carb-plates and incubated over night at 37ºC. Next day, single colonies were picked for DNA-miniprep and sequence analysis.

Correct sequences were transfected into HEK293 cells as described in Example 4.

Protein was purified using immobilized metal affinity chromatography (IMAC) according to the following. 95ml Supernatant was used (~4ml of all is kept for analysis (IPC)).

Used Material:

Nickel-NTA Agarose, Qiagen, Cat No./ID: 30230, Poly-Prep Chromatography Columns, empty, BioRad, No. 731-1550, IMAC A Buffer pH7.4 (containing 20mM $NaPO_4$-buffer and 50mM Imidazol). IMAC B Buffer pH7.4 (containing 20mM $NaPO_4$-buffer and 300mM Imidazol). TBS (10x-conc. diluted to 1x conc. With MilliQ-Water). Amicon Ultra-4 Centrifugal Filter Unit with Ultracel-10 membrane, 10K, UFC801096.

Process steps:

1. Columns were prepared with 1ml Nickel-NTA-Agarose of Qiagen (= 0.5ml CV);
2. Equilibration with 10 CV IMAC A;
3. Loading of 15/45 ml SN on column (collect flow through);
4. Washing with 10 CV IMAC A (collect in 15ml Falcon tube);
5. Elution in 6.5 CV of IMAC B;
6. Determination of concentration of eluate;

7. Concentration of 3.5 ml sample to ~400µl with Amicon Ultra-4 Centrifugal Filter Unit 10K;

8. Buffer exchange by adding TBS and centrifugation 5000;

Samples were analyzed using analytical SEC with 40µl of each sample and using protein gel with 12 µl of each sample.

The resulting protein was stored.

(b) Results and interpretation

The results are shown in Table 18.

Table 18. Result overview

Name	Yield (mg/l)	IPC (app, mg/l)	Aggregation (% monomeric peak)
EP14xEP19	6.85	4.5	75.1
EP17xEP19	13.35	11.5	68.9
EP14xEP17	17.27	11.5	69.2
EP10xEP19_H436D	7.42	4.3	74.3
EP19 w/o H436D	8.28	2.5	55.6
EP1xEP17	13.46	13.2	77.4
EP28	7.8	2.8	57.5

Protease sites:

There was no/very low yield when Matriptase was inserted. With Furin site, there was ~40% yield (but for transfection only 50% of DNA has been used as well, as it was a co-transfection with Furin plasmid).

IL2-truncations:

All truncations where aa1-3 are included give a comparable result, aa1-3 only might be slightly lower compared to the others, but this might be a variation from sample to sample. Truncation aa4-12 lead to no protein expression. No difference could be found between EP28 that contains, like all other EP-variants, a TSS linker between IL2-start and the hCD39-protein.

Combinations:

Combinations with EP19 (L424Q) did not lead to a significant improvement of protein expression.

Combination with EP1 (R113M) displayed a lower aggregation in analytical SEC. NEG726 was well expressed, but showed worst aggregation of all tested (~37%). Combination of EP14xEP17 did not lead to any further improvement (F365S + Y412F).

7. Example 6: Cloning of final candidates

A selection of clinical candidates as set forth in Table 19 below, were expressed for further testing.

Table 19. Overview of final candidates.

Construct	Combination of clones	IL2 leader	Main Sequence
1	EP1xEP14xEP19aa1-3	SEQ ID NO: 137	SEQ ID NO: 233
2	EP1xEP17xEP19 aa1-3	SEQ ID NO: 137	SEQ ID NO: 217
3	EP14aa1-3	SEQ ID NO: 137	SEQ ID NO: 229
4	EP17aa1-3	SEQ ID NO: 137	SEQ ID NO: 237
5	EP19aa1-3	SEQ ID NO: 137	SEQ ID NO: 243
6	EP28aa1-3 (lead/parental)	SEQ ID NO: 137	SEQ ID NO: 58
7	EP1xEP14xEP19 aa1-6	SEQ ID NO: 135	SEQ ID NO: 235
8	EP1xEP17xEP19 aa1-6	SEQ ID NO: 135	SEQ ID NO: 219
9	EP14aa1-6	SEQ ID NO: 135	SEQ ID NO: 231
10	EP17aa1-6	SEQ ID NO: 135	SEQ ID NO: 239
11	EP19aa1-6	SEQ ID NO: 135	SEQ ID NO: 245
12	EP28aa1-6 (lead/parental)	SEQ ID NO: 135	SEQ ID NO: 80

The following primers were used:

Table 20. Primers

Primer	Sequence
R113Mtempl	SEQ ID NO: 191
R113MFW	SEQ ID NO: 192
R113MRev	SEQ ID NO: 193

F330Stempl	SEQ ID NO: 194
F330SFW	SEQ ID NO: 195
F330SRev	SEQ ID NO: 196
Y377Ftempl	SEQ ID NO: 197
L389Ctempl	SEQ ID NO: 198
Y377F/L389Qtempl	SEQ ID NO: 199
FW	SEQ ID NO: 200
Rev	SEQ ID NO: 201
WT	SEQ ID NO: 202

A PCR reaction was set up using the following pipetting scheme:

0.25 µl DMSO,

20 ng vector

1.5 µl insert (45 ng/ µl),

2 µl 5 x HF buffer,

0.1 µl Phusion pol,

0.08 µl dNTP mix

10-X µl ddH_2O

The PCR cycling parameters according to Table 17 were used.

Table 21. PCR cycling parameters

	No. of cycles	Temp	Time
1	1	98ºC	3 min
2	25	98ºC	30 sec
		60ºC	30 sec
		72ºC	5 min 46 sec
3	1	72ºC	10 min

Directly after reaction, 0.5 µl DpnI-Enzyme was added to each reaction, mixed and incubated for 2 h at 37ºC.

Transformation into XL10-gold ultra-competent cells was performed as follows. Cells were thawed on ice. 45 µl/transformation was used, and 2 µl B-ME was added to each vial. Then, 3 µl DpnI-digested PCR product was added, and incubated for 30 min on ice in 15 ml BD tubes. Thereafter, the samples were heat shocked for 40 seconds and incubated on ice for 2 min. Next, 950 µl SOC media was added, followed by incubation

for 1.5 h at 37ºC in a shaking incubator. Finally, cells were plated on LB-carb-plates and incubated over night at 37ºC. Next day, single colonies were picked for DNA-miniprep and sequence analysis.

All constructs were subcloned into new vector background to ensure that sequences were correct. For this, all constructs were amplified with PCR, with G4S-linkers inserted, followed by digestion with HindIII/EcoRI.

The resulting protein was stored.

8. Example 7: Generation of comparator proteins

(1) Null mutations

In order to generate negative control proteins for *in vivo* studies, one / two mutations were inserted into the parental human CD39ΔMIL protein (EP28). This mutations have been described in the literature to remove or lower the Enzyme activity of this protein. Mutation positions are E174A and S218A.

The following primers were used:

Table 22. Primers

Primer	Sequence
P910	SEQ ID NO: 203
P911	SEQ ID NO: 204
P914	SEQ ID NO: 205
P915	SEQ ID NO: 206

A PCR reaction was set up using the following pipetting scheme:

5 µl of 10x reaction buffer,

1 µl ds-DNA-template (stock conc. 100 ng/µl),

1.5 µl primer 1,

1.5 µl primer 2,

1 µl dNTP mix

1.5 µl QuickSolution reagent,

35.5 µl H_2O (for final volume of 50 µl), and

1 µl QuickChange Lightning Enzyme.

The PCR cycling parameters according to Table 17 were used.

Table 23. PCR cycling parameters

	No. of cycles	Temp	Time
1	1	96ºC	2 min

2	18	96ºC	20 sec
		60ºC	10 sec
		68ºC	3 min (30 sec/kb)
3	1	68ºC	6 min

Directly after reaction, 2 µl DpnI-Enzyme was added to each reaction, mixed and incubated for 5 min at 37ºC.

Transformation into XL10-gold ultra-competent cells was performed as follows. Cells were thawed on ice. 45 µl/transformation was used, and 2 µl B-ME was added to each vial. Then, 3 µl DpnI-digested PCR product was added, and incubated for 30 min on ice in 15 ml BD tubes. Thereafter, the samples were heat shocked for 40 seconds and incubated on ice for 2 min. Next, 950 µl SOC media was added, followed by incubation for 1.5 h at 37ºC in a shaking incubator. Finally, cells were plated on LB-carb-plates and incubated over night at 37ºC. Next day, single colonies were picked for DNA-miniprep and sequence analysis.

Correct sequences were transfected into HEK293 cells according to the following protocol.

A digestion buffer was prepared, using 10 µg vector-DNA, 0.4 µl HindIII (100 U/µl, NEB), 2 µl EcoRI (20 U/µl, NEB), 5 µl Cutsmart buffer 10x conc. (NEB), and H_2O to a final volume of 50 µl. The digestion reaction was run for 3 h at 37ºC.

Immediately after digestion, a dephosphorylating reaction was run. Calf intestinal alkaline phosphatase (10U/µl, CIP, NEB, No. M0290L) was added (3µl) to the digested vector mix and incubated for 30 min at 37ºC.

The digested and dephosphorylated vector was sub cloned to check the sequence.

Correct sequences were transfected into HEK293 cells according to the following protocol.

7 days of expression was performed using the following material; 1. Human Embryonic Kidney cells constitutively expressing the SV40 large T antigen (HEK293-T, ATCC11268); 2. Polyethylenimine "MAX" MW 40.000 (PEI) (Polysciences, Cat. 24765).

The PEI solution is prepared by carefully dissolving 1g PEI in 900ml cell culture grade water at room temperature (RT). Then it is neutralized with NaOH for a final pH of 7.05. Finally the volume is adjusted to 1L and the solution filtered through a 0.22µm filter, distributed in aliquots and frozen at -80°C until further use. Once thawed, an aliquot can be re-frozen up to 3 times at -20°C but should not be stored long term at -20°C.

M11V3 serum-free culture medium (Bioconcept, CH, Cat: V3-K).

All cell culture work for the transient transfections is carried out using suspension adapted HEK293-Tcells growing in serum-free M11V3 medium.

For small scale (<5L) transfections cells are grown in Corning shake flasks (Corning, USA) on an orbital shaker (100 rpm) in a humidified CO_2-incubator with 5% CO_2 (seed flasks).

In general, cells in the seed cultures should be in the exponential growth phase (cell density between $5x10^5$ and $3x10^6$/ml) and have a viability of >90%. Cell densities outside of this range will result in either a lag phase after splitting or reduced transfection efficacy.

For small scale (here 2L) transfection an aliquot of cells is taken out of the seed cultures and adjusted to $1.4x10^6$ cells/ml in 36 % of the final volume with M11V3 medium.

The DNA solution (solution 1) is prepared by diluting 1mg/L final volume DNA in 7% final volume M11V3 and gentle mixing. To prevent contamination of the cultures, this solution might be filtered using a 0.22µm filter (e.g. Millipore Stericup). Here because of the small volume no sterile filtration has been done. Then 3mg/L final volume PEI solution is diluted in 7% final volume M11V3 and mixed gently (solution 2). Both solutions are incubated for 5-10 min at room temperature (RT). Thereafter solution 2 is added to solution 1 with gentle mixing and incubated another 5-15 minutes at RT (do not mix again during incubation time, as PEI covers/condenses DNA into positively charged particles, which bind to anionic cell surface residues and are brought into the cell via endocytosis). After the incubation the transfection mix is added to the cells and the culture is cultivated for four hours (10rpm, 37°C, 6% CO_2).

Finally the culture is fed with the remaining 50% final volume M11V3 medium according to the following example: Inoculation volume: 36 ml with $1.4x10^6$ cells /ml.

Solution 1: 7 ml M11V3 medium with 100 µg plasmid DNA. Solution 2: 7 ml M11V3 medium with 300 µg PEI (300 µl)

Feed: 50 ml M11V3, Total 100 ml.

Protein was purified using immobilized metal affinity chromatography (IMAC) according to the following. 95ml Supernatant was used (~4ml of all is kept for analysis (IPC)).

Used Material:

Nickel-NTA Agarose, Qiagen, Cat No./ID: 30230, Poly-Prep Chromatography Columns, empty, BioRad, No. 731-1550, IMAC A Buffer pH7.4 (containing 20mM $NaPO_4$-buffer and 50mM Imidazol). IMAC B Buffer pH7.4 (containing 20mM $NaPO_4$-buffer and 300mM Imidazol). TBS (10x-conc. diluted to 1x conc. With MilliQ-Water). Amicon Ultra-4 Centrifugal Filter Unit with Ultracel-10 membrane, 10K, UFC801096.

Process steps:

1. Columns were prepared with 1ml Nickel-NTA-Agarose of Qiagen (= 0.5ml CV);
2. Equilibration with 10 CV IMAC A;
3. Loading of 15/45 ml SN on column (collect flow through);
4. Washing with 10 CV IMAC A (collect in 15ml Falcon tube);
5. Elution in 6.5 CV of IMAC B;
6. Determination of concentration of eluate;
7. Concentration of 3.5 ml sample to ~400µl with Amicon Ultra-4 Centrifugal Filter Unit 10K;
8. Buffer exchange by adding TBS and centrifugation 5000;

Samples were analyzed using analytical SEC with 40µl of each sample and using protein gel with 12 µl of each sample.

The resulting protein was stored.

(2) plusMIL

Cloning of EP14aa1-3 with Membrane Interaction Loop (aa193-204) with Overlap extension PCR was performed.

The following primers were used:

Table 24. Primers

Primer	Sequence
FW	SEQ ID NO: 207
REV	SEQ ID NO: 208
Rev-sense	SEQ ID NO: 98

A PCR reaction was set up using the following pipetting scheme:

1.2 µl Phusion Hot Start Polymerase,

24 µl 5x HF-buffer,

0.96 µl 100mM dNTPs (25mM of each dNTP),

0.6 µl Fw primer,

0.6 µl Rev primer,

92.64 µl DEPC H_2O.

The PCR cycling parameters according to Table 17 were used.

Table 25. PCR cycling parameters

	No. of cycles	Temp	Time
1	1	98ºC	30 sec
2	30	98ºC	10 sec

		50-70ºC gradient	30 sec
		72ºC	30 sec
3	1	72ºC	10 min

Directly after reaction, 2 µl DpnI-Enzyme was added to each reaction, mixed and incubated for 2 h at 37ºC.

Transformation was performed by transferring 2 µl PCR product to a 96-well PCR plate and cool down on ice. 20 µl STELLAR chemical component bacteria was added and carefully mixed by pipetting once up-and-down. The samples were incubated 30 min on ice, and then 45 sec at 42ºC in a PCR machine, followed by another 60 sec incubation on ice. Finally, 90 µl SOC medium was added and incubated 1 hr at 37ºC. The whole transfection mix was plated on LB-Ampicilin or LB-Carbencilin plates and grown over night at 37ºC.

The resulting protein EP14_plusMIL, with an amino acid sequence according to SEQ ID NO: 155, was stored.

9. Example 8: Enzymatic activity

The candidates generated in previous examples, were characterized using an enzymatic activity assay.

The following reagents were used: Pi free buffer, a phosphate-free physiological saline solution (140mM NaCl, 5mM KCl, 1mM MgCl2, 2mM CaCl2, 10mM Hepes, pH7.4); and Pi free buffer + 2% BSA, a phosphate-free physiological saline solution with 20 mg/ml BSA; CD39 protein (according to SEQ ID NO: 1); ATP.

Duplicate CD39 solution was prepared at 2 µg/ml. Duplicate ATP solution was prepared at 1000 µM from a 15 µl ATP stock + 1185 µl buffer, total 1.2 ml.

The enzymatic reaction was studied by mixing the 60 µl ATP with 60 µl CD39 or 60 µl with Pi free buffer for the controls, in 48 well PCR plates filled with 120 µl final/well. The final concentration was 500 µM ATP and 1 µg/ml CD39.

Samples were incubated at 37°C for 0, 5, 15, 30, 60, 90, and 150 minutes, respectively. Then, samples were evaluated either by Pi release assay or HPLC.

(1) Pi release assay

(a) Materials and methods

Reagents were prepared from a standard Pi detection kit according the manufacturers instructions.

A standard curve with Pi was prepared by dilution in water. A 1:2 serial dilution of the Pi stock (100 µM) was prepared: 450 µl + 450 µl water. The standard curve concentration was: 50 µM / 25 µM / 12.5 µM / 6.25 µM / 3.1 µM / 1.5 µM / 0 µM.

Gold reagent mix was prepared: 4 ml gold reagent + 40 µl accelerator (for 3 plates). In a 96 well plate, the samples were diluted 1:10 in H_2O (Dilution in water: 10 µl sample + 90 µl H2O). 50 µl, 1:10 diluted sample was distributed in each well of a 96 half-area well plate (Corning, 3690). 12.5 µl Gold reagent mix was added to each well (25% sample volume) and the samples were incubated 10min at room temperature. Absorbance was read at 635 nm.

(b) Results and interpretation

Comparative results for candidates are shown in Table 26.

Table 26. Comparative results for candidates.

	Construct	IL-2 start	SEQ ID	Yield after ALC	Monomeric % after ALC	Melting Temp (ºC)	In vitro enzyme activity (relative to EP28)
1	EP14aa1-3	SEQ ID NO: 137	SEQ ID NO: 229	33.1	83.8	62	4
2	EP1xEP14aa1-3	SEQ ID NO: 137	SEQ ID NO: 221	3.7	50.6	65.5	4
3	EP1xEP17aa1-3	SEQ ID NO: 137	SEQ ID NO: 211	95.8	91.9	61	1.5
4	EP17xEP19 aa1-3	SEQ ID NO: 137	SEQ ID NO: 227	3.5	38.9	60.5	1.5
5	EP1xEP17xEP19aa1-3	SEQ ID NO: 137	SEQ ID NO: 217	153.2	89.7	60.75	1.5
6	EP1 aa1-3	SEQ ID NO: 137	SEQ ID NO: 209	6.0	9.2	59.75	1
7	EP1xEP14 aa1-6	SEQ ID NO: 135	SEQ ID NO: 223	148.8	91.8	64	4

8	EP1xEP17 aa1-6	SEQ ID NO: 135	SEQ ID NO: 213	59.4	86.1	59.5	1.5
9	EP17xEP19 aa1-6	SEQ ID NO: 135	SEQ ID NO: 227	2.7	13.7	60	1.5
10	EP1xEP17xEP19 aa1-6	SEQ ID NO: 135	SEQ ID NO: 219	30.9	88.4	60.75	1.5
11	EP1xEP17_K405N aa1-15	SEQ ID NO: 133	SEQ ID NO: 215	156.3	86.4	62.25	1.5
12	EP28aa1-3	SEQ ID NO: 137	SEQ ID NO: 58	2.7	10	60.5	1
13	EP28aa1-16	SEQ ID NO: 131	SEQ ID NO: 72	4.7	45	61.8	1

Enzymatic activity was measured by adding 500µM ATP to the enzyme and analyzing the concentration of ATP, ADP, AMP with HPLC (method description below) over time. The resulting kinetic curves where fitted with the model in Figure 6 to obtain the enzymatic constants. In terms of the enzymatic constant Kcat the enzymes show the following order (low activity to high activity): EP28 (wt), EP17, EP14, EP15.

Figure 7 shows kinetic data and model fit for EP28. Figure 8 shows kinetic data and model fit for EP14. Figure 9 shows kinetic data and model fit for EP15.

An overview of enzyme constants for EP28 (wt), EP14, EP15 and EP17 is shown in **Table 27**. Compared to the wild type (WT) the three novel variants show increased catalytic activity. Importantly, the new variants show a clear increase in the catalytic rate constant (kcat) catalytic efficiency (kcat/Km). As the reported ATP and ADP substrate concentration during tissue damage and thrombosis are above the reported Km, this increase in kcat and kcat/Km will likely translate in higher activity in vivo.

Table 27. Enzyme constants

	ATP -> ADP + P			**ADP -> AMP + P**			**inhibition**
	k^T_{cat}	K^T_M	k^T_{cat}/K^T_M	k^D_{cat}	K^D_M	k^D_{cat}/K^D_M	K^M_d
WT	65.3	0.7	89.7	40.0	0.1	400.3	0.2
EP14	380.2	1.1	352.6	90.3	Fixed to 0.1	903.0	556.8

EP15	734.9	1.1	658.1	128.7	0.1	1287.1	584.9
EP17	180.7	1.0	178.1	67.0	0.1	670.0	3.0

(2) HPLC validation assay (kinetic and dose response)

(a) Materials and methods

The candidates were tested with HPLC validation assay. 70 µl of each sample was transferred into glass vials for HPLC.

Calibration samples were prepared with Stock-Solutions 5 mM as shown in **Table 28**.

Table 28. Stock solutions

	5 mM	weight	H_2O
Adenosine	1336.2 µg/mL	1.862 mg	1394 µL
Inosine	1341.2 µg/mL	2.668 mg	1989 µL
AMP	1736.1 µg/mL	2.182 mg	1257 µL
ADP	2506.6 µg/mL	2.500 mg	997 µL
ATP	2755.7 µg/mL	4.834 mg	1754 µL

1000 µM	20 µL of each stock-solutions were mixed in a HPLC vial
500 µM	20 µL 1 mM + 20 µL H_2O
100 µM	10 µL 1 mM + 90 µL H_2O
10 µM	10 µL 100 µM + 90 µL H_2O
1 µM	10 µL 10 µM + 90 µL H_2O

HPLC Separation was done using an Agilent 1100 System with a CapPump (G1376A), Degasser (G1379A), ALS (G1329A), Thermostat (G1330B, ColComp (G1316A) and a DAD (G1315A). Solvent A: 10 mM KH_2PO_4 (04243, Riedel-de Haën) + 2 mM TBA bromide, pH7.0 (86857-10G-F, Fluka) and Solvent B: 10 mM KH2PO4 / ACN 1/1 + 2 mM TBA bromide, pH5.5. Column: Nucleodur 300-5 C18 ec, 2 x 150 mm, 5 µm, Macherey-Nagel 760185.20 Batch E14100258 36654055. The column temperature was 40°C, injection volume 10 µL, flow rate was 0.3 ml/min and the gradient was 0-3': 0% B; 3-23': 0-95% B, linear; 23-28': 95% B, linear; 28-29': 95-0% B, linear; 5' Post Time". DAD: 247 nm and 259 nm.

UPLC Separation was done using a Waters UPLC I class. Solvent A: 10 mM KH_2PO_4 / 10 mM K_2HPO_4 1/1 + 2 mM TBA bromide, pH 7.0. Solvent B: 10 mM KH_2PO_4 / ACN 1/1 + 2 mM TBA bromide, pH 5.5. Column: Fortis Bio C18, 2.1 x 50 mm, 5 µm,

di2chrom BIO318-020301 SN H03161210-2. Column temperature was 40°C, injection volume was 10 µL, flow rate was 0.5 ml/min and gradient was 0-1': 0% B; 1-8': 0-55% B, linear; 8-10': 55% B; 10-11': 55-0% B, linear; 14' Stop Time. DAD was 247 nm and 259 nm.

(b) Results

The results can be seen in Figures 7, 8, 9 and 11, showing kinetic data and model fit for candidates according to different embodiments.

Example 9: *In vitro* activity, initial screen

The CD39 versions EP1 to EP24, described in previous examples, were cloned in mammalian expression vector pRS5a_Leader_APP_His (Figure 5), without IL2-leader and without IL2-start.

(a) Materials and methods

A small scale expression (20/50ml scale) of EP-Hits in HEK293 (PEI-Transfection) for 7 days was performed, followed by IPC on APP-HPLC (as described supra).

Protein purification of 15/45ml cell supernatant with Ni-NTA-columns (0.5ml CV);
Elution with 6 CV IMAC B buffer (20mM NaPO4-buffer, 300mM Imidazol, pH7.4);
Concentration and rebuffering of purified protein in TBS, pH7.4;
Analysis of protein with protein gel, analytical SEC;
Delivery of all variants and three controls (parental hCD39-dMIL, or EP28, with and without IL2-start, and 8M-version without IL2-start): 90-200ul of purified protein in TBS, pH7.4

(b) Results and interpretation

The results are summarized in **Table 29** below.

All samples are in TBS pH7.4 and have an APP- (SEQ ID N: 247) and a His-Tag (SEQ ID NO: 249)

Only parental human CD39ΔMIL (EP28) has a 15 amino acid long IL2-start, aa1-15 (SEQ ID NO: 133).

Pi release assay BOENKTH1-0252824, double det. For 60 and 180 min. values

Table 29. In vitro activity

					Pi release assay, 0.25ug/ml + 500uM ATP		
Date of purification	Name	conc. [mg/ml]	conc. [umolar]	total vol. [ml]	0 min.	mean 60 min.	mean 180 min
17.06.2016	EP1	0.19	3.7	0.11	10.35	20.90	45.99
14.06.2016	EP2	0.15	2.8	0.10	11.35	23.65	53.92
14.06.2016	EP3	0.11	2.2	0.10	8.92	19.22	40.76
14.06.2016	EP4	0.25	4.8	0.10	7.99	18.59	37.47
14.06.2016	EP5	0.11	2.1	0.10	17.36	39.59	72.09
17.06.2016	EP6	0.14	2.7	0.15	11.57	32.73	69.63
21.06.2016	EP7	0.41	7.8	0.11	9.47	21.19	43.68
21.06.2016	EP8	0.31	5.9	0.11	7.92	15.23	33.94
14.06.2016	EP9	0.15	2.9	0.10	5.56	13.39	31.38
21.06.2016	EP10	0.33	6.3	0.11	9.32	21.91	54.07
14.06.2016	EP11	0.23	4.4	0.10	10.24	21.27	46.21
21.06.2016	EP12	0.37	7.1	0.11	10.55	21.99	50.80
21.06.2016	EP13	0.13	2.5	0.11	4.93	3.13	3.54
21.06.2016	EP14	0.34	6.5	0.11	19.07	66.35	104.80
14.06.2016	EP15	0.19	3.7	0.10	11.11	29.26	89.92
14.06.2016	EP17	0.28	5.3	0.10	12.49	30.30	102.81
14.06.2016	EP18	0.15	2.9	0.10	3.91	9.70	23.49
17.06.2016	EP19	0.55	10.6	0.12	14.36	26.38	69.93
14.06.2016	EP20	0.14	2.7	0.10	3.36	2.22	3.60
14.06.2016	EP21	0.22	4.2	0.10	7.17	16.37	24.27
17.06.2016	EP22	0.17	3.3	0.11	8.06	15.33	37.30
21.06.2016	EP23.1	0.28	5.4	0.11	12.62	23.58	62.78
17.06.2016	EP24	0.10	2.0	0.19	3.10	3.45	4.83
14.06.2016	EP25 hCD39-dMIL parental	0.23	4.4	0.10	4.98	11.46	24.30
17.06.2016	EP26 hCD39-8M	0.19	3.7	0.15	3.66	8.41	24.15
17.06.2016	EP28-IL2start-hCD39 par	2.19	42.0	0.14	10.25	23.48	52.73
21.06.2016	EP1repet.	0.49	9.5	0.11	10.03	17.84	40.33
17.06.2016	EP2 repet.	0.55	10.6	0.12	12.80	28.22	66.88
17.06.2016	EP3 repet.	0.56	10.8	0.12	18.05	33.35	79.53
17.06.2016	EP4 repet.	0.61	11.7	0.16	15.98	29.47	68.39
17.06.2016	EP5 repet.	0.66	12.6	0.15	25.53	46.10	91.32
21.06.2016	EP23.4	0.29	5.5	0.11	10.43	22.45	56.53

11. Example 10: *In vitro* activity, refined screen

A subset of 12 mutants were tested a second time, but with IL-2 start allowing a larger expression scale.

(a) Materials and methods

The mammalian expression vector pRS5a_Leader_APP_His, with a 15 amino acid long IL2-start, aa1-15 (SEQ ID NO: 133) (Figure 5). Small scale expression (50/100ml scale) of EP-Hits in HEK293 (PEI-Transfection) for 7 days followed by IPC on APP-HPLC (as described supra).

Protein purification of 45/95ml cell supernatant with Ni-NTA-columns (0.5ml CV)

Elution with 6 CV IMAC B buffer (20mM NaPO4-buffer, 300mM Imidazol, pH7.4)

Concentration and rebuffering of purified protein in TBS, pH7.4,

Analysis of protein with protein gel, analytical SEC

Delivery of all variants and control (parental hCD39-dMIL, or EP28, with IL2-start aa1-15 (SEQ ID NO: 133)):

500ul of purified protein in TBS, pH7.4

(b) Results and interpretation

The results are summarized in Table 30, Table 32 and Table 33 below.

Table 30. Protein purifications of EP-Hits 06.07.2016, part 1

Name	conc. [mg/ml]	conc. [umolar]	total vol. [ml]	yield/46 or 16ml [mg]	Yield (mg/l)	IPC (APP, mg/l)
EP2	0.64	12.3	0.5	0.32	7.13	6.9
EP3	0.72	13.9	0.5	0.36	8.02	8.6
EP4	0.86	16.4	0.5	0.43	9.49	8.6
EP5	0.89	17.0	0.5	0.44	9.84	10.1
EP6	0.40	7.7	0.5	0.20	4.46	4.3
EP9	0.57	11.0	0.5	0.29	6.35	6.0
EP11	0.74	14.2	0.5	0.37	8.18	8.3
EP12	0.85	16.3	0.5	0.42	9.40	8.2
EP14	0.82	15.7	0.5	0.41	9.09	7.8
EP17	0.94	18.0	0.5	0.47	13.04	13.3
EP18	0.70	13.4	0.5	0.35	7.75	6.4
EP24	0.65	12.4	0.5	0.32	8.99	10.8

EP28 with IL2-start	0.27	5.2	0.5	0.14	9.01	6.6

Table 31. Protein purifications of EP-Hits 06.07.2016, part 2

Name	Expr. vol. (ml)	Aggregation (%) (Anal. SEC)	Monomeric peak (%) (Anal. SEC)	Degradation (%) (Anal. SEC)	Pi Assay: 1ug/ml Enzyme, 500uM ATP, 60 min (1:10)
EP2	50	15.7	69.5	14.9	53.572
EP3	50	14.9	67.6	17.5	62.6725
EP4	50	11.3	72.5	16.3	52.1195
EP5	50	15.1	67.8	17	75.1995
EP6	50	17.2	59.3	23.5	72.517
EP9	50	21.7	57.5	20.8	63.7175
EP11	50	12.3	72.2	15.6	59.0205
EP12	50	19.9	63.1	17.1	48.358
EP14	50	14.9	66.6	18.5	88.3785
EP17	40	17.3	68.9	13.8	89.8415
EP18	50	15.4	67.2	17.4	61.495
EP24	40	8.9	73	18	74.713
EP28 with IL2-start	20	17.8	56.4	25.8	53.6735

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Table 32. Protein purifications EP-Hits 15.07.2016

Name	MW [kD]	e [M-1*cm-1]	conc. [mg/ml]	conc. [umolar]	total volume [ml]	delivered amount	Expression volume (ml)
EP8	52.08	70875	0.02	0.5	0.5	0.01	50
EP10	52.08	70875	0.76	14.7	0.5	0.38	50
EP14	52.08	70875	0.21	4.0	0.5	0.10	50
EP15	52.08	70875	0.81	15.6	1	0.81	100
EP17	52.08	70875	0.22	4.3	0.5	0.11	40
EP19	52.08	70875	1.10	21.2	0.5	0.55	50
EP23	52.08	70875	0.46	8.8	0.5	0.23	50
EP28-parental control	52.08	70875	0.77	14.7	1	0.77	100

Table 33. Point mutations, in relation to the wild type CD39 sequence according to SEQ ID NO: 1.

No. Muta-tions	Mutation Pos. 1	Mutation Pos. 2	Mutation Pos. 3	Mutation Pos. 4	Sequence found	Pi Assay: 1ug/ml Enzyme, 500uM ATP, 60 min., 1:10
1	151: V->A				2x	4.309
1	319: I->T				2x	54.866
1	365: F->S				unique	69.0195
4	292: N->K	365: F->S	424: L->P	463: P->S	unique	78.81
2	405: K->N	412: Y->F			unique	89.415
2	424: L->Q	436: H->D			unique	62.912
4	254: L->M	263: W->R	439: F->S	469: S->R	unique	88.282

12. Example 11: *In vivo* activity, pK

(a) Materials and methods

For in-vivo PK 10 mg/kg compound at a final concentration of 10 mg/ml in PBS buffer was administered intravenously (1 ml/kg) via the tail vein to 4 conscious female C57BL/6 mice. Mice were obtained from WIGA and had a bodyweight of around 22 g. All in-life work was conducted under the Swiss animal welfare law.

Whole blood was collected (50 µL per time point) 0.25, 3, 8, 24 and 48 h post dose in

small volume serum tubes using POCT Minivettes. Serum was separated and used for concentration determination.

The Gyrolab technology is an automated immunoassay at nanoliter scale using an affinity flow-through format which works through centrifugal forces and laser-induced fluorescence detection. Streptavidin-coated beads are pre-packed in affinity columns on a Gyrolab Bioaffy CD. Each CD contains 112 columns. The affinity-capture columns per microstructure comprise 15 nl. The injected samples enter by capillary action. The biotinylated capture reagent binds to the Streptavidin coated beads. Afterwards, the analyte solution is injected, which binds to the captured molecules. Finally, the fluorophore-labeled detection reagent is applied. In the case of CD39, two different assay read-outs were used depending on the availability of an APP tag.

1) anti-CD39 (40035) and anti-APP (27431) is seen in Figure 10A.

2) Fab (40035) and anti-Fc/anti-CD39 (40044) 1:1 pre-mix (all EP28aa1-16 constructs) is seen in Figure 10B. Antibody 40044 loses activity when biotinylated by amine coupling, therefore, only antibody 40035 was biotinylated.

All standard curves for the CD39 constructs were diluted in Rexxip A containing 5% (v/v) mouse serum in a dilution series of 1:2. The applied concentration range for the APP tagged constructs was 5000 ng/ml - 9.77 ng/ml and for EP28aa1-16 it was 10000 ng/ml - 9.77 ng/ml. All mouse sera samples were diluted 1:100 in Rexxip A containing 5% (v/v) mouse serum. The QC samples of the CD39 constructs were diluted in Rexxip A containing 5% (v/v) mouse serum (50 and 500 ng/ml for constructs with APP tag, and 500 and 1000 ng/ml for EP28aa1-16). The final concentration for all biotinylated capture reagents was 0.1 mg/ml and the fluorescently labelled detection antibody was diluted to 10 nM in Rexxip F.

(b) Result and interpretation

The results are summarized in Table 34. As can be seen, all candidates show the same PK. Therefore, the selection of the candidate was not based on PK properties.

Table 34. pK values

Construct	SEQ ID	Animal 1	Animal 2	Animal 3	Animal 4	Mean t/2 (d)
EP28aa1-16	SEQ ID NO: 72	1.1	1.3	1.0	1.1	1.1
EP1xEP14aa 1-6	SEQ ID NO: 223	0.9	0.7	0.7	0.3	0.7

EP28aa1-3	SEQ ID NO: 58	0.6	0.7	0.9	0.8	0.8
EP14aa1-3	SEQ ID NO: 229	0.7	1.0	0.6	1.1	0.9
EP14aa1-6	SEQ ID NO: 231	0.7	0.7	0.7	0.8	0.7
EP17aa1-3	SEQ ID NO: 237	0.9	0.8	0.9	0.8	0.9
EP17aa1-15	SEQ ID NO: 241	0.8	0.9	0.9	0.6	0.8

13. Example 12: *In vivo* activity, AKI model

(a) Materials and methods

A nephrectomy of the right kidney is performed prior to the start of I/R setting. The second kidney is removed to avoid compensatory mechanisms that change the entire dynamic of the biology. Spontaneously breathing anesthetized animals are placed on the homeothermic blanket of a homeothermic monitor system and covered by sterile gauze. The body temperature is recorded through a rectal probe and controlled in the range of 36.5-37.5°C to avoid hypothermia. Animals are anaesthetized, shaved and disinfected (Betaseptic). Following mid-line incision / laparotomy the abdominal contents are retracted to the left and the right kidney is removed. The ureter and blood vessels are disconnected and ligated (9-0 Ethicon), the kidney is then removed.

I/R injury induction: Immediately after the nephrectomy of the right kidney abdominal contents are retracted to the right and the left renal artery is dissected free for renal ischemia induction.

Micro-aneurysm clips are *used* to clamp the pedicle to block the blood flow to the kidney and induce renal ischemia. The duration of the kidney ischemia starts from the time of clamping. Successful ischemia is confirmed by color change of the kidney from red to dark purple in a few seconds. After the ischemia, the micro-aneurysm clips are removed and reperfusion is indicated by a kidney color change to red.

(b) Result and interpretation

The result is seen in Figure 12. The candidates show a dose response *in vivo* which correlate to their specific *in vitro* activity. Figure 12A shows results for the parental EP28, Figure 12B shows results for EP1xEP17 and Figure 12C shows results for EP14.

As can be seen, EP28 and EP1xEP17 show similar dose responses, whereas EP14 with higher *in vitro* activity shows full efficacy with a lower dose.

14. Example 13: Titer, yield and developability

In order to manufacture selected candidates in a commercial scale, it is important to be able to express them with relatively high yield. For therapeutic proteins, this might be less straightforward compared to therapeutic antibodies, due to format complexity in addition to lack of enrichment technology which enables selection of high producing clones.

Both candidates, EP14aa1-3 and EP28aa1-3, had comparable technical characteristics, which were challenging. Particularly, low expression titers of early expression batches (data not shown) impacts production costs or might even be even lower after upscaling because of the control of host cell proteins is not robust.

In order to try to improve protein expression by early clone selection for both candidates a tailor-made purification process required was required. To this end, pools of cells expressing the candidates EP28aa1-3 and EP14aa1-3 were generated.

A parental CHO cell line was used as host cell line for the production of the EP28aa1-16/EP14aa1-3 expressing cell line. The host cell line was derived from the CHO-K1 cell line, well known to a person skilled in the art, in a way described e.g. in the patent applications WO2015092737 and WO2015092735, both incorporated by reference in their entirety. A single vial from the CHO line was used to prepare the EP28aa1-16/EP14aa1-3 recombinant cell line.

The cells were grown in chemically defined cultivation medium. One µg of SwaI linearized plasmid DNA, expression vector encoding for EP28aa1-16/EP14aa1-3, was added per transfection. The transfection reaction was performed in chemically defined cultivation medium.

Transfections were performed by electroporation using an AMAXA Gene Pulser, according to the manufactures instructions. The parental CHO cells used for transfection were in exponential growth phase with cell viabilities higher than 95%. In total, three transfections were performed with $5x10^6$ cells per transfection. Immediately after transfection, cells were transferred into Shake Flasks, containing medium chemically defined cultivation medium.

Cell pools were incubated for 48 hours at 36.5°C and 10% CO_2 before starting the selection process. A selection procedure was carried out using the selection marker encoded in the expression vector. 48 hours after transfection and growth under low folate conditions, additional selective pressure was applied by adding 10 nM MTX to the

chemically defined cultivation medium. 21 days after the start of MTX selection, pool populations consisting predominantly of MTX resistant cells have emerged. After pool recovery cells were frozen. Standard fed batches in chemically defined cultivation medium were set up for determination of concentration of the EP28aa1-16/EP14aa1-3. A reversed phase chromatography (RPC) was used to determine the product concentration. CHO cell pools producing EP28aa1-16/EP14aa1-3 were used for a FACS single cell sorting/Cell printer procedure to obtain individualized clonal cell lines.

15. Example 14: Therapeutic use

Extracellular ATP, activating $P2X_7R$, have been clearly linked several diseases, such as enhancing graft-versus-host disease (Wilhelm et al. Graft-versus-host disease is enhanced by extracellular ATP activating $P2X_7R$. Nature Medicine 16:12, pages 1434-1439 (2010).)

Furthermore, both in vitro and in vivo studies indicate that CD39 represents an important apyrase in cardiovascular health by regulating levels of ADP. Apyrase is known to inhibit platelet aggregation by metabolizing extracellular ADP.

Human apyrase does not covalently bind to platelets as opposed to other therapies like clopidogrel (Plavix™), which irreversibly bind to ADP receptor on the platelet. This allows a faster disappearance of the therapeutic blockade and therefore a safer approach to patients with excessive platelet activation. This provides a safer approach to patients with excessive platelet activation.

Thus, there is a clear basis for therapeutic use of compounds which reduce levels of extracellular ATP, such as the compounds according to the invention.

Specific non-limiting examples of therapeutic uses of the compounds according to the invention are acute organ damage due to trauma and/or hypoxia, such as acute respiratory distress syndrome (ARDS), lung injury, renal failure, acute kidney injury (AKI), including acute kidney injury following coronary artery bypass graft surgery, delayed graft function after transplantation (including xenotransplantation) of kidney or other solid organs, or vascular disease, such as occlusive vascular disease, transplantation, and xenotransplantation, treatment of individuals who suffer from stroke, coronary artery disease or injury resulting from myocardial infarction, atherosclerosis, arteriosclerosis, embolism, preeclampsia, angioplasty, vessel injury, transplantation, neonatal hypoxic ischemic encephalopathy, platelet-associated ischemic disorders including lung ischemia, coronary ischemia and cerebral ischemia, ischemia-reperfusion injury (IRI) thrombotic disorders including, coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, and venous thrombosis delayed graft function after transplantation (including xenotransplantation) of kidney or other solid

organs. Other non-limiting examples of therapeutic uses of compounds according to the invention are treatment of burns or radiation damage, sepsis, improving wound healing, decrease bleeding or the risk of bleeding, prevention organ damage, graft-versus-host disease, or prevention of transplant rejection.

Particularly preferred therapeutic uses of the compounds according to the invention is acute kidney injury (AKI), such as acute kidney injury following coronary artery bypass graft surgery or sepsis or rhabdomyolysis. This condition increases patient mortality and there is no standard of care (SoC). The main causes of AKI in the intensive care unit are: sepsis (47.5%), major surgery (34%), cardiogenic shock (27%), hypovolemia (26%) and nephrotoxic compounds (19%). Furthermore, AKI is an independent strong risk factor for developing chronic kidney disease (CKD). 20-30% of major cardiac surgeries patients acquire acute kidney injury. Another preferred embodiment relates to the use an isolated apyrase according to the invention for the treatment of cardiac surgery associated acute kidney injury.

In another embodiment, the disclosure relates to an isolated apyrase according to the invention for use in the treatment of delayed graft function (DGF), acute respiratory distress syndrome (ARDS), acute myocardial infarction (AMI), traumatic brain injury (TBI) /acute ischemic stroke (AIS), or combinations thereof often referred to as multi-organ failures (MOF).

16. Acute kidney injury (AKI) is a common complication of sepsis. 28% of sepsis patients acquire AKI. In an additional preferred embodiment the disclosure relates to the use an isolated apyrase according to the invention for the treatment of sepsis associated acute kidney injury. Example 15: Therapeutic compositions

Therapeutic proteins are typically formulated either in aqueous form ready for administration or as lyophilisate for reconstitution with a suitable diluent prior to administration. A protein may be formulated either as a lyophilisate, or as an aqueous composition, for example in pre-filled syringes.

Suitable formulation can provide an aqueous pharmaceutical composition or a lyophilisate which can be reconstituted to give a solution with a high concentration of the therapeutic protein active ingredient and a low level of protein aggregation for delivery to a patient. High concentrations of protein are useful as they reduce the amount of material which must be delivered to a patient (the dose). Reduced dosing volumes minimize the time taken to deliver a fixed dose to the patient. The aqueous compositions of the invention with high concentration of proteins are particularly suitable for subcutaneous administration.

Thus the invention provides an aqueous pharmaceutical composition, suitable for administration in a subject, e.g., for subcutaneous administration, comprising a therapeutic protein.

The therapeutic protein may be used as a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may contain, in addition to a therapeutic protein, carriers, various diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The characteristics of the carrier will depend on the route of administration. The pharmaceutical compositions for use in the disclosed methods may also contain additional therapeutic agents for treatment of the particular targeted disorder.

17. Example 16: Route of administration

Typically, the proteins according to the invention are administered by injection, for example, either intravenously, intraperitoneally, or subcutaneously. Methods to accomplish this administration are known to those of ordinary skill in the art. It may also be possible to obtain compositions that may be topically or orally administered, or which may be capable of transmission across mucous membranes. As will be appreciated by a person skilled in the art, any suitable means for administering can be used, as appropriate for a particular selected route of administration.

Examples of possible routes of administration include parenteral, (e.g., intravenous (I.V. or IV), intramuscular (IM), intradermal, subcutaneous (S.C. or SC), or infusion), oral and pulmonary (e.g., inhalation), nasal, transdermal (topical), transmucosal, intra-arterial, continuous infusion, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerin, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes, or multiple dose vials made of glass or plastic.

An apyrase therapy can be initiated by administering a "loading dose" of the proteins according to the invention to the subject in need therapy. By "loading dose" is intended an initial dose of the proteins according to the invention that is administered to the subject, where the dose of the proteins according to the invention administered falls

within the higher dosing range. The "loading dose" can be administered as a single administration, for example, a single infusion where the proteins are administered IV, or as multiple administrations, for example, multiple infusions where the proteins are administered IV, so long as the complete "loading dose" is administered within about a 24-hour period (or within the first month if multiple intravenous administration are needed, based on the severity of the disease). Following administration of the "loading dose", the subject is then administered one or more additional therapeutically effective doses of the proteins according to the invention. Subsequent therapeutically effective doses can be administered, for example, according to a weekly dosing schedule, or once every two weeks, once every three weeks, or once every four weeks. In such embodiments, the subsequent therapeutically effective doses generally fall within the lower dosing range.

Alternatively, in some embodiments, following the "loading dose", the subsequent therapeutically effective doses of the proteins according to the invention are administered according to a "maintenance schedule", wherein the therapeutically effective dose of the proteins according to the invention is administered once a month, once every 6 weeks, once every two months, once every 10 weeks, once every three months, once every 14 weeks, once every four months, once every 18 weeks, once every five months, once every 22 weeks, once every six months, once every 7 months, once every 8 months, once every 9 months, once every 10 months, once every 11 months, or once every 12 months. In such embodiments, the therapeutically effective doses of the proteins according to the invention fall within the lower dosing range, particularly when the subsequent doses are administered at more frequent intervals, for example, once every two weeks to once every month, or within the higher dosing range, particularly when the subsequent doses are administered at less frequent intervals, for example, where subsequent doses are administered one month to 12 months apart.

The timing of dosing is generally measured from the day of the first dose of the active compound, which is also known as “baseline”. However, different health care providers use different naming conventions.

Notably, week zero may be referred to as week 1 by some health care providers, while day zero may be referred to as day one by some health care providers. Thus, it is possible that different physicians will designate, e.g., a dose as being given during week 3 / on day 21, during week 3 / on day 22, during week 4 / on day 21, during week 4 / on day 22, while referring to the same dosing schedule. For consistency, the first week of dosing will be referred to herein as week 0, while the first day of dosing will be referred to as day 1. However, it will be understood by a skilled artisan that this naming convention is simply used for consistency and should not be construed as limiting, i.e., weekly

dosing is the provision of a weekly dose of the protein regardless of whether the physician refers to a particular week as “week 1” or “week 2”. Example of dosage regimes as noted herein are found in Figure 1 and 2. It will be understood that a dose need not be provided at an exact time point, e.g., a dose due approximately on day 29 could be provided, e.g., on day 24 to day 34, e.g. day 30, as long as it is provided in the appropriate week.

As used herein, the phrase “container having a sufficient amount of the protein to allow delivery of [a designated dose]” is used to mean that a given container (e.g., vial, pen, syringe) has disposed therein a volume of a protein (e.g., as part of a pharmaceutical composition) that can be used to provide a desired dose. As an example, if a desired dose is 500 mg, then a clinician may use 2 ml from a container that contains a protein formulation with a concentration of 250 mg/ml, 1 ml from a container that contains a protein formulation with a concentration of 500 mg/ml, 0.5 ml from a container contains a protein formulation with a concentration of 1000 mg/ml, etc. In each such case, these containers have a sufficient amount of the protein to allow delivery of the desired 500 mg dose.

As used herein, the phrase “formulated at a dosage to allow [route of administration] delivery of [a designated dose]” is used to mean that a given pharmaceutical composition can be used to provide a desired dose of a protein via a designated route of administration (e.g., s.c. or i.v.). As an example, if a desired subcutaneous dose is 500 mg, then a clinician may use 2 ml of a protein formulation having a concentration of 250 mg/ml, 1 ml of a protein formulation having a concentration of 500 mg/ml, 0.5 ml of a protein formulation having a concentration of 1000 mg/ml, etc. In each such case, these protein formulations are at a concentration high enough to allow subcutaneous delivery of the protein. Subcutaneous delivery typically requires delivery of volumes of less than about 2 ml, preferably a volume of about 1ml or less. However, higher volumes may be delivered over time using, e.g., a patch/pump mechanism.

Disclosed herein is the use of a protein for the manufacture of a medicament for the treatment of tissue damage in a patient, wherein the medicament is formulated to comprise containers, each container having a sufficient amount of the protein to allow delivery of at least about 75 mg, 150 mg, 300 mg or 600 mg protein per unit dose.

Disclosed herein is the use of a protein for the manufacture of a medicament for the treatment of tissue damage in a patient, wherein the medicament is formulated at a dosage to allow systemic delivery (e.g., i.v. or s.c. delivery) 75 mg, 150 mg, 300 mg of 600 mg protein per unit dose.

18. Example 17: Kits

The disclosure also encompasses kits for treating a patient with tissue damage (as the case may be) with a protein. Such kits comprise a protein (e.g., in liquid or lyophilized form) or a pharmaceutical composition comprising the protein (described supra). Additionally, such kits may comprise means for administering the protein (e.g., a syringe and vial, a prefilled syringe, a prefilled pen, a patch/pump) and instructions for use. The instructions may disclose providing the protein to the patient as part of a specific dosing regimen. These kits may also contain additional therapeutic agents (described supra) for treating psoriasis, e.g., for delivery in combination with the enclosed protein.

The phrase “means for administering” is used to indicate any available implement for systemically administering a drug top a patient, including, but not limited to, a pre-filled syringe, a vial and syringe, an injection pen, an autoinjector, an i.v. drip and bag, a pump, patch/pump, etc. With such items, a patient may self-administer the drug (i.e., administer the drug on their own behalf) or a care-giver or a physician may administer the drug.

Disclosed herein are kits for the treatment of a patient having tissue damage, comprising: a) a pharmaceutical composition comprising a therapeutically effective amount of a protein; b) means for administering the protein to the patient; and c) instructions providing subcutaneously administering a protein to a patient in need thereof.

SEQUENCE TABLE

Useful amino acid and nucleotide sequences for practicing the invention are disclosed in Table 35.

Table 35. Sequences useful for practicing the invention.

SEQ ID Number	Feature	Sequence
Wild type human CD39		
SEQ ID NO: 1	Amino acid	MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVL DAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGI YLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVV ERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYET

		NNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHS FLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCT KRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPL QGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYA GVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLG YMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLIFHKPSYFW KDMV
Wild type rat CD39		
SEQ ID NO: 2	Amino acid	MEDIKDSKVKRFCSKNILIILGFSSVLAVIALIAVGLTHNKPLPENVKYGIVLD AGSSHTNLYIYKWPAEKENDTGVVQLLEECQVKGPGISKYAQKTDEIAAY LAECMKMSTERIPASKQHQTPVYLGATAGMRLLRMESKQSADEVLAAVS RSLKSYPFDFQGAKIITGQEEGAYGWITINYLLGRFTQEQSWLNFISDSQK QATFGALDLGGSSTQVTFVPLNQTLEAPETSLQFRLYGTDYTVYTHSFLC YGKDQALWQKLAQDIQVSSGGILKDPCFYPGYKKVVNVSELYGTPCTKR FEKKLPFNQFQVQGTGDYEQCHQSILKFFNNSHCPYSQCAFNGVFLPPL QGSFGAFSAFYFVMDFFKKMANDSVSSQEKMTEITKNFCSKPWEEVKAS YPTVKEKYLSEYCFSGTYILSLLLQGYNFTGTSWDQIHFMGKIKDSNAGW TLGYMLNLTNMIPAEQPLSPPLPHSTYISLMVLFSLVLVAMVITGLFIFSKPS YFWKEAV
CD39L3		
SEQ ID NO: 3	Amino acid	QIHKQEVLPPGLKYGIVLDAGSSRTTVYVYQWPAEKENNTGVVSQTFKCS VKGSGISSYGNNPQDVPRAFEECMQKVKGQVPSHLHGSTPIHLGATAGM RLLRLQNETAANEVLESIQSYFKSQPFDFRGAQIISGQEEGVYGWITANYL MGNFLEKNLWHMWVHPHGVETTGALDLGGASTQISFVAGEKMDLNTSDI MQVSLYGYVYTLYTHSFQCYGRNEAEKKFLAMLLQNSPTKNHLTNPCYP RDYSISFTMGHVFDSLCTVDQRPESYNPNDVITFEGTGDPSLCKEKVASIF DFKACHDQETCSFDGVYQPKIKGPFVAFAGFYYTASALNLSGSFSLDTFN SSTWNFCSQNWSQLPLLLPKFDEVYARSYCFSANYIYHLFVNGYKFTEET WPQIHFEKEVGNSSIAWSLGYMLSLTNQIPAESPLIRLPIEP
EP28		
SEQ ID NO: 4	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST

SEQ ID NO: 5	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1		
SEQ ID NO: 6	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 7	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG

		CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP2		
SEQ ID NO: 8	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVMDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLG KFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNV YTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYK TPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIF LPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 9	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA

		GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGATGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAAGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP3		
SEQ ID NO: 10	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKGFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLRTPLSHST
SEQ ID NO: 11	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC

		GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGGGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGAT CCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAAC TGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGC ATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTT CTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGCGCACACCTCTGAGC CACAGCACC
EP4		
SEQ ID NO: 12	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFAQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLRTPLSHST
SEQ ID NO: 13	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGCGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT

		TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGGACACCTCTGAGC CACAGCACC
EP5		
SEQ ID NO: 14	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVMDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIDKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 15	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGATGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA

		GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGACAAG ATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATCT GACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGCC ACAGCACC
EP6		
SEQ ID NO: 16	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGISLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVMDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALRQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 17	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTCCCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGATGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG

		CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGCGGCAGAAGCTGGCCAAGG ACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCAC CCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCC CTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGAT CCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAAC TGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGC ATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTT CTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP7		
SEQ ID NO: 18	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEEENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLSDCMERAREVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDAVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGTGNYQQCHQSILELFNTSYCPYSQCAFNGIF LPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 19	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGGAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTG CAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACG AGATCGGCATCTACCTGTCCGACTGCATGGAACGGGCCAGGGAAGTG ATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCAC CGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGAC CGGGTGCTGGACGCGGTGGAAAGAAGCCTGAGCAACTACCCATTCGA TTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACG GCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATC AGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTG ACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCT GCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCT TTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAG

		GACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCA CCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCC CCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAG ATCCAGGGCACCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGA ACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACG GCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCC TTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCC CAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTG GGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGA GCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAG GGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGG CAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGA ATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTG AGCCACAGCACC
EP8		
SEQ ID NO: 20	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDAVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 21	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TTCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGCGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGTAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTAGTGAACGTGTCCGACCTGTACAAGACCCCC

		TGCACCAAGAGATTCGAGATGACCCTGCCATTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP9		
SEQ ID NO: 22	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALRQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 23	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGAGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT

		GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP10		
SEQ ID NO: 24	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGTGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 25	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTATGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCACCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC

		TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCTTTGAGCACACCTCTGAGC CACAGCACC
EP11		
SEQ ID NO: 26	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGTGNYQQCHQSILELFNTSYCPYSQCAFNGIF LPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 27	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCACCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACTAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA

		GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP12		
SEQ ID NO: 28	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNDILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGTGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 29	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGATATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCACCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC

		TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP13		
SEQ ID NO: 30	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLPQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 31	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCCGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC

		TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14		
SEQ ID NO: 32	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 33	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCTTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGTTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC

EP15		
SEQ ID NO: 34	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVKVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLPQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMISAEQPLSTPLSHST
SEQ ID NO: 35	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCGCTGTGGCAGAAGCTGGCCAAGG ACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCAC CCCGGCTACAAGAAAGTCGTGAAGGTGTCCGACCTGTACAAGACCCC CTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGAT CCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAAC TGTTCAACACCAGCTACTGCCCATACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCCGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCTCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP17		

SEQ ID NO: 36	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 37	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAACCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAACGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP17.1		
SEQ ID NO: 38	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR

		MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 39	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP18		
SEQ ID NO: 40	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIDIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT

		HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 41	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGACATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP19		
SEQ ID NO: 42	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP

		PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEDIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 43	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGGACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP20		
SEQ ID NO: 44	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNGILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS

		YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHSIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 45	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGGGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTCCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP21		
SEQ ID NO: 46	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLRTPLSHST

SEQ ID NO: 47	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGCGCACACCTCTGAGC CACAGCACC
EP22		
SEQ ID NO: 48	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNGILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLGTPLSHST
SEQ ID NO: 49	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG

		CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGGGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGTTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGGGCACACCTCTGAGC CACAGCACC
EP23		
SEQ ID NO: 50	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFMCYGKDQALRQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHSIGKIQGSDAGWT LGYMLNLTNMIPAEQPLRTPLSHST
SEQ ID NO: 51	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA

		GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT ATGTGCTACGGAAAGGACCAGGCTCTGAGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGTACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTCCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGAACACCTCTGAGC CACAGCACC
EP24		
SEQ ID NO: 52	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAKEVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHNHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 53	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAAGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC

		GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACAACCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1xEP1 7_K405N		
SEQ ID NO: 54	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 55	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC

		GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAACCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAACGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1xEP1 7		
SEQ ID NO: 56	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 57	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT

		TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP28aa1-3		
SEQ ID NO: 58	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 59	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGACGCCGGCTCCTCCCACACCTCCCTGTACATCTACAA GTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCACCAAGTG GAAGAGTGCAGAGTGAAGGGCCCCGGCATCTCCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA GAGAAGTGATCCCTCGGTCCCAGCACCAGGAAACCCCTGTCTACCTG GGCGCCACCGCCGGCATGCGGCTGCTGCGGATGGAATCCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAACGGTCCCTGTCCAACTAC CCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAGGG

		CGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCTCCC AGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCCAG CACCCAAGTCACATTCGTGCCCCAGAACCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAACGTGTAC ACCCACAGCTTTCTGTGCTACGGCAAGGACCAGGCCCTGTGGCAGAA GCTGGCCAAGGACATCCAAGTGGCCTCCAACGAGATCCTGCGGGACC CCTGCTTCCACCCCGGCTACAAGAAAGTGGTCAACGTGTCCGACCTG TACAAGACCCCTTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAG CAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCAGTC CATCCTGGAACTGTTCAACACCTCCTACTGCCCCTACTCCCAGTGCGC CTTCAACGGCATCTTCCTGCCTCCACTGCAGGGCGACTTCGGCGCCT TCTCCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCTCCGAGA AAGTGTCCCAGGAAAAAGTGACCGAGATGATGAAGAAGTTCTGCGCC CAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAA GTACCTGTCCGAGTACTGCTTCTCCGGCACCTACATCCTGTCCCTGCT GCTGCAGGGCTACCACTTCACCGCCGACAGCTGGGAGCACATCCACT TCATCGGCAAGATCCAGGGATCCGACGCTGGCTGGACCCTGGGCTAC ATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGTCCAC CCCTCTGTCTCACTCCACC
EP14xEP 17		
SEQ ID NO: 60	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 61	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA

		GGAAACCTTCGGCGCCTTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGTTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP10xEP19_H436D		
SEQ ID NO: 62	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGTGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEDIHFIGKIQGSDAG WTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 63	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA

		GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCACCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGGACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14xEP19		
SEQ ID NO: 64	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 65	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCTTGGACCTGGGCGGAGCTTCTACCCAAGTGA

		CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGTTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP28aa1-15		
SEQ ID NO: 66	Amino acid	APTSSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKEN DTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQE TPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQE EGAYGWITINYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDN ALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHP GYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNT SYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEM MKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWE HIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 67	DNA	GCCCCTACCAGCAGCAGCACCAAGAAAACCCAGCTGACCAGCAGCAC CCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCTGG ATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTGCC GAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGCAG AGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGAGA TCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGATC CCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACCGC CGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACCGG GTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGATTTT CAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGGCT GGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCAG GAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGAC

		CTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGC AGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTTC TGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGAC ATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCC CGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCT GCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP17xEP19_H436D		
SEQ ID NO: 68	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEDIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 69	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA

		CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGGACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP17xEP 19		
SEQ ID NO: 70	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 71	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG

		CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP28aa1-16		
SEQ ID NO: 72	Amino acid	APTSSSTKKTQLTSSGTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKE NDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQ ETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQ EEGAYGWITINYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPD NALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFH PGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFN TSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTE MMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSW EHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 73	DNA	GCCCCTACCTCCTCCAGCACCAAGAAAACCCAGCTGACCTCCAGCGG CACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGC TGGACGCCGGCTCCTCCCACACCTCCCTGTACATCTACAAGTGGCCT GCCGAGAAAGAAAACGACACCGGCGTGGTGCACCAAGTGGAAGAGT GCAGAGTGAAGGGCCCCGGCATCTCCAAGTTCGTGCAGAAAGTGAAC GAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGAGAAGT GATCCCTCGGTCCCAGCACCAGGAAACCCCTGTCTACCTGGGCGCCA CCGCCGGCATGCGGCTGCTGCGGATGGAATCCGAGGAACTGGCCGA CCGGGTGCTGGACGTGGTGGAACGGTCCCTGTCCAACTACCCATTCG ATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAGGGCGCCTAC GGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCTCCCAGAAGAAT CAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCCAGCACCCAAG TCACATTCGTGCCCCAGAACCAGACCATCGAGAGCCCCGACAACGCC

		CTGCAGTTCCGGCTGTACGGCAAGGACTACAACGTGTACACCCACAG CTTTCTGTGCTACGGCAAGGACCAGGCCCTGTGGCAGAAGCTGGCCA AGGACATCCAAGTGGCCTCCAACGAGATCCTGCGGGACCCCTGCTTC CACCCCGGCTACAAGAAAGTGGTCAACGTGTCCGACCTGTACAAGAC CCCTTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGA GATCCAGGGCATCGGCAACTACCAGCAGTGCCACCAGTCCATCCTGG AACTGTTCAACACCTCCTACTGCCCCTACTCCCAGTGCGCCTTCAACG GCATCTTCCTGCCTCCACTGCAGGGCGACTTCGGCGCCTTCTCCGCC TTCTACTTCGTGATGAAGTTCCTGAACCTGACCTCCGAGAAAGTGTCC CAGGAAAAAGTGACCGAGATGATGAAGAAGTTCTGCGCCCAGCCCTG GGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGT CCGAGTACTGCTTCTCCGGCACCTACATCCTGTCCCTGCTGCTGCAG GGCTACCACTTCACCGCCGACAGCTGGGAGCACATCCACTTCATCGG CAAGATCCAGGGATCCGACGCTGGCTGGACCCTGGGCTACATGCTGA ATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGTCCACCCCTCTG TCTCACTCCACC
EP1xEP1 4xEP19		
SEQ ID NO: 74	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSDAG WTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 75	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT

		CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1xEP1 7xEP19		
SEQ ID NO: 76	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSDAG WTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 77	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA

		CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTTCTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCAGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1xEP1 4		
SEQ ID NO: 78	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGMRLL RMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGK FSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVY THSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKT PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKT SYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGW TLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 79	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCTTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC

		CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGTTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP28aa1-6		
SEQ ID NO: 80	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITI NYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK DYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVS DLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCA FNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQG SDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 81	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT

		CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCC TGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAG CACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGAC ACTGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGC CCCTGAGCACACCTCTGAGCCACAGCACC
EP28_E174A		
SEQ ID NO: 82	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEAGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 83	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGCCGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC

		CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCG AGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP28_E174A_S218A		
SEQ ID NO: 84	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEAGAYGWITINYLLGKF SQKNQETFGALDLGGAATQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 85	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGCCGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTGCTACCCAAGTG ACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCT GCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCT TTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAG GACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCA CCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCC CCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAG

		ATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGA ACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACG GCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCC TTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCC CAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTG GGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGA GCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAG GGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGG CAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGA ATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTG AGCCACAGCACC
EP14_N73Q		
SEQ ID NO: 86	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKEQDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 87	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAACAGGACACCGGCGTGGTGCATCAGGTGGAAGAGTG CAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACG AGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTG ATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCAC CGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGAC CGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGA TTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACG GCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATC AGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTG ACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCT GCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCT TTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAG GACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCA CCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCC CCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAG ATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGA

		ACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACG GCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCC TTCTACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCC CAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTG GGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGA GCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAG GGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGG CAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGA ATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTG AGCCACAGCACC
EP14_T2 29A		
SEQ ID NO: 88	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQAIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 89	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGGCCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA

		TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14_N2 92Q		
SEQ ID NO: 90	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVQVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 91	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGCAGGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC

		TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14_N3 27Q		
SEQ ID NO: 92	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFQTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 93	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCCAGACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA

		GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14_N371Q		
SEQ ID NO: 94	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLQLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 95	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGCAGCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG

		AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP14_N4 57Q		
SEQ ID NO: 96	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLQLTNMIPAEQPLSTPLSHST
SEQ ID NO: 97	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGA CATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACC CCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCC TGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTCCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGC

		GAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGG CTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGCAG CTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAG CCACAGCACC
SEQ ID NO: 98	plusMILr evsense primer	TGCCCTACGAGACAAACAATCAGGAAACCTTCGGCGCCCTGGACCTG GGCGGAGCTTCTACCCAAGTGA
CD39(aa39-469)		
SEQ ID NO: 99	Amino acid	QNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQF RLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKK VVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPY SQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFC AQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIG KIQGSDAGWTLGYMLNLTNMIPAEQPLS
SEQ ID NO: 100	DNA	CAGAACAAAGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCTGGA TGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTGCCG AGAAAGAAAACGATACCGGTGTCGTGCACCAGGTGGAAGAGTGCAGA GTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGAGAT CGGCATCTACCTGACCGACTGCATGGAACGGGCCAGAGAAGTGATCC CCAGAAGCCAGCACCAGGAAACCCCCGTGTACCTGGGAGCCACAGC CGGCATGAGACTGCTGCGGATGGAAAGCGAGGAACTGGCCGACAGA GTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGATTTT CAAGGGGCCAGAATCATCACCGGCCAGGAAGAGGGCGCTTACGGCT GGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAAACCCGG TGGTTCAGCATCGTGCCCTACGAGACAAACAATCAGGAAACCTTCGGA GCCCTGGACCTGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCA GAATCAGACCATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGT ACGGCAAGGACTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAA AGGACCAGGCCCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGC CAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGA AAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGA TTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGG CAACTACCAGCAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCA GCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCA CCTCTGCAGGGGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGAT

		GAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGA CAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAG ACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTT CAGCGGTACCTACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCA CCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAAGATTCAGGGC AGCGACGCCGGCTGGACACTGGGCTACATGCTGAATCTGACCAACAT GATCCCCGCCGAGCAGCCCCTGAGC
CD39(aa46-476)		
SEQ ID NO: 101	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAF NGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPW EEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGS DAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 102	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG

		CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTG AGCACACCTCTGTCTCACAGCACC
CD39(aa46-461)		
SEQ ID NO: 103	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAF NGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPW EEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGS DAGWTLGYMLNLTNM
SEQ ID NO: 104	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)		
SEQ ID NO: 105	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 106	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGC CCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAG ATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAA CGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGA CCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAG CAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCC CTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGG GGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGA ACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATG AAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGC

		TGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCT ACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGC TGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGG CTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_delta cys1		
SEQ ID NO: 107	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEARVKGPGISKFV QKVNEIGIYLTDAMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAF NGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPW EEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGS DAGWTLGYMLNLTNM
SEQ ID NO: 108	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGGCCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACGC CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_deltacys2		
SEQ ID NO: 109	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPAFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQAHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNM
SEQ ID NO: 110	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTGCCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGGCCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_deltacys3		
SEQ ID NO: 111	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLAYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPATKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNM
SEQ ID NO: 112	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGGCCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCGCCACCAAGAGATTCGAGATGACCCTGCCCTT CCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACC AGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_deltacys4		
SEQ ID NO: 113	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYAPYSQAAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNM
SEQ ID NO: 114	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACGCCCCCTACAGCCAGG CCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_deltacys5		
SEQ ID NO: 115	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRW FSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD YNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSD LYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAF NGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFAAQPW EEIKTSYAGVKEKYLSEYAFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGS DAGWTLGYMLNLTNM
SEQ ID NO: 116	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAACCCGGTGGTTCAGCATCGTGCCCTACG AGACAAACAATCAGGAAACCTTCGGAGCCCTGGACCTGGGCGGAGCC TCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCC CGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGT ACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCCCTGTGGCAG AAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGG ACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGAC CTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTC CAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCA GAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGT GCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCGC CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG

		AGAAGTACCTGAGCGAGTACGCCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)_delta cys1		
SEQ ID NO: 117	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEARVKGPGISKFV QKVNEIGIYLTDAMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 118	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGGCCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACGC CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGC CCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAG ATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAA CGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGA CCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAG CAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCC CTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGG GGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGA ACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATG

		AAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGC TGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCT ACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGC TGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGG CTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)_delta cys2		
SEQ ID NO: 119	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPAFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQAHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 120	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGC CCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAG ATCCTGCGGGACCCTGCCTTCCACCCCGGCTACAAGAAAGTCGTGAA CGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGA CCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAG CAGGCCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCC CTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGG GGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGA

		ACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATG AAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGC TGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCT ACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGC TGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGG CTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)_delta cys3		
SEQ ID NO: 121	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLAYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPATKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 122	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGGCCTACGGAAAGGACCAGG CCCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGA GATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGA ACGTGTCCGACCTGTACAAGACCCCCGCCACCAAGAGATTCGAGATG ACCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCA GCAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCC CCTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAG

		GGGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTG AACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGAT GAAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACG CTGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACC TACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAG CTGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCG GCTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)_delta cys4		
SEQ ID NO: 123	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYAPYSQAAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 124	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGC CCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAG ATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAA CGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGA CCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAG CAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACGCCCC

		CTACAGCCAGGCCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGG GGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGA ACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATG AAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGC TGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCT ACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGC TGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGG CTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa46-461)_dMIL(193-204)_delta cys5		
SEQ ID NO: 125	Amino acid	NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFAAQPWEEIKTSYAGVKEKYL SEYAFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN M
SEQ ID NO: 126	DNA	AACGTGAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAG CCTGTACATCTACAAGTGGCCTGCCGAGAAAGAAAACGATACCGGTGT CGTGCACCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGC AAGTTCGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTG CATGGAACGGGCCAGAGAAGTGATCCCCAGAAGCCAGCACCAGGAAA CCCCCGTGTACCTGGGAGCCACAGCCGGCATGAGACTGCTGCGGAT GGAAAGCGAGGAACTGGCCGACAGAGTGCTGGACGTGGTGGAAAGA AGCCTGAGCAACTACCCATTCGATTTTCAAGGGGCCAGAATCATCACC GGCCAGGAAGAGGGCGCTTACGGCTGGATCACCATCAACTACCTGCT GGGCAAGTTCAGCCAGAAAAATCAGGAAACCTTCGGAGCCCTGGACC TGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACC ATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGA CTACAATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGC CCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAG ATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAA CGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGA CCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAACTACCAG

		CAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCC CTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGG GGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGA ACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATG AAGAAGTTCGCCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGC TGGCGTGAAAGAGAAGTACCTGAGCGAGTACGCCTTCAGCGGTACCT ACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGC TGGGAGCACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGG CTGGACACTGGGCTACATGCTGAATCTGACCAACATG
CD39(aa38-476)_delta337-344		
SEQ ID NO: 127	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQF RLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKK VVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSFNGI FLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIK TSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAG WTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 128	DNA	ACACAGAACAAAGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGATACCGGTGTCGTGCACCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGAGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTACCTGGGAGCCACA GCCGGCATGAGACTGCTGCGGATGGAAAGCGAGGAACTGGCCGACA GAGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGGGCCAGAATCATCACCGGCCAGGAAGAGGGCGCTTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAAACCC GGTGGTTCAGCATCGTGCCCTACGAGACAAACAATCAGGAAACCTTC GGAGCCCTGGACCTGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCC CCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGC TGTACGGCAAGGACTACAATGTGTACACCCACAGCTTTCTGTGCTACG GAAAGGACCAGGCCCTGTGGCAGAAGCTGGCCAAGGACATCCAGGT GGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCCCGGCTACA AGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCTGCACCAAG AGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCAT

		CGGCAACTACCAGCAGTGCCACCAGAGCATCCTGGAACTGTTCAACA CCAGCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGACTTCGGC GCTTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGC GAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTG CGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAG AGAAGTACCTGAGCGAGTACTGCTTCAGCGGTACCTACATCCTGAGC CTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACAT CCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGG GCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTG AGCACACCTCTGTCTCACAGCACC
CD39(aa38-476)_C338A_C343A		
SEQ ID NO: 129	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQF RLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKK VVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYAPY SQAAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFC AQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIG KIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 130	DNA	ACACAGAACAAAGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGATACCGGTGTCGTGCACCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGAGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTACCTGGGAGCCACA GCCGGCATGAGACTGCTGCGGATGGAAAGCGAGGAACTGGCCGACA GAGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGGGCCAGAATCATCACCGGCCAGGAAGAGGGCGCTTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAAACCC GGTGGTTCAGCATCGTGCCCTACGAGACAAACAATCAGGAAACCTTC GGAGCCCTGGACCTGGGCGGAGCCTCTACCCAAGTGACCTTCGTGCC CCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGC TGTACGGCAAGGACTACAATGTGTACACCCACAGCTTTCTGTGCTACG GAAAGGACCAGGCCCTGTGGCAGAAGCTGGCCAAGGACATCCAGGT GGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCCCGGCTACA

		AGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCTGCACCAAG AGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCAT CGGCAACTACCAGCAGTGCCACCAGAGCATCCTGGAACTGTTCAACA CCAGCTACGCCCCCTACAGCCAGGCCGCCTTCAACGGCATCTTCCTG CCACCTCTGCAGGGGGACTTCGGCGCTTTCAGCGCCTTCTACTTCGT GATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAG TGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATC AAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCGAGTACTG CTTCAGCGGTACCTACATCCTGAGCCTGCTGCTGCAGGGCTACCACTT CACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAAGATTCAGG GCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATCTGACCAAC ATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGTCTCACAGCAC C
Expression tag aa1-16		
SEQ ID NO: 131	Amino acid	APTSSSTKKTQLTSSG
SEQ ID NO: 132	DNA	GCCCCCACCAGCAGCAGCACCAAGAAGACCCAGCTGACCAGCAGCG GC
Expression tag aa1-15		
SEQ ID NO: 133	Amino acid	APTSSSTKKTQLTSS
SEQ ID NO: 134	DNA	GCCCCTACCAGCAGCAGCACCAAGAAAACCCAGCTGACCAGCAGC
Expression tag aa1-6		
SEQ ID NO: 135	Amino acid	APTSSS
SEQ ID NO: 136	DNA	GCCCCTACCAGCAGCAGC

Expression tag aa1-3		
SEQ ID NO: 137	Amino acid	APT
SEQ ID NO: 138	DNA	GCCCCTACC
Expression tag aa1-9		
SEQ ID NO: 139	Amino acid	APTSSSTKK
SEQ ID NO: 140	DNA	GCCCCTACCAGCAGCAGCACCAAGAAA
Expression tag aa1-12		
SEQ ID NO: 141	Amino acid	APTSSSTKKTQL
SEQ ID NO: 142	DNA	GCCCCTACCAGCAGCAGCACCAAGAAAACCCAGCTG
Expression tag aa4-12		
SEQ ID NO: 143	Amino acid	SSSTKKTQL
SEQ ID NO: 144	DNA	AGCAGCAGCACCAAGAAAACCCAGCTG
EP28_8M		
SEQ ID NO: 145	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQDEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGRDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSNFYYVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS

		YAGQERWLRDYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 146	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGAGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGACGAGGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCA GGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGA CCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTG CAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTT CTGTGCTACGGCCGGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGG ACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCAC CCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCC CTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGAT CCAGGGCATCGGCAACTACCAGCAGTGCCACCAGAGCATCCTGGAAC TGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGC ATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCAACTTC TACTACGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCA GGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGG AGGAAATCAAGACCTCTTACGCCGGACAGGAACGGTGGCTGCGGGAC TACTGTTTCAGCGGCACCTACATCCTGTCCCTGCTGCTGCAGGGCTAC CACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAAGATT CAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATCTGAC CAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGTCTCACA GCACC
CD39(aa38-476)_dMIL(193-204)_CKAPPA		
SEQ ID NO: 147	Amino acid	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEGGGGSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTG VVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPV

		YLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGA YGWITINYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQ FRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYK KVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCP YSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKF CAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFI GKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 148	DNA	ACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCA GCTGAAGAGCGGCACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCT ACCCCCGGGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCA GAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTA CGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTG TCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCGAGGGAGGCGGAG GATCTACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATC GTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTG GCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAA GAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGT GAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGG AAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGA GCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGG CCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCA TTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGC CTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGA AGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACC CAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAA CGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCC ACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTG GCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTG CTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAA GACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGT TCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATC CTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTC AACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAG CGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGT GTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGC CCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTAC CTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCT GCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCA TCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACAT

		GCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACAC CTCTGAGCCACAGCACC
CD39(aa38-476)_dMIL(193-204)_UBI		
SEQ ID NO: 149	Amino acid	MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLED GRTLSDYNIQKESTLHLVLRLRGGGGGGSTQNKALPENVKYGIVLDAGSS HTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDC MERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS NYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQETFGALDLGGAST QVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK DIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGI GNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKF LNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYI LSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLST PLSHST
SEQ ID NO: 150	DNA	ATGCAAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCCTCGAG GTGGAGCCCAGTGACACCATCGAGAATGTCAAGGCAAAGATCCAAGA TAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAA ACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAG AGTCCACTCTGCACTTGGTCCTGCGCTTGAGGGGGGGTGGAGGCGG AGGATCTACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCA TCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAG TGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGA AGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAG TGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGG GAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGG AGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTG GCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACC CATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGC GCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCA GAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTA CCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGAC AACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACAC CCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGC TGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCT TGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTA CAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGC

		AGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGC ATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGC CTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCT TCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGA AGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCC CAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAA GTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGC TGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCAC TTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTA CATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCA CACCTCTGAGCCACAGCACC
CD39(aa38-476)_dMIL(193-204)_HSAl	HSA Domain I-G4S-CD39-dMIL	
SEQ ID NO: 151	Amino acid	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFA KTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERN ECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYF YAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRGGGGSTQNKALPE NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFV QKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELA DRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKNQET FGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK DQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMT LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGA FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYL SEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTN MIPAEQPLSTPLSHST
SEQ ID NO: 152	DNA	GACGCCCACAAGAGCGAGGTGGCCCACCGGTTCAAGGACCTGGGCG AGGAAAACTTCAAGGCCCTGGTGCTGATCGCCTTCGCCCAGTACCTG CAGCAGAGCCCCTTCGAAGATCACGTAAAGTTAGTCAACGAGGTTACG GAATTCGCAAAGACATGCGTTGCTGACGAATCCGCTGAGAATTGTGAC AAGAGTTTGCACACTTTATTCGGAGATAAGTTGTGTACTGTAGCTACTT TGAGAGAGACTTACGGTGAAATGGCTGACTGCTGTGCAAAACAGGAA CCAGAACGTAACGAATGTTTCCTTCAGCATAAGGATGATAACCCTAAC CTTCCAAGGCTTGTTAGGCCAGAAGTCGACGTGATGTGCACCGCCTT CCATGATAATGAAGAGACTTTTCTTAAAAAGTACCTATACGAGATTGCA AGGCGTCATCCATATTTTTACGCCCCAGAGCTGTTGTTTTTCGCAAAG

		AGATACAAAGCTGCATTTACTGAGTGTTGCCAAGCTGCCGACAAGGCC GCTTGTTTGCTACCAAAGTTGGACGAATTGAGAGGAGGCGGAGGATC TACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGC TGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCT GCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGT GCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAAC GAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGT GATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCA CCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGA CCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCG ATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTAC GGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAA TCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAG TGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCC CTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAG CTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCA AGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTC CACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGAC CCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCG AGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTG GAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAAC GGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGC CTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTC CCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAGCCCT GGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACCTG AGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCA GGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCG GCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCT GAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTC TGAGCCACAGCACC
CD39(aa38-476)_dMIL(193-204)_HSAII		
SEQ ID NO: 153	Amino acid	DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLV TDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEK SHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYAR RHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPGGGGST

		QNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT HSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLP PLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTS YAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWT LGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 154	DNA	GACGAGGGTAAGGCATCATCTGCCAAGCAGAGATTAAAATGTGCATCT TTGCAAAAATTTGGAGAGAGAGCTTTTAAGGCATGGGCTGTTGCCCGA CTAAGCCAAAGATTCCCAAAAGCCGAATTTGCTGAAGTATCCAAGCTG GTGACTGATTTGACTAAAGTACATACAGAATGTTGCCATGGCGACCTT TTAGAATGTGCTGATGACAGAGCAGATTTGGCTAAGTATATCTGCGAA AATCAAGATTCAATCAGCTCTAAGCTGAAGGAATGTTGCGAGAAACCA CTGTTAGAAAAATCGCATTGTATTGCTGAAGTTGAAAATGATGAGATGC CTGCTGACTTGCCTTCTCTTGCCGCTGATTTTGTTGAGTCGAAGGATG TCTGTAAGAATTATGCTGAAGCTAAAGACGTTTTCCTGGGTATGTTCTT ATATGAGTACGCAAGACGTCACCCAGATTACTCTGTGGTTCTGCTACT GAGATTGGCTAAAACATACGAGACAACGCTGGAGAAGTGCTGTGCTG CCGCTGACCCTCATGAGTGCTATGCAAAGGTTTTTGATGAATTCAAAC CAGGAGGCGGAGGATCTACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG

		CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCC TGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAG CACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGAC ACTGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGC CCCTGAGCACACCTCTGAGCCACAGCACC
EP14_plusMIL		
SEQ ID NO: 155	Amino acid	TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVK GPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLR MESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF SQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQF RLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKK VVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPY SQCAFNGIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFC AQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIG KIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 156	DNA	ACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCT GGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTG CCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGC AGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGA GATCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGA TCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACC GCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACC GGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGAT TTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGG CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGACCA GATGGTTCAGCATCGTGCCCTACGAGACAAACAATCAGGAAACCTTCG GCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGACCTTCGTGCCC CAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGCAGTTCCGGCT GTACGGCAAGGACTACAATGTGTACACCCACAGCTTTCTGTGCTACGG AAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGACATCCAGGTGG CCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCCCGGCTACAAG AAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCTGCACCAAGAG ATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATCCAGGGCATCG GCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACTGTTCAACACCA GCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCATCTTCCTGCCA

		CCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTCTACTCCGTGAT GAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAGGAAAAAGTGA CAGAGATGATGAAGAAGTTCTGCGCCCAGCCCTGGGAGGAAATCAAG ACCTCCTACGCTGGCGTGAAAGAGAAGTACCTGAGCGAGTACTGCTT CAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGCTACCACTTCA CCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAAGATTCAGGGC AGCGACGCCGGCTGGACACTGGGCTACATGCTGAATCTGACCAACAT GATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGCCACAGCACC
SEQ ID NO: 157	Forward primer	TCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCAGCAGCAGCACC AAGAAAACCCAGCTGACCAGCAGCACCCAGAACAAGGCCCTGC
SEQ ID NO: 158	Reverse primer	TAGAAGGCACAGTCGAGG
SEQ ID NO: 159	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCAGCAGCA GCACCCAGAACAAGGCCCTG
SEQ ID NO: 160	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCAGCAGCA GCACCCAGAACAAGGCCCTG
SEQ ID NO: 161	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCACCCAGAA CAAGGCCCTG
SEQ ID NO: 162	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCAGCAGCA GCACCAAGAAAACCCAGAACAAGGCCCTG
SEQ ID NO: 163	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCGCCCCTACCAGCAGCA GCACCAAGAAAACCCAGCTGACCCAGAACAAGGCCCTG
SEQ ID NO: 164	Forward primer	CTGGTCGCGATCCTGGAAGGCGTGCACTGCAGCAGCAGCACCAAGAA AACCCAGCTGACCCAGAACAAGGCCCTG
SEQ ID NO: 165	Primer P270	CATACGATTTAGGTGA
SEQ ID NO: 166	Primer P271	TAGAAGGCACAGTCGAGG
SEQ ID NO: 167	Ubiquitin tag	MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLED GRTLSDYNIQKESTLHLVLRLRGG
SEQ ID NO: 168	CKappa tag	TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGE
SEQ ID NO: 169	HSA Domain I tag	DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQSPFEDHVKLVNEVTEFA KTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERN ECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYF YAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELR
SEQ ID NO: 170	HSA Domain II tag	DEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLV TDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEK

		SHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYAR RHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKP
SEQ ID NO: 171	P928 primer	CTGCCGAGAAAGAACAGGACACCGGCGTGG
SEQ ID NO: 172	P929 primer	CCACGCCGGTGTCCTGTTCTTTCTCGGCAG
SEQ ID NO: 173	P930 primer	CGTGCCCCAGAATCAGGCCATCGAGAGCC
SEQ ID NO: 174	P931 primer	GGCTCTCGATGGCCTGATTCTGGGGCACG
SEQ ID NO: 175	P932 primer	GGCTACAAGAAAGTCGTGCAGGTGTCCGACCTGTACAAGAC
SEQ ID NO: 176	P933 primer	GTCTTGTACAGGTCGGACACCTGCACGACTTTCTTGTAGCC
SEQ ID NO: 177	P934 primer	GCATCCTGGAACTGTTCCAGACCAGCTACTGCCCC
SEQ ID NO: 178	P935 primer	GGGGCAGTAGCTGGTCTGGAACAGTTCCAGGATGC
SEQ ID NO: 179	P936 primer	CCGTGATGAAGTTCCTGCAGCTGACCAGCGAGAAG
SEQ ID NO: 180	P937 primer	CTTCTCGCTGGTCAGCTGCAGGAACTTCATCACGG
SEQ ID NO: 181	P938 primer	CACTGGGCTACATGCTGCAGCTGACCAACATGATCC
SEQ ID NO: 182	P939 primer	GGATCATGTTGGTCAGCTGCAGCATGTAGCCCAGTG
SEQ ID NO: 183	P878 primer	CTACATCCTGAGCCTGCTGCAGCAGGGCTACCACTTCAC
SEQ ID NO: 184	P879 primer	GTGAAGTGGTAGCCCTGCTGCAGCAGGCTCAGGATGTAG
SEQ ID NO: 185	P880 primer	GAGAAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCC
SEQ ID NO: 186	P881 primer	GGATGTAGGTGCCGCTGAAGCAAAACTCGCTCAGGTACTTCTC
SEQ ID NO: 187	P882 primer	GTTCGAGATCCAGGGCACCGGCAATTACCAGCAGTG
SEQ ID NO: 188	P883 primer	CACTGCTGGTAATTGCCGGTGCCCTGGATCTCGAAC
SEQ ID NO: 189	P884 primer	CGCCGATAGCTGGGAGCACATCCACTTCATCGGCAAG

SEQ ID NO: 190	P885 primer	CTTGCCGATGAAGTGGATGTGCTCCCAGCTATCGGCG
SEQ ID NO: 191	R113Mt empl	GAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGT GATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCA CCGCCGGCATGAGACTGCTGAGAATG
SEQ ID NO: 192	R113MF W	GAGATCGGCATCTACCTGACCGACT
SEQ ID NO: 193	R113M Rev	CATTCTCAGCAGTCTCAT
SEQ ID NO: 194	F330Ste mpl	CTTCAGCGCCTTCTACTcCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGAC
SEQ ID NO: 195	F330S FW	CTTCAGCGCCTTCTACTCC
SEQ ID NO: 196	F330S Rev	GGTCTTGATTTCCTCCCAG
SEQ ID NO: 197	Y377F templ	CTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACC TGAGCGAGTtCTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGC AGGGCTACCACTTCACCGCCGATA
SEQ ID NO: 198	L389C templ	CTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACC TGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCaG CAGGGCTACCACTTCACCGCCGATA
SEQ ID NO: 199	Y377F/L 389Q templ	CTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACC TGAGCGAGTTCTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCaG CAGGGCTACCACTTCACCGCCGATA
SEQ ID NO: 200	FW primer	CTGGGAGGAAATCAAGACC
SEQ ID NO: 201	Rev primer	TATCGGCGGTGAAGTGGTA
SEQ ID NO: 202	WT primer	CTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAAGTACC TGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTG CAGGGCTACCACTTCACCGCCGATA
SEQ ID NO: 203	fwMut17 4	CACCGGCCAGGAAGCCGGCGCCTACG
SEQ ID NO: 204	revMut1 74	CGTAGGCGCCGGCTTCCTGGCCGGTG
SEQ ID NO: 205	fwMut21 8	GGACCTGGGCGGAGCTGCTACCCAAGTGACCTTC
SEQ ID NO: 206	revMut2 18	GAAGGTCACTTGGGTAGCAGCTCCGCCCAGGTCC

SEQ ID NO: 207	plusMILfw	CTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGACCA GATGGTTCAGCATCGTGCCCTACGAGACAAACA
SEQ ID NO: 208	plusMILrev	TCACTTGGGTAGAAGCTCCGCCCAGGTCCAGGGCGCCGAAGGTTTCC TGATTGTTTGTCTCGTAGGGCA
EP1aa1-3		
SEQ ID NO: 209	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 210	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA TGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCT GCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCC ACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGC

		TACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAG CACACCTCTGAGCCACAGCACC
EP1xEP1 7aa1-3		
SEQ ID NO: 211	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 212	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA TGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTG CTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCA CTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCT

		ACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGC ACACCTCTGAGCCACAGCACC
EP1xEP1 7aa1-6		
SEQ ID NO: 213	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGAT AGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWIT INYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYG KDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNV SDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQC AFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQG SDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 214	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCATGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCC GTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAG CGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTG AGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAG GAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAA GTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCG GAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGA GCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAAT GTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTG GCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGC GGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCC GACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCC CTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCC ACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCC AGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTC GGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACC AGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTT CTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGA AAGAGAAGTACCTGAGCGAGTTCTGCTTCAGCGGCACCTACATCCTGA GCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCAC ATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACT

		GGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCC TGAGCACACCTCTGAGCCACAGCACC
EP1xEP17_K405N aa1-15		
SEQ ID NO: 215	Amino acid	APTSSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKEN DTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQE TPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQE EGAYGWITINYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDN ALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHP GYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNT SYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEM MKKFCAQPWEEIKTSYAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWE HIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 216	DNA	GCCCCTACCAGCAGCAGCACCAAGAAAACCCAGCTGACCAGCAGCAC CCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCTGG ATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTGCC GAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGCAG AGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGAGA TCGGCATCTACCTGACCGACTGCATGGAACGGGCCATGGAAGTGATC CCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACCGC CGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACCGG GTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGATTTT CAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGGCT GGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCAG GAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGAC CTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGC AGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTTC TGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGAC ATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCC CGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCT GCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAACCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAACGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA

		GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP1xEP1 7xEP19a a1-3		
SEQ ID NO: 217	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 218	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA TGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTTCTGCTTCAGCGGCACCTACATCCTGAGCCT GCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCC

		ACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGC TACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAG CACACCTCTGAGCCACAGCACC
EP1xEP17xEP19aa1-6		
SEQ ID NO: 219	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGAT AGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWIT INYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYG KDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNV SDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQC AFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQ GSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 220	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCATGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCC GTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAG CGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTG AGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAG GAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAA GTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCG GAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGA GCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAAT GTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTG GCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGC GGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCC GACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCC CTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCC ACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCC AGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTC GGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACC AGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTT CTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGA AAGAGAAGTACCTGAGCGAGTTCTGCTTCAGCGGCACCTACATCCTGA GCCTGCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCAC

		ATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACT GGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCC TGAGCACACCTCTGAGCCACAGCACC
EP1xEP1 4aa1-3		
SEQ ID NO: 221	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 222	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA TGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCTTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCT GCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCC ACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGT

		TACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAG CACACCTCTGAGCCACAGCACC
EP1xEP1 4aa1-6		
SEQ ID NO: 223	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGAT AGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWIT INYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYG KDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNV SDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQC AFNGIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQG SDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 224	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCATGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCC GTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAG CGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTG AGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAG GAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAA GTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCTTGGACCTGGGCG GAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGA GCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAAT GTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTG GCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGC GGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCC GACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCC CTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCC ACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCC AGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTC GGCGCCTTCAGCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGACC AGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTT CTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGA AAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTG AGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCA CATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACAC

		TGGGTTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCC CTGAGCACACCTCTGAGCCACAGCACC
EP17xEP 19aa1-3		
SEQ ID NO: 225	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 226	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA GGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTG CTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCA CTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCT

		ACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGC ACACCTCTGAGCCACAGCACC
EP17xEP 19aa1-6		
SEQ ID NO: 227	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITI NYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK DYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVS DLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCA FNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEFCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQ GSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 228	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAAAGAGAAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCCT GAGCCTGCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGC ACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACA

		CTGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCC CCTGAGCACACCTCTGAGCCACAGCACC
EP14aa1-3		
SEQ ID NO: 229	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 230	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGACGCCGGCTCCTCCCACACCTCCCTGTACATCTACAA GTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCACCAAGTG GAAGAGTGCAGAGTGAAGGGCCCCGGCATCTCCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA GAGAAGTGATCCCTCGGTCCCAGCACCAGGAAACCCCTGTCTACCTG GGCGCCACCGCCGGCATGCGGCTGCTGCGGATGGAATCCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAACGGTCCCTGTCCAACTAC CCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAGGG CGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCTCCC AGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCCAG CACCCAAGTCACATTCGTGCCCCAGAACCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAACGTGTAC ACCCACAGCTTTCTGTGCTACGGCAAGGACCAGGCCCTGTGGCAGAA GCTGGCCAAGGACATCCAAGTGGCCTCCAACGAGATCCTGCGGGACC CCTGCTTCCACCCCGGCTACAAGAAAGTGGTCAACGTGTCCGACCTG TACAAGACCCCTTGCACCAAGAGATTCGAGATGACCCTGCCCTTCCAG CAGTTCGAGATCCAGGGCATCGGCAACTACCAGCAGTGCCACCAGTC CATCCTGGAACTGTTCAACACCTCCTACTGCCCCTACTCCCAGTGCGC CTTCAACGGCATCTTCCTGCCTCCACTGCAGGGCGACTTCGGCGCCT TCTCCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGACCTCCGAGA AAGTGTCCCAGGAAAAAGTGACCGAGATGATGAAGAAGTTCTGCGCC CAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAGAA GTACCTGTCCGAGTACTGCTTCTCCGGCACCTACATCCTGTCCCTGCT GCTGCAGGGCTACCACTTCACCGCCGACAGCTGGGAGCACATCCACT TCATCGGCAAGATCCAGGGATCCGACGCTGGCTGGACCCTGGGCTAC

		ATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGTCCAC CCCTCTGTCTCACTCCACC
EP14aa1-6		
SEQ ID NO: 231	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITI NYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK DYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVS DLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCA FNGIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQG SDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 232	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCTTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCC TGAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAG CACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGAC

		ACTGGGTTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGC CCCTGAGCACACCTCTGAGCCACAGCACC
EP1xEP14xEP19aa1-3		
SEQ ID NO: 233	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 234	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA TGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCT GCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCC ACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGC

		TACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAG CACACCTCTGAGCCACAGCACC
EP1xEP14xEP19aa1-6		
SEQ ID NO: 235	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAMEVIPRSQHQETPVYLGAT AGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWIT INYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYG KDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNV SDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQC AFNGIFLPPLQGDFGAFSAFYSVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEHIHFIGKIQ GSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 236	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCATGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCC GTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAG CGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTG AGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAG GAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAA GTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCG GAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGA GCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAAT GTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTG GCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGC GGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCC GACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCC CTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCC ACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCC AGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTC GGCGCCTTCAGCGCCTTCTACTCCGTGATGAAGTTCCTGAACCTGACC AGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTT CTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGA AAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTG AGCCTGCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCA CATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACAC

		TGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCC CTGAGCACACCTCTGAGCCACAGCACC
EP17aa1-3		
SEQ ID NO: 237	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 238	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA GGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAACCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAACGAG AAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTG CTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGCACATCCA CTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGCT

		ACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAGC ACACCTCTGAGCCACAGCACC
EP17aa1-6		
SEQ ID NO: 239	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITI NYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK DYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVS DLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCA FNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWEHIHFIGKIQG SDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 240	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAACCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAACGAGAAGTACCTGAGCGAGTTTTGCTTCAGCGGCACCTACATCCT GAGCCTGCTGCTGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGC ACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACA

		CTGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCC CCTGAGCACACCTCTGAGCCACAGCACC
EP17aa1-15		
SEQ ID NO: 241	Amino acid	APTSSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKEN DTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQE TPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQE EGAYGWITINYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDN ALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHP GYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNT SYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEM MKKFCAQPWEEIKTSYAGVNEKYLSEFCFSGTYILSLLLQGYHFTADSWE HIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 242	DNA	GCCCCTACCAGCAGCAGCACCAAGAAAACCCAGCTGACCAGCAGCAC CCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGGCATCGTGCTGG ATGCCGGCAGCAGCCACACCAGCCTGTACATCTACAAGTGGCCTGCC GAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTGGAAGAGTGCAG AGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAAAGTGAACGAGA TCGGCATCTACCTGACCGACTGCATGGAACGGGCCAGGGAAGTGATC CCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTGGGAGCCACCGC CGGCATGAGACTGCTGAGAATGGAAAGCGAGGAACTGGCCGACCGG GTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTACCCATTCGATTTT CAAGGCGCCAGAATCATCACCGGCCAGGAAGAAGGCGCCTACGGCT GGATCACCATCAACTACCTGCTGGGCAAGTTCAGCCAGAAGAATCAG GAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTCTACCCAAGTGAC CTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCGACAACGCCCTGC AGTTCCGGCTGTACGGCAAGGACTACAATGTGTACACCCACAGCTTTC TGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAAGCTGGCCAAGGAC ATCCAGGTGGCCAGCAACGAGATCCTGCGGGACCCTTGCTTCCACCC CGGCTACAAGAAAGTCGTGAACGTGTCCGACCTGTACAAGACCCCCT GCACCAAGAGATTCGAGATGACCCTGCCCTTCCAGCAGTTCGAGATC CAGGGCATCGGCAATTACCAGCAGTGCCACCAGAGCATCCTGGAACT GTTCAACACCAGCTACTGCCCCTACAGCCAGTGCGCCTTCAACGGCA TCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGCCTTCAGCGCCTTC TACTTCGTGATGAAGTTCCTGAACCTGACCAGCGAGAAGGTGTCCCAG GAAAAAGTGACAGAGATGATGAAGAAGTTCTGCGCCCAACCCTGGGA GGAAATCAAGACCTCCTACGCTGGCGTGAACGAGAAGTACCTGAGCG AGTTTTGCTTCAGCGGCACCTACATCCTGAGCCTGCTGCTGCAGGGC TACCACTTCACCGCCGATAGCTGGGAGCACATCCACTTCATCGGCAA GATTCAGGGCAGCGACGCCGGCTGGACACTGGGCTACATGCTGAATC

		TGACCAACATGATCCCCGCCGAGCAGCCCCTGAGCACACCTCTGAGC CACAGCACC
EP19aa1-3		
SEQ ID NO: 243	Amino acid	APTTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEEC RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGM RLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYL LGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDY NVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDL YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFN GIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWE EIKTSYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEDIHFIGKIQGSD AGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 244	DNA	GCCCCTACCACCCAGAACAAGGCCCTGCCCGAGAACGTGAAGTACGG CATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGTACATCTACA AGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTGCATCAGGTG GAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTTCGTGCAGAA AGTGAACGAGATCGGCATCTACCTGACCGACTGCATGGAACGGGCCA GGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCCCGTGTATCTG GGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAAGCGAGGAAC TGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCTGAGCAACTA CCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCAGGAAGAAG GCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCAAGTTCAGC CAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGCGGAGCTTC TACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGAGAGCCCCG ACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACAATGTGTAC ACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGTGGCAGAA GCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCTGCGGGAC CCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGTCCGACCT GTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTGCCCTTCC AGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTGCCACCAG AGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAGCCAGTGC GCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATTTCGGCGC CTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGACCAGCGA GAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAGTTCTGCG CCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGTGAAAGAG AAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCCTGAGCCT GCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAGGACATCC ACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGACACTGGGC

		TACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGCCCCTGAG CACACCTCTGAGCCACAGCACC
EP19aa1-6		
SEQ ID NO: 245	Amino acid	APTSSSTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQV EECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITI NYLLGKFSQKNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK DYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVS DLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCA FNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQP WEEIKTSYAGVKEKYLSEYCFSGTYILSLLQQGYHFTADSWEDIHFIGKIQ GSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST
SEQ ID NO: 246	DNA	GCCCCTACCAGCAGCAGCACCCAGAACAAGGCCCTGCCCGAGAACGT GAAGTACGGCATCGTGCTGGATGCCGGCAGCAGCCACACCAGCCTGT ACATCTACAAGTGGCCTGCCGAGAAAGAAAACGACACCGGCGTGGTG CATCAGGTGGAAGAGTGCAGAGTGAAGGGCCCTGGCATCAGCAAGTT CGTGCAGAAAGTGAACGAGATCGGCATCTACCTGACCGACTGCATGG AACGGGCCAGGGAAGTGATCCCCAGAAGCCAGCACCAGGAAACCCC CGTGTATCTGGGAGCCACCGCCGGCATGAGACTGCTGAGAATGGAAA GCGAGGAACTGGCCGACCGGGTGCTGGACGTGGTGGAAAGAAGCCT GAGCAACTACCCATTCGATTTTCAAGGCGCCAGAATCATCACCGGCCA GGAAGAAGGCGCCTACGGCTGGATCACCATCAACTACCTGCTGGGCA AGTTCAGCCAGAAGAATCAGGAAACCTTCGGCGCCCTGGACCTGGGC GGAGCTTCTACCCAAGTGACCTTCGTGCCCCAGAATCAGACCATCGA GAGCCCCGACAACGCCCTGCAGTTCCGGCTGTACGGCAAGGACTACA ATGTGTACACCCACAGCTTTCTGTGCTACGGAAAGGACCAGGCTCTGT GGCAGAAGCTGGCCAAGGACATCCAGGTGGCCAGCAACGAGATCCT GCGGGACCCTTGCTTCCACCCCGGCTACAAGAAAGTCGTGAACGTGT CCGACCTGTACAAGACCCCCTGCACCAAGAGATTCGAGATGACCCTG CCCTTCCAGCAGTTCGAGATCCAGGGCATCGGCAATTACCAGCAGTG CCACCAGAGCATCCTGGAACTGTTCAACACCAGCTACTGCCCCTACAG CCAGTGCGCCTTCAACGGCATCTTCCTGCCACCTCTGCAGGGGGATT TCGGCGCCTTCAGCGCCTTCTACTTCGTGATGAAGTTCCTGAACCTGA CCAGCGAGAAGGTGTCCCAGGAAAAAGTGACAGAGATGATGAAGAAG TTCTGCGCCCAGCCCTGGGAGGAAATCAAGACCTCCTACGCTGGCGT GAAAGAGAAGTACCTGAGCGAGTACTGCTTCAGCGGCACCTACATCC TGAGCCTGCTGCAGCAGGGCTACCACTTCACCGCCGATAGCTGGGAG GACATCCACTTCATCGGCAAGATTCAGGGCAGCGACGCCGGCTGGAC

		ACTGGGCTACATGCTGAATCTGACCAACATGATCCCCGCCGAGCAGC CCCTGAGCACACCTCTGAGCCACAGCACC
SEQ ID NO: 247	Amino acid	EFRHDS
SEQ ID NO: 248	DNA	GAATTCCGGCACGACAGC
SEQ ID NO: 249	Amino acid	HHHHHH
SEQ ID NO: 250	DNA	CATCATCATCATCATCAC

CLAIMS

1. A solubilized human apyrase with modifications of: N terminal deletion, C terminal deletion and central modification, wherein
a) the N terminal deletion is between 30 and 50 amino acids long,
b) the C terminal deletion is between 20 and 40 amino acids long, and
c) the central modification comprises a deletion of 10 to 15 consecutive amino acids, wherein the deletion is a deletion of amino acids number 193 to 204 in relation to the wild type CD39 sequence according to SEQ ID NO: 1,
and wherein the central modification comprises a point mutation comprising one, two, three, four, or five point mutation(s) in relation to the wild type CD39 sequence according to SEQ ID NO: 1, selected from the group consisting of K71E, N73Q, V95A, G102D, Y104S, T106S, R113M, L149M, V151A, E173D, T229A, L254M, K258R, W263R, E276D, N292Q, R304G, I319T, N327Q, A362N, F365S, N371Q, K405N, Y412F, L424Q, H436D, I437N, F439S, G441D, N457Q, P463S, and S469R.

2. The solubilized human apyrase of claim 1, comprising a sequence selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 32, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 70, SEQ ID NO: 76, and SEQ ID NO: 78.

3. The solubilized human apyrase of claim 1 or claim 2, comprising a sequence selected from the group consisting of SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139 and SEQ ID NO: 141.

4. The solubilized human apyrase of claim 3, comprising or consisting of a sequence selected from the group consisting of SEQ ID NO: 213, SEQ ID NO: 227, SEQ ID NO: 219, SEQ ID NO: 225, SEQ ID NO: 217, SEQ ID NO: 209, SEQ ID NO: 221, SEQ ID NO: 72, SEQ ID NO: 215, SEQ ID NO: 223, SEQ ID NO: 211, SEQ ID NO: 58 and SEQ ID NO: 229.

5. The solubilized human apyrase of claim 4, consisting of a sequence selected from the group consisting of SEQ ID NO: 58, SEQ ID NO: 72 and SEQ ID NO: 229.

6. A pharmaceutical composition comprising a therapeutically effective dose of the apyrase of any one of claims 1 to 5 and one or more pharmaceutically acceptable carriers.

7. The pharmaceutical composition of claim 6, further comprising one or more additional active ingredients.

8. An isolated apyrase of any one of claims 1 to 5 for use as a medicament.

9. Use of an isolated apyrase of any one of claims 1 to 5 in the manufacture of a medicament for the treatment of tissue damage.

10. Use according to claim 9, wherein the tissue damage is acute brain injury (stroke); acute multi-organ failure; delayed graft function after transplantation of kidney or other solid organs; burn damage; radiation damage; acute damage due to trauma and/or hypoxia, such as acute respiratory distress syndrome (ARDS) or lung injury; acute kidney injury, such as acute kidney injury secondary to thoracic surgery (e.g. aortic valve replacement, coronary artery bypass surgery) or sepsis or rhabdomyolysis or toxic effects of antibiotics or other medication; acute myocardial injury.

11. Use of an isolated apyrase of any one of claims 1 to 5 in the manufacture of a medicament for the treatment of cardiac surgery associated acute kidney injury.

12. Use of an isolated apyrase of any one of claims 1 to 5 in the manufacture of a medicament for the treatment of delayed graft function (DGF), acute respiratory distress syndrome (ARDS), acute myocardial infarction (AMI), traumatic brain injury (TBI) / acute ischemic stroke (AIS), ischemia-reperfusion injury (IRI), or combinations

thereof often referred to as multi-organ failures (MOF).

13. Use of an isolated apyrase of any one of claims 1 to 5 in the manufacture of a medicament for the treatment of sepsis associated acute kidney injury.

14. An isolated nucleic acid molecule encoding an apyrase of any one of claims 1 to 5.

15. A cloning or expression vector comprising one or more nucleic acid sequences according to claim 14, wherein the vector is suitable for the recombinant production of isolated apyrase of any one of claims 1 to 5.

16. A host cell comprising one or more cloning or expression vectors according to claim 15.

17. A process for the production of an apyrase of any one of claims 1 to 5, comprising culturing a host cell according to claim 16, purifying and recovering said apyrase.