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(72) Inventeurs/Inventors:
CHARRETIER, YANNICK, FR;
CHARRIER, JEAN-PHILIPPE, FR;
FRANCESCHI, CHRISTINE, FR;
ZAMBARDI, GILLES, FR;
DEGOUT-CHARMETTE, ELODIE, FR;
CECCHINI, TIPHAINE, FR

(73) Propriétaire/Owner:
BIOMERIEUX INC., US

(74) Agent: ROBIC

(54) Titre : PROCEDE DE DETECTION D'AU MOINS UN MECANISME DE RESISTANCE AUX CARBAPENEMES PAR SPECTROMETRIE DE MASSE

(54) Title: METHOD OF DETECTING AT LEAST ONE MECHANISM OF RESISTANCE TO CARBAPENEMS BY MASS SPECTROMETRY

(57) Abrégé/Abstract:
The invention relates to a method for the mass spectrometry-based detection of at least one marker of at least one mechanism of resistance to at least one antimicrobial agent, for at least one microorganism included in a sample. The method is characterised in that the antimicrobial agent is a carbapenem, and said resistance markers are proteins or peptides. Preferably, the proteins or peptides are proteins from said microorganism.

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(71) Déposant *(pour tous les États désignés sauf US)* : **BIOMERIEUX INC.** [US/US]; 100 Rodolphe Street, Durham, North Carolina 27712 (US).

(72) Inventeurs; et

(75) Inventeurs/Déposants *(pour US seulement)* : **CHARRETIER, Yannick** [FR/FR]; Le Georges, F-69690 Courzieu (FR). **CHARRIER, Jean-Philippe** [FR/FR]; 28 rue Barthélémy Thimonnier, F-69160 Tassin La Demi-Lune (FR). **FRANCESCHI, Christine** [FR/FR]; Les Portes de la Dombe II, 1 rue des Carronnières, F-01800 Meximieux (FR). **ZAMBARDI, Gilles** [FR/FR]; 10 Impasse Pré Guillaud, F-38300 Chezeneuve (FR).

(74) Mandataire : **SPRUGNOLI, Claude**; bioMérieux, Département Propriété Industrielle, Chemin de l'Orme, F-69280 Marcy L'Etoile (FR).

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(54) Title : METHOD FOR DETECTING AT LEAST ONE CARBAPENEM RESISTANCE MECHANISM BY MEANS OF MASS SPECTROMETRY

(54) Titre : PROCEDE DE DETECTION D'AU MOINS UN MECANISME DE RESISTANCE AUX CARBAPENEMES PAR SPECTROMETRIE DE MASSE

(57) Abstract : The invention relates to a method for the mass spectrometry-based detection of at least one marker of at least one mechanism of resistance to at least one antimicrobial agent, for at least one microorganism included in a sample. The method is characterised in that the antimicrobial agent is a carbapenem, and said resistance markers are proteins or peptides. Preferably, the proteins or peptides are proteins from said microorganism.

(57) Abrégé : L'invention porte sur un procédé de détection, par spectrométrie de masse, d'au moins un marqueur d'au moins un mécanisme de résistance à au moins un antimicrobien, résistance d'au moins un microorganisme compris dans un échantillon, caractérisé en ce que l'antimicrobien est un carbapénème, et lesdits marqueurs de résistance sont des protéines ou des peptides. De façon préférentielle, lesdits protéines ou peptides sont des protéines dudit microorganisme.

Method of detecting at least one mechanism of resistance to carbapenems by mass spectrometry

The present invention relates to the field of microbiology. More precisely, the invention relates to the detection of at least one mechanism of resistance to carbapenems of at least one microorganism from a sample by using mass spectrometry.

Since Pasteur's discovery of microbes, microorganisms have been studied by microscopy and biochemical analyses. These conventional methods are often long and tedious, and analytical alternatives were sought very early on. This is why the analysis of bacteria by mass spectrometry was initiated from 1975 by J. Anhalt and C. Fenselau [1].

This preliminary work was followed by the study of fatty acids from the wall of the microorganisms using gas chromatography combined with mass spectrometry (GC-MS) [2]. This method was popularised under the English term FAME, standing for Fatty Acid Methyl Ester. It currently constitutes a reference method for taxonomic studies. However, its use remains limited to certain specialised laboratories dealing with the treatment of the sample by saponification, hydrolysis and derivation.

In 1996, the works by M. Claydon et al. [3] as well as by T. Krishnamurthy and P. Ross [4] demonstrated the possibility of identifying different bacterial species with a MALDI-TOF mass spectrometer (English acronym for Matrix Assisted Laser Desorption Ionization – Time Of Flight). The analysis combines the acquisition of a mass spectrum and the interpretation of expert software. It is extremely simple and can be carried out in a few minutes. However it has only been making it into medical analysis laboratories fairly recently [5]. Its clinical use is currently limited to the identification of bacteria and yeast species. It is not routinely used to identify resistances to antimicrobials.

Yet the identification of resistances to antimicrobials such as antibiotics is an essential element in ensuring optimal patient care.

Other mass spectrometry methods, particularly in tandem, have been proposed to meet these needs. By way of example, it is possible to cite the work of C. Fenselau et al. for identifying β-Lactamase with a quadripole-TOF (Q-TOF) [6].

However these research results are not applicable to routine clinical use. They were obtained with research instruments requiring highly qualified personnel. The analysis

times, often greater than one hour per sample, are incompatible with the workload of a microbiological analysis laboratory.

More recently, S. Hofstadler et al. [7] proposed a method combining a microbial genome amplification by PCR to a detection of the PCR products by electrospray-TOF (ESI-TOF). This method is now fully automated [8]. However, it requires a PCR amplification with the flaws inherent in molecular biology, namely extraction yield, cost of the probes, etc.

In this context, the objective of the present invention is to propose a method of detecting mechanisms of resistance to carbapenems which makes it possible to overcome the disadvantages of the prior art methods, namely providing an inexpensive method, without reagents specific to each species, particularly compared to molecular biology methods, which gives a result in a short amount of time, less than one hour, and which can be used in routine clinical work, without requiring highly qualified personnel.

To this end, the invention proposes a new method of detecting, by mass spectrometry, at least one mechanism of resistance to at least one antimicrobial of at least one microorganism from a sample, characterised in that the antimicrobial is a carbapenem and in that proteins and/or peptides are detected as markers of said mechanism of resistance to at least one carbapenem-class antibiotic.

Preferably, the resistance markers are proteins from said at least one microorganism.

Advantageously, markers of resistance to several different antimicrobials can be detected simultaneously.

As indicated in application PCT/FR2010/052181, markers of type and/or virulence of said microorganisms can be detected in the same way by mass spectrometry prior to or at the same time as the detection of the resistance mechanism markers.

Markers of resistance to at least one carbapenem-class antimicrobial is understood to mean molecules of protein origin which are characteristic of said properties.

Carbapenems are antibiotics belonging to the beta-lactam family and their main representatives are imipenem, meropenem, ertapenem and doripenem. These molecules are broken down by the beta-lactamases 2df, 2f and 3a of the classification by Bush and Jacoby ([9], Antimicrobial Agents and Chemotherapy, 2010; 54 (3): 969-976).

Determination of the resistance to at least one antimicrobial is understood to mean determining the susceptibility of a microorganism to being destroyed by an antimicrobial. The proteins involved in the resistance mechanisms will differ depending on the family and the species.

The nomenclature of the beta-lactamases, beta-lactam-resistant bacterial enzymes, is not standardised. They are either classified in four molecular classes (A to D) on the basis of their primary structure, or in functional groups on the basis of the target substrates and their resistance to inhibitors (for an overview, see [9] Bush and Jacoby, *supra*). For molecular classification, sequencing techniques have made more precise classification possible: for example, 183 variants of the TEM protein have been described (labelled TEM-i, with i being between 1 and 183). For the functional classification, Bush and Jacoby (*supra*) have proposed new functional subgroups:

- the group 1 enzymes are cephalosporinases belonging to the molecular class C. CMY and FOX are plasmid-borne enzymes, belonging to this subgroup.
- the group 2 enzymes belong to molecular classes A and D. This group is itself subdivided into subgroups, 2b, 2be, 2br, 2ber, 2d, 2de, 2df, 2f, etc. CTX-M (2be) and TEM (including 2be, 2br) are enzymes belonging to this subgroup. The subgroup 2b corresponds to broad-spectrum beta-lactamases which are inhibited by clavulanic acid, sulfobactam, or tazobactam. The subgroup 2be corresponds to extended-spectrum beta-lactamases (ESBL), which are also inhibited by clavulanic acid, sulfobactam or tazobactam. The subgroup 2br corresponds to beta-lactamases from the subgroup 2b which are insensitive to inhibition by clavulanic acid, sulfobactam or tazobactam. The subgroup 2df includes OXAs having a spectrum extended to carbapenems. Group 2f corresponds to carbapenemase beta-lactamases such as KPC.
- group 3 encompasses the metallo-beta-lactamases which hydrolyse carbapenems, such as IMP, VIM, SPM, GIM, SIM, AIM, KHM, DIM or NDM.

NDM-1 beta-lactamase was described in 2010 (Kumarasamy et al., 2010, Lancet Infect. Dis., 10:597-602). It corresponds to a metallo-beta-lactamase which confers a resistance to all beta-lactams except aztreonam.

KPC beta-lactamases were described from 2001 in the United States (Yigit et al., 2001, Antimicrobio. Agents Chemother., 45:1151-1161) and then throughout the world. They correspond to class-A beta-lactamases which confer a resistance to cephalosporins and to carbapenems, in particular to imipenem and to meropenem.

IMP beta-lactamases were described from 1994 in Japan (Osano et al., 1994, Antimicrobio. Agents Chemother., 38:71-78) and then throughout the world. They correspond to metallo-beta-lactamases which confer a resistance to cephalosporins and to carbapenems, but which do not confer resistance to Temocillin and to aztreonam.

VIM beta-lactamases were described from 1999 in Europe (Lauretti et al., 1999, Antimicrobio. Agents Chemother., 43:1584-1590) and then throughout the world. They correspond to metallo-beta-lactamases which confer a resistance to cephalosporins and to carbapenems, but which do not confer resistance to aztreonam.

The first GES beta-lactamase was isolated in 1998 in French Guiana (Poirel et al., 2000, Antimicrobio. Agents Chemother., 43:622-632). This enzyme (GES-1) conferred an ESBL resistance. The second isolate from a bacterium bearing a GES beta-lactamase was achieved in 2000 in South Africa (Poirel et al., 2001, Antimicrobio. Agents Chemother., 45:2598-2603). This enzyme (GES-2) conferred a resistance to cephalosporins and to carbapenems such as imipenem.

IND beta-lactamases were described for the first time in 1999 (Bellais et al., 1999, FEMS Microbio. Lett., 171:127-132). They correspond to metallo-beta-lactamases which confer a resistance to cephalosporins and to carbapenems.

SME beta-lactamases were described for the first time in 1994 (Naas et al., 1994, Antimicrobio. Agents Chemother., 38:1262-1270). They correspond to class-A beta-lactamases which confer a resistance to cephalosporins and to carbapenems.

OXA beta-lactamases (or oxacillinases) correspond to Class-D beta-lactamases. According to their primary sequence, they can confer resistances to cephalosporins or to cephalosporins and to carbapenems (Poirel et al., 2010, Antimicrobio. Agents Chemother., 54:24-38).

The method of the invention can be employed to detect mechanisms of resistance to carbapenems in bacteria. Thus, for example, as bacteria in which it is possible to seek a mechanism of resistance to carbapenems according to the method of the invention, non-exhaustive mention may be made of: *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, Bacillus* spp, *Stenotrophomonas maltophilia, Aeromonas* spp, *Bacteroides fragilis, Pseudomonas otitidis* and *Enterobacter cloacae*, and more generally, the Enterobacteriaceae, which

carry the bla_{NDM-1} or bla_{KPC} resistance gene. It should further be noted that the strains known to be resistant to carbapenems are also resistant to cephalosporins and to penicillins.

Thus, the method according to the invention also makes it possible to detect a mechanism of resistance to said antibiotics.

The sample on which the method of the invention can be employed is any sample susceptible of containing a target microorganism. The sample can be of biological origin, either animal, vegetable or human. In this case it may correspond to a specimen of biological fluid (whole blood, serum, plasma, urine, cerebrospinal fluid, organic secretion, for example), a tissue specimen or isolated cells. This specimen can be used such as it is, insofar as the markers of mechanisms of bacterial resistance to beta-lactams are available in the sample tested, or it can, prior to the analysis, undergo preparation by enrichment, extraction, concentration, purification, culturing, in accordance with methods known to the person skilled in the art.

The sample can be of industrial origin, or, according to a non-exhaustive list, can be an air specimen, a water specimen, a surface specimen, a part or a manufactured product, or a food product. Amongst the food samples, non-exhaustive mention can be made of a sample of a dairy product (yogurts, cheeses), of meat, of fish, of egg, of fruit, of vegetable, of water, of a beverage (milk, fruit juice, soda, etc.). These food samples can also come from sauces or ready meals. Finally, a food sample can come from an animal feed, such as animal meals.

Upstream of the detection by mass spectrometry, the sample to be analysed is preferably pretreated to produce peptides from the entirety of the proteins present in the sample to fragment these proteins into peptides, for example by digestion with a proteolytic enzyme (protease), or by the action of a chemical reagent. In fact, the cleaving of the protein can be performed by a physico-chemical treatment, by a biological treatment or by a combination of the two treatments. Amongst the useable treatments, mention can be made of treatment by hydroxyl radicals, in particular with H_2O_2. Treatment by hydroxyl radicals results in a cutting of the peptide bonds which takes place randomly on any of the protein's peptide bonds. The hydroxyl radical concentration determines the number of cleavages performed, and therefore the length of the peptide fragments obtained. Other chemical treatments can also be used such as, for example, cyanogen bromide (CNBr) treatment which specifically splits the peptide bonds at the carboxyl group of the methionyl residues. It is also

possible to perform partial acid cleaving at the aspartyl residues by heating a solution of proteins in trifluoroacetic acid to 1000°C.

Treatment of the proteins by enzymatic digestion is nevertheless preferred over physico-chemical treatment because it preserves more of the structure of the protein, and is easier to control. "Enzymatic digestion" is understood to mean the single or combined action of one or more enzymes under appropriate reaction conditions. The enzymes carrying out the proteolysis, which are called proteases, cut the proteins at specific locations. Each protease generally recognises a sequence of amino acids within which it always makes the same cut. Certain proteases recognise a single amino acid or a sequence of two amino acids between which they perform a cleavage, whereas other proteases only recognise longer sequences. These proteases can be endoproteases or exoproteases. Amongst the known proteases, mention may be made of the following as described in WO2005/098071:

- specific enzymes such as trypsin which splits the peptide bond at the carboxyl group of the Arg and Lys residues, endolysin which cleaves the peptide bond of the -CO group of the lysines, chymotrypsin which hydrolyses the peptide bond at the carboxylic group of the aromatic residues (Phe, Tyr and Trp), pepsin which makes a cut at the NH_2 group of the aromatic residues (Phe, Tyr and Trp), the protease V8 from the V8 strain of *Staphylococcus aureus* which cleaves the peptide bond at the carboxylic group of the Glu residue;
- the non-specific enzymes such as thermolysin from the bacteria *Bacillus thermoproteolyticus* which hydrolyses the peptide bond of the NH_2 group of hydrophobic amino acids (Xaa-The, Xaa-Ile, Xaa-Phe), subtilisin and pronase which are bacterial proteases which hydrolyse practically all the bonds and can transform the proteins into oligopeptides under controlled reaction conditions (enzyme concentration and duration of reaction).

Several proteases may be used simultaneously, if their modes of action are compatible, or they may be used successively. Within the framework of the invention, the digestion of the sample is preferably performed by the action of a protease enzyme, for example trypsin.

The generation of peptides using a chemical reagent or a protease can be obtained by means of a simple reaction in solution. It can also be performed with a microwave oven [10], or under pressure [11], or even with an ultrasound device [12]. In these three latter cases, the protocol will be much faster.

Amongst the peptides thus obtained, the peptides specific to the protein are referred to as proteotypic peptides. It is these which will be assayed by mass spectrometry.

According to the invention, the markers of the mechanisms of bacterial resistance to carbapenems are proteins from the bacterium in which the mechanisms of resistance to cephalosporins are to be sought. In particular, said proteins are digested into peptides, preferably by an enzyme, and more preferably by trypsin.

Similarly, the sample containing protein markers characterising mechanisms of bacterial resistance to carbapenems can also be pretreated for the purposes of purification. This purification pretreatment can be employed before or after the peptide production step as described above.

The sample purification pretreatment is widely known to the person skilled in the art and may in particular employ the techniques of centrifugation, filtration, electrophoresis or chromatography. These separating techniques can be used alone or in combination with one another to obtain a multidimensional separation. For example, multidimensional chromatography can be used by combining separation by ion exchange chromatography with reversed-phase chromatography, as described by T. Fortin et al. [13], or H. Keshishian et al. [14]. In these publications, the chromatography medium can be in a column or in a cartridge (solid-phase extraction).

The electrophoretic or chromatographic fraction (or the retention time in monodimensional or multidimensional chromatography) of the proteotypic peptides is characteristic of each peptide, and employing these techniques therefore makes it possible to select the proteotypic peptide or peptides to be assayed. Such a fractionation of the produced peptides makes it possible to increase the specificity of the subsequent assay by mass spectrometry.

An alternative to the electrophoresis or chromatography techniques for the fractionation of the peptides consists in specifically purifying the N-glycopeptides ([15] and patent application WO 2008/066629). However, such a purification only makes it possible to quantify the peptides which have undergone an N-glycosylation post-translational modification. Not all proteins are glycosylated though, which therefore limits its use.

The mass spectrometry to be employed in the method of the invention is widely known to the person skilled in the art as a powerful tool for analysing and detecting different types of molecules. Generally, any type of molecule able to be ionised can

be detected according to its molecular mass with the aid of a mass spectrometer. According to the nature of the molecule to be detected, whether of protein or metabolic origin, certain mass spectrometry technologies can be more suitable. Nevertheless, whatever mass spectrometry method is used for the detection, this latter includes a step of ionising the target molecule into so-called molecular ions, in the present case a step of ionising the characterising markers, and a step of separating the molecular ions obtained according to their mass.

All mass spectrometers therefore comprise:

- an ionising source intended to ionise the markers present in the sample to be analysed, i.e. to confer a positive or negative charge upon these markers;
- a mass analyser intended to separate the ionised markers, or molecular ions, according to their mass-to-charge ratio (m/z);
- a detector intended to measure the signal produced either directly by the molecular ions, or by ions produced from molecular ions as detailed hereafter.

The ionisation step necessary for employing mass spectrometry can be performed via any method known to the person skilled in the art. The ionising source makes it possible to transform the molecules to be assayed into a gaseous and ionised state. An ionising source can be used either in positive mode to study the positive ions, or in negative mode to study the negative ions. Several types of sources exist and will be used depending on the result sought and the molecules analysed. In particular, mention may be made of:

- electron ionisation (EI), chemical ionisation (CI) and desorption chemical ionisation (DCI)
- fast atom bombardment (FAB), metastable atom bombardment (MAB) or ion bombardment (SIMS, LSIMS)
- inductively coupled plasma (ICP)
- atmospheric-pressure chemical ionisation (APCI) and atmospheric-pressure photoionisation (APPI)
- electronebulisation or electrospray (ESI)
- matrix-assisted laser desorption/ionisation (MALDI), surface-activated laser desorption/ionisation (SELDI) or desorption/ionisation on silicon (DIOS)
- ionisation/desorption by interaction with metastable species (DART)

In particular, ionisation can be employed as follows: the sample containing the target molecules is introduced into an ionisation source, where the molecules are ionised in gaseous state and thus transformed into molecular ions which correspond to the initial molecules. An electrospray ionisation (ESI) source makes it possible to ionise a molecule by making it pass from a liquid state into a gaseous state. The molecular ions obtained therefore correspond to the molecules present in liquid state, with, in positive mode, one, two, or even three or more additional protons and therefore carry one, two, or even three or more charges. For example, when the target molecule is a protein, an ionisation of the proteotypic peptides obtained after fractionation of the target protein, by means of an electrospray source functioning in positive mode, leads to polypeptide ions in gaseous state, with one, two, or even three or more additional protons and which therefore carry one, two, or even three or more charges, and makes it possible to move from a liquid state to a gaseous state [16]. This type of source is particularly well suited when the target molecules or proteotypic peptides obtained are separated beforehand by reversed-phase liquid chromatography. Nevertheless, the ionisation yield of the molecules present in the sample may vary depending on the concentration and the nature of the different species present. This phenomenon leads to a matrix effect well known to the person skilled in the art.

A MALDI ionisation source will allow ionisation of the molecules from a solid-state sample.

The mass analyser in which the step of separating the ionised markers according to their mass-to-charge ratio (m/z) is performed is any mass analyser known to the person skilled in the art. Mention can be made of low-resolution analysers, quadripole or quadrupole (Q), 3D ion trap (IT) or linear ion trap (LIT), also called ion trap, and high-resolution analysers which make it possible to measure the exact mass of the analytes and which in particular use the magnetic sector linked to an electric sector, the time of flight (TOF), Fourier transform ion cyclotron resonance (FT-ICR), orbitrap.

The separation of the molecular ions depending upon their m/z ratio can be employed just once (single mass spectrometry or MS), or several successive MS separations can be conducted. When two successive MS separations are carried out, the analysis is called MS/MS or MS^2. When three successive MS separations are

carried out, the analysis is called MS/MS/MS or MS^3, and more generally, when n successive MS separations are carried out, the analysis is called MS^n.

Amongst the techniques which employ several successive separations, SRM (Selected Reaction Monitoring) mode when detecting or assaying a single target molecule, or MRM (Multiple Reaction Monitoring) mode when detecting or assaying several target molecules are particular uses of MS^2 separation. Similarly the MRM^3 mode is a particular use of MS/MS/MS separation. This is referred to as targeted mass spectrometry.

In the case of a detection in single MS mode, it is the mass-to-charge ratio of the molecular ions obtained which is correlated to the target molecule to be detected.

In the case of detection in MS/MS mode, essentially two steps are added, compared to an MS assay, which are:

- a fragmentation of the molecular ions, then called precursor ions, to give ions called 1^{st} generation fragment ions, and
- a separation of the ions called 1^{st} generation fragment ions according to their mass $(m/z)_2$, the ratio $(m/z)_1$ corresponding to the ratio (m/z) of the precursor ions.

It is therefore the mass-to-charge ratio of the 1^{st} generation fragment ions thus obtained which is correlated to the target molecule to be detected. First-generation fragment ion is understood to be an ion derived from the precursor ion, following a fragmentation step and of which the mass-to-charge ratio m/z is different from the precursor ion.

The $(m/z)_1$ and $(m/z)_2$ pairs are called transitions and are representative of the characteristic ions to be detected.

The choice of the characteristic ions which are detected to be correlated to the target molecule is made by the person skilled in the art in accordance with the standard methods. Their selection will advantageously lead to the most sensitive, specific and robust assays possible, in terms of reproducibility and reliability. In the methods developed for the selection of proteotypic peptides $(m/z)_1$, and of the first-generation fragment $(m/z)_2$, the choice is essentially based on the intensity of the response. For more details, it is possible to refer to V. Fusaro et al. [17]. Commercially available software, such as the MIDAS and MRM Pilot software from Applied Biosystems or MRMaid [18] can be used by the person skilled in the art to allow him to predict all the possible transition pairs. He can also make use of a database called PeptideAtlas

constructed by F Desiere et al. [19] to compile all of the MRM transitions of peptides described by the scientific community. This database PeptideAtlas is freely available on the internet. For non-protein molecules, it is also possible to use databases, such as, for example, the one accessible through the Cliquid software from the company Applied Biosystems (United States of America).

An alternative approach to selecting the proteotypic peptides $(m/z)_1$ and $(m/z)_2$ consists in using MS/MS fragmentation spectra obtained during other work. This work can be, for example, the phases of biomarker discovery and identification by proteomic analysis. This approach was proposed by Thermo Scientific during user conferences [18]. It makes it possible to generate a list of candidate transitions from the peptides identified through testing by the SIEVE (Thermo Scientific) software. Certain criteria were detailed by J. Mead et al. [18] for the choice of the ions $(m/z)_1$ and $(m/z)_2$ and are detailed hereafter:

- peptides with internal cleavage sites, i.e. with internal Lysine or Arginine, must be avoided, unless the Lysine or Arginine is followed by Proline,
- peptides with Aspargine or Glutamine must be avoided because they may deaminate,
- peptides with Glutamine or Glutamic Acid at the N-terminal must be avoided because they may cyclise spontaneously,
- peptides with Methionine must be avoided because they may be oxidised,
- peptides with Cysteine must be avoided because they may be non-reproducibly modified during a potential step of denaturation, reduction and blocking of the thiol functions,
- peptides with Proline may be considered to be favourable because they generally produce intense fragments in MS/MS with a very strong single peak. However, a very strong single fragment does not make it possible to validate the identity of the transition in a complex mixture. Indeed, only the simultaneous presence of several characteristic fragments makes it possible to verify that the precursor ion sought has actually been detected,
- the peptides having a Proline adjacent to the C-terminal (Position n-1) or in second position relative to the C-terminal (position n-2) should be avoided because, in this case, the size of the first-generation peptide fragment is generally considered to be too small to be sufficiently specific,

- the selection of fragments having a mass greater than the precursor should be given preference in order to promote specificity. To this end, it is necessary to select a dicharged precursor ion and select the most intense first-generation ion fragment having a mass greater than the precursor, i.e. a monocharged first-generation fragment ion.

The fragmentation of the selected precursor ions is performed in a fragmentation cell such as the triple quadripole model [20], ion trap model [21], or time-of-flight (TOF) model [22], which also make it possible to separate ions. The fragmentation or fragmentations will be conventionally performed by collision with an inert gas such as argon or nitrogen, within an electrical field, by photo-excitation or photo-dissociation using an intense light source, collision with electrons or radical species, by applying a potential difference, for example in a time-of-flight tube, or by any other activation mode. The characteristics of the electrical field determine the intensity and nature of the fragmentation. Thus, the electrical field applied in the presence of an inert gas, for example in a quadripole, determines the collision energy provided to the ions. This collision energy will be optimised, by the person skilled in the art, to increase the sensitivity of the transition to be assayed. By way of example, it is possible to vary the collision energy between 5 and 180 eV in q2 in an AB SCIEX QTRAP® 5500 mass spectrometer from the company Applied Biosystems (Foster City, United States of America). Similarly, the duration of the collision step and the excitation energy within, for example, an ion trap will be optimised by the person skilled in the art to lead to the most sensitive assay. By way of example, it is possible to vary this duration, called excitation time, between 0.010 et 50 ms and the excitation energy between 0 and 1 (arbitrary unit) in Q3 in an AB SCIEX QTRAP® 5500 mass spectrometer by the company Applied Biosystems.

Finally, the detection of the selected characteristic ions takes place in the conventional manner, particularly by means of a detector and a processing system. The detector collects the ions and produces an electrical signal whose intensity depends on the amount of ions collected. The signal obtained is then amplified such that it can be processed by computer. A computer data processing assembly makes it possible to transform the information received by the mass spectrum detector.

The principle of the SRM mode, or even of the MRM mode, is to specifically select a precursor ion, fragment it, and then specifically select one of its fragment ions. For

such applications, triple quadripole or hybrid triple quadripole/ion trap devices are generally used.

In the case of a triple quadripole device (Q1q2Q3) used in MS^2 mode, with a view to assaying or detecting a target protein, the first quadripole (Q1) makes it possible to filter the molecular ions corresponding to the proteotypic peptides characteristic of the protein to be assayed and obtained during an earlier digestion step, depending on their mass-to-charge ratio (m/z). Only the peptides having the mass-to-charge ratio of the proteotypic peptide sought, which ratio is called $(m/z)_1$, are transmitted into the second quadripole (q2) and act as precursor ions for the subsequent fragmentation. The analyser q2 can fragment the peptides of mass-to-charge ratio $(m/z)_1$ into first-generation fragment ions. Fragmentation is generally obtained through collision of the precursor peptides with an inert gas, such as nitrogen or argon in q2. The first-generation fragment ions are transmitted into a third quadripole (Q3) which filters the first-generation fragment ions depending on a specific mass-to-charge ratio, called $(m/z)_2$. Only the first-generation fragment ions having the mass-to-charge ratio of a fragment characteristic of the sought proteotypic peptide $(m/z)_2$ are transmitted into the detector in order to be detected, or even quantified.

This mode of operation exhibits a double selectivity, with regard to the selection of the precursor ion on the one hand, and the selection of the first-generation fragment ion on the other hand. Mass spectrometry in SRM or MRM mode is therefore advantageous for quantification.

When the mass spectrometry employed in the method according to invention is tandem mass spectrometry (MS^2, MS^3, MS^4 or MS^5), several mass analysers can be linked to one another. For example, a first analyser separates the ions, a collision cell makes it possible to fragment the ions, and a second analyser separates the fragment ions. Certain analysers, such as the ion traps or the FT-ICR, constitute several analysers in one and make it possible to fragment the ions and analyse the fragments directly.

According to preferred embodiments of the invention, the method of the invention comprises one or more of the following characteristics:

- the mass spectrometry employed for the properties of potential resistance to at least one antimicrobial is MS/MS spectrometry, which has the advantage of producing a fragment which is specific to the molecule to be

detected or quantified, and thus of providing great specificity to the assaying method;

- the MS/MS spectrometry is MRM which has the advantage of using an analysis cycle time in the mass spectrometer of several tens of milliseconds, which makes it possible to detect or quantify, with a high degree of sensitivity, a large number of different molecules in a multiplexed manner;
- where applicable, the determination of the type properties and of the virulence factor is performed in the same mass spectrometry apparatus as the determination of the markers of resistance to at least one antimicrobial, preferably simultaneously, which has the advantage of reducing the analysis time and the cost of the instrument, which also facilitates the processing and the yielding of the results.

In addition to determining the resistance to an antibiotic, it is necessary to identify the microorganism or microorganisms present in the sample to be tested.

The methods of identifying microorganisms are widely known to the person skilled in the art, as described for example by Murray P. R. et al. in Manual of Clinical Microbiology, 2007, 9th edition, and especially in Vol. I, Section III, chapters 15 and 16 for bacteria and yeasts, Vol. II, Section VI, chapter 82 for viruses, and Vol. II, Section X, chapter 135 for protozoa. As an example of conventional identification methods, mention can be made of the determination of the biological profile, by using the Vitek 2 (bioMérieux) identification cards, for example, or even by using molecular biology techniques with identification criteria based on the study of the presence of certain genes, and on the study of their sequence.

Identification can be performed directly from the sample in which the identification is made, or the microorganisms contained in the sample can be cultured using methods well known to the person skilled in the art with optimal culture media and culturing conditions tailored to the species of microorganisms to be sought, as described by Murray P. R. et al. in Manual of Clinical Microbiology, 2007, 9th edition, Vol. I, Section III, chapter 14, and in particular in Vol. I, Section IV, chapter 21 for bacteria, and Vol. II, Section VI, chapter 81 for viruses, Vol. II, Section VIII, chapter 117 for yeasts, and Vol. II, Section X, chapter 134 for protozoa.

Thus, generally, in the case of an identification using a biochemical method of a bacterium in a specimen, it is first necessary to obtain it in a pure culture, for example

after seeding on agar. Molecular biology (PCR) can in certain cases be applied directly to the sample to be analysed.

Instead of cultivating the microorganisms, they can be concentrated by capture directly in the sample by means of active surfaces. Such a method was described by W.-J. Chen et al. [10] who captured different bacterial species with the aid of magnetic beads with an Fe_3O_4/TiO_2-activated surface. Capture by other means is also possible, such as a capture by lectins [23], or by antibodies [24], or by Vancomycin [25]. The capture makes it possible to concentrate the microorganisms and thus to reduce or even eliminate the culture step. This results in a considerable time saving.

The identification may also be performed by mass spectrometry, in accordance with the techniques described previously, preferably by MS, by MS/MS, or even by MS followed by MS/MS spectrometry, which constitutes one embodiment of the invention. In this case too, the sample can be subjected to a culture step beforehand, such as seeding on agar.

The use of an MS identification method is advantageous in that it may be carried out in a few minutes, and in that it requires a mass spectrometer with a single analyser, i.e. a less complex instrument than a tandem mass spectrometer used in MS/MS.

The use of a method of identification by MS followed by MS/MS spectrometry is also advantageous. It makes it possible to check the identity of the ions observed by MS, which increases the specificity of the analysis.

The use of an MRM-type MS/MS identification method has the advantage of being more sensitive and simpler than the conventional MS followed by MS/MS approaches. This method requires neither a high-performance software to process the information between the acquisition of the MS spectrum and of the MS/MS spectrum, nor a change in the setting of the machine parameters for linking up MS then MS/MS spectra.

The method of identification by MS may be employed with an electrospray source on a raw sample, as described by S. Vaidyanathan et al. [26] or by R. Everley et al. [27] after chromatographic separation. Different m/z ranges thus make it possible to identify the microorganisms. S. Vaidyanathan et al. used a window of between 200 and 2000 Th, and R. Everley et al. used a window of between 620 and 2450 Th. The mass spectra may also be deconvoluted to access the mass of the proteins independently of their charge state. R. Everley et al. therefore used masses of

between about 5,000 and 50,000 Da. Alternatively, the method of identification by MS can also be employed with the aid of a MALDI-TOF, as described by Claydon et al. [3] and T. Krishnamurthy and P. Ross [4]. The analysis combines acquisition of a mass spectrum and interpretation of expert software. It is extremely simple and can be carried out in a few minutes. This method of identification is currently becoming more widespread in medical analysis laboratories [28].

The identification of bacteria by MS followed by MS/MS via their proteins present in the sample has been applied widely by a number of teams. By way of example, mention can be made of the recent work of Manes N. et al. [29], who studied the peptidome of *Salmonella enterica*, or the work of R. Nandakumar et al. [30] or of L. Hernychova et al. [31] who have studied the proteome of bacteria after digestion of the proteins with trypsin. The conventional approach consists in i) acquiring an MS spectrum, ii) successively selecting each precursor ion observed on the MS spectrum with an intense signal, iii) successively fragmenting each precursor ion and acquiring its MS/MS spectrum, iv) interrogating protein databases such as SWISS-PROT or NCBI, through software such as Mascot (Matrix Science, London, United Kingdom) or SEQUEST (Thermo Scientific, Waltham, United States of America), to identify the peptide which has a strong probability of matching the MS/MS spectrum observed. This method may lead to the identification of a microorganism if a protein or a peptide characteristic of the species is identified.

One of the advantages of the use of mass spectrometry lies in that it is particularly useful for quantifying molecules, in the present case the markers of the mechanisms of bacterial resistance to beta-lactams. To this end, the current intensity detected is used, which is proportional to the quantity of target molecule. The current intensity thus measured may serve as a quantitative measurement making it possible to determine the quantity of target molecule present, which is characterised by its expression in International System (SI) mol/m^3 or kg/m^3 units, or by multiples or sub-multiples of these units, or by the usual derivatives of the SI units, including multiples or sub-multiples thereof. As a non-limiting example, the units such as ng/ml or fmol/l are units characterising a quantitative measurement.

A calibration is nevertheless necessary in order to be able to correlate the measured area of the peak, which corresponds to the current intensity induced by the detected ions, to the quantity of target molecule to be assayed. For this purpose, the calibrations conventionally used in mass spectrometry may be employed, within the

framework of the invention. MRM assays are conventionally calibrated with the aid of external standards or, preferably, with the aid of internal standards such as described by T. Fortin et al. [13]. If the target molecule is a proteotypic peptide which permits the assaying of a protein of interest, the correlation between the quantitative measurement and the quantity of target proteotypic peptide, and subsequently of protein of interest, is obtained by calibrating the measured signal relative to a standard signal for which the quantity to be assayed is known. The calibration may be performed using a calibration curve, for example obtained by successive injections of standard proteotypic peptide at different concentrations (external calibration), or preferably by internal calibration using a heavy peptide as an internal standard, for example in accordance with the AQUA, QconCAT or PSAQ methods detailed below. "Heavy peptide" is understood to mean a peptide corresponding to the proteotypic peptide, but in which one or more atoms of carbon 12 (^{12}C) is (are) replaced by carbon 13 (^{13}C), and/or one or more atoms of nitrogen 14 (^{14}N) is (are) replaced by nitrogen 15 (^{15}N).

The use of heavy peptides as internal standards (AQUA) was also proposed in US patent application 2004/0229283. The principle is to artificially synthesise proteotypic peptides with amino acids containing isotopes which are heavier than the usual natural isotopes. Such amino acids are obtained, for example, by replacing some of the atoms of carbon 12 (^{12}C) with carbon 13 (^{13}C), or by replacing some of the atoms of nitrogen 14 (^{14}N) with nitrogen 15 (^{15}N). The artificial peptide (AQUA) thus synthesised has strictly the same physicochemical properties as the natural peptide (with the exception of a higher mass). It is generally added, at a given concentration, to the sample, upstream of assaying by mass spectroscopy, for example between the treatment entailing the cleaving of the proteins in the sample of interest and the fractionation of the peptides obtained after the treatment step. Thus, the AQUA peptide is co-purified with the natural peptide to be assayed, during fractionation of the peptides. The two peptides are therefore injected simultaneously into the mass spectrometer, for assaying. They then undergo the same ionisation yield in the source. The comparison of the peak areas of the natural and AQUA peptides, whose concentration is known, makes it possible to calculate the concentration of the natural peptide and thus the concentration of the protein to be assayed. A variation of the AQUA technique was proposed by J.-M. Pratt et al. [32] under the name QconCat. This variant is also described in patent application WO 2006/128492. It

consists in concatenating various AQUA peptides and producing the artificial polypeptide in the form of a heavy recombinant protein. The recombinant protein is synthesised with amino acids comprising heavy isotopes. In this way, it is possible to obtain a standard to calibrate the simultaneous assay of several proteins at lower cost. The QconCAT standard is added from the start, upstream of the treatment entailing the cleaving of the proteins and prior to the steps of protein fractionation, denaturation, reduction and blocking of the protein thiol functions, if these are present. The QconCAT standard therefore undergoes the same treatment cycle entailing the cleaving of the proteins as the natural protein, which makes it possible to take account of the yield from the treatment step which entails the cleaving of the proteins. In fact, the treatment, particularly by digestion, of the natural protein may not be complete. In this case, the use of an AQUA standard would lead to underestimating the quantity of natural protein. For full assaying, it may therefore be important to take into account the yields from treatment which entails the cleaving of the proteins. However, V. Brun et al. [33] have shown that the QconQAT standards sometimes do not exactly reproduce the treatment yield particularly by digestion of the natural protein, undoubtedly due to a three-dimensional conformation different from the QconCAT protein.

V. Brun et al. [33] then proposed the use of a method dubbed PSAQ, and described in patent application WO 2008/145763. In this case, the internal standard is a recombinant protein having the same sequence as the natural protein but synthesised with heavy amino acids. The synthesis is performed ex-vivo with heavy amino acids. This standard has strictly the same physicochemical properties as the natural protein (with the exception of a higher mass). It is added from the start, before the protein fractionation step, when the latter is present. It is therefore co-purified with the native protein, during the protein fractionation step. It exhibits the same treatment yield, particularly by digestion, as the native protein. The heavy peptide obtained after cleaving is also co-purified with the natural peptide, if a peptide fractionation step is performed. The two peptides are therefore injected simultaneously into the mass spectrometer, to be quantitatively assayed. They then undergo the same ionisation yields in the source. Comparison of the peak areas of the natural and the reference peptides in the PSAQ method makes it possible to calculate the concentration of the protein to be assayed taking into account all of the steps of the assay method.

All of these techniques, namely AQUA, QconCAT or PSAQ or any other calibration technique, used in the mass spectrometry assays and in particular in MRM or MS assays, may be employed to carry out calibration, within the framework of the invention.

Preferably, the mass spectrometry used in the detection method according to the invention is MS/MS. More preferably, the mass spectrometry is MRM.

The method of the invention makes it possible to detect resistances to carbapenems, characterised by the detection of at least one peptide as a resistance marker. Said resistance marker peptide preferably belongs to the proteins NDM, KPC, GES, IMP, IND, SME, VIM or OXA.

In some embodiments, described herein are one or more of the following items:

1. A method of detecting at least one carbapenem resistance marker in a sample, the method comprising: subjecting the sample to MS/MS spectrometry in MRM mode, and detecting whether at least one of the carbapenem resistance marker is present in the sample, wherein the at least one carbapenem resistance marker comprises a KPC peptide of SEQ ID NO: 20-33, 1094, 1096, or 1097.
2. The method of item 1, wherein the at least one carbapenem resistance marker comprises a KPC peptide of SEQ ID NO: 20, 21, 23, 25, 28, 29, 31, or 32.
3. The method of item 1 or 2, wherein at least one of the carbapenem resistance markers are from a microorganism in the sample.
4. The method of any one of items 1 to 3, further comprising, before performing MS/MS spectrometry in MRM mode, digesting proteins in the sample to produce peptides.
5. The method of item 4, wherein the digestion is performed by an enzyme.
6. The method of item 5, wherein the enzyme is trypsin.

7. The method of any one of items 1 to 6, wherein the carbapenem resistance markers further comprise proteins or peptides of NDM, GES, IMP, IND, SME, VIM, OXA type, or any combination thereof.
8. The method of item 7, wherein the carbapenem resistance markers comprise one or more NDM peptides of SEQ ID NO: 2-9 or 1083.
9. The method of item 8, wherein the carbapenem resistance markers comprise one or more NDM peptides of SEQ ID NO: 2, 3, 5, or 7.
10. The method of any one of items 7 to 9, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 51, 52, 54-58, 61-75, or 77-79.
11. The method of item 10, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 51, 61, 64, 70, 73, 74, or 79.
12. The method of item 10, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 54, 55, 66, 67, 68, 69, 71, 77, or 78.
13. The method of any one of items 7 to 12, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 106, 108-130, 133-173, or 175-180.
14. The method of item 13, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 106, 108, 109, 110, 112, 113, 115, 116, 117, 118, 121, 124, 126, 127, 128, 129, 130, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 175, 176, 177, 179, or 180.
15. The method of item 13, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 109, 143, 144, 148, 149, 150, 151, 154, 155, 156, 159, 165, 169, 170, 171, 172, or 173.
16. The method of any one of items 7 to 15, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188-197, 200, 201, or 203-262.

17. The method of item 16, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188, 189, 190, 191, 192, 193, 194, 195, 197, 201, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 215, 216, 218, 219, 220, 221, 222, 225, 226, 227, 228, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.
18. The method of item 16, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188, 193, 207, 242, 243, 246, 256, or 260.
19. The method of any one of items 7 to 18, wherein the carbapenem resistance markers comprise one or more SME peptides of SEQ ID NO: 266-281 or 283-287.
20. The method of item 19, wherein the carbapenem resistance markers comprise one or more SME peptides of SEQ ID NO: 266, 268, 269, 270, 273, 274, 277, 279, or 281.
21. The method of any one of items 7 to 20, wherein the carbapenem resistance markers comprise one or more VIM peptides of SEQ ID NO: 314-318, or 320-346.
22. The method of item 21, wherein the carbapenem resistance markers comprise one or more VIM peptides of SEQ ID NO: 316, 318, 321, 341, 342, 344, or 346.
23. The method of any one of items 7 to 22, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 509-523, 525-572, 574-604, 606-618, 620-696, 698-1077, or 1098-1109.
24. The method of item 23, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 509, 510, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 525, 526, 528, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 571, 572, 574, 575, 576, 577, 578, 580, 581, 583, 584, 586, 587, 588, 589, 590, 591, 593, 594, 595, 596, 597, 598, 599, 600,

601, 602, 604, 606, 607, 609, 611, 612, 613, 614, 615, 616, 618, 620, 622, 623, 624, 625, 626, 627, 632, 633, 635, 636, 637, 638, 639, 640, 641, 642, 643, 645, 648, 649, 651, 652, 653, 654, 655, 656, 659, 660, 664, 665, 666, 667, 669, 670, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 696, 698, 699, 700, 701, 702, 703, 706, 707, 710, 714, 717, 719, 720, 722, 725, 726, 727, 728, 729, 732, 735, 736, 737, 738, 740, 741, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 759, 760, 762, 763, 766, 767, 768, 769, 770, 771, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 785, 786, 787, 788, 789, 790, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 803, 804, 805, 806, 807, 809, 810, 811, 812, 813, 814, 815, 818, 821, 822, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 840, 841, 842, 844, 845, 846, 847, 848, 849, 850, 851, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 865, 866, 867, 868, 869, 871, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 912, 913, 914, 918, 920, 921, 922, 923, 928, 930, 932, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 953, 954, 955, 956, 958, 961, 962, 963, 964, 967, 968, 970, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 988, 990, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1003, 1004, 1005, 1008, 1009, 1011, 1012, 1013, 1014, 1015, 1018, 1019, 1020, 1022, 1024, 1025, 1026, 1027, 1028, 1030, 1031, 1034, 1036, 1041, 1042, 1044, 1045, 1046, 1048, 1049, 1050, 1052, 1053, 1054, 1058, 1059, 1060, 1062, 1063, 1064, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, or 1109.

25. The method of item 24, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 510, 512, 513, 514, 520, 521, 522, 523, 525, 530, 532, 537, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 556, 557, 558, 559, 560, 561, 562, 574, 581, 582, 583, 584, 596, 597, 598, 599, 600, 601, 602, 607, 609, 632, 633, 635, 636, 649,

655, 656, 667, 674, 675, 689, 690, 698, 714, 719, 720, 722, 727, 729, 741, 746, 748, 750, 751, 752, 755, 756, 757, 763, 767, 768, 772, 775, 781, 782, 790, 792, 793, 794, 795, 796, 797, 798, 801, 809, 811, 812, 813, 814, 824, 832, 834, 837, 838, 847, 851, 853, 854, 855, 856, 857, 858, 859, 860, 862, 868, 869, 870, 874, 875, 876, 877, 879, 880, 881, 882, 894, 895, 898, 902, 903, 904, 906, 907, 908, 912, 913, 914, 920, 922, 923, 937, 938, 939, 945, 946, 948, 949, 950, 951, 954, 956, 962, 964, 967, 969, 971, 972, 974, 975, 979, 980, 985, 988, 990, 993, 994, 995, 996, 997, 1000, 1001, 1003, 1004, 1005, 1011, 1013, 1015, 1018, 1019, 1027, 1030, 1034, 1035, 1036, 1042, 1048, 1052, 1058, 1060, 1070, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, or 1109.

26. The method of item 24, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 1098, 1100, 1102, 1103, 1104, 1105, 1107, 1108, or 1109.

In particular, the detection of a mechanism of resistance to carbapenems induced by the expression of an NDM protein is characterised by the detection of at least one peptide belonging to an NDM protein and its different sequence variants SEQ ID No. 1 and SEQ ID No. 1078 to SEQ ID No. 1080.

SEQ ID No. 1:

MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGDLVFRQ
LAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLVVDTAWTDDQTAQILNWIK
QEINLPVALAVVTHAHQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQH
SLTFAANGWVEPATAPNFGPLKVFYPGPGHTSDNITVGIDGTDIAFGGCLIKDSK
AKSLGNLGDADTEHYAASARAFGAAFPKASMIVMSHSAPDSRAAITHTARMAD
KLR

SEQ ID No. 1078

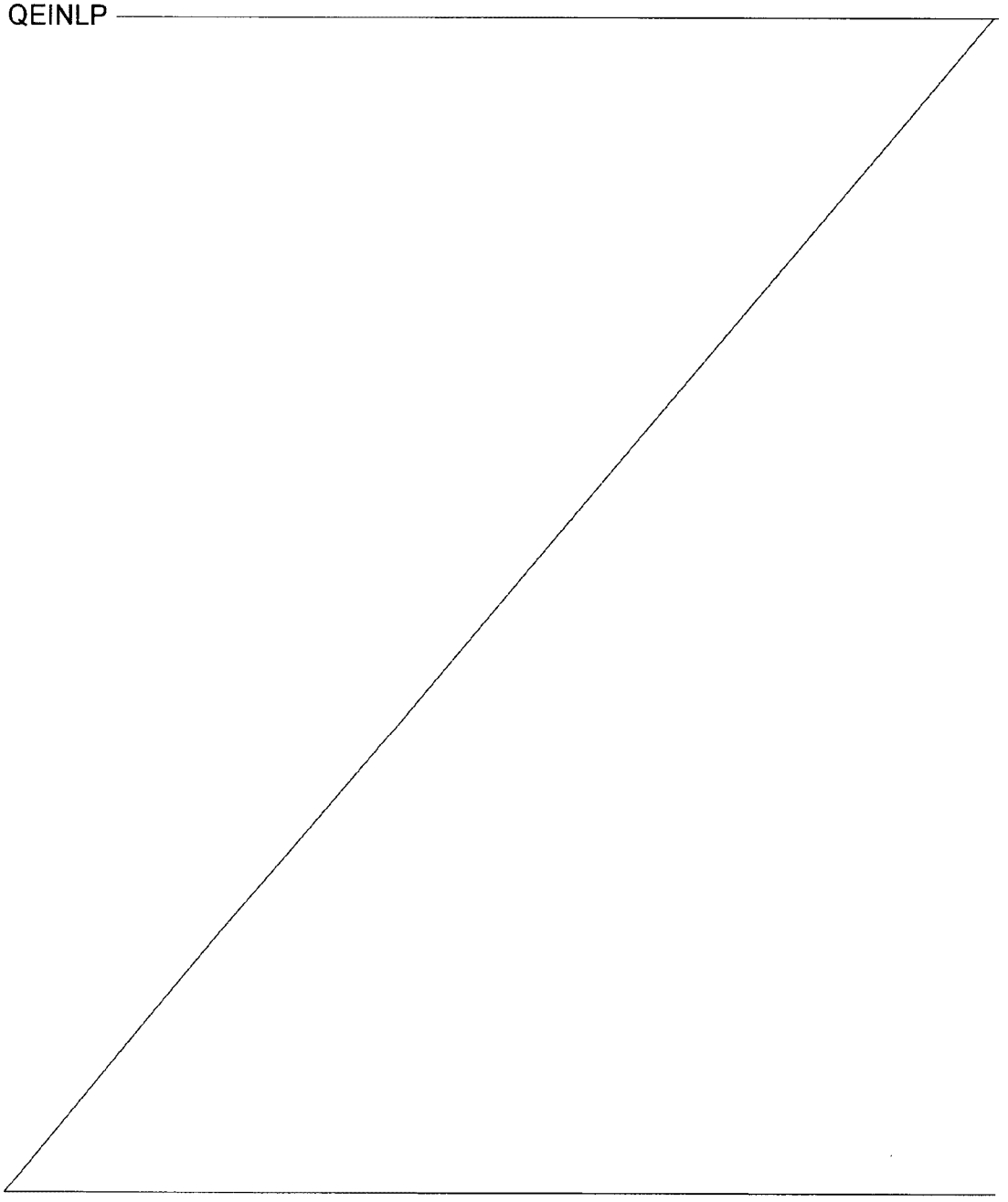
MELPNIMHPVAKLSTALAAALMLSGCMAGEIRPTIGQQMETGDQRFGDLVFRQ
LAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLVVDTAWTDDQTAQILNWIK
QEINLPVALAVVTHAHQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQH
SLTFAANGWVEPATAPNFGPLKVFYPGPGHTSDNITVGIDGTDIAFGGCLIKDSK
AKSLGNLGDADTEHYAASARAFGAAFPKASMIVMSHSAPDSRAAITHTARMAD
KLR

SEQ ID No. 1079

MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGDLVFRQ
LAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLLVDTAWTDDQTAQILNWIK
QEINLPVALAVVTHAHQDKMGGMDALHAAGIATYANALSNQLAPQEGLVAAQH
SLTFAANGWVEPATAPNFGPLKVFYPGPGHTSDNITVGIDGTDIAFGGCLIKDSK
AKSLGNLGDADTEHYAASARAFGAAFPKASMIVMSHSAPDSRAAITHTARMAD
KLR

SEQ ID No. 1080

MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGDLVFRQ
LAPNVWQHTSYLDMPGFGAVASNGLIVRDGGRVLVVDTAWTDDQTAQILNWIK
QEINLP



VALAVVTHAHQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQHSLTFAANG
WVEPATAPNFGPLKVFYPGPGHTSDNITVGIDGTDIAFGGCLIKDSKAKSLGNLGDA
DTEHYAASARAFGAAFPKASMIVMSHSAPDSRAAITHTARMADKLR

said peptides being chosen, preferably, from the peptides of sequence **SEQ ID No. 2** to **SEQ ID No. 9** and **SEQ ID No. 1083** as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the NDM protein(s)
SEQ ID No. 2	AAITHTAR	257-264 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 3	AFGAAFPK	235-242 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 4	ASMIVMSHSAPDSR	243-256 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 5	FGDLVFR	46-52 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 6	MELPNIMHPVAK	1-12 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 7	QEINLPVALAVVTHAHQDK	107-125 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 8	SLGNLGDADTEHYAASAR	217-234 for the proteins of SEQ No. 1, 1078, 1079, 1080
SEQ ID No. 9	VLVVDTAWTDDQTAQILNWIK	86-106 for the proteins of SEQ No. 1, 1078, 1080
SEQ ID No. 1081	LSTALAAALMLSGCMAGEIR	13-32 for the protein of SEQ No. 1078
SEQ ID No. 1082	LSTALAAALMLSGCMPGEIR	13-32 for the protein of SEQ No. 1, 1079, 1080
SEQ ID No. 1083	VLLVDTAWTDDQTAQILNWIK	86-106 for the protein of SEQ No. 1079

Preferably, the resistance markers are NDM markers, chosen from the peptides of sequence SEQ ID No. 2, SEQ ID No. 3, SEQ ID No. 5, or SEQ ID No. 7.

The detection of a mechanism of resistance to carbapenems induced by the expression of a KPC protein is characterised by the detection of at least one peptide belonging to a KPC protein and to its different sequence variants **SEQ ID No. 10** to **SEQ ID No. 19** and **SEQ ID No. 1084** to **SEQ ID No. 1093**.

SEQ ID No. 10:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 11:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 12:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 13:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 14:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 15:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAIDTGSGATV
SYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTT
GMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELNS
AIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPA
DWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAA
RLALEGLGVNGQ

SEQ ID No. 16:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 17:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGAYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLG

SEQ ID No. 18:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 19:

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVLWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA

ARLALEGLGVNGQ

SEQ ID No. 1084

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1085

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1086

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1087

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1088

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPSDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP

ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1089

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELEMN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1090

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1091

MSLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGAT
VSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEKYLT
TGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELN
SAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVP
ADWAVGDKTGTCGVYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAA
ARLALEGLGVNGQ

SEQ ID No. 1092

RLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYRA
EERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVPWSPISEKYLTTGMTV
AELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWELELNSAIPGD
ARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRAAVPADWAV
GDKTGTCGAYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALE
GLG

SEQ ID No. 1093

SLYRRLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGS
GATVSYRAEERFPLCSSFKGFLAAAVLARSQQQAGLLDTPIRYGKNALVRWSPISEK
YLTTGMTVAELSAAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFRLDRWEL

ELNSAIPGDARDTSSPRAVTESLQKLTLGSALAAPQRQQFVDWLKGNTTGNHRIRA
AVPADWAVGDKTGTCGGYGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKHSEAVI
AAAARLALEGLGVNGQ

said peptides being chosen, preferably, from the peptides of sequence **SEQ ID No. 20** to **SEQ ID No. 33** and **SEQ ID No. 1094** to **SEQ ID No. 1097** as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the KPC protein(s)
SEQ ID No. 20	AAVPADWAVGDK	221-232 for the protein of SEQ No. 1093; 222-233 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 21	APIVLAVYTR	254-263 for the protein of SEQ No. 1093; 255-264 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 22	AVTESLQK	183-190 for the protein of SEQ No. 1093; 184-191 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 23	ELGGPAGLTAFMR	139-151 for the protein of SEQ No. 1093; 140-152 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 24	FPLCSSFK	64-71 for the protein of SEQ No. 1093; 65-72 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 25	GFLAAAVLAR	72-81 for the protein of SEQ No. 1093; 73-82 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 26	GNTTGNHR	211-218 for the protein of SEQ No. 1093; 212-219 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 27	LALEGLGVNGQ	282-292 for the protein of SEQ No. 1093; 283-293 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091
SEQ ID No. 28	LTLGSALAAPQR	191-202 for the protein of SEQ No. 1093; 192-203 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 29	NALVPWSPISEK	94-105 for the protein of SEQ No. 1092; 99-110 for the proteins of sequence SEQ ID No. 10, 11, 14, 15, 16, 17, 1084, 1085, 1086, 1087, 1088, 1089
SEQ ID No. 30	QQFVDWLK	203-210 for the protein of SEQ No. 1093; 204-211 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092

SEQ ID No. 31	SIGDTTFR	152-159 for the protein of SEQ No. 1093; 153-160 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 32	SQQQAGLLDTPIR	82-94 for the protein of SEQ No. 1093; 83-95 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092
SEQ ID No. 33	WELELNSAIPGDAR	163-176 for the protein of SEQ No. 1093; 164-177 for the proteins of sequence SEQ ID No. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 1084, 1085, 1086, 1087, 1090, 1091, 1092
SEQ ID No. 1094	NALVR	98-102 for the proteins of SEQ No. 1093; 99-103 for the proteins of sequence SEQ ID No. 12, 13, 18, 1090, 1091
SEQ ID No. 1095	TGTCGAYGTANDYAVVWPTGR	229-249 for the protein of SEQ No. 1092; 234-254 for the protein of sequence SEQ ID No. 17
SEQ ID No. 1096	WELELNSAIPSDAR	164-177 for the protein of SEQ No. 1088
SEQ ID No. 1097	WELEMNSAIPGDAR	164-177 for the protein of SEQ No. 1089

Preferably, the resistance markers are KPC markers, chosen from the peptides of sequence SEQ ID No. 20, SEQ ID No. 21, SEQ ID No. 23, SEQ ID No. 25, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 31, or SEQ ID No. 32.

The detection of a mechanism of resistance to carbapenems and/or to cephalosporins induced by the expression of a GES protein is characterised by the detection of at least one peptide belonging to a GES protein and to its different sequence variants **SEQ ID No. 34** to **SEQ ID No. 50**.

SEQ ID No. 34:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 35:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 36:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQLAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 37:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMNDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 38:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 39:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 40:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGSRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 41:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGARNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 42:
MRFIHALLLAGTAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRTAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV

LEAAQAAVQLCDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 43:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMNDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 44:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKESEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 45:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGARNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 46:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAEIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 47:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGARNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 48:
MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRTAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG

EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 49:

MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRTAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVKWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMSDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGTCANGGRNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

SEQ ID No. 50:

MRFIHALLLAGIAHSAYASEKLTFKTDLEKLEREKAAQIGVAIVDPQGEIVAGHRMAQ
RFAMCSTFKFPLAALVFERIDSGTERGDRKLSYGPDMIVEWSPATERFLASGHMTV
LEAAQAAVQLSDNGATNLLLREIGGPAAMTQYFRKIGDSVSRLDRKEPEMGDNTPG
DLRDTTTPIAMARTVAKVLYGGALTSTSTHTIERWLIGNQTGDATLRAGFPKDWVVG
EKTGACANGARNDIGFFKAQERDYAVAVYTTAPKLSAVERDELVASVGQVITQLILS
TDK

said peptides being chosen, preferably, from the peptides of sequence **SEQ ID No. 51** to **SEQ ID No. 79** as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the GES protein(s)	Clinical interest
SEQ ID No. 51	AAEIGVAIVDPQGEIVAGH R	36-55 for the protein of SEQ No. 46	carba
SEQ ID No. 52	AAQIGVAIVDPQGEIVAGH R	36-55 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 48, 49, 50	ESBL
SEQ ID No. 53	AGFPK	218-222 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 54	DTTTPIAMAR	174-183 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 55	DWVVGEK	223-229 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 56	DYAVAVYTTAPK	250-261 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 57	EIGGPAAMTQYFR	136-148 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 58	EPEMGDNTPGDLR	161-173 for the proteins of SEQ No. 34, 35, 36, 40, 41, 42, 47, 48, 50	ESBL

SEQ ID No. 59	EPEMNDNTPGDLR	161-173 for the proteins of SEQ No. 37, 43	carba
SEQ ID No. 60	EPEMSDNTPGDLR	161-173 for the proteins of SEQ No. 38, 39, 45, 46, 49	carba
SEQ ID No. 61	ESEMSDNTPGDLR	161-173 for the protein of SEQ No. 44	carba
SEQ ID No. 62	FAMCSTFK	60-67 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 63	FIHALLLAGIAHSAYASEK	3-21 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 64	FIHALLLAGTAHSAYASEK	3-21 for the protein of SEQ No. 42	carba
SEQ ID No. 65	FPLAALVFER	68-77 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 66	IDSGTER	78-84 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 67	IGDSVSR	150-156 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 68	LSAVER	262-267 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 69	LSYGPDMIVEWSPATER	89-105 for the proteins of SEQ No. 34, 36, 37, 38, 40, 41, 42, 44, 45, 46, 50	ESBL
SEQ ID No. 70	LSYGPDMIVK	89-98 for the proteins of SEQ No. 35, 39, 43, 47, 48, 49	carba
SEQ ID No. 71	NDIGFFK	239-245 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 72	TDLEK	26-30 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 73	TGACANGAR	230-238 for the protein of SEQ No. 50	carba
SEQ ID No. 74	TGTCANGAR	230-238 for the proteins of SEQ No. 41, 45, 47	carba
SEQ ID No. 75	TGTCANGGR	230-238 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 42, 43, 44, 46, 48, 49	ESBL
SEQ ID No. 76	TGTCANGSR	230-238 for the protein of SEQ No. 40	carba
SEQ ID No. 77	VLYGGALTSTSTHTIER	188-204 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 78	WLIGNQTGDATLR	205-217 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	ESBL
SEQ ID No. 79	WSPATER	99-105 for the proteins of SEQ No. 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50	carba

In the clinical interest column, the ESBL and carba entries correspond to the GES beta-lactamase activities which the corresponding peptide makes it possible to detect. Therefore, the detection of a carba peptide will indicate the presence of a carbapenemase beta-lactamase capable of hydrolysing carbapenems.

If no peptide referred to as carba is detected, the detection of a peptide referred to as ESBL will indicate the presence of a beta-lactamase with an extended spectrum (ESBL) capable of hydrolysing penicillins, first-generation cephalosporins such as cephaloridine and cefalotin, and at least one antibiotic from the oxyimino-beta-lactam class such as cefotaxime, ceftazidime or monobactams such as aztreonam.

The detection of a mechanism of resistance to carbapenems induced by a GES protein is thus characterised by the detection of at least one resistance-marking carba peptide chosen from the sequences **SEQ ID No. 51, 59, 60, 61, 64, 70, 73, 74, 76, 79.**

The detection of a mechanism of resistance to carbapenems induced by the expression of an IMP protein is characterised by the detection of at least one peptide belonging to an IMP protein and to its different sequence variants **SEQ ID No. 80** to **SEQ ID No. 105**.

SEQ ID No. 80:
MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL
FGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 81:
MKKLSVFFMFLFCSIAASGEALPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVL
VNTDAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGASYWLVKKKIEIFYPGPGHTPDNVVVWLPEHRV
LFGGCFVKPYGLGNLGDANLEAWPKSAKLLVSKYGKAKLVVPSHSEVGDASLLKRT
LEQAVKGLNESKKLSKPSN

SEQ ID No. 82:
MSKLSVFFIFLFCSIATAAEPLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLV
DAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SELTNELLKKDGKVQAKNSFGGVNYWLVKNKIEVFYPGPGHTPDNLVVWLPERKIL

FGGCFIKPYGLGNLGDANLEAWPKSAKLLISKYGKAKLVVPSHSEAGDASLLKLTLE
QAVKGLNESKKPSKLSN

SEQ ID No. 83:

MKKLFVLCVCFLCSITAAGAALPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKI
LFGGCFVKPDGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSEIGDASLLKRT
WEQAVKGLNESKKPSQPSN

SEQ ID No. 84:

MSKLFVFFMFLFCSITAAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVL
VNTEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGASYWLVKKKIEVFYPGPGHTPDNVVVWLPENRV
LFGGCFVKPYGLGNLGDANVEAWPKSAKLLMSKYGKAKLVVPSHSEVGDASLLKR
TLEQAVKGLNESKKPSKPSN

SEQ ID No. 85:

MSKLFVFFMFLFCSITAAGESLPDLKIEKLDEGVYVHTSFEEVNGWGVIPKHGLVVLV
NTDAYLIDTPFTAKDTENLVNWFVERGYRIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SELTNELLKKDGKVQAKYSFSGVSYWLVKKKIEVFYPGPGHAPDNVVVWLPENRVL
FGGCFVKPYGLGNLGDANLEAWPKSAKLLMSKYSKAKLVVPSHSDIGDSSLLKLTW
EQTVKGFNESKKSTTAH

SEQ ID No. 86:

MKKLFVLCVFFFCNIAVAEESLPDLKIEKLEEGVYVHTSFEEVKGWSVVTKHGLVVL
VKNDAYLIDTPITAKDTEKLVNWFVERGYKIKGSISTHFHGDSTAGIEWLNSQSIPTY
ASELTNELLKKDNKVQAKHSFNGVSYSLIKNKIEVFYPGPGHTQDNVVVWLPEKKIL
FGGCFVKPDGLGYLGDANLEAWPKSAKILMSKYGKAKLVVSSHSDIGDVSLLKRTW
EQAVKGLNESKKSSQPSD

SEQ ID No. 87:

MNKLSVFFMFMFCSITAAGESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVV
LVNTEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPT
YASELTNELLKKDGKVQAKNSFSGGSYWLVNNKIEVFYPGPGHTPDNVVVWLPEN
RVLFGGCFVKPYGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSETGNASLLK
LTWEQAVKGLKESKKPSLPSN

SEQ ID No. 88:

MKKLFVLCVFFLCNIAAADDSLPDLKIEKLEKGVYVHTSFEEVKGWGVVTKHGLVVL
VKNDAYLIDTPITAKDTEKLVNWFIEHGYRIKGSISTHFHGDSTAGIEWLNSQSISTYA
SELTNELLKKDNKVQATNSFSGVSYSLIKNKIEVFYPGPGHTQDNVVVWLPEKKILF
GGCFVKPDGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSEIGNASLLQRTWE
QAVKGLNESKKPLQPSS

SEQ ID No. 89:

MKKLFVLCVFLFCSITAAGESLPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVILV
NTDAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SELTNDLLKQNGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKIL

FGGCFVKPYGLGNLDDANVVAWPHSAEILMSRYGNAKLVVPSHSDIGDASLLKLTW
EQAVKGLKESKKPSEPSN

SEQ ID No. 90:
MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFKEVNGWGVVPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL
FGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 91:
MKKLFVLCVCFLCSITAAGAALPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKI
LFGGCFVKPDGLGNLGDANLEAWPKSAKILMSKYVKAKLVVSSHSEIGDASLLKRT
WEQAVKGLNESKKPSQPSN

SEQ ID No. 92:
MKKLFVLCVCFLCSITAAGAALPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKI
LFGGCFVKPDGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSEIGDASLLKRT
WEQAVKGLNESRKPSQPSN

SEQ ID No. 93:
MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL
FGGCFIKPYGLGNLSDANIEAWPKSAKLLKSKYGKAKLVVPGHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 94:
MSKLSVFFIFLFCSIATAAEPLPDLKIEKLDEGVYVHTSFEEVNGWGVFPKHGLVVLV
DAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SELTNELLKKDGKVQAKNSFGGVNYWLVKNKIEVFYPGPGHTPDNLVVWLPERKIL
FGGCFIKPYGLGNLGDANLEAWPKSAKLLISKYGKAKLVVPSHSEAGDASLLKLTLE
QAVKGLNESKKPSKLSN

SEQ ID No. 95:
MKKLFVLCVFVFCSITVAGETLPNLRVEKLEEGVYVHTSYEEVKGWGVVTKHGLVVL
IGADAYLIDTPFTAKDTEKLVNWFVERGYKIKGTVSSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFDGVSYWLAKDKIEVFYPGPGHTQDNVVVWLPEKEI
LFGGCFVKPHGLGNLGDANLEAWPESAKILMEKYGKAKLVVSGHSETGDATHLKRT
WEQAVKGLKESKKTLQPSN

SEQ ID No. 96:
MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIGWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL

FGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPGHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 97:

MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL
FGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPGHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 98:

MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVFPKHGLVVLV
NAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYA
SELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKIL
FGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLE
QAVKGLNESKKPSKPSN

SEQ ID No. 99:

MKKLFVLCIFLFCSITAAGASLPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVLV
NTDAYLIDTPFTAKDTEKLVNWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SVLTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPKNKIL
FGGCFVKPYGLGNLDDANVEAWPHSAEKLISKYGNAKLVVPSHSDIGDASLLKLTW
EQAVKGLNESKKSNTVH

SEQ ID No. 100:

MKKLFVLCVCFLCSITAAGAALPDLKIEKLEEGVYVHTSFEEVNGWGVFSKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKI
LFGGCFVKPDGLGNLGDANLEAWPKSAKILMSKYVKAKLVVSSHSEIGDASLLKRT
WEQAVKGLNESKKPSQPSN

SEQ ID No. 101:

MKKLFVLCIFLFCSITAAGASLPDLKIEKLEEGVYVHTSFEEVNGWGVASKHGLVVLV
NTDAYLIDTPFTAKDTEKLVNWFVERGYKIKGSISSHFHSDSTGGIEWLNSQSIPTYA
SVLTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPKNKIL
FGGCFVKPYGLGNLDDANVEAWPHSAEKLISKYGNAKLVVPSHSDIGDASLLKLTW
EQAVKGLNESKKSNTVH

SEQ ID No. 102:

MKKLFVLCVCFLCSITAAGARLPDLKIEKLEEGVYVHTSFEEVNGWGVVSKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYKIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKDGKVQAKNSFSGVSYWLVKNKIEVFYPGPGHTQDNVVVWLPEKKI
LFGGCFVKPDGLGNLGDANLEAWPKSAKILMSKYVKAKLVVSSHSEIGDASLLKRT
WEQAVKGLNESKKPSQPSN

SEQ ID No. 103:

MKKLFVLCIFLFLSITASGEVLPDLKIEKLEEGVYLHTSFEEVSGWGVVTKHGLVVLV
NNDAYLIDTPFTNKDTEKLVAWFVGRGFTIKGSVSSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKNGKVQATNSFSGVSYWLVKNKIEIFYPGPGHTQDNVVVWLPENKIL

FGGCFVKPDGLGNLDDANLKAWPKSAKILMSKYGKAKLVVSGHSEIGNASLLKLTW
EQAVKGLKESKKPLLPSN

SEQ ID No. 104:
MKKLFVLCVCFFCSITAAGAALPDLKIEKLEEGVFVHTSFEEVNGWGVVTKHGLVVL
VNTDAYLIDTPFTATDTEKLVNWFVERGYEIKGTISSHFHSDSTGGIEWLNSQSIPTY
ASELTNELLKKSGKVQAKYSFSEVSYWLVKNKIEVFYPGPGHTQDNLVVWLPESKIL
FGGCFIKPHGLGNLGDANLEAWPKSAKILMSKYGKAKLVVSSHSEKGDASLMKRT
WEQALKGLKESKKTSSPSN

SEQ ID No. 105:
MKKLFVLCIFLFCSITAAGESLPDLKIEKLEDGVYVHTSFEEVNGWGVVTKHGLVFLV
NTDAYLIDTPFAAKDTEKLVNWFVERGYKIKGSISSHFHSDSSGGIEWLNSQSIPTYA
SELTNELLKKNGKVQAKNSFSGVSYWLLKNKIEIFYPGPGHTQDNVVVWLPEKKILF
GGCFVKPYGLGNLDDANVEAWPHSAEILMSRYGNAKLVVPSHSDVGDASLLKLTW
EQAVKGLKESKKPSQPSN

said peptides being chosen, preferably, from the peptides of sequence SEQ ID No. 106, SEQ ID No. 108 to SEQ ID No. 130, SEQ ID No. 133 to SEQ ID No. 173, SEQ ID No. 175 to SEQ ID No. 180, as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the IMP protein(s)
SEQ ID No. 106	DTENLVNWFVER	73-84 for the protein of SEQ No. 85
SEQ ID No. 107	EILFGGCFVK	170-179 for the protein of SEQ No. 95
SEQ ID No. 108	EVNGWGVVPK	42-51 for the proteins of SEQ No. 80, 81, 82, 84, 87, 90, 93, 96, 97
SEQ ID No. 109	GDASLMK	219-225 for the protein of SEQ No. 104
SEQ ID No. 110	GFNESK	234-239 for the protein of SEQ No. 85
SEQ ID No. 111	GFTIK	85-89 for the protein of SEQ No. 103

SEQ ID No. 112	GLNESK	234-239 for the proteins of SEQ No. 80, 81, 82, 83, 84, 86, 88, 90, 91, 93, 94, 96, 97, 98, 99, 100, 101, 102
SEQ ID No. 113	GLNESR	234-239 for the protein of SEQ No. 92
SEQ ID No. 114	GSISSHFHSDSTGGIEWLNSR	90-110 for the proteins of SEQ No. 80, 90, 93, 97, 98
SEQ ID No. 115	GSISSHFHSDSTGGIGWLNSR	90-110 for the protein of SEQ No. 96
SEQ ID No. 116	GVYVHTSFEEVK	33-44 for the proteins of SEQ No. 86, 88
SEQ ID No. 117	GWGVVTK	45-51 for the proteins of SEQ No. 88, 95, 103, 104, 105
SEQ ID No. 118	GWSVVTK	45-51 for the protein of SEQ No. 86
SEQ ID No. 119	GYEIK	85-89 for the protein of SEQ No. 104
SEQ ID No. 120	HGLVFLVNTDAYLIDTPFAAK	52-72 for the protein of SEQ No. 105
SEQ ID No. 121	HGLVILVNTDAYLIDTPFTAK	52-72 for the protein of SEQ No. 89
SEQ ID No. 122	HGLVVLIGADAYLIDTPFTAK	52-72 for the protein of SEQ No. 95
SEQ ID No. 123	HGLVVLVDAEAYLIDTPFTAK	52-72 for the proteins of SEQ No. 82, 94
SEQ ID No. 124	HGLVVLVK	52-59 for the proteins of SEQ No. 86, 88
SEQ ID No. 125	HGLVVLVNAEAYLIDTPFTAK	52-72 for the proteins of SEQ No. 80, 90, 93, 96, 97, 98

SEQ ID No. 126	HGLVVLVNNDAYLIDTPFTNK	52-72 for the protein of SEQ No. 103
SEQ ID No. 127	HGLVVLVNTDAYLIDTPFTAK	52-72 for the proteins of SEQ No. 81, 85, 99, 101
SEQ ID No. 128	HGLVVLVNTEAYLIDTPFTAK	52-72 for the proteins of SEQ No. 84, 87
SEQ ID No. 129	HSFNGVSYSLIK	134-145 for the protein of SEQ No. 86
SEQ ID No. 130	IEVFYPGPGHTQDNVVVWLPK	148-168 for the proteins of SEQ No. 99, 101
SEQ ID No. 131	ILFGGCFIK	171-179 for the proteins of SEQ No. 80, 82, 90, 93, 94, 96, 97, 98, 104
SEQ ID No. 132	ILFGGCFVK	171-179 for the proteins of SEQ No. 83, 86, 88, 89, 91, 92, 95, 99, 100, 101, 102, 103, 105
SEQ ID No. 133	ILMEK	200-204 for the protein of SEQ No. 95
SEQ ID No. 134	ILMSK	200-204 for the proteins of SEQ No. 83, 86, 87, 88, 91, 92, 100, 102, 103, 104
SEQ ID No. 135	LDEGVYVHTSFK	30-41 for the protein of SEQ No. 90
SEQ ID No. 136	LEEGVYVHTSFEEVK	30-44 for the protein of SEQ No. 86
SEQ ID No. 137	LEEGVYVHTSYEEVK	30-44 for the protein of SEQ No. 95
SEQ ID No. 138	LFVLCVCFLCSITAAGAR	4-21 for the protein of SEQ No. 102
SEQ ID No. 139	LLISK	200-204 for the proteins of SEQ No. 82, 94

SEQ ID No. 140	LLMSK	200-204 for the proteins of SEQ No. 84, 85
SEQ ID No. 141	LLVSK	200-204 for the protein of SEQ No. 81
SEQ ID No. 142	LPDLK	22-26 for the proteins of SEQ No. 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105
SEQ ID No. 143	LTLEQAVK	226-233 for the proteins of SEQ No. 80, 82, 90, 93, 94, 96, 97, 98
SEQ ID No. 144	LTWEQAVK	226-233 for the proteins of SEQ No. 87, 89, 99, 101, 103, 105
SEQ ID No. 145	LTWEQTVK	226-233 for the protein of SEQ No. 85
SEQ ID No. 146	LVAWFVGR	77-84 for the protein of SEQ No. 103
SEQ ID No. 147	LVNWFIEHGYR	77-87 for the protein of SEQ No. 88
SEQ ID No. 148	LVNWFVER	77-84 for the proteins of SEQ No. 83, 85, 86, 91, 92, 95, 99, 100, 101, 102, 104, 105
SEQ ID No. 149	LVTWFVER	77-84 for the proteins of SEQ No. 80, 81, 82, 84, 87, 89, 90, 93, 94, 96, 97, 98
SEQ ID No. 150	LVVPGHSEVGDASLLK	210-225 for the proteins of SEQ No. 93, 96, 97
SEQ ID No. 151	LVVPSHSDIGDASLLK	210-225 for the proteins of SEQ No. 89, 99, 101
SEQ ID No. 152	LVVPSHSDIGDSSLLK	210-225 for the protein of SEQ No. 85
SEQ ID No. 153	LVVPSHSDVGDASLLK	210-225 for the protein of SEQ No. 105

SEQ ID No. 154	LVVPSHSEAGDASLLK	210-225 for the proteins of SEQ No. 82, 94
SEQ ID No. 155	LVVPSHSEVGDASLLK	210-225 for the proteins of SEQ No. 80, 81, 84, 90, 98
SEQ ID No. 156	LVVSGHSEIGNASLLK	210-225 for the protein of SEQ No. 103
SEQ ID No. 157	LVVSGHSETGDATHLK	210-225 for the protein of SEQ No. 95
SEQ ID No. 158	LVVSSHSDIGDVSLLK	210-225 for the protein of SEQ No. 86
SEQ ID No. 159	LVVSSHSEIGDASLLK	210-225 for the proteins of SEQ No. 83, 91, 92, 100, 102
SEQ ID No. 160	LVVSSHSEIGNASLLQR	210-226 for the protein of SEQ No. 88
SEQ ID No. 161	LVVSSHSEK	210-218 for the protein of SEQ No. 104
SEQ ID No. 162	LVVSSHSETGNASLLK	210-225 for the protein of SEQ No. 87
SEQ ID No. 163	NDAYLIDTPITAK	60-72 for the proteins of SEQ No. 86, 88
SEQ ID No. 164	NSFDGVSYWLAK	134-145 for the protein of SEQ No. 95
SEQ ID No. 165	NSFGGVNYWLVK	134-145 for the proteins of SEQ No. 82, 94
SEQ ID No. 166	NSFSGASYWLVK	134-145 for the proteins of SEQ No. 81, 84
SEQ ID No. 167	NSFSGGSYWLVNNK	134-147 for the protein of SEQ No. 87

SEQ ID No. 168	NSFSGVSYWLLK	134-145 for the protein of SEQ No. 105
SEQ ID No. 169	NSFSGVSYWLVK	134-145 for the proteins of SEQ No. 83, 89, 91, 92, 99, 100, 101, 102, 103
SEQ ID No. 170	SIPTYASELTNELLK	111-125 for the proteins of SEQ No. 80, 81, 82, 83, 84, 85, 86, 87, 90, 91, 92, 93, 94, 95, 96, 97, 98, 100, 102, 103, 104, 105
SEQ ID No. 171	TLEQAVK	227-233 for the proteins of SEQ No. 80, 81, 82, 84, 90, 93, 94, 96, 97, 98
SEQ ID No. 172	TWEQALK	227-233 for the protein of SEQ No. 104
SEQ ID No. 173	TWEQAVK	227-233 for the proteins of SEQ No. 83, 86, 87, 88, 89, 91, 92, 95, 99, 100, 101, 102, 103, 105
SEQ ID No. 174	VLFGGCFVK	171-179 for the proteins of SEQ No. 81, 84, 85, 87
SEQ ID No. 175	VQATNSFSGVNYWLVK	130-145 for the proteins of SEQ No. 80, 90, 93, 96, 97, 98
SEQ ID No. 176	VQATNSFSGVSYSLIK	130-145 for the protein of SEQ No. 88
SEQ ID No. 177	VQATNSFSGVSYWLVK	130-145 for the protein of SEQ No. 103
SEQ ID No. 178	YGNAK	205-209 for the proteins of SEQ No. 89, 99, 101, 105
SEQ ID No. 179	YSFSEVSYWLVK	134-145 for the protein of SEQ No. 104
SEQ ID No. 180	YSFSGVSYWLVK	134-145 for the protein of SEQ No. 85

The detection of a mechanism of resistance to carbapenems induced by the expression of the IND protein is characterised by the detection of at least one peptide

belonging to the IND protein and to its different sequence variants **SEQ ID No. 181** to **SEQ ID No. 187**.

SEQ ID No. 181:
MKKSIRFFIVSILLSPFASAQVKDFVIEPPIKNNLHIYKTFGVFGGKEYSANSMYLVTK
KGVVLFDVPWEKIQYQSLMDTIKKRHNLPVVAVFATHSHDDRAGDLSFFNNKGIKTY
ATAKTNEFLKKDGKATSTEIIKTGKPYRIGGEEFVVDFLGEGHTADNVVVWFPKYNV
LDGGCLVKSNSATDLGYIKEANVEQWPKTINKLKAKYSKATLIIPGHDEWKGGGHVE
HTLELLNKK

SEQ ID No. 182:
MKKSIQLLMMSMFLSPLINAQVKDFVIEPPVKPNLYLYKSFGVFGGKEYSANAVYLT
TKKGVVLFDVPWQKEQYQTLMDTIQKRHHLPVIAVFATHSHDDRAGDLSFYNQKGI
KTYATAKTNELLKKDGKATSTEIIKTGKPYKIGGEEFMVDFLGEGHTVDNVVVWFPK
YKVLDGGCLVKSRTATDLGYTGEANVKQWPETMRKLKTKYAQATLVIPGHDEWKG
GGHVQHTLDLLDKNKKPE

SEQ ID No. 183:
MKKSIQLLMMSMFLSPLINAQVKDFVIEPPVKPNLYLYKSFGVFGGKEYSANAVYLT
TKKGVVLFDVPWQKEQYQTLMDTIQKRHHLPVIAVFATHSHDDRAGDLSFYNQKGI
KTYATAKTNELLKKDGKATSTEIIKTGKPYKIGGEEFMVDFLGEGHTVDNVVVWFPK
YKVLDGGCLVKSRTATDLGYTGEANVKQWPETMRKLKTKYAQATLVIPGHEEWKG
GGHVQHTLDLLDKNKKPE

SEQ ID No. 184:
MKKRIQFFMVSMMLSSLFSAQVKDFVIEPPIKKNLHIYKTFGVFGGKEYSANSVYLVT
QKGVVLFDVPWEKVQYQSLMDTIQKRHNLPVIAVFATHSHDDRAGDLSFFNNKGIK
TYATSKTNEFLKKDGKATSTEIIKTGKPYRIGGEEFVVDFLGEGHTADNVVVWFPKY
NVLDGGCLVKSKAATDLGYIKEANVEQWPKTINKLKSKYSKASLVIPGHDEWKGGG
HVKHTLELLNKK

SEQ ID No. 185:
MRKNVRIFTVLSLFLINFFNAQARDFVIEQPFGKQLYLYKTFGVFDGKEYSTNALYLV
TKKGVVLFDVPWQKTQYQSLMDTIKKRHNLPVIAVFATHSHSDRAGDLSFYNKKGIP
TYATAKTNELLKKEGKATSSKLTKIGKKYKIGGEEFTVDFLGEGHTADNVVVWFPKY
NVLDGGCLVKSSAAVDLGYTGEANVEQWPATMKKLQAKYPSTAKVIPGHDEWKGN
DHVKHTLELLDQQKQ

SEQ ID No. 186:
MKKRIQFFMVSMMLAPMFNAQVKDFVIEPPIKNNLHIYKTFGVFGGKEYSANSVYLV
TKKGVVLFDVPWEKAQYQSLMDTIKKRHNLPVIAVFATHSHDDRAGDLSFFNNKGIK
TYATSKTNEFLKKDGKATSTEIIKTGKPYRIGGEEFTVDFLGEGHTADNVVVWFPKY
NVLDGGCLVKSNSATDLGYIKEANVEQWPITIDKLKAKYSKATLIIPGHDDWKGGGH
VEHTLELLNKK

SEQ ID No. 187:
MKRRIQFFMVSMMLTPLFSAQVKDFVIEPPIKKNLYIYKTFGVFGGKEYSANSVYLVT
KTGVVLFDVPWEKAQYQSLMDTIKKRHNLPVVAVFATHSHDDRAGDLSFFNNKGIK
TYATPKTNQFLKRDGKATSTELIKPGKPYRFGGEEFVVDFLGEGHTADNVVVWFPK

YKVLDGGCLVKSNSATDLGYIKEANLEQWPKTMHKLKTKYSEAVLIIPGHDEWKGG GHVEHTLELLDKK

said peptides being chosen, preferably, from the peptides of sequence SEQ ID No. 188 to SEQ ID No. 197, SEQ ID No. 200, SEQ ID No. 201, SEQ ID No. 203 to SEQ ID No. 262, as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the IND protein(s)
SEQ ID No. 188	AATDLGYIK	184-192 for the protein of SEQ No. 184
SEQ ID No. 189	AGDLSFFNNK	102-111 for the proteins of SEQ No. 181, 184, 186, 187
SEQ ID No. 190	AGDLSFYNK	103-111 for the protein of SEQ No. 185
SEQ ID No. 191	AGDLSFYNQK	102-111 for the proteins of SEQ No. 182, 183
SEQ ID No. 192	AQYQSLMDTIK	72-82 for the proteins of SEQ No. 186, 187
SEQ ID No. 193	ASLVIPGHDEWK	213-224 for the protein of SEQ No. 184
SEQ ID No. 194	ATLIIPGHDDWK	213-224 for the protein of SEQ No. 186
SEQ ID No. 195	ATLIIPGHDEWK	213-224 for the protein of SEQ No. 181
SEQ ID No. 196	ATSSK	132-136 for the protein of SEQ No. 185
SEQ ID No. 197	ATSTEIIK	131-138 for the proteins of SEQ No. 181, 182, 183, 184, 186
SEQ ID No. 198	ATSTELIK	131-138 for the protein of SEQ No. 187

SEQ ID No. 199	ATSTELIKPGK	131-141 for the protein of SEQ No. 187
SEQ ID No. 200	ATSTELIKPGKPYR	131-144 for the protein of SEQ No. 187
SEQ ID No. 201	DFVIEPPIK	24-32 for the proteins of SEQ No. 181, 184, 186, 187
SEQ ID No. 202	DFVIEPPVK	24-32 for the proteins of SEQ No. 182, 183
SEQ ID No. 203	DFVIEPPVKPNLYLYK	24-39 for the proteins of SEQ No. 182, 183
SEQ ID No. 204	DFVIEQPFGK	25-34 for the protein of SEQ No. 185
SEQ ID No. 205	EANLEQWPK	193-201 for the protein of SEQ No. 187
SEQ ID No. 206	EANVEQWPITIDK	193-205 for the protein of SEQ No. 186
SEQ ID No. 207	EANVEQWPK	193-201 for the proteins of SEQ No. 181, 184
SEQ ID No. 208	EQYQTLMDTIQK	72-83 for the proteins of SEQ No. 182, 183
SEQ ID No. 209	EYSANAVYLTTK	48-59 for the proteins of SEQ No. 182, 183
SEQ ID No. 210	EYSANSMYLVTK	48-59 for the protein of SEQ No. 181
SEQ ID No. 211	EYSANSVYLVTK	48-59 for the proteins of SEQ No. 186, 187
SEQ ID No. 212	EYSANSVYLVTQK	48-60 for the protein of SEQ No. 184

SEQ ID No. 213	EYSTNALYLVTK	49-60 for the protein of SEQ No. 185
SEQ ID No. 214	FFIVSILLSPFASAQVK	7-23 for the protein of SEQ No. 181
SEQ ID No. 215	GGGHVEHTLELLDK	225-238 for the protein of SEQ No. 187
SEQ ID No. 216	GGGHVEHTLELLNK	225-238 for the proteins of SEQ No. 181, 186
SEQ ID No. 217	GGGHVK	225-230 for the protein of SEQ No. 184
SEQ ID No. 218	GGGHVQHTLDLLDK	225-238 for the proteins of SEQ No. 182, 183
SEQ ID No. 219	GIPTYATAK	113-121 for the protein of SEQ No. 185
SEQ ID No. 220	GNDHVK	226-231 for the protein of SEQ No. 185
SEQ ID No. 221	GVVLFDVPWEK	61-71 for the proteins of SEQ No. 181, 184, 186, 187
SEQ ID No. 222	GVVLFDVPWQK	62-72 for the protein of SEQ No. 185; 61-71 for the protein of sequence SEQ ID No. 182; 61-71 for the protein of sequence SEQ ID No. 183
SEQ ID No. 223	HHLPVIAVFATHSHDDR	85-101 for the proteins of SEQ No. 182, 183
SEQ ID No. 224	HNLPVIAVFATHSHDDR	85-101 for the proteins of SEQ No. 184, 186
SEQ ID No. 225	HNLPVIAVFATHSHSDR	86-102 for the protein of SEQ No. 185
SEQ ID No. 226	HNLPVVAVFATHSHDDR	85-101 for the proteins of SEQ No. 181, 187

SEQ ID No. 227	HTLELLDQQK	232-241 for the protein of SEQ No. 185
SEQ ID No. 228	HTLELLNK	231-238 for the proteins of SEQ No. 181, 184, 186
SEQ ID No. 229	IFTVLSLFLINFFNAQAR	7-24 for the protein of SEQ No. 185
SEQ ID No. 230	IQFFMVSMMLAPMFNAQVK	5-23 for the protein of SEQ No. 186
SEQ ID No. 231	IQFFMVSMMLSSLFSAQVK	5-23 for the protein of SEQ No. 184
SEQ ID No. 232	IQFFMVSMMLTPLFSAQVK	5-23 for the protein of SEQ No. 187
SEQ ID No. 233	IQYQSLMDTIK	72-82 for the protein of SEQ No. 181
SEQ ID No. 234	NLHIYK	34-39 for the proteins of SEQ No. 181, 184, 186
SEQ ID No. 235	NLYIYK	34-39 for the protein of SEQ No. 187
SEQ ID No. 236	NNLHIYK	33-39 for the proteins of SEQ No. 181, 186
SEQ ID No. 237	QLYLYK	35-40 for the protein of SEQ No. 185
SEQ ID No. 238	QWPETMR	198-204 for the proteins of SEQ No. 182, 183
SEQ ID No. 239	SFGVFGGK	40-47 for the proteins of SEQ No. 182, 183
SEQ ID No. 240	SIQLLMMSMFLSPLINAQVK	4-23 for the proteins of SEQ No. 182, 183

SEQ ID No. 241	SNSATDLGYIK	182-192 for the proteins of SEQ No. 181, 186, 187
SEQ ID No. 242	TATDLGYTGEANVK	184-197 for the proteins of SEQ No. 182, 183
SEQ ID No. 243	TFGVFDGK	41-48 for the protein of SEQ No. 185
SEQ ID No. 244	TFGVFGGK	40-47 for the proteins of SEQ No. 181, 184, 186, 187
SEQ ID No. 245	TGKPYK	139-144 for the proteins of SEQ No. 182, 183
SEQ ID No. 246	TGKPYR	139-144 for the proteins of SEQ No. 181, 184, 186
SEQ ID No. 247	TGVVLFDVPWEK	60-71 for the protein of SEQ No. 187
SEQ ID No. 248	TNEFLK	121-126 for the proteins of SEQ No. 181, 184, 186
SEQ ID No. 249	TNELLK	122-127 for the protein of SEQ No. 185; 121-126 for the proteins of sequence SEQ ID No. 182, 183
SEQ ID No. 250	TNQFLK	121-126 for the protein of SEQ No. 187
SEQ ID No. 251	TQYQSLMDTIK	73-83 for the protein of SEQ No. 185
SEQ ID No. 252	TYATAK	116-121 for the protein of SEQ No. 185; 115-120 for the proteins of sequence SEQ ID No. 181, 182, 183
SEQ ID No. 253	TYATPK	115-120 for the protein of SEQ No. 187
SEQ ID No. 254	TYATSK	115-120 for the proteins of SEQ No. 184, 186

SEQ ID No. 255	VIPGHDEWK	217-225 for the protein of SEQ No. 185; 216-224 for the protein of sequence SEQ ID No. 182; 216-224 for the protein of sequence SEQ ID No. 184
SEQ ID No. 256	VLDGGCLVK	173-181 for the proteins of SEQ No. 181, 182, 183, 184, 186, 187; 174-182 for the protein of sequence SEQ ID No. 185
SEQ ID No. 257	VQYQSLMDTIQK	72-83 for the protein of SEQ No. 184
SEQ ID No. 258	YAQATLVIPGHDEWK	210-224 for the protein of SEQ No. 182
SEQ ID No. 259	YAQATLVIPGHEEWK	210-224 for the protein of SEQ No. 183
SEQ ID No. 260	YNVLDGGCLVK	171-181 for the proteins of SEQ No. 181, 184, 186; 172-182 for the protein of sequence SEQ ID No. 185
SEQ ID No. 261	YPSTAK	211-216 for the protein of SEQ No. 185
SEQ ID No. 262	YSEAVLIIPGHDEWK	210-224 for the protein of SEQ No. 187

The detection of a mechanism of resistance to carbapenems induced by the expression of the SME protein is characterised by the detection of at least one peptide belonging to the SME protein and to its different sequence variants **SEQ ID No. 263** to **SEQ ID No. 265**.

SEQ ID No 263:
MSNKVNFKTASFLFSVCLALSAFNAHANKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFG
YRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKVKYESRDLEYHSPITTKYKGSGMTLGD
MASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTS
TPKAVANSLNKLALGNVLNAKEKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAY
GTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID

SEQ ID No. 264:
MSNKVNFKTASFLFSVCLALSAFNAHANKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFG
YRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKVKYESRDLEYYSPITTKYKGSGMTLGD
MASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTS
TPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAY
GTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID

SEQ ID No. 265:
MSNKVNFKTASFLFSVCLALSAFNAHANKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFG
YRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKVKYESRDLEYHSPITTKYKGSGMTLGD
MASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTS
TPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAIG
TANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID

said peptides being chosen, preferably, from the peptides of sequence **SEQ ID No. 266** to **SEQ ID No. 287** as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the SME protein(s)
SEQ ID No. 266	AIYQNWLK	209-216 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 267	APLIVSIYTTR	260-270 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 268	ASVPADWVVGDK	227-238 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 269	AVANSLNK	189-196 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 270	DLEYHSPITTK	104-114 for the proteins of SEQ No. 263, 265
SEQ ID No. 271	DLEYYSPITTK	104-114 for the protein of SEQ No. 264
SEQ ID No. 272	DTSTPK	183-188 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 273	FLGGPEGMTK	145-154 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 274	GFLAAAVLER	77-86 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 275	GNTTGDAR	217-224 for the proteins of SEQ No. 263, 264, 265

SEQ ID No. 276	IGVFAIDTGSGNTFGYR	48-64 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 277	LALGNVLNAK	197-206 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 278	LDINQK	92-97 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 279	LEEDFDGR	40-47 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 280	SDAAAK	30-35 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 281	SIGDNEFR	158-165 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 282	TASFLFSVCLALSAFNAHANK	9-29 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 283	TGSCGAIGTANDYAVIWPK	239-257 for the protein of SEQ No. 265
SEQ ID No. 284	TGSCGAYGTANDYAVIWPK	239-257 for the proteins of SEQ No. 263, 264
SEQ ID No. 285	TIAEASR	281-287 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 286	WELELNTAIPGDK	169-181 for the proteins of SEQ No. 263, 264, 265
SEQ ID No. 287	FPLCSSFK	69-76 for the proteins of SEQ No. 263, 264, 265

The detection of a mechanism of resistance to carbapenems induced by the expression of a VIM protein is characterised by the detection of at least one peptide belonging to a VIM protein and to its different sequence variants **SEQ ID No. 288** to **SEQ ID No. 313**.

SEQ ID No. 288:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 289:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
KSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 290:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVHELSRTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 291:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRKAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVLALSRTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVTAHKNRSVAE

SEQ ID No. 292:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
RSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 293:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSARRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 294:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSIRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELFY
PGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYP
EAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 295:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQYVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 296:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGSEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 297:
MLKVISSLLVYMTASVMAVASPLAHSGEPSSEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVHELSRTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 298:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVHELSSTSAGNVADADLAEWPTSIERIQ
QHYPEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 299:
MLKVISSLLFYMTASLMAVASPLAHSGESRGEYPTVSEIPVGEVRLYQIDDGVWSHI
ATHTFDGVVYPSNGLIVRDGDELLLIDTAWGTKNTVALLAEIEKQIGLPVTRSVSTHF
HDDRVGGVDALRAAGVATYASPSTRRLAEAEGNEVPTHSLEGLSSSGDAVRFGPV
ELFYPGAAHSTDNLVVYVPSANVLYGGCAVLELSRTSAGNVADADLAEWPGSVERI
QQHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHTNRSVAE

SEQ ID No. 300:
MFKLLSKLLVYLTASMMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIA
TQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFH
DDRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVEL
FYPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQH
YPEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 301:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLFGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 302:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWLHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 303:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSSTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 304:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSAKVLYGGCAVHELSRTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 305:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSLTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 306:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRKAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVLALSRTSAGNVADADLAEWPTSVERIQ
KHYPEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 307:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
STQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVHELSSTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 308:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVLELSRTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 309:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVNEIPVGEVRLYQIADGVWSHIAT
QSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLAEVEGNEIPTHSLEGLSSSGDAVRFGPVELF
YPGAAHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHY
PEAQFVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 310:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVHELSSTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

SEQ ID No. 311:
MFQIRSFLVGISAFVMAVLGSAAYSAQPGGEYPTVDDIPVGEVRLYKIGDGVWSHIA
TQKLGDTVYSSNGLIVRDADELLLIDTAWGAKNTVALLAEIEKQIGLPVTRSISTHFHD
DRVGGVDVLRAAGVATYTSPLTRQLAEAAGNEVPAHSLKALSSSGDVVRFGPVEVF
YPGAAHSGDNLVVYVPAVRVLFGGCAVHEASRESAGNVADANLAEWPATIKRIQQ
RYPEAEVVIPGHGLPGGLELLQHTTNVVKTHKVRPVAE

SEQ ID No. 312:
MFKLLSKLLVYLTASIMAIASPLAFSVDSSGEYPTVSEIPVGEVRLYQIADGVWSHIAT
RSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHFHD
DRVGGVDVLRAAGVATYASPSTRRLANEIPTHSLEGLSSSGDAVRFGPVELFYPGA
AHSTDNLVVYVPSASVLYGGCAIYELSRTSAGNVADADLAEWPTSIERIQQHYPEAQ
FVIPGHGLPGGLDLLKHTTNVVKAHTNRSVVE

SEQ ID No. 313:
MLKVISSLLVYMTASVMAVASPLAHSGEPSGEYPTVNEIPVGEVRLYQIADGVWSHI
ATQSFDGAVYPSNGLIVRDGDELLLIDTAWGAKNTAALLAEIEKQIGLPVTRAVSTHF
HDDRVGGVDVLRAAGVATYASPSTRRLAEAEGNEIPTHSLEGLSSSGDAVRFGPVE
LFYPGAAHSTDNLVVYVPSANVLYGGCAVLELSSTSAGNVADADLAEWPTSVERIQ
KHYPEAEVVIPGHGLPGGLDLLQHTANVVKAHKNRSVAE

said peptides being chosen, preferably, from the peptides of sequence **SEQ ID No. 314** to **SEQ ID No. 346** as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the VIM protein(s)
SEQ ID No. 314	AAGVATYASPSAR	128-140 for the protein of SEQ No. 293
SEQ ID No. 315	AAGVATYASPSIR	128-140 for the protein of SEQ No. 294

SEQ ID No. 316	AAGVATYASPSTR	128-140 for the proteins of SEQ No. 288, 289, 290, 292, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 307, 308, 309, 310, 312, 313
SEQ ID No. 317	AAGVATYTSPLTR	127-139 for the protein of SEQ No. 311
SEQ ID No. 318	AGVATYASPSTR	129-140 for the proteins of SEQ No. 288, 289, 290, 291, 292, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313
SEQ ID No. 319	AHTNR	254-258 for the protein of SEQ No. 312; 258-262 for the proteins of sequence SEQ ID No. 288, 289, 292, 293, 294, 295, 296, 298, 299, 300, 301, 302, 303, 305, 306, 309
SEQ ID No. 320	ALSSSGDVVR	156-165 for the protein of SEQ No. 311
SEQ ID No. 321	AVSTHFHDDR	110-119 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313
SEQ ID No. 322	DADELLLIDTAWGAK	75-89 for the protein of SEQ No. 311
SEQ ID No. 323	DGDELLLIDTAWGAK	76-90 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313
SEQ ID No. 324	DGDELLLIDTAWGTK	76-90 for the protein of SEQ No. 299
SEQ ID No. 325	ESAGNVADANLAEWPATIK	205-223 for the protein of SEQ No. 311
SEQ ID No. 326	GEYPTVSEIPVGEVR	31-45 for the proteins of SEQ No. 288, 289, 292, 293, 294, 295, 296, 299, 300, 301, 302, 303, 305, 312
SEQ ID No. 327	HTTNVVK	247-253 for the protein of SEQ No. 312; 251-257 for the proteins of sequence SEQ ID No. 288, 289, 292, 293, 294, 295, 296, 298, 300, 301, 302, 303, 305, 306, 309; 250-256 for the protein of sequence SEQ ID No. 311
SEQ ID No. 328	IGDGVWSHIATQK	48-60 for the protein of SEQ No. 311
SEQ ID No. 329	LANEIPTHSLEGLSSSGDAVR	142-162 for the protein of SEQ No. 312

SEQ ID No. 330	LGDTVYSSNGLIVR	61-74 for the protein of SEQ No. 311
SEQ ID No. 331	LYQIADGVWSHIATK	46-60 for the protein of SEQ No. 289
SEQ ID No. 332	LYQIADGVWSHIATR	46-60 for the proteins of SEQ No. 292, 312
SEQ ID No. 333	NTAALLAEIEK	91-101 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313
SEQ ID No. 334	NTVALLAEIEK	90-100 for the protein of SEQ No. 311; 91-101 for the protein of sequence SEQ ID No. 299
SEQ ID No. 335	QIGLPVTR	102-109 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313; 101-108 for the protein of sequence SEQ ID No. 311
SEQ ID No. 336	QLAEAAGNEVPAHSLK	140-155 for the protein of SEQ No. 311
SEQ ID No. 337	SFDGAVYPSNGLIVR	61-75 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313
SEQ ID No. 338	SISTHFHDDR	109-118 for the protein of SEQ No. 311
SEQ ID No. 339	SVSTHFHDDR	110-119 for the protein of SEQ No. 299
SEQ ID No. 340	TSAGNVADADLAEWPGSVER	206-225 for the protein of SEQ No. 299
SEQ ID No. 341	TSAGNVADADLAEWPTSIER	202-221 for the protein of SEQ No. 312; 206-225 for the protein of sequence SEQ ID No. 288, 289, 292, 293, 294, 295, 296, 298, 300, 301, 302, 303, 305, 309
SEQ ID No. 342	TSAGNVADADLAEWPTSVER	206-225 for the proteins of SEQ No. 290, 291, 297, 304, 306, 307, 308, 310, 313
SEQ ID No. 343	VGGVDALR	120-127 for the protein of SEQ No. 299

SEQ ID No. 344	VGGVDVLR	120-127 for the proteins of SEQ No. 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 312, 313; 119-126 for the protein of sequence SEQ ID No. 311
SEQ ID No. 345	VLFGGCAVHEASR	192-204 for the protein of SEQ No. 311
SEQ ID No. 346	VLYGGCAVHELSR	193-205 for the proteins of SEQ No. 290, 297, 304

The detection of a mechanism of resistance to carbapenems and/or to cephalosporins induced by the expression of an OXA protein is characterised by the detection of at least one peptide belonging to an OXA protein and to its different sequence variants **SEQ ID No. 347** to **SEQ ID No. 508**.

SEQ ID No. 347:
MSRLLLSGLLATGLLCAVPASAASGCFLYADGNGQTLSSEGDCSSQLPPASTFKIPL
ALMGYDSGFLVNEEHPALPYKPSYDGWLPAWRETTTPRRWETYSVVWFSQQITE
WLGMERFQQYVDRFDYGNRDLSGNPGKHDGLTQAWLSSSLAISPEEQARFLGKM
VSGKLPVSAQTLQYTANILKVSEVEGWQIHGKTGMGYPKKLDGSLNRDQQIGWFV
GWASKPGKQLIFVHTVVQKPGKQFASIKAKEEVLAALPAQLKKL
SEQ ID No. 348:
IACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPA
STFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQI
AREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEDQLRISAVNQVEFLESLYLNKLSA
SKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFF
AFNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 349:
MKKILLLHMLVFVSATLPISSVASDEVETLKCTIIADAITGNTLYETGECARRVSPCSS
FKLPLAIMGFDSGILQSPKSPTWELKPEYNPSPRDRTYKQVYPALWQSDSVVWFSQ
QLTSRLGVDRFTEYVKKFEYGNQDVSGDSGKHNGLTQSWLMSSLTISPKEQIQFLL
RFVAHKLPVSEAAYDMAYATIPQYQAAEGWAVHGKSGSGWLRDNNGKINESRPQ
GWFVGWAEKNGRQVVFARLEIGKEKSDIPGGSKAREDILVELPVLMGNK
SEQ ID No. 350:
MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTWVYELFAKEIGDDKARRYLKKIDYGNAGPSTSNGDYWIEGSLAISAQE
QIAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR
SEQ ID No. 351:
MQRSLSMSGKRHFIFAVSFVISTVCLTFSPANAAQKLSCTLVIDEASGDLLHREGSC
DKAFAPMSTFKLPLAIMGYDADILLDATTPRWDYKPEFNGYKSQQKPTDPTIWLKDS
IVWYSQELTRRLGESRFSDYVQRFDYGNKDVSGDPGKHNGLTHAWLASSLKISPEE
QVRFLRRFLRGELPVSEDALEMTKAVVPHFEAGDWDVQGKTGTGSLSDAKGGKAP
IGWFIGWATRDDRRVVFARLTVGARKGEQPAGPAARDEFLNTLPALSENF

SEQ ID No. 352:
MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLAR
ASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVS
AVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLE
SLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 353:
IACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPA
STFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIT
REVGEVRMQKYLKKFSYGNQNISGGIDKFWLEDQLRISAVNQVEFLESLYLNKLSAS
KENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFA
FNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 354:
IACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPA
STFKIPSAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIA
REVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLESLYLNKLSAS
KENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFA
FNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 355:
MIIRFLALLFSAVVLVSLGHAQEKTHESSNWGKYFSDFNAKGTIVVVDERTNGNSTS
VYNESRAQQRYSPASTFKIPHTLFALDAGAVRDEFHVFRWDGAKRSFAGHNQDQN
LRSAMRNSTVWVYQLFAKEIGENKARSYLEKLNYGNADPSTKSGDYWIDGNLAISA
NEQISILKKLYRNELPFRVEHQRLVKDLMIVEAKRDWILRAKTGWDGQMGWWVGW
VEWPTGPVFFALNIDTPNRMEDLHKREAIARAILQSVNALPPN
SEQ ID No. 356:
MAIRIFAILFSTFVFGTFAHAQEGMRERSDWRKFFSEFQAKGTIVVADERQTDRVILV
FDQVRSEKRYSPASTFKIPHTLFALDAGAARDEFQVFRWDGIKRSFAAHNQDQDLR
SAMRNSTVWIYELFAKEIGEDKARRYLKQIDYGNADPSTSNGDYWIDGNLAIAAQEQ
IAFLRKLYHNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRIGWWVGWVEW
PTGPVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR
SEQ ID No. 357:
MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPSAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFL
ESLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWV
EKGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 358:
MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEDQLRISAVNQVEFLE
SLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 359:
MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFGLEGQLRISAVNQVEFLE
SLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 360:
MKNTIHINFAIFLIIANIIYSSASASTDISTVASPLFEGTEGCFLLYDASTNAEIAQFNKA

KCATQMAPDSTFKIALSLMAFDAEIIDQKTIFKWDKTPKGMEIWNSNHTPKTWMQFS
VVWVSQEITQKIGLNKIKNYLKDFDYGNQDFSGDKERNNGLTEAWLESSLKISPEEQ
IQFLRKIINHNLPVKNSAIENTIENMYLQDLDNSTKLYGKTGAGFTANRTLQNGWFEG
FIISKSGHKYVFVSALTGNLGSNLTSSIKAKKNAITILNTLNL

SEQ ID No. 361:

ANIIYSSASASTDISTVASPLFEGTEGCFLLYDVSTNAEIAQFNKAKCATQMAPDSTF
KIALSLMAFDAEIIDQKTIFKWDKTPKGMEIWNSNHTPKTWMQFSVVWVSQEITQKI
GLNKIKNYLKDFDYGNQDFSGDKERNNGLTEAWLESSLKISPEEQIQFLRKIINHNLP
VKNSAIENTIENMYLQDLENSTKLYGKTGAGFTANRTLQNGWFEGFIISKSGHKYVF
VSALTGNLGSNLTSSIKAKKNAITIL

SEQ ID No. 362:

IFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLVFDPVRSKKR
YSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLRSAMRNSTV
WVYELFAKEIGDDKARRYLKKIDYGNAYPSTSNGDYWIEGSLAISAQEQIAFLRKLYR
NELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVEWPTGSVFFA
LNIDTPNRMDDLFKREAIVRAIL

SEQ ID No. 363:

MIIRFLALLFSAVVLVSLGHAQDKTHESSNWGKYFSDFNAKGTIVVVDERTNGNSTS
VYNESRAQQRYSPASTFKIPHTLFALDAGAVRDEFHVFRWDGAKRSFAGHNQDQN
LRSAMRNSTVWVYQLFAKEIGENKARSYLEKLNYGNADPSTKSGDYWIDGNLAISA
NEQISILKKLYRNELPFRVEHQRLVKDLMIVEAKRDWILRAKTGWDGQMGWWVGW
VEWPTGPVFFALNIDTPNRMEDLHKREAIARAILQSVNALPPN

SEQ ID No. 364:

MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGK
NLSTYGNALARANKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEK
DMTLGEAMALSAVPVYQELARRTGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPL
KITPVQEVNFADDLAHNRLPFKLETQEEVEKMLLIKEVNGSKIYAKSGWGMGVTPQV
GWLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKLLENLGII

SEQ ID No. 365:

MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGK
NLSTYGNALARANKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEK
DMTLGEAMALSAVPVYQELARRTGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPL
KITPVQEVNFADDLAHNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMGVTPQV
GWLTGWVEQANGKKIPFSLNLEMKEGMTGSIRNEITYKSLENLGII

SEQ ID No. 366:

MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKADINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALKMEMRSEMPASIRNELLMKSLKQLNII

SEQ ID No. 367:

MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGNADPSTSNGDYCIEGSLAISAQEQ
IAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAIL

SEQ ID No. 368:

MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFL

ESLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWV
EKGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG

SEQ ID No. 369:

MAIRFLTILLSTFFLTSFVHAQEHVLERSDWKKFFSDLRAEGAIVISDERQAEHALLVF
GQERAAKRYSPASTFKLPHTLFALDADAVRDEFQVFRWDGVKRSFAGHNQDQDLR
SAMRNSAVWVYELFAKEIGKDKARHYLKQIDYGNADPSTIKGDYWIDGNLEISAHEQ
ISFLRKLYRNQLPFQVEHQRLVKDLMITEAGRNWILRAKTGWEGRFGWWVGWVE
WPTGPVFFALNIDTPNRTDDLFKREAIARAILRSIDALPPN

SEQ ID No. 370:

MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGNADPSTSNGDYWIEGSIAISAQEQ
IAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR

SEQ ID No. 371:

MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGK
NLSTYGNALARANKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEK
DMTLGEAMALSAVPVYQELARRTGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPL
KITPVQEVNFADDLAHNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMGVTPQV
GWLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKSLENLGII

SEQ ID No. 372:

MAIRFLTILLSTFFLTSFVHAQEHVLERSDWKKFFSDLRAEGAIVISDERQAEHALLVF
GQERAAKRYSPASTFKLPHTLFALDADAVRDEFQVFRWDGVKRSFAGHNQDQDLR
SAMRNSAVWVYELFAKEIGEDKARRYLKQIDYGNADPSTIKGDYWIDGNLEISAHEQ
ISFLRKLYRNQLPFQVEHQRLVKDLMITEAGRNWILRAKTGWEGRFGWWVGWVE
WPTGPVFFALNIDTPNRTDDLFKREAIARAILRSIDALPPN

SEQ ID No. 373:

MAIRFFTILLSTFFLTSFVYAQEHVVIRSDWKKFFSDLQAEGAIVIADERQAKHTLSVF
DQERAAKRYSPASTFKIPHTLFALDADAVRDEFQVFRWDGVNRSFAGHNQDQDLR
SAMRNSTVWVYELFAKDIGEDKARRYLKQIDYGNVDPSTIKGDYWIDGNLKISAHEQ
ILFLRKLYRNQLPFKVEHQRLVKDLMITEAGRSWILRAKTGWEGRFGWWVGWIEW
PTGPVFFALNIDTPNRTDDLFKREAIARAILRSIDALPPN

SEQ ID No. 374:

MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVERIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAAMDIKPQ
VGWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII

SEQ ID No. 375:

MAIQIFAILFSTFVLATFAHAQDGTLERSDWGKFFSDFQAKGTIVVADERQADHAILV
FDQARSMKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVKRSFAGHNKDQDLR
SAMRNSTVWVYELFAKEIGDGKARRYLKQIGYGNADPSTSHGDYWIEGSLAISAQE
QIAFLRKLYQNDLPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGSMGWWVGWV
EWPTGPVFFALNIDTPNRMDDLFKREAIARAILLSIEALPPNPAVHSDAAR

SEQ ID No. 376:

MKNTIHINFAIFLIIANIIYSSASASTDISTVASQLFEGTEGCFLLYDASTNAEIAQFNKA
KCAAQMAPDSTFKIALSLMAFDAEIIDQKTIFKWDKIPKGMEIWNSNHTPKTWMQFS
VVWVSQEITQKIGLNKIKNYLKDFDYGNQDFSGDKERNNGLTEAWLESSLKISPEEQ
IQFLRKIINHNLPVRNSAIENTIDNMYLQDLENSTKLYGKTGAGFTANRTLQNGWFEG
FIISKSGHKYVFVSALTGSLGSNLTSSIKAKKNAITILNTLNL

SEQ ID No. 377:
MLLFMFSIISFGNENQFMKEIFERKGLNGTFVVYDLKNDKIDYYNLDRANERFYPASS
FKIFNTLIGLENGIVKNVDEMFYYYDGSKVFLDSWAKDSNLRYAIKVSQVPAYKKLAR
ELGKERMQEGLNKLNYGNKEIGSEIDKFWLEGPLKISAMEQVKLLNLLSQSKLPFKL
ENQEQVKDITILEKKDDFILHGKTGWATDNIVVPIGWFVGWIETSDNIYSFAINLDISD
SKFLPKREEIVREYFKNINVIK
SEQ ID No. 378:
MRVLALSAVFLVASIIGMPAVAKEWQENKSWNAHFTEHKSQGVVVLWNENKQQGF
TNNLKRANQAFLPASTFKIPNSLIALDLGVVKDEHQVFKWDGQTRDIATWNRDHNLI
TAMKYSVVPVYQEFARQIGEARMSKMLHAFDYGNEDISGNVDSFWLDGGIRISATE
QISFLRKLYHNKLHVSERSQRIVKQAMLTEANGDYIIRAKTGYSTRIEPKIGWWVGW
VELDDNVWFFAMNMDMPTSDGLGLRQAITKEVLKQEKIIP
SEQ ID No. 379:
MLSRYSKTLAFAVVACTLAISTATAHAELVVRNDLKRVFDDAGVSGTFVLMDITADR
TYVVDPARAARSIHPASTFKIPNSLIAFDTGAVRDDQEVLPYGGKPQPYEQWEHDM
ALPEAIRLSAVPIYQEVARRVGFERMQAYVDAFDYGNRQLGSAIDQFWLRGPLEISA
FEEARFTSRMALKQLPVKPRTWDMVQRMLLIEQQGDAALYAKTGVATEYQPEIGW
WAGWVERAGHVYAFALNIDMPREGDMAKRIPLGKQLMRALEVWPAP
SEQ ID No. 380:
MRPLLFSALLLLSGHTQASEWNDSQAVDKLFGAAGVKGTFVLYDVQRQRYVGHDR
ERAETRFVPASTYKVANSLIGLSTGAVRSADEVLPYGGKPQRFKAWEHDMSLRDAI
KASNVPVYQELARRIGLERMRANVSRLGYGNAEIGQVVDNFWLVGPLKISAMEQTR
FLLRLAQGELPFPAPVQSTVRAMTLLESGPGWELHGKTGWCFDCTPELGWWVGW
VKRNERLYGFALNIDMPGGEADIGKRVELGKASLKALGILP
SEQ ID No. 381:
MNKGLHRKRLSKRLLLPMLLCLLAQQTQAVAAEQTKVSDVCSEVTAEGWQEVRRW
DKLFESAGVKGSLLLWDQKRSLGLSNNLSRAAEGFIPASTFKLPSSLIALETGAVRD
ETSRFSWDGKVREIAVWNRDQSFRTAMKYSVVPVYQQLAREIGPKVMAAMVRQLE
YGNQDIGGQADSFWLDGQLRITAFQQVDFLRQLHDNKLPVSERSQRIVKQMMLTE
ASTDYIIRAKTGYGVRRTPAIGWWVGWLELDDNTVYFAVNLDLASASQLPLRQQLV
KQVLKQEQLLP
SEQ ID No. 382:
MNTIISRRWRAGLWRRLVGAVVLPATLAATPAAYAADVPKAALGRITERADWGKLF
AAEGVKGTIVVLDARTQTYQAYDAARAEKRMSPASTYKIFNSLLALDSGALDNERAII
PWDGKPRRIKNWNAAMDLRTAFRVSCLPCYQVVSHKIGRRYAQAKLNEVGYGNRT
IGGAPDAYWVDDSLQISAREQVDFVQRLARGTLPFSARSQDIVRQMSIVEATPDYVL
HGKTGWFVDKKPDIGWWVGWIERDGNITSVAINIDMLSEADAPKRARIVKAVLKDLK
LI
SEQ ID No. 383:
MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQIFKWDGKPRAMKQWERDLSLRGAIQVS
AVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLE
SLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KGAEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 384:
MRVLALSAVLVVASIVGMPAMANEWQEKPSWNTHFSEHKAQGVIVLWNENKQQGF
TNNLKRANQAFLPASTFKIPNSLIALDLGVVKDEHQVFKWDGQTRDIAAWNRDHDLI
TAMKYSVVPVYQEFARQIGQARMSKMLHAFDYGNEDISGNLDSFWLDGGIRISATE
QVAFLRKLYHNKLHVSERSQRIVKQAMLTEANSDYIIRAKTGYSTRIEPQIGWWVGW
VELDDNVWFFAMNMDMPTADGLGLRQAITKEVLKQEKIIP

SEQ ID No. 385:
MKKITLFLLFLNLVFGQDKILNNWFKEYNTSGTFVFYDGKTWASNDFSRAMETFSPA
STFKIFNALIALDSGVIKTKKEIFYHYRGEKVFLSSWAQDMNLSSAIKYSNVLAFKEVA
RRIGIKTMQEYLNKLHYGNAKISKIDTFWLDNSLKISAKEQAILLFRLSQNSLPFSQEA
MNSVKEMIYLKNMENLELFGKTGFNDGQKIAWIVGFVYLKDENKYKAFALNLDIDKF
EDLYKREKILEKYLDELVKKVKNDG
SEQ ID No. 386:
MSKKNFILIFIFVILISCKNTEKISNETTLIDNIFTNSNAEGTLVIYNLNDDKYIIHNKERAE
QRFYPASTFKIYNSLIGLNEKAVKDVDEVFYKLMAKSFLESWAKDSNLRYAIKNSQV
PAYKELARRIGIKKMKENIEKLDFGNKSIGDSVDTFWLEGPLEISAMEQVKLLTKLAQ
NELQYPIEIQKAISDITITRANLHITLHGKTGLADSKNMTTEPIGWFVGWLEENDNIYV
FALNIDNINSDDLAKRINIVKESLKALNLLK
SEQ ID No. 387:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALKMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 388:
MNIQALLLITSAIFISACSPYIVTANPNYSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRIGYGNADIGTQVDNFWLVGPLKI
TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGISSSVRKEITYRGLEQLGIL
SEQ ID No. 389:
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TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
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SEQ ID No. 390:
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DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
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SEQ ID No. 391:
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GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 392:
MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQEVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 393:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ

TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGEKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 394:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDKKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWNGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQHEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 395:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKTTTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 396:
MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTAVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGTPSSVRKEITYKSLEQLGIL

SEQ ID No. 397:
MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLPRRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 398:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEKLGIL

SEQ ID No. 399:
MNIKTLLLITSTIFISACSPYIVTANPNHSTSKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASIEYVPASTFKMLNALIGLEHHKATTTEIFKWDGQKRLFPEWEKD
MTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKIT
PQQEAQFAYKLANKTLPFSLKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQVG
WLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 400:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAISVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLAGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 401:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
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KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 402:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGEKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGSVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 403:

MNIKTLLLITSTIFISACSPYIVTANPNHSTSKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASIEYVPASTFKMLNALIGLEHHKATTTEIFKWDGQKRLFPEWEKD
MTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKIT
PQQEAQFAYKLANKTLPFSLKAQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQVG
WLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 404:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDKKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 405:

MNIKTLLLITSAIFISACSHYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFTYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 406:

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 407:

MNIKALLLITSTIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
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DMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 408:

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DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPHGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 409:

MNIKALFLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
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DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 410:
MKLLKILSLVCLSISIGACAEHSMSRAKTSTIPQVNNSIIDQNVQALFNEISADAVFVTY
DGQNIKKYGTHLDRAKTAYIPASTFKIANALIGLENHKATSTEIFKWDGKPRFFKAWD
KDFTLGEAMQASTVPVYQELARRIGPSLMQSELQRIGYGNMQMGTEVDQFWLKGP
LTITPIQEVKFVYDLAQGQLPFKPEVQQQVKEMLYVERRGENRLYAKSGWGMAVD
PQVGWYVGFVEKADGQVVAFALNMQMKAGDDIALRKQLSLDVLDKLGVFHYL
SEQ ID No. 411:
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TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEIFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
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GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 412:
MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIRQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
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GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 413:
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KDFTLGEAMQASTVPVYQELARRIGPSLMQSELQRIGYGNMQIGTEVDQFWLKGPL
TITPIQEVKFVYDLAQGQLPFKPEVQQQVKEMLYVERRGENRLYAKSGWGMAVDP
QVGWYVGFVEKADGQVVAFALNMQMKAGDDIALRKQLSLDVLDKLGVFHYL
SEQ ID No. 414:
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NLSTYGNALARANKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEK
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KITPVQEVNFADDLAHNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMDVTPQV
GWLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKSLENLGII
SEQ ID No. 415:
MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGNADPSTSNGDYWIESSLAISAQE
QIAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR
SEQ ID No. 416:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 417:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAILVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 418:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDKKAEKIKNLFNEAHTTGVLVIQQGQ

TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWNGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 419:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGEKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 420:

MNIKALLLITSAIFISACSPYIVTTNPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNTDIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 421:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIQVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 422:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGEKRLFPEWEK
NMTLGDAMKASALPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPL
KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 423:

MNIKTLLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
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DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEMNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 424:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGEKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFPLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 425:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGGDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 426:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
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DMTLGDAMKASAILVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKI

TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 427:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
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DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 428:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKTTTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 429:

MSKKNFILIFIFVILISCKNTEKISNETTLIDNIFTNSNAEGTLVIYNLNDDKYIIHNKERAE
QRFYPASTFKIYNSLIGLNEKAVKDVDEVFYKYNGEKVFLESWAKDSNLRYAIKNSQ
VPAYKELARRIGLKKMKENIEKLDFGNKSIGDSVDTFWLEGPLEISAMEQVKLLTKLA
QNELPYPIEIQKAVSDITILEQTYNYTLHGKTGLADSKNMTTEPIGWFVGWLEENDNI
YVFALNIDNINSDDLAKRINIVKESLKALNLLK

SEQ ID No. 430:

MSKKNFILIFIFVILTSCKNTEKISNETTLIDNIFTNSNAEGTLVIYNLNDDKYIIHNKERA
EQRFYPASTFKIYNSLIGLNEKAVKDVDEVFYKYNGEKVFLESWAKDSNLRYAIKNS
QVPAYKELARRIGLKKMKENIEKLDFGNKSIGDSVDTFWLEGPLEISAMEQIKLLTKL
AQNELPYPIEIQKAVSDITILEQTYNYTLHGKTGLADSKNMTTEPIGWFVGWLEENDN
IYVFALNIDNINSDDLAKRINIVKESLKALNLLK

SEQ ID No. 431:

LLITSAIFISACSPYIVSANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIQQGQTQQSY
GNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEKNMTLG
DAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLKITPQQ
EAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQVGWLT
GWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSL

SEQ ID No. 432:

LLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQTQQSY
GNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEKNMTLG
DAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLKITPQQ
EAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQVGWLT
EWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSL

SEQ ID No. 433:

MTVRRLSCALGAALSLSALGGGPVQAAVLCTVVADAADGRILFQQGTQQACAERYT
PASTFKLAIALMGADAGILQGPHEPVWNYQPAYPDWGGDAWRQPTDPARWIKYSV
VWYSQLTAKALGQDRFQRYTSAFGYGNADVSGEPGKHNGTDGAWIISSLRISPLEQ
LAFLRKLVNRQLPVKAAAYELAENLFEAGQADGWRLYGKTGTGSPGSNGVYTAAN
AYGWFVGWARKDGRQLVYARLLQDERATRPNAGLRARDELVRDWPAMAGAWRP

SEQ ID No. 434:

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNVLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQEVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 435:
MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLAR
ASKEYLPASTFKIPSAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVS
AVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEK
ETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 436:
MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 437:
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TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 438:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
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KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNQ
QVGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 439:
MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEMTYKSLEQLGIL
SEQ ID No. 440:
MNKYFTCYVVASLFFSGCTVQHNLINETQSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTTWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVERIDFGNAEIGQQVDNFWLIGPLK
VTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEENNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 441:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAAMDIKPQ
VGWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 442:
MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFLLEGQLRISAVNQVEFLE
SLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 443:
MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV

FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGDADPSTSNGDYWIEGSLAISAQE
QIAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR

SEQ ID No. 444:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDKKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKASTTEVFKWNGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVKSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 445:

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKHVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 446:

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKHVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 447:

MKKFILPILSISTLLSVSACSSIQTKFEDTFHTSNQQHEKAIKSYFDEAQTQGVIIIKKG
KNISTYGNNLTRAHTEYVPASTFKMLNALIGLENHKATTTEIFKWDGKKRSYPMWEK
DMTLGDAMALSAVPVYQELARRTGLDLMQKEVKRVGFGNMNIGTQVDNFWLVGPL
KITPIQEVNFADDFANNRLPFKLETQEEVKKMLLIKEFNGSKIYAKSGWGMDVTPQV
GWLTGWVEKSNGEKVAFSLNIEMKQGMPGSIRNEITYKSLENLGII

SEQ ID No. 448:

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQEVQDEVQSILFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 449:

MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGK
NLSTYGNALARANKEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRTYPMWEK
DMTLGEAMALSAVPVYQELARRTGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPL
KITPVQEVNFADDLAHNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMGVTSQV
GWLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKSLENLGII

SEQ ID No. 450:

MRVLALSAVFLVASIIGMPAVAKEWQENKSWNAHFTEHKSQGVVVLWNENKQQGF
TNNLKRANQAFLPASTFKIPNSLIALDLGVVKDEHQVFKWDGQTRDIATWNRDHNLI
TAMKYSVVPVYQEFARQIGEARMSKMLHAFDYGNEDISGNVDSFWLDGGIRISATE
QISFLRKLYHNKLHVSERSQRIVKQAMLTEANGDYIIRAKTGYSARIEPKIGWWVGW
VELDDNVWFFAMNMDMPTSDGLGLRQAITKEVLKQEKIIP

SEQ ID No. 451:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAVPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPL

KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGLDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 452:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAVPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPL
KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGLDVNLQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 453:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEKLGIL

SEQ ID No. 454:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIRNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 455:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDSKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 456:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDGVQSMLFIEEKNGNKIYAKSGWGWDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 457:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDSKKRLFPEWEK
DMTLGDAMKASAILVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKI
TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 458:

MKLLKILSLVCLSISIGACAEHSMSRAKTSTIPQVNNSIIDQNVQALFNEISADAVFVTY
DGQNIKKYGTHLDRAKTAYIPASTFKIANALIGLENHKATSTEIFKWDGKPRFLKAWD
KDFTLGEAMQASTVPVYQELARRIGPSLMQSELQRIGYGNMQIGTEVDQFWLKGPL
TITPIQEVKFVYDLAQGQLPFKPEVQQQVKEMLYVERRGENRLYAKSGWGMAVDP
QVGWYVGFVEKADGQVVAFALNMQMKAGDDIALRKQLSLDVLDKLGVFHYL

SEQ ID No. 459:

MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDVKPQ
VGWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII

SEQ ID No. 460:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGALVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 461:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELMMKSLKQLNII
SEQ ID No. 462:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLAGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 463:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDERNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 464:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEKSNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 465:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASTRNELLMKSLKQLNII
SEQ ID No. 466:
MKKFILPIFSISILLSLSACSSIQTKFEDTFHISNQKHEKAIKSYFDEAQTQGVIIIKEGKN
ISSYGNNLVRAHTEYVPASTFKMLNALIGLENHKATTNEIFKWDGKKRSYPMWEKD
MTLGEAMALSAVPVYQDLARRIGLNLMQKEVKRVGFGNMNIGTQVDNFWLIGPLKI
TPIQEVNFADDLANNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMDVSPQVG
WLTGWVEKSNGEKVSFSLNIEMKQGMSGSIRNEITYKSLENLGII
SEQ ID No. 467:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIAVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 468:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ

TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAIKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKI
TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 469:

MKILIFLPLLSCLGLTACSLPVSSLPSQSISTQAIASLFDQAQSSGVLVIQRDQQVQVY
GNDLNRANTEYVPASTFKMLNALIGLQHGKATTNEIFKWDGKKRSFTAWEKDMTLG
QAMQASAVPVYQELARRIGLELMQQEVQRIQFGNQQIGQQVDNFWLVGPLKVTPK
QEVQFVSALAREQLAFDPQVQQQVKAMLFLQERKAYRLYVKSGWGMDVEPQVGW
LTGWVETPQAEIVAFSLNMQMQNGIDPAIRLEILQQALAELGLYPKAEG

SEQ ID No. 470:

MHKHMSKLFIAFLAFLLSVPAAAEDQTLAELFAQQGIDGTIVISSLHNGKTFIHNDPRA
KQRFSTASTFKILNTLISLEEKAISGKDDVLKWDGHIYDFPDWNRDQTLESAFKVSCV
WCYQALARQVGAEKYRNYLRKSVYGELREPFEETTFWLDGSLQISAIEQVNFLKKV
HLRTLPFSASSYETLRQIMLIEQTPAFTLRAKTGWATRVKPQVGWYVGHVETPTDV
WFFATNIEVRDEKDLPLRQKLTRKALQAKGIIE

SEQ ID No. 471:

MKTFAAYVITACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGTDKFWLEDQLRISAVNQVEFL
ESLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWV
EKGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG

SEQ ID No. 472:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAILVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKI
TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGLDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 473:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIQVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 474:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAMPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPL
KITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 475:

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 476:

MRVLALSAVFLVASIIGMPAVAKEWQENKSWNAHFTEHKSQGVVVLWNENKQQGF
TNNLKRANQAFLPASTFKIPNSLIALDLGVVKDEHQVFKWDGQTRDIATWNRDHNLI
TAMKYSVVPVYQEFARQIGEARMSKMLHAFDYGNEDISGNVDSFWLDGGIRISATE

QISFLRKLYHNKLHVSERSQRIVKQAMLTEANGDYIIRAKTGYDTKIGWWVGWVELD
DNVWFFAMNMDMPTSDGLGLRQAITKEVLKQEKIIP

SEQ ID No. 477:

MSKKNFILIFIFVILISCKNTEKTSNETTLIDNIFTNSNAEGTLVIYNLNDDKYIIHNKERA
EQRFYPASTFKIYNSLIGLNEKAVKDVDEVFYKYNGEKVFLESWAKDSNLRYAIKNS
QVPAYKELARRIGLEKMKENIEKLDFGNKNIGDSVDTFWLEGPLEISAMEQVKLLTKL
AQNELPYPIEIQKAVSDITILEQTDNYTLHGKTGLADSENMTTEPIGWLVGWLEENNN
IYVFALNIDNINSDDLAKRINIVKESLKALNLLK

SEQ ID No. 478:

MNIKALFLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 479:

MNIKALFLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPSSQKVQDEVQSMLFIEEKNGNKMYAKSGWGWDVNPQ
VGWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 480:

MNIKALFLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEIAYKSLEQLGIL

SEQ ID No. 481:

MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGNADPSTSNGDCWIEGSLAISAQE
QIAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR

SEQ ID No. 482:

MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWVVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 483:

MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEYHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 484:

MAIRFLTILLSTFFLTSFVHAQEHVVVRSDWKKFFSDLQAEGAIVIADERQAEHALLV
FGQERAAKRYSPASTFKLPHTLFALDAGAVRDEFQVFRWDGVKRSFAGHNQDQDL
RSAMRNSAVWVYELFAKEIGEDNARRYLKQIDYGNADPSTIKGNYWIDGNLEISAHE
QISFLRKLYRNQLPFQVEHQRLVKYLMITEAGRNWILRAKTGWEGRFGWWIGWVE
WPTGPVFFALNIDTPNRTDDLFKREAIARAILRSIDALPPN

SEQ ID No. 485:
MRVLALSAVFLVASIIGMPAVAKEWQENKSWNAHFTEHKSQGVVVLWNENKQQGF
TNNLKRANQAFLPASTFKIPNSLIALDLGVVKDEHQVFKWDGQTRDIAAWNRDHDLI
TAMKYSVVPVYQEFARQIGEARMSKMLHAFDYGNEDISGNVDSFWLDGGIRISATQ
QIAFLRKLYHNKLHVSERSQRIVKQAMLTEANGDYIIRAKTGYSTRIEPKIGWWVGW
VELDDNVWFFAMNMDMPTSDGLGLRQAITKEVLKQEKIIP
SEQ ID No. 486:
MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKSQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII
SEQ ID No. 487:
MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAISVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL
SEQ ID No. 488:
MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLV
FDPVRSKKRYSPASTFKIPHTLFALDAGAVRDEFQIFRWDGVNRGFAGHNQDQDLR
SAMRNSTVWVYELFAKEIGDDKARRYLKKIDYGNADPSTSNGDYWIEGSLAISAQE
QIAFLRKLYRNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGSVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR
SEQ ID No. 489:
MKTIAAYLVLVFYASTALSESISENLAWNKEFSSESVHGVFVLCKSSSNSCTTNNAA
RASTAYIPASTFKIPNALIGLETGAIKDERQVFKWDGKPRAMKQWEKDLKLRGAIQV
SAVPVFQQIAREVGEIRMQKYLNLFSYGNANIGGGIDKFWLEGQLRISAFNQVKFLE
SLYLNNLPASKANQLIVKEAIVTEATPEYIVHSKTGYSGVGTESSPGVAWWVGWVE
KGTEVYFFAFNMDIDNESKLPSRKSISTKIMASEGIIIGG
SEQ ID No. 490:
MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNGVFVLCKSSSKLACATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQIFKWDGKPRAMKQWERDLSLRGAIQVS
AVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLE
SLFLNKLSASKENQLIVKEALVTEAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEK
GAEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG
SEQ ID No. 491:
MAIRIFAILFSTFVFGTFAHAQEGMRERSDWRKFFSEFQAKGTIVVADERQTDRVILV
FDQVRSEKRYSPASTFKIPHTLFALDAGAARDEFQVFRWDGIKRSFAAHNQDQDLR
SAMRNSTVWIYELFAKEIGEDKARRYLKQIDYGNADPSTSNGDYWIDGNLAIAAQEQ
IAFLRKLYHNELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWWVGWVE
WPTGPVFFALNIDTPNRMDDLFKREAIVRAILRSIEALPPNPAVNSDAAR
SEQ ID No. 492:
MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLAR
ASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVS
AVPVFQQIAREVGEVRMQKYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEK
ETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIGG
SEQ ID No. 493

MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQT
DKKINLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWE
KDMTLGEAMKLSAVPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPL
KVTPIQEVEFVSQLAHTQLPFSEKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQV
GWLTGWVEQPDGKIVAFALNMEMRSEMPASIRNELLMKSLKQLNII

SEQ ID No. 494

MKKLSVLLWLTLFYCGTIWAQSTCFLVQENQTVLKHEGKDCNKRFAPESTFKIALSL
MGFDSGILKDTLNPEWPYKKEYELYLNVWKYPHNPRTWIRDSCVWYSQVLTQQLG
MTRFKNYVDAFHYGNQDISGDKGQNNGLTHSWLSSSLAISPSEQIQFLQKIVNKKLS
VNPKAFTMTKDILYIQELAGGWKLYGKTGNGRQLTKDKSQKLSLQHGWFIGWIEKD
GRVITFTKHIADSKKHVTFASFRAKNETLNQLFYLINELEK

SEQ ID No. 495

MNIKTLLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEVHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSPKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 496

MKFRHALSSAFVLLGCIAASAHAKTICTAIADAGTGKLLVQDGDCGRRASPASTFKIA
ISLMGYDAGFLRNEHDPVLPYRDSYIAWGGEAWKQPTDPTRWLKYSVVWYSQQV
AHHLGAQRFAQYAKAFGYGNADVSGDPGQNNGLDRAWIGSSLQISPLEQLEFLGK
MLNRKLPVSPTAVDMTERIVESTTLADGTVVHGKTGVSYPLLADGTRDWARGSGW
FVGWIVRGNQTLVFARLTQDERKQPVSAGIRTREAFLRDLPRLLAAR

SEQ ID No. 497

MKFRHALSSAFVLLGCIAASAHAKTICTAIADAGTGKLLVQDGDCGRRASPASTFKIA
ISLMGYDAGFLRNEHDPVLPYRDSYIAWGGEAWKQPTDPTRWLKYPVVWYSQQV
AHHLGAQRFAQYAKAFGYGNADVSGDPGQNNGLDRAWIGSSLQISPLEQLEFLGK
MLNRKLPVSPTAVDMTERIVESTTLADGTVVHGKTGVSYPLLADGTRDWARGSGW
FVGWIVRGKQTLVFARLTQDERKQPVSAGIRTREAFLRDLPRLLAAR

SEQ ID No. 498

MRGKHTVILGAALSALFAGAAGAQMLECTLVADAASGQELYRKGACDKAFAPMSTF
KVPLAVMGYDAGILVDAHNPRWDYKPEFNGYKFQQKTTDPTIWEKDSIVWYSQQLT
RKMGQKRFAAYVAGFGYGNGDISGEPGKSNGLTHSWLGSSLKISPEGQVRFVRDL
LSAKLPASKDAQQMTVSILPHFAAGDWAVQGKTGTGSFIDARGAKAPLGWFIGWAT
HEERRVVFARMTAGGKKGEQPAGPAARDAFLKALPDLAKRF

SEQ ID No. 499

MKFRHALSSAFVLLGCIAASAHAKTICTAIADAGTGKLLVQDGDCGRRASPASTFKIA
ISLMGYDAGFLRNEHDPVLPYRDSYIAWGGEAWKQPTDPTRWLKYSVVWYSQQV
AHHLGAQRFAQYAKAFGYGNADVSGDPGQNNGLDRAWIGSSLQISPLEQLEFLGK
MLDRKLPVSPTAVDMTERIVESTTLADGTVVHGKTGVSYPLLADGTRDWARGSGW
FVGWIVRGKQTLVFARLTQDERKQPVSAGIRTREAFLRDLPRLLAAR

SEQ ID No. 500

MKFRHALSSAFVLLGCIAASAHAKTICTAIADAGTGKLLVQDGDCGRRASPASTFKIA
ISLMGYDAGFLRNEHDPVLPYRDSYIAWGGEAWKQPTDPTRWLKYSVVWYSQQV
AHHLGAQRFAQYAKAFGYGNADVSGDPGQNNGLDRAWIGSSLQISPLEQLEFLGK
MLNRKLPVSPTAVDMTERIVESTTLADGTVVHGKTGVSYPLLADGTRDWARGSGW
FVGWIVRGKQTLVFARLTQDERKQPVSAGIRTREAFLRDLPRLLAAR

SEQ ID No. 501

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLAR
ASKEYLPVSTFKIPSAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVS

AVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLE
SLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVE
KETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIGG

SEQ ID No. 502

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGKKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 503

MNIKALLLITSAIFISACSPYIVSANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
NMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVNPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 504

MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNGVFVLCKSSSKSCATNNLA
RASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLSLRGAIQV
SAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFL
ESLFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWV
EKGTEVYFFAFNMDIDNENKLPLRKSIPTKIMASEGIIGG

SEQ ID No. 505

MKTIAAYLVLVFFAGTALSESISENLAWNKEFSSESVHGVFVLCKSSSNSCTTNNAT
RASTAYIPASTFKIPNALIGLETGAIKDARQVFKWDGKPRAMKQWEKDLTLRGAIQV
SAVPVFQQIARDIGKKRMQKYLNLFSYGNANIGGGIDKFWLEGQLRISAVNQVKFLE
SLYLNNLPASKANQLIVKEAIVTEATPEYIVHSKTGYSGVGTESNPGVAWWVGWVE
KGTEVYFFAFNMDIDNESKLPSRKSIPTKIMASEGIIIGG

SEQ ID No. 506

MKKFILPIFSISILVSLSACSSIKTKSEDNFHISSQQHEKAIKSYFDEAQTQGVIIIKEGK
NLSTYGNALARANKEYVPASTFKMLIALIGLENHKATTNEIFKWDGKKRTYPMWEKD
MTLGEAMALSAVPVYQELARRTGLELMQKEVKRVNFGNTNIGTQVDNFWLVGPLKI
TPVQEVNFADDLAHNRLPFKLETQEEVKKMLLIKEVNGSKIYAKSGWGMGVTPQVG
WLTGWVEQANGKKIPFSLNLEMKEGMSGSIRNEITYKSLENLGII

SEQ ID No. 507

MNIKALLLITSAIFISACSPYIVTANPNHSASKSDDKAEKIKNLFNEAHTTGVLVIHQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWNGQKRLFPEWEK
DMTLGDAMKASAIPVYQDLARRIGLELMSNEVKRVGYGNADIGTQVDNFWLVGPLK
ITPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

SEQ ID No. 508

MNIKALLLITSAISISACSPYIVTANPNHSASKSDEKAEKIKNLFNEAHTTGVLVIQQGQ
TQQSYGNDLARASTEYVPASTFKMLNALIGLEHHKATTTEVFKWDGQKRLFPEWEK
DMTLGDAIKASAIPVYQDLARRIGLELMSKEVKRVGYGNADIGTQVDNFWLVGPLKI
TPQQEAQFAYKLANKTLPFSQKVQDEVQSMLFIEEKNGNKIYAKSGWGWDVDPQV
GWLTGWVVQPQGNIVAFSLNLEMKKGIPSSVRKEITYKSLEQLGIL

said peptides being chosen, preferably, from the peptides of sequence SEQ ID No. 509 to SEQ ID No. 523, SEQ ID No. 525 to SEQ ID No. 572, SEQ ID No. 574

to SEQ ID No. 604, SEQ ID No. 606 to SEQ ID No. 618, SEQ ID No. 620 to SEQ ID No. 696, SEQ ID No. 698 to SEQ ID No. 1077 and SEQ ID No. 1098 to SEQ ID No. 1109, as defined hereafter:

Peptide SEQ ID No.	Amino acid sequence	Position of the peptide in the OXA protein(s)	Clinical interest
SEQ ID No. 509	AAAYELAENLFEAGQADGWR	183-202 for the protein of SEQ No. 433	2d
SEQ ID No. 510	AAEGFIPASTFK	86-97 for the protein of SEQ No. 381	2df
SEQ ID No. 511	AALGR	41-45 for the protein of SEQ No. 382	2df
SEQ ID No. 512	ADGQVVAFALNMQMK	241-255 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 513	ADINEIFK	95-102 for the protein of SEQ No. 366	2df
SEQ ID No. 514	ADWGK	50-54 for the protein of SEQ No. 382	2df
SEQ ID No. 515	AEGAIVISDER	40-50 for the proteins of SEQ No. 369, 372	OXA
SEQ ID No. 516	AFALNLDIDK	222-231 for the protein of SEQ No. 385	2d
SEQ ID No. 517	AFAPMSTFK	49-57 for the protein of SEQ No. 498; 60-68 for the protein of sequence SEQ ID No. 351	OXA
SEQ ID No. 518	AFGYGNADVSGDPGQNNGLDR	127-147 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 519	AFTMTK	174-179 for the protein of SEQ No. 494	2de
SEQ ID No. 520	AGDDIALR	256-263 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 521	AGHVYAFALNIDMPR	233-247 for the protein of SEQ No. 379	2df
SEQ ID No. 522	AGLWR	11-15 for the protein of SEQ No. 382	2df
SEQ ID No. 523	AHTEYVPASTFK	73-84 for the proteins of SEQ No. 447, 466	2df
SEQ ID No. 524	AIIPWDGK	112-119 for the protein of SEQ No. 382	2df
SEQ ID No. 525	AIIPWDGKPR	112-121 for the protein of SEQ No. 382	2df

SEQ ID No. 526	AISDITITR	190-198 for the protein of SEQ No. 386	2d
SEQ ID No. 527	AISGK	82-86 for the protein of SEQ No. 470	2df
SEQ ID No. 528	ALGQDR	121-126 for the protein of SEQ No. 433	2d
SEQ ID No. 529	ALPDLAK	256-262 for the protein of SEQ No. 498	2d
SEQ ID No. 530	ALQAK	254-258 for the protein of SEQ No. 470	2df
SEQ ID No. 531	AMETFSPASTFK	50-61 for the protein of SEQ No. 385	2d
SEQ ID No. 532	AMLFLQER	196-203 for the protein of SEQ No. 469	2df
SEQ ID No. 533	AMLVFDPVR	55-63 for the proteins of SEQ No. 350, 367, 370, 415, 443, 481, 488; 44-52 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 534	AMTLLESGPGWELHGK	189-204 for the protein of SEQ No. 380	2d
SEQ ID No. 535	ANLHITLHGK	199-208 for the protein of SEQ No. 386	2d
SEQ ID No. 536	ANQLIVK	183-189 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 537	ANTEYVPASTFK	71-82 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493; 66-77 for the protein of sequence SEQ ID No. 469	2df
SEQ ID No. 538	ANVSR	133-137 for the protein of SEQ No. 380	2d
SEQ ID No. 539	APIGWFIGWATR	224-235 for the protein of SEQ No. 351	2de
SEQ ID No. 540	APLGWFIGWATHEER	213-227 for the protein of SEQ No. 498	2d
SEQ ID No. 541	AQDEVQSMLFIEEK	196-209 for the protein of SEQ No. 403	2df
SEQ ID No. 542	AQGVIVLWNENK	40-51 for the protein of SEQ No. 384	2df
SEQ ID No. 543	ASAIAVYQDLAR	126-137 for the protein of SEQ No. 467	2df
SEQ ID No. 544	ASAILVYQDLAR	126-137 for the proteins of SEQ No. 417, 426, 457, 472	2df
SEQ ID No. 545	ASAIPVYQDLAR	126-137 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 398, 399, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 418, 419, 420, 423, 424, 425, 427, 428, 434, 436, 437, 439, 444, 445, 446, 448, 453, 454, 455, 456, 468, 475, 478, 479,	2df

		480, 482, 483, 495, 502, 503, 507, 508; 120-131 for the proteins of sequence SEQ ID No. 431, 432	
SEQ ID No. 546	ASAIPVYQDLPR	126-137 for the protein of SEQ No. 397	2df
SEQ ID No. 547	ASAIQVYQDLAR	126-137 for the proteins of SEQ No. 421, 473	2df
SEQ ID No. 548	ASAISVYQDLAR	126-137 for the proteins of SEQ No. 400, 487	2df
SEQ ID No. 549	ASALPVYQDLAR	126-137 for the proteins of SEQ No. 401, 422	2df
SEQ ID No. 550	ASAMPVYQDLAR	126-137 for the protein of SEQ No. 474	2df
SEQ ID No. 551	ASAVPVYQDLAR	126-137 for the proteins of SEQ No. 438, 451, 452	2df
SEQ ID No. 552	ASIEYVPASTFK	72-83 for the proteins of SEQ No. 399, 403	2df
SEQ ID No. 553	ASNVPVYQELAR	113-124 for the protein of SEQ No. 380	2d
SEQ ID No. 554	ASPASTFK	49-56 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 555	ASTAYIPASTFK	59-70 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 556	ASTEYVPASTFK	72-83 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 400, 401, 402, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 66-77 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 557	ASTTEVFK	96-103 for the protein of SEQ No. 444	2df
SEQ ID No. 558	ATSTEIFK	99-106 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 559	ATTNEIFK	97-104 for the proteins of SEQ No. 364, 365, 371, 414, 449, 466, 506; 90-97 for the protein of sequence SEQ ID No. 469	2df
SEQ ID No. 560	ATTTAVFK	96-103 for the protein of SEQ No. 396	2df
SEQ ID No. 561	ATTTEIFK	97-104 for the protein of SEQ No. 447; 96-103 for the proteins of sequence SEQ ID No. 399, 403, 411	2df
SEQ ID No. 562	ATTTEVFK	96-103 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 397, 398, 400, 401, 402, 404, 405, 406, 407, 408, 409, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 434, 436, 437, 438, 439, 445, 446,	2df

		448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 90-97 for the proteins of sequence SEQ ID No. 431, 432	
SEQ ID No. 563	AVSDITILEQTDNYTLHGK	191-209 for the protein of SEQ No. 477	OXA
SEQ ID No. 564	AVSDITILEQTYNYTLHGK	191-209 for the proteins of SEQ No. 429, 430	2d
SEQ ID No. 565	AVVPHFEAGDWDVQGK	195-210 for the protein of SEQ No. 351	2de
SEQ ID No. 566	AWEHDMSLR	100-108 for the protein of SEQ No. 380	2d
SEQ ID No. 567	AWIGSSLQISPLEQLEFLGK	148-167 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 568	CAAQMAPDSTFK	63-74 for the protein of SEQ No. 376	2d
SEQ ID No. 569	CATQMAPDSTFK	48-59 for the protein of SEQ No. 361; 63-74 for the protein of sequence SEQ ID No. 360	2d
SEQ ID No. 570	CTHADAITGNTLYETGECAR	32-52 for the protein of SEQ No. 349	2d
SEQ ID No. 571	DAFLK	251-255 for the protein of SEQ No. 498	2d
SEQ ID No. 572	DDFILHGK	189-196 for the protein of SEQ No. 377	2d
SEQ ID No. 573	DDQEVLPYGGK	92-102 for the protein of SEQ No. 379	2df
SEQ ID No. 574	DDVLK	87-91 for the protein of SEQ No. 470	2df
SEQ ID No. 575	DEFHVFR	90-96 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 576	DEFQIFR	90-96 for the proteins of SEQ No. 350, 367, 370, 375, 415, 443, 481, 488; 79-85 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 577	DEFQVFR	90-96 for the proteins of SEQ No. 356, 369, 372, 373, 484, 491	2d
SEQ ID No. 578	DELVR	260-264 for the protein of SEQ No. 433	2d
SEQ ID No. 579	DETSR	112-116 for the protein of SEQ No. 381	2df
SEQ ID No. 580	DFDYGNQDFSGDK	141-153 for the proteins of SEQ No. 360, 376; 126-138 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 581	DFTLGEAMQASTVPVYQELAR	120-140 for the proteins of SEQ No. 410, 413, 458	2df

SEQ ID No. 582	DGNITSVAINIDMLSEADAPK	250-270 for the protein of SEQ No. 382	2df
SEQ ID No. 583	DHDLITAMK	108-116 for the proteins of SEQ No. 384, 485	2df
SEQ ID No. 584	DIAAWNR	101-107 for the proteins of SEQ No. 384, 485	2df
SEQ ID No. 585	DIGEDK	131-136 for the protein of SEQ No. 373	2d
SEQ ID No. 586	DILYIQELAGGWK	180-192 for the protein of SEQ No. 494	2de
SEQ ID No. 587	DITILEK	181-187 for the protein of SEQ No. 377	2d
SEQ ID No. 588	DLLSAK	166-171 for the protein of SEQ No. 498	2d
SEQ ID No. 589	DLMITEAGR	195-203 for the proteins of SEQ No. 369, 372, 373	2d
SEQ ID No. 590	DLMIVEAGR	195-203 for the proteins of SEQ No. 350, 356, 367, 370, 375, 415, 443, 481, 488, 491; 184-192 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 591	DLMIVEAK	195-202 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 592	DLPLR	243-247 for the protein of SEQ No. 470	2df
SEQ ID No. 593	DLSGNPGK	131-138 for the protein of SEQ No. 347	2d
SEQ ID No. 594	DLSLR	105-109 for the proteins of SEQ No. 357, 358, 359, 368, 383, 442, 471, 504; 106-110 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 595	DLTLR	105-109 for the proteins of SEQ No. 352, 435, 492, 501, 505; 96-100 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 596	DMTLGDAIK	117-125 for the proteins of SEQ No. 468, 508	2df
SEQ ID No. 597	DMTLGDAMALSAVPVYQELAR	118-138 for the protein of SEQ No. 447	2df
SEQ ID No. 598	DMTLGDAMK	117-125 for the proteins of SEQ No. 389, 390, 391, 394, 395, 398, 399, 400, 401, 403, 404, 407, 408, 409, 411, 412, 417, 418, 420, 421, 423, 425, 426, 427, 428, 436, 437, 438, 439, 444, 451, 452, 453, 454, 455, 456, 457, 467, 472, 473, 474, 478, 479, 480, 482, 483, 487, 495, 502, 507	2df
SEQ ID No. 599	DMTLGEAMALSAVPVYQDLAR	118-138 for the protein of SEQ No. 466	2df
SEQ ID No. 600	DMTLGEAMALSAVPVYQELAR	118-138 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df

SEQ ID No. 601	DMTLGEAMK	116-124 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 602	DMTLGQAMQASAVPVYQELAR	111-131 for the protein of SEQ No. 469	2df
SEQ ID No. 603	DNNGK	214-218 for the protein of SEQ No. 349	2d
SEQ ID No. 604	DQDLR	110-114 for the proteins of SEQ No. 350, 356, 367, 369, 370, 372, 373, 375, 415, 443, 481, 484, 488, 491; 99-103 for the protein of sequence SEQ ID No. 362	2d
SEQ ID No. 605	DQQIGWFVGWASK	213-225 for the protein of SEQ No. 347	2d
SEQ ID No. 606	DQQIGWFVGWASKPGK	213-228 for the protein of SEQ No. 347	2d
SEQ ID No. 607	DQQVQVYGNDLNR	53-65 for the protein of SEQ No. 469	2df
SEQ ID No. 608	DQSFR	132-136 for the protein of SEQ No. 381	2df
SEQ ID No. 609	DQTLESAFK	105-113 for the protein of SEQ No. 470	2df
SEQ ID No. 610	DSCVWYSQVLTQQLGMTR	98-115 for the protein of SEQ No. 494	2de
SEQ ID No. 611	DSIVWYSQELTR	113-124 for the protein of SEQ No. 351	2de
SEQ ID No. 612	DSIVWYSQQLTR	102-113 for the protein of SEQ No. 498	2d
SEQ ID No. 613	DSNLR	109-113 for the proteins of SEQ No. 429, 430, 477; 96-100 for the proteins of sequence SEQ ID No. 377, 386	2d
SEQ ID No. 614	DSYIAWGGEAWK	81-92 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 615	DTLNPEWPYK	67-76 for the protein of SEQ No. 494	2de
SEQ ID No. 616	DVDEVFYK	88-95 for the proteins of SEQ No. 386, 429, 430, 477	2d
SEQ ID No. 617	DVSGDPGK	144-151 for the protein of SEQ No. 351	2de
SEQ ID No. 618	DWILR	204-208 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 619	DWPAMAGAWR	265-274 for the protein of SEQ No. 433	2d
SEQ ID No. 620	EAFLR	256-260 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 621	EAIAR	250-254 for the proteins of SEQ No. 355, 363, 369, 372, 373, 375, 484	2d

SEQ ID No. 622	EAIVR	250-254 for the proteins of SEQ No. 350, 356, 367, 370, 415, 443, 481, 488, 491; 239-243 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 623	EAIVTEATPEYIVHSK	190-205 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 624	EALVTEAAPEYLVHSK	190-205 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 492, 501, 504; 181-196 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 625	EALVTEAPEYLVHSK	191-205 for the protein of SEQ No. 490	2d
SEQ ID No. 626	EEIVR	240-244 for the protein of SEQ No. 377	2d
SEQ ID No. 627	EEVLAALPAQLK	251-262 for the protein of SEQ No. 347	2d
SEQ ID No. 628	EFNGSK	209-214 for the protein of SEQ No. 447	2df
SEQ ID No. 629	EFSAEAVNGVFVLCK	31-45 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 490, 492, 501, 504; 22-36 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 630	EFSSESVHGVFVLCK	31-45 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 631	EGDMAK	248-253 for the protein of SEQ No. 379	2df
SEQ ID No. 632	EGMSGSIR	254-261 for the proteins of SEQ No. 364, 371, 414, 449, 506	2df
SEQ ID No. 633	EGMTGSIR	254-261 for the protein of SEQ No. 365	2df
SEQ ID No. 634	EGSCDK	54-59 for the protein of SEQ No. 351	2de
SEQ ID No. 635	EIAVWNR	125-131 for the protein of SEQ No. 381	2df
SEQ ID No. 636	EIAYK	262-266 for the protein of SEQ No. 480	2df
SEQ ID No. 637	EIFER	20-24 for the protein of SEQ No. 377	2d
SEQ ID No. 638	EIFYHYR	79-85 for the protein of SEQ No. 385	2d
SEQ ID No. 639	EIGDDK	131-136 for the proteins of SEQ No. 350, 367, 370, 415, 443, 481, 488; 120-125 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 640	EIGDGK	131-136 for the protein of SEQ No. 375	2d
SEQ ID No. 641	EIGEDK	131-136 for the proteins of SEQ No. 356, 372, 491	2d

SEQ ID No. 642	EIGEDNAR	131-138 for the protein of SEQ No. 484	OXA
SEQ ID No. 643	EIGENK	131-136 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 644	EIGPK	153-157 for the protein of SEQ No. 381	2df
SEQ ID No. 645	EIGSEIDK	136-143 for the protein of SEQ No. 377	2d
SEQ ID No. 646	EITYK	262-266 for the proteins of SEQ No. 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 482, 483, 487, 495, 502, 503, 507, 508; 263-267 for the proteins of sequence SEQ ID No. 364, 365, 371, 414, 447, 449, 466, 506; 256-260 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 647	EITYR	262-266 for the protein of SEQ No. 388	2df
SEQ ID No. 648	EMIYLK	181-186 for the protein of SEQ No. 385	2d
SEQ ID No. 649	EMLYVER	205-211 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 650	EMTYK	262-266 for the protein of SEQ No. 439	2df
SEQ ID No. 651	ENIEK	138-142 for the proteins of SEQ No. 429, 430, 477; 137-141 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 652	ENQLIVK	183-189 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 492, 501, 504; 174-180 for the proteins of sequence SEQ ID No. 348, 353, 354; 184-190 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 653	EQAILLFR	156-163 for the protein of SEQ No. 385	2d
SEQ ID No. 654	EQIQFLLR	165-172 for the protein of SEQ No. 349	2d
SEQ ID No. 655	EQLAFDPQVQQQVK	182-195 for the protein of SEQ No. 469	2df
SEQ ID No. 656	EQVDFVQR	189-196 for the protein of SEQ No. 382	2df
SEQ ID No. 657	ETEVYFFAFNMDIDNESK	229-246 for the proteins of SEQ No. 352, 435, 492, 501; 220-237 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 658	ETTTPR	90-95 for the protein of SEQ No. 347	2d

SEQ ID No. 659	EVGEIR	126-131 for the protein of SEQ No. 489	2d
SEQ ID No. 660	EVGEVR	126-131 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 492, 501, 504; 117-122 for the proteins of sequence SEQ ID No. 348, 353, 354; 127-132 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 661	EVNGSK	209-214 for the proteins of SEQ No. 364, 365, 371, 414, 449, 466, 506	2df
SEQ ID No. 662	EWQENK	24-29 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 663	EYELYLNVWK	78-87 for the protein of SEQ No. 494	2de
SEQ ID No. 664	EYLPASTFK	62-70 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 492, 504; 53-61 for the proteins of sequence SEQ ID No. 348, 353, 354; 63-71 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 665	EYLPVSTFK	62-70 for the protein of SEQ No. 501	2de
SEQ ID No. 666	EYNTSGTFVFYDGK	27-40 for the protein of SEQ No. 385	2d
SEQ ID No. 667	EYVPASTFK	75-83 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 69-77 for the proteins of sequence SEQ ID No. 431, 432, 469; 74-82 for the proteins of sequence SEQ ID No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493; 76-84 for the proteins of sequence SEQ ID No. 364, 365, 371, 414, 447, 449, 466, 506	2df
SEQ ID No. 668	FAAYVAGFGYGNGDISGEPGK	120-140 for the protein of SEQ No. 498	2d
SEQ ID No. 669	FAPESTFK	45-52 for the protein of SEQ No. 494	2de
SEQ ID No. 670	FAQYAK	121-126 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 671	FDYGNK	138-143 for the protein of SEQ No. 351	2de
SEQ ID No. 672	FDYGNR	146-151 for the protein of SEQ No. 379; 125-130 for the protein of sequence SEQ ID No. 347	2d
SEQ ID No. 673	FEDLYK	232-237 for the protein of SEQ No. 385	2d

SEQ ID No. 674	FEDTFHHSNQK	27-37 for the protein of SEQ No. 466	2df
SEQ ID No. 675	FEDTFHTSNQQHEK	27-40 for the protein of SEQ No. 447	2df
SEQ ID No. 676	FEYGNQDVSGDSGK	133-146 for the protein of SEQ No. 349	2d
SEQ ID No. 677	FFSDFQAK	34-41 for the protein of SEQ No. 375	2d
SEQ ID No. 678	FFSDLQAEGAIVIADER	34-50 for the proteins of SEQ No. 373, 484	2d
SEQ ID No. 679	FFSDLR	34-39 for the proteins of SEQ No. 369, 372	OXA
SEQ ID No. 680	FFSEFQAK	34-41 for the proteins of SEQ No. 350, 356, 367, 370, 415, 443, 481, 488, 491; 23-30 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 681	FGLEGQLR	153-160 for the protein of SEQ No. 359	2de
SEQ ID No. 682	FILPIFSISILVSLSACSSIK	4-24 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 683	FLALLFSAVVLVSLGHAQDK	5-24 for the protein of SEQ No. 363	2d
SEQ ID No. 684	FLALLFSAVVLVSLGHAQEK	5-24 for the protein of SEQ No. 355	2d
SEQ ID No. 685	FLESLYLNNLPASK	169-182 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 686	FLLEGQLR	153-160 for the protein of SEQ No. 442	2de
SEQ ID No. 687	FQQYVDR	118-124 for the protein of SEQ No. 347	2d
SEQ ID No. 688	FSDYVQR	131-137 for the protein of SEQ No. 351	2de
SEQ ID No. 689	FSTASTFK	63-70 for the protein of SEQ No. 470	2df
SEQ ID No. 690	FSWDGK	117-122 for the protein of SEQ No. 381	2df
SEQ ID No. 691	FSYGNQNISGGIDK	139-152 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 501, 504; 130-143 for the proteins of sequence SEQ ID No. 348, 353, 354; 140-153 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 692	FSYGNQNISGGTDK	139-152 for the protein of SEQ No. 471	2de
SEQ ID No. 693	FSYGSQNISGGIDK	139-152 for the protein of SEQ No. 492	2de

SEQ ID No. 694	FTEYVK	126-131 for the protein of SEQ No. 349	2d
SEQ ID No. 695	FVAHK	173-177 for the protein of SEQ No. 349	2d
SEQ ID No. 696	FVPASTYK	62-69 for the protein of SEQ No. 380	2d
SEQ ID No. 697	FVYDLAQGQLPFK	184-196 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 698	FVYDLAQGQLPFKPEVQQQVK	184-204 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 699	FWLEDQLR	153-160 for the proteins of SEQ No. 358, 435, 471, 492; 144-151 for the proteins of sequence SEQ ID No. 348, 353	2de
SEQ ID No. 700	FWLEGPLK	144-151 for the protein of SEQ No. 377	2d
SEQ ID No. 701	FWLEGQLR	153-160 for the proteins of SEQ No. 352, 357, 368, 383, 489, 501, 504, 505; 144-151 for the protein of sequence SEQ ID No. 354; 154-161 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 702	FYPASSFK	53-60 for the protein of SEQ No. 377	2d
SEQ ID No. 703	FYPASTFK	66-73 for the proteins of SEQ No. 386, 429, 430, 477	2d
SEQ ID No. 704	GACDK	44-48 for the protein of SEQ No. 498	2d
SEQ ID No. 705	GAEVYFFAFNMDIDNENK	229-246 for the proteins of SEQ No. 383, 490	2d
SEQ ID No. 706	GAIQVSAVPVFQQIAR	110-125 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 489, 492, 501, 504, 505; 101-116 for the proteins of sequence SEQ ID No. 348, 354; 111-126 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 707	GAIQVSAVPVFQQITR	101-116 for the protein of SEQ No. 353	2de
SEQ ID No. 708	GDYWIDGNLEISAHEQISFLR	156-176 for the proteins of SEQ No. 369, 372	OXA
SEQ ID No. 709	GDYWIDGNLK	156-165 for the protein of SEQ No. 373	2d
SEQ ID No. 710	GELPVSEDALEMTK	181-194 for the protein of SEQ No. 351	2de
SEQ ID No. 711	GEQPAGPAAR	241-250 for the protein of SEQ No. 498; 252-261 for the protein of sequence SEQ ID No. 351	OXA
SEQ ID No. 712	GFAGHNQDQDLR	103-114 for the proteins of SEQ No. 350, 367, 370, 415, 443, 481, 488; 92-103 for the protein of sequence SEQ ID No. 362	OXA

SEQ ID No. 713	GIPSSVR	254-260 for the proteins of SEQ No. 389, 390, 391, 392, 393, 394, 395, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 248-254 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 714	GISSSVR	254-260 for the protein of SEQ No. 388	2df
SEQ ID No. 715	GLNGTFVVYDLK	26-37 for the protein of SEQ No. 377	2d
SEQ ID No. 716	GMEIWNSNHTPK	101-112 for the proteins of SEQ No. 360, 376; 86-97 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 717	GNQTLVFAR	230-238 for the protein of SEQ No. 496	2d
SEQ ID No. 718	GNYWIDGNLEISAHEQISFLR	156-176 for the protein of SEQ No. 484	OXA
SEQ ID No. 719	GPLEISAFEEAR	164-175 for the protein of SEQ No. 379	2df
SEQ ID No. 720	GPLTITPIQEVK	172-183 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 721	GSGWFVGWIVR	219-229 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 722	GSLLLWDQK	66-74 for the protein of SEQ No. 381	2df
SEQ ID No. 723	GTEVYFFAFNMDIDNENK	229-246 for the proteins of SEQ No. 357, 358, 359, 368, 442, 471, 504	OXA
SEQ ID No. 724	GTEVYFFAFNMDIDNESK	229-246 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 725	GTFVLYDVQR	38-47 for the protein of SEQ No. 380	2d
SEQ ID No. 726	GTIVVADER	42-50 for the proteins of SEQ No. 350, 356, 367, 370, 375, 415, 443, 481, 488, 491; 31-39 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 727	GTIVVLDAR	63-71 for the protein of SEQ No. 382	2df
SEQ ID No. 728	GTIVVVDER	42-50 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 729	GTLPFSAR	200-207 for the protein of SEQ No. 382	2df
SEQ ID No. 730	GTPSSVR	254-260 for the protein of SEQ No. 396	2df
SEQ ID No. 731	HALSSAFVLLGCIAASAHAK	5-24 for the proteins of SEQ No. 496, 497, 499, 500	2d

SEQ ID No. 732	HIADSK	234-239 for the protein of SEQ No. 494	2de
SEQ ID No. 733	HNGLTHAWLASSLK	152-165 for the protein of SEQ No. 351	2de
SEQ ID No. 734	HNGLTQSWLMSSLTISPK	147-164 for the protein of SEQ No. 349	2d
SEQ ID No. 735	HNGTDGAWHSSLR	148-161 for the protein of SEQ No. 433	2d
SEQ ID No. 736	HTLSVFDQER	54-63 for the protein of SEQ No. 373	2d
SEQ ID No. 737	HVTFASFR	241-248 for the protein of SEQ No. 494	2de
SEQ ID No. 738	IAISLMGYDAGFLR	57-70 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 739	IALSLMAFDAEHDQK	75-90 for the proteins of SEQ No. 360, 376; 60-75 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 740	IALSLMGFDSGILK	53-66 for the protein of SEQ No. 494	2de
SEQ ID No. 741	IANALIGLENHK	87-98 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 742	IAWIVGFVYLK	205-215 for the protein of SEQ No. 385	2d
SEQ ID No. 743	IDTFWLDNSLK	141-151 for the protein of SEQ No. 385	2d
SEQ ID No. 744	IDYYNLDR	41-48 for the protein of SEQ No. 377	2d
SEQ ID No. 745	IFNALIALDSGVIK	62-75 for the protein of SEQ No. 385	2d
SEQ ID No. 746	IFNSLLALDSGALDNER	95-111 for the protein of SEQ No. 382	2df
SEQ ID No. 747	IFNTLIGLENGIVK	61-74 for the protein of SEQ No. 377	2d
SEQ ID No. 748	IGLDLMQK	138-145 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 749	IGLEK	131-135 for the protein of SEQ No. 477	OXA
SEQ ID No. 750	IGLELMQQEVQR	133-144 for the protein of SEQ No. 469	2df
SEQ ID No. 751	IGLELMSK	139-146 for the proteins of SEQ No. 389, 390, 391, 393, 395, 398, 399, 400, 401, 402, 403, 404, 408, 409, 411, 412, 417, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 436, 437, 438, 439, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 478, 479, 480, 482, 483, 487, 495, 502, 508	2df

SEQ ID No. 752	IGLELMSNEVK	139-149 for the proteins of SEQ No. 388, 392, 394, 396, 397, 405, 406, 407, 416, 418, 434, 444, 445, 446, 448, 475, 503, 507; 133-143 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 753	IGLER	126-130 for the protein of SEQ No. 380	2d
SEQ ID No. 754	IGLNK	130-134 for the proteins of SEQ No. 360, 376; 115-119 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 755	IGLNLMQK	140-147 for the protein of SEQ No. 466	2df
SEQ ID No. 756	IGPSLMQSELQR	142-153 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 757	IGYGNMQIGTEVDQFWLK	154-171 for the proteins of SEQ No. 413, 458	2df
SEQ ID No. 758	IGYGNMQMGTEVDQFWLK	154-171 for the protein of SEQ No. 410	2df
SEQ ID No. 759	IINHNLPVK	167-175 for the protein of SEQ No. 361; 182-190 for the protein of sequence SEQ ID No. 360	2d
SEQ ID No. 760	IINHNLPVR	182-190 for the protein of SEQ No. 376	2d
SEQ ID No. 761	ILFQQGTQQACAER	41-54 for the protein of SEQ No. 433	2d
SEQ ID No. 762	ILNNWFK	20-26 for the protein of SEQ No. 385	2d
SEQ ID No. 763	ILNTLISLEEK	71-81 for the protein of SEQ No. 470	2df
SEQ ID No. 764	ILSLVCLSISIGACAEHSMSR	6-26 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 765	INESR	219-223 for the protein of SEQ No. 349	2d
SEQ ID No. 766	INIVK	255-259 for the proteins of SEQ No. 429, 430, 477; 254-258 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 767	INLYGNALSR	61-70 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 768	IPFSLNLEMK	244-253 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 769	IPHTLFALDADAVR	76-89 for the protein of SEQ No. 373	2d
SEQ ID No. 770	IPHTLFALDAGAAR	76-89 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 771	IPHTLFALDAGAVR	76-89 for the proteins of SEQ No. 350, 355, 363, 367, 370, 375, 415, 443, 481, 488; 65-78 for the protein of sequence SEQ ID No. 362	OXA

SEQ ID No. 772	IPLGK	255-259 for the protein of SEQ No. 379	2df
SEQ ID No. 773	IPNAIIGLETGVIK	71-84 for the proteins of SEQ No. 352, 358, 359, 368, 383, 442, 471, 492, 504; 62-75 for the proteins of sequence SEQ ID No. 348, 353; 72-85 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 774	IPNALIGLETGAIK	71-84 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 775	IPNSLIAFDTGAVR	78-91 for the protein of SEQ No. 379	2df
SEQ ID No. 776	IPSAIIGLETGVIK	71-84 for the proteins of SEQ No. 357, 435, 501; 62-75 for the protein of sequence SEQ ID No. 354	2de
SEQ ID No. 777	ISAFNQVK	161-168 for the protein of SEQ No. 489	2d
SEQ ID No. 778	ISAHEQILFLR	166-176 for the protein of SEQ No. 373	2d
SEQ ID No. 779	ISAMEQTR	160-167 for the protein of SEQ No. 380	2d
SEQ ID No. 780	ISAMEQVK	165-172 for the proteins of SEQ No. 429, 477; 152-159 for the protein of sequence SEQ ID No. 377; 164-171 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 781	ISATEQVAFLR	164-174 for the protein of SEQ No. 384	2df
SEQ ID No. 782	ISATQQIAFLR	164-174 for the protein of SEQ No. 485	2df
SEQ ID No. 783	ISAVNQVEFLESLFLNK	161-177 for the proteins of SEQ No. 357, 358, 359, 368, 383, 442, 471, 504; 162-178 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 784	ISAVNQVEFLESLYLNK	161-177 for the proteins of SEQ No. 352, 435, 492, 501; 152-168 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 785	ISAVNQVK	161-168 for the protein of SEQ No. 505	2de
SEQ ID No. 786	ISPEEQIQFLR	170-180 for the proteins of SEQ No. 360, 376; 155-165 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 787	ISPEEQVR	166-173 for the protein of SEQ No. 351	2de
SEQ ID No. 788	ISPEGQVR	155-162 for the protein of SEQ No. 498	2d
SEQ ID No. 789	ISPLEQLAFLR	162-172 for the protein of SEQ No. 433	2d
SEQ ID No. 790	ITAFQQVDFLR	188-198 for the protein of SEQ No. 381	2df
SEQ ID No. 791	ITLFLLFLNLVFGQDK	4-19 for the protein of SEQ No. 385	2d

SEQ ID No. 792	ITPIQEVNFADDFANNR	174-190 for the protein of SEQ No. 447	2df
SEQ ID No. 793	ITPIQEVNFADDLANNR	174-190 for the protein of SEQ No. 466	2df
SEQ ID No. 794	ITPQQEAQFAYK	173-184 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 167-178 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 795	ITPQQEAQFTYK	173-184 for the protein of SEQ No. 405	2df
SEQ ID No. 796	ITPVQEVNFADDLAHNR	174-190 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 797	IVAFALK	241-247 for the proteins of SEQ No. 366, 387	2df
SEQ ID No. 798	IVAFALNMEMR	241-251 for the proteins of SEQ No. 440, 459, 460, 461, 462, 463, 464, 465, 486, 493; 242-252 for the proteins of sequence SEQ ID No. 374, 441	2df
SEQ ID No. 799	IVESTTLADGTVVHGK	186-201 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 800	IYNSLIGLNEK	74-84 for the proteins of SEQ No. 386, 429, 430, 477	2d
SEQ ID No. 801	KPDIGWWVGWIER	237-249 for the protein of SEQ No. 382	2df
SEQ ID No. 802	LACATNNLAR	50-59 for the protein of SEQ No. 490	2d
SEQ ID No. 803	LAQGELPFPAPVQSTVR	172-188 for the protein of SEQ No. 380	2d
SEQ ID No. 804	LAQNELPYPIEIQK	177-190 for the proteins of SEQ No. 429, 430, 477	2d
SEQ ID No. 805	LAQNELQYPIEIQK	176-189 for the protein of SEQ No. 386	2d
SEQ ID No. 806	LDFGNK	143-148 for the proteins of SEQ No. 429, 430, 477; 142-147 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 807	LDGSLNR	206-212 for the protein of SEQ No. 347	2d
SEQ ID No. 808	LEIGK	244-248 for the protein of SEQ No. 349	2d
SEQ ID No. 809	LEILQQALAELGLYPK	255-270 for the protein of SEQ No. 469	2df

SEQ ID No. 810	LENQEQVK	173-180 for the protein of SEQ No. 377	2d
SEQ ID No. 811	LETQEEVEK	195-203 for the protein of SEQ No. 364	2df
SEQ ID No. 812	LETQEEVK	195-202 for the proteins of SEQ No. 365, 371, 414, 447, 449, 466, 506	2df
SEQ ID No. 813	LFAAEGVK	55-62 for the protein of SEQ No. 382	2df
SEQ ID No. 814	LFESAGVK	58-65 for the protein of SEQ No. 381	2df
SEQ ID No. 815	LFGAAGVK	30-37 for the protein of SEQ No. 380	2d
SEQ ID No. 816	LFPEWEK	110-116 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 104-110 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 817	LGESR	126-130 for the protein of SEQ No. 351	2de
SEQ ID No. 818	LGVDR	121-125 for the protein of SEQ No. 349	2d
SEQ ID No. 819	LHVSER	181-186 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 820	LHYGNAK	131-137 for the protein of SEQ No. 385	2d
SEQ ID No. 821	LLNLLSQSK	160-168 for the protein of SEQ No. 377	2d
SEQ ID No. 822	LLQDER	243-248 for the protein of SEQ No. 433	2d
SEQ ID No. 823	LLVQDGDCGR	38-47 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 824	LNEVGYGNR	160-168 for the protein of SEQ No. 382	2df
SEQ ID No. 825	LNYGNADPSTK	144-154 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 826	LNYGNK	130-135 for the protein of SEQ No. 377	2d
SEQ ID No. 827	LPASK	178-182 for the proteins of SEQ No. 489, 505; 172-176 for the protein of sequence SEQ ID No. 498	2d
SEQ ID No. 828	LPHTLFALDADAVR	76-89 for the proteins of SEQ No. 369, 372	OXA

SEQ ID No. 829	LPHTLFALDAGAVR	76-89 for the protein of SEQ No. 484	OXA
SEQ ID No. 830	LPLAIMGFDSGILQSPK	62-78 for the protein of SEQ No. 349	2d
SEQ ID No. 831	LPLAIMGYDADILLDATTPR	69-88 for the protein of SEQ No. 351	2de
SEQ ID No. 832	LPSSLIALETGAVR	98-111 for the protein of SEQ No. 381	2df
SEQ ID No. 833	LPVSAQTLQYTANILK	170-185 for the protein of SEQ No. 347	2d
SEQ ID No. 834	LPVSER	205-210 for the protein of SEQ No. 381	2df
SEQ ID No. 835	LPVSPTAVDMTER	173-185 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 836	LSASK	178-182 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 492, 501, 504; 169-173 for the proteins of sequence SEQ ID No. 348, 353, 354; 179-183 for the protein of sequence SEQ ID No. 490	OXA
SEQ ID No. 837	LSAVPIYQEVAR	121-132 for the protein of SEQ No. 379	2df
SEQ ID No. 838	LSAVPVYQELAR	127-138 for the proteins of SEQ No. 364, 365, 371, 414, 447, 449, 506; 125-136 for the proteins of sequence SEQ ID No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 839	LSCTLVIDEASGDLLHR	37-53 for the protein of SEQ No. 351	2de
SEQ ID No. 840	LSLQHGWFIGWIEK	211-224 for the protein of SEQ No. 494	2de
SEQ ID No. 841	LSQNSLPFSQEAMNSVK	164-180 for the protein of SEQ No. 385	2d
SEQ ID No. 842	LSVNPK	168-173 for the protein of SEQ No. 494	2de
SEQ ID No. 843	LTQDER	239-244 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 844	LTVGAR	245-250 for the protein of SEQ No. 351	2de
SEQ ID No. 845	LYGFALNIDMPGGEADIGK	228-246 for the protein of SEQ No. 380	2d
SEQ ID No. 846	LYHNELPFR	178-186 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 847	LYHNK	176-180 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df

SEQ ID No. 848	LYQNDLPFR	178-186 for the protein of SEQ No. 375	2d
SEQ ID No. 849	MDDLFK	243-248 for the proteins of SEQ No. 350, 356, 367, 370, 375, 415, 443, 481, 488, 491; 232-237 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 850	MEDLHK	243-248 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 851	MLIALIGLENHK	85-96 for the protein of SEQ No. 506	2df
SEQ ID No. 852	MLLIEQQGDAALYAK	198-212 for the protein of SEQ No. 379	2df
SEQ ID No. 853	MLLIK	204-208 for the proteins of SEQ No. 364, 365, 371, 414, 447, 449, 466, 506	2df
SEQ ID No. 854	MLNALIGLEHHK	84-95 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 487, 495, 502, 503, 507, 508; 78-89 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 855	MLNALIGLENHK	85-96 for the proteins of SEQ No. 364, 365, 371, 414, 447, 449, 466	2df
SEQ ID No. 856	MLNALIGLENQK	83-94 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 857	MLNALIGLEYHK	84-95 for the protein of SEQ No. 483	2df
SEQ ID No. 858	MLNALIGLQHGK	78-89 for the protein of SEQ No. 469	2df
SEQ ID No. 859	MLNALISLEHHK	84-95 for the protein of SEQ No. 407	2df
SEQ ID No. 860	MQAYVDAFDYGNR	139-151 for the protein of SEQ No. 379	2df
SEQ ID No. 861	MQEGLNK	123-129 for the protein of SEQ No. 377	2d
SEQ ID No. 862	MSPASTYK	87-94 for the protein of SEQ No. 382	2df
SEQ ID No. 863	MTAGGK	234-239 for the protein of SEQ No. 498	2d
SEQ ID No. 864	MVSGK	165-169 for the protein of SEQ No. 347	2d
SEQ ID No. 865	NEHDPVLPYR	71-80 for the proteins of SEQ No. 496, 497, 499, 500	2d

SEQ ID No. 866	NEHQIFK	86-92 for the protein of SEQ No. 490; 85-91 for the protein of sequence SEQ ID No. 383	2d
SEQ ID No. 867	NEHQVFK	85-91 for the proteins of SEQ No. 352, 357, 358, 359, 368, 435, 442, 471, 492, 501, 504; 76-82 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 868	NEITYK	262-267 for the proteins of SEQ No. 364, 365, 371, 414, 447, 449, 466, 506	2df
SEQ ID No. 869	NELLMK	260-265 for the proteins of SEQ No. 366, 387, 440, 459, 460, 462, 463, 464, 465, 486, 493; 261-266 for the proteins of sequence SEQ ID No. 374, 441	2df
SEQ ID No. 870	NELMMK	260-265 for the protein of SEQ No. 461	2df
SEQ ID No. 871	NELPFR	181-186 for the proteins of SEQ No. 350, 355, 356, 363, 367, 370, 415, 443, 481, 488, 491; 170-175 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 872	NFILIFIFVILISCK	5-19 for the proteins of SEQ No. 386, 429, 477	2d
SEQ ID No. 873	NFILIFIFVILTSCK	5-19 for the protein of SEQ No. 430	2d
SEQ ID No. 874	NISSYGNNLVR	62-72 for the protein of SEQ No. 466	2df
SEQ ID No. 875	NISTYGNNLTR	62-72 for the protein of SEQ No. 447	2df
SEQ ID No. 876	NLFNEVHTTGVLVIR	43-57 for the protein of SEQ No. 412	2df
SEQ ID No. 877	NLSTYGNALAR	62-72 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 878	NMENLELFGK	187-196 for the protein of SEQ No. 385	2d
SEQ ID No. 879	NMLLLEENNGYK	201-212 for the protein of SEQ No. 440	2df
SEQ ID No. 880	NMLLLEESNGYK	201-212 for the proteins of SEQ No. 366, 374, 387, 441, 459, 460, 461, 462, 463, 465, 486, 493	2df
SEQ ID No. 881	NMLLLEK	201-207 for the protein of SEQ No. 464	2df
SEQ ID No. 882	NMTLGDAMK	117-125 for the proteins of SEQ No. 388, 392, 393, 396, 397, 402, 405, 406, 416, 419, 422, 424, 434, 445, 446, 448, 475, 503; 111-119 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 883	NNGLTEAWLESSLK	156-169 for the proteins of SEQ No. 360, 376; 141-154 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 884	NQLPFK	181-186 for the protein of SEQ No. 373	2d

SEQ ID No. 885	NQLPFQVEHQR	181-191 for the proteins of SEQ No. 369, 372, 484	OXA
SEQ ID No. 886	NSAIENTIDNMYLQDLENSTK	191-211 for the protein of SEQ No. 376	2d
SEQ ID No. 887	NSAIENTIENMYLQDLDNSTK	191-211 for the protein of SEQ No. 360	2d
SEQ ID No. 888	NSAIENTIENMYLQDLENSTK	176-196 for the protein of SEQ No. 361	2d
SEQ ID No. 889	NSAVWVYELFAK	119-130 for the proteins of SEQ No. 369, 372, 484	OXA
SEQ ID No. 890	NSQVPAYK	118-125 for the proteins of SEQ No. 429, 430, 477; 117-124 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 891	NSTVWIYELFAK	119-130 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 892	NSTVWVYELFAK	119-130 for the proteins of SEQ No. 350, 367, 370, 373, 375, 415, 443, 481, 488; 108-119 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 893	NSTVWVYQLFAK	119-130 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 894	NTSGALVIQTDK	48-59 for the protein of SEQ No. 460	2df
SEQ ID No. 895	NTSGVLVIQTDK	48-59 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 896	NVDEMFYYYDGSK	75-87 for the protein of SEQ No. 377	2d
SEQ ID No. 897	NWILR	204-208 for the proteins of SEQ No. 350, 356, 367, 369, 370, 372, 375, 415, 443, 481, 484, 488, 491; 193-197 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 898	NWNAAMDLR	125-133 for the protein of SEQ No. 382	2df
SEQ ID No. 899	NYVDAFHYGNQDISGDK	118-134 for the protein of SEQ No. 494	2de
SEQ ID No. 900	QADHAILVFDQAR	51-63 for the protein of SEQ No. 375	2d
SEQ ID No. 901	QAEHALLVFGQER	51-63 for the proteins of SEQ No. 369, 372, 484	OXA
SEQ ID No. 902	QAITK	251-255 for the proteins of SEQ No. 378, 384, 450, 485; 247-251 for the protein of sequence SEQ ID No. 476	2df
SEQ ID No. 903	QAMLTEANSDYIIR	193-206 for the protein of SEQ No. 384	2df
SEQ ID No. 904	QEVQFVSALAR	171-181 for the protein of SEQ No. 469	2df

SEQ ID No. 905	QFASIK	243-248 for the protein of SEQ No. 347	2d
SEQ ID No. 906	QGMPGSIR	254-261 for the protein of SEQ No. 447	2df
SEQ ID No. 907	QGMSGSIR	254-261 for the protein of SEQ No. 466	2df
SEQ ID No. 908	QGQTQQSYGNDLAR	58-71 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 412, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 436, 437, 438, 439, 444, 445, 446, 448, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 52-65 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 909	QIDYGNADPSTIK	143-155 for the proteins of SEQ No. 369, 372, 484	OXA
SEQ ID No. 910	QIDYGNVDPSTIK	143-155 for the protein of SEQ No. 373	2d
SEQ ID No. 911	QIGEAR	129-134 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 912	QIGQAR	129-134 for the protein of SEQ No. 384	2df
SEQ ID No. 913	QIMLIEQTPAFTLR	190-203 for the protein of SEQ No. 470	2df
SEQ ID No. 914	QLGSAIDQFWLR	152-163 for the protein of SEQ No. 379	2df
SEQ ID No. 915	QLHDNK	199-204 for the protein of SEQ No. 381	2df
SEQ ID No. 916	QLIFVHTVVQK	229-239 for the protein of SEQ No. 347	2d
SEQ ID No. 917	QLIFVHTVVQKPGK	229-242 for the protein of SEQ No. 347	2d
SEQ ID No. 918	QLPVK	178-182 for the protein of SEQ No. 433; 184-188 for the protein of sequence SEQ ID No. 379	OXA
SEQ ID No. 919	QLPVKPR	184-190 for the protein of SEQ No. 379	2df
SEQ ID No. 920	QLSLDVLDK	265-273 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 921	QLVYAR	237-242 for the protein of SEQ No. 433	2d
SEQ ID No. 922	QMMLTEASTDYIIR	217-230 for the protein of SEQ No. 381	2df
SEQ ID No. 923	QMSIVEATPDYVLHGK	214-229 for the protein of SEQ No. 382	2df

SEQ ID No. 924	QPTDPAR	99-105 for the protein of SEQ No. 433	2d
SEQ ID No. 925	QPTDPTR	93-99 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 926	QPVSAGIR	246-253 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 927	QQLVK	275-279 for the protein of SEQ No. 381	2df
SEQ ID No. 928	QTLVFAR	232-238 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 929	QVGAEK	126-131 for the protein of SEQ No. 470	2df
SEQ ID No. 930	QVVFAR	238-243 for the protein of SEQ No. 349	2d
SEQ ID No. 931	SADEVLPYGGK	84-94 for the protein of SEQ No. 380	2d
SEQ ID No. 932	SADEVLPYGGKPQR	84-97 for the protein of SEQ No. 380	2d
SEQ ID No. 933	SCATNDLAR	50-58 for the proteins of SEQ No. 352, 435, 492, 501; 41-49 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 934	SCATNNLAR	50-58 for the proteins of SEQ No. 357, 358, 359, 368, 383, 442, 471, 504	OXA
SEQ ID No. 935	SDIPGGSK	251-258 for the protein of SEQ No. 349	2d
SEQ ID No. 936	SDWGK	29-33 for the protein of SEQ No. 375	2d
SEQ ID No. 937	SEDNFHISSQQHEK	27-40 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 938	SEMPASIR	252-259 for the proteins of SEQ No. 366, 387, 440, 459, 460, 461, 462, 463, 464, 486, 493; 253-260 for the proteins of sequence SEQ ID No. 374, 441	2df
SEQ ID No. 939	SEMPASTR	252-259 for the protein of SEQ No. 465	2df
SEQ ID No. 940	SFAAHNQDQDLR	103-114 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 941	SFAGHNK	103-109 for the protein of SEQ No. 375	2d
SEQ ID No. 942	SFAGHNQDQDLR	103-114 for the proteins of SEQ No. 369, 372, 373, 484	2d
SEQ ID No. 943	SFAGHNQDQNLR	103-114 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 944	SFLESWAK	100-107 for the protein of SEQ No. 386	2d

SEQ ID No. 945	SFTAWEK	109-115 for the proteins of SEQ No. 366, 374, 387, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493; 104-110 for the protein of sequence SEQ ID No. 469	2df
SEQ ID No. 946	SFTTWEK	109-115 for the protein of SEQ No. 440	2df
SEQ ID No. 947	SGSGWLR	207-213 for the protein of SEQ No. 349	2d
SEQ ID No. 948	SGWGMAVDPQVGWYVGFVEK	221-240 for the proteins of SEQ No. 410, 413, 458	2df
SEQ ID No. 949	SGWGMDVSPQVGWLTGWVEK	219-238 for the protein of SEQ No. 466	2df
SEQ ID No. 950	SGWGMDVTPQVGWLTGWVEK	219-238 for the protein of SEQ No. 447	2df
SEQ ID No. 951	SIHPASTFK	69-77 for the protein of SEQ No. 379	2df
SEQ ID No. 952	SIPTK	252-256 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 490, 492, 501, 504, 505; 243-247 for the proteins of sequence SEQ ID No. 348, 353, 354	OXA
SEQ ID No. 953	SISTK	252-256 for the protein of SEQ No. 489	2d
SEQ ID No. 954	SLGLSNNLSR	76-85 for the protein of SEQ No. 381	2df
SEQ ID No. 955	SLSMSGK	4-10 for the protein of SEQ No. 351	2de
SEQ ID No. 956	SMLFIEEK	202-209 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 411, 416, 417, 418, 419, 420, 421, 422, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 444, 445, 446, 451, 452, 453, 454, 455, 456, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 196-203 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 957	SNGEK	239-243 for the proteins of SEQ No. 447, 466	2df
SEQ ID No. 958	SNGLTHSWLGSSLK	141-154 for the protein of SEQ No. 498	2d
SEQ ID No. 959	SNGYK	208-212 for the proteins of SEQ No. 366, 374, 387, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 960	SPTWELK	79-85 for the protein of SEQ No. 349	2d
SEQ ID No. 961	SPTWELKPEYNPSPR	79-93 for the protein of SEQ No. 349	2d
SEQ ID No. 962	SQDIVR	208-213 for the protein of SEQ No. 382	2df

SEQ ID No. 963	SQQKPTDPTIWLK	100-112 for the protein of SEQ No. 351	2de
SEQ ID No. 964	SQVGWLTGWVEQPDGK	225-240 for the protein of SEQ No. 486	2df
SEQ ID No. 965	SSSNSCTTNNAAR	46-58 for the protein of SEQ No. 489	2d
SEQ ID No. 966	SSSNSCTTNNATR	46-58 for the protein of SEQ No. 505	2de
SEQ ID No. 967	SVYGELR	139-145 for the protein of SEQ No. 470	2df
SEQ ID No. 968	SWILR	204-208 for the protein of SEQ No. 373	2d
SEQ ID No. 969	SYFDEAQTQGVIIIK	44-58 for the proteins of SEQ No. 364, 365, 371, 414, 447, 449, 466, 506	2df
SEQ ID No. 970	SYLEK	139-143 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 971	SYPMWEK	111-117 for the proteins of SEQ No. 447, 466	2df
SEQ ID No. 972	TAYIPASTFK	61-70 for the proteins of SEQ No. 489, 505; 77-86 for the proteins of sequence SEQ ID No. 410, 413, 458	2df
SEQ ID No. 973	TDDLFK	243-248 for the proteins of SEQ No. 369, 372, 373, 484	2d
SEQ ID No. 974	TDINEIFK	95-102 for the proteins of SEQ No. 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 975	TFIHNDPR	51-58 for the protein of SEQ No. 470	2df
SEQ ID No. 976	TGAGFTANR	216-224 for the proteins of SEQ No. 360, 376; 201-209 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 977	TGFNDGQK	197-204 for the protein of SEQ No. 385	2d
SEQ ID No. 978	TGLADSK	210-216 for the proteins of SEQ No. 429, 430; 209-215 for the protein of sequence SEQ ID No. 386	2d
SEQ ID No. 979	TGLDLMQK	140-147 for the protein of SEQ No. 447	2df
SEQ ID No. 980	TGLELMQK	140-147 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 981	TGMGYPK	198-204 for the protein of SEQ No. 347	2d
SEQ ID No. 982	TGNGR	197-201 for the protein of SEQ No. 494	2de
SEQ ID No. 983	TGTGSFIDAR	200-209 for the protein of SEQ No. 498	2d

SEQ ID No. 984	TGTGSLSDAK	211-220 for the protein of SEQ No. 351	2de
SEQ ID No. 985	TGVATEYQPEIGWWAGWVER	213-232 for the protein of SEQ No. 379	2df
SEQ ID No. 986	TGVSYPLLADGTR	202-214 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 987	TGWAAMDIK	217-225 for the proteins of SEQ No. 374, 441	2df
SEQ ID No. 988	TGWAMDIK	217-224 for the proteins of SEQ No. 366, 387, 440, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 989	TGWAMDVK	217-224 for the protein of SEQ No. 459	2df
SEQ ID No. 990	TGWATR	206-211 for the protein of SEQ No. 470	2df
SEQ ID No. 991	TGWCFDCTPELGWWVGWVK	205-223 for the protein of SEQ No. 380	2d
SEQ ID No. 992	TGWEGR	211-216 for the proteins of SEQ No. 350, 356, 367, 369, 370, 372, 373, 415, 443, 481, 484, 488, 491; 200-205 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 993	TGWFVDK	230-236 for the protein of SEQ No. 382	2df
SEQ ID No. 994	TGYDTK	209-214 for the protein of SEQ No. 476	2df
SEQ ID No. 995	TGYGVR	233-238 for the protein of SEQ No. 381	2df
SEQ ID No. 996	TGYSAR	209-214 for the protein of SEQ No. 450	2df
SEQ ID No. 997	TGYSTR	209-214 for the proteins of SEQ No. 378, 384, 485	2df
SEQ ID No. 998	THESSNWGK	25-33 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 999	TICTAIADAGTGK	25-37 for the proteins of SEQ No. 496, 497, 499, 500	2d
SEQ ID No. 1000	TIGGAPDAYWVDDSLQISAR	169-188 for the protein of SEQ No. 382	2df
SEQ ID No. 1001	TLPFSASSYETLR	177-189 for the protein of SEQ No. 470	2df
SEQ ID No. 1002	TLPFSLK	189-195 for the proteins of SEQ No. 399, 403, 411	2df
SEQ ID No. 1003	TLPFSPK	189-195 for the proteins of SEQ No. 389, 395, 412, 423, 428, 439, 445, 467, 482, 483, 495	2df
SEQ ID No. 1004	TLPFSQEVQDEVQSILFIEEK	189-209 for the protein of SEQ No. 448	2df

SEQ ID No. 1005	TLPFSQEVQDEVQSMLFIEEK	189-209 for the proteins of SEQ No. 392, 434	2df
SEQ ID No. 1006	TLPFSQK	189-195 for the proteins of SEQ No. 388, 390, 391, 393, 394, 396, 397, 398, 400, 401, 402, 404, 405, 406, 407, 408, 409, 416, 417, 418, 419, 420, 421, 422, 424, 425, 426, 427, 436, 437, 438, 444, 446, 451, 452, 453, 454, 455, 456, 457, 468, 472, 473, 474, 475, 478, 480, 487, 502, 503, 507, 508; 183-189 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 1007	TLPSSQK	189-195 for the protein of SEQ No. 479	2df
SEQ ID No. 1008	TLQNGWFEGFIISK	225-238 for the proteins of SEQ No. 360, 376; 210-223 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 1009	TMQEYLNK	123-130 for the protein of SEQ No. 385	2d
SEQ ID No. 1010	TNGNSTSVYNESR	51-63 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 1011	TQTYQAYDAAR	72-82 for the protein of SEQ No. 382	2df
SEQ ID No. 1012	TTDPTIWEK	93-101 for the protein of SEQ No. 498	2d
SEQ ID No. 1013	TTTTEVFK	96-103 for the proteins of SEQ No. 395, 428	2df
SEQ ID No. 1014	TWASNDFSR	41-49 for the protein of SEQ No. 385	2d
SEQ ID No. 1015	TWDMVQR	191-197 for the protein of SEQ No. 379	2df
SEQ ID No. 1016	TWMQFSVVWVSQEITQK	113-129 for the proteins of SEQ No. 360, 376; 98-114 for the protein of sequence SEQ ID No. 361	2d
SEQ ID No. 1017	TYPMWEK	111-117 for the proteins of SEQ No. 364, 365, 371, 414, 449, 506	2df
SEQ ID No. 1018	TYVVDPAR	58-65 for the protein of SEQ No. 379	2df
SEQ ID No. 1019	VAFSLNIEMK	244-253 for the protein of SEQ No. 447	2df
SEQ ID No. 1020	VANSLIGLSTGAVR	70-83 for the protein of SEQ No. 380	2d
SEQ ID No. 1021	VEHQR	187-191 for the proteins of SEQ No. 350, 355, 356, 363, 367, 369, 370, 372, 373, 375, 415, 443, 481, 484, 488, 491; 176-180 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 1022	VELGK	248-252 for the protein of SEQ No. 380	2d
SEQ ID No. 1023	VFDDAGVSGTFVLMDITADR	38-57 for the protein of SEQ No. 379	2df

SEQ ID No. 1024	VFLDSWAK	88-95 for the protein of SEQ No. 377	2d
SEQ ID No. 1025	VFLESWAK	101-108 for the proteins of SEQ No. 429, 430, 477	2d
SEQ ID No. 1026	VFLSSWAQDMNLSSAIK	89-105 for the protein of SEQ No. 385	2d
SEQ ID No. 1027	VGFER	134-138 for the protein of SEQ No. 379	2df
SEQ ID No. 1028	VILVFDQVR	55-63 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 1029	VITFTK	228-233 for the protein of SEQ No. 494	2de
SEQ ID No. 1030	VMAAMVR	158-164 for the protein of SEQ No. 381	2df
SEQ ID No. 1031	VPLAVMGYDAGILVDAHNPR	58-77 for the protein of SEQ No. 498	2d
SEQ ID No. 1032	VQANVK	195-200 for the proteins of SEQ No. 366, 374, 387, 440, 441, 459, 460, 461, 462, 463, 464, 465, 486, 493	2df
SEQ ID No. 1033	VQDEVK	196-201 for the protein of SEQ No. 444	2df
SEQ ID No. 1034	VQDEVQSMLFIEEK	196-209 for the proteins of SEQ No. 388, 389, 390, 391, 392, 393, 395, 396, 397, 398, 399, 400, 401, 402, 404, 405, 406, 407, 408, 409, 411, 416, 417, 418, 419, 420, 421, 422, 424, 425, 426, 427, 428, 434, 436, 437, 438, 439, 445, 446, 451, 452, 453, 454, 455, 457, 467, 468, 472, 473, 474, 475, 478, 479, 480, 482, 483, 487, 495, 502, 503, 507, 508; 190-203 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 1035	VQDEVQSMLFIEEMNGNK	196-213 for the proteins of SEQ No. 412, 423	2df
SEQ ID No. 1036	VQDGVQSMLFIEEK	196-209 for the protein of SEQ No. 456	2df
SEQ ID No. 1037	VQHEVQSMLFIEEK	196-209 for the protein of SEQ No. 394	2df
SEQ ID No. 1038	VSCLPCYQVVSHK	138-150 for the protein of SEQ No. 382	2df
SEQ ID No. 1039	VSCVWCYQALAR	114-125 for the protein of SEQ No. 470	2df
SEQ ID No. 1040	VSDVCSEVTAEGWQEVR	37-53 for the protein of SEQ No. 381	2df
SEQ ID No. 1041	VSEVEGWQIHGK	186-197 for the protein of SEQ No. 347	2d
SEQ ID No. 1042	VSFSLNIEMK	244-253 for the protein of SEQ No. 466	2df

SEQ ID No. 1043	VSPCSSFK	54-61 for the protein of SEQ No. 349	2d
SEQ ID No. 1044	VSQVPAYK	105-112 for the protein of SEQ No. 377	2d
SEQ ID No. 1045	VVFAR	229-233 for the protein of SEQ No. 498; 239-243 for the proteins of sequence SEQ ID No. 349,351	OXA
SEQ ID No. 1046	WDGAK	97-101 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 1047	WDGEK	104-108 for the proteins of SEQ No. 393, 402, 419, 422, 424	2df
SEQ ID No. 1048	WDGHIYDFPDWNR	92-104 for the protein of SEQ No. 470	2df
SEQ ID No. 1049	WDGIK	97-101 for the proteins of SEQ No. 356, 491	2d
SEQ ID No. 1050	WDGKPR	92-97 for the proteins of SEQ No. 352, 357, 358, 359, 368, 383, 435, 442, 471, 489, 492, 501, 504, 505; 83-88 for the proteins of sequence SEQ ID No. 348, 353, 354; 107-112 for the proteins of sequence SEQ ID No. 410, 413, 458; 93-98 for the protein of sequence SEQ ID No. 490; 116-121 for the protein of sequence SEQ ID No. 382;	OXA
SEQ ID No. 1051	WDGQK	104-108 for the proteins of SEQ No. 388, 389, 392, 395, 396, 397, 399, 403, 405, 406, 407, 411, 412, 423, 428, 434, 439, 445, 446, 448, 467, 468, 482, 483, 495, 503, 508; 98-102 for the proteins of sequence SEQ ID No. 431, 432	2df
SEQ ID No. 1052	WDGQTR	95-100 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 1053	WDGVK	97-101 for the proteins of SEQ No. 369, 372, 375, 484	2d
SEQ ID No. 1054	WDGVNR	97-102 for the proteins of SEQ No. 350, 367, 370, 373, 415, 443, 481, 488; 86-91 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 1055	WDYKPEFNGYK	78-88 for the protein of SEQ No. 498; 89-99 for the protein of sequence SEQ ID No. 351	OXA
SEQ ID No. 1056	WETYSVVWFSQQITEWLGMER	97-117 for the protein of SEQ No. 347	2d
SEQ ID No. 1057	WNGQK	104-108 for the proteins of SEQ No. 394, 418, 444, 507	2df
SEQ ID No. 1058	YAQAK	155-159 for the protein of SEQ No. 382	2df
SEQ ID No. 1059	YFSDFNAK	34-41 for the proteins of SEQ No. 355, 363	2d
SEQ ID No. 1060	YGTHLDR	68-74 for the proteins of SEQ No. 410, 413, 458	2df

SEQ ID No. 1061	YIIINK	54-59 for the proteins of SEQ No. 386, 429, 430, 477	2d
SEQ ID No. 1062	YLDELVK	245-251 for the protein of SEQ No. 385	2d
SEQ ID No. 1063	YLMITEAGR	195-203 for the protein of SEQ No. 484	OXA
SEQ ID No. 1064	YLNLFSYGNANIGGGIDK	135-152 for the proteins of SEQ No. 489, 505	OXA
SEQ ID No. 1065	YNGEK	96-100 for the proteins of SEQ No. 429, 430, 477	2d
SEQ ID No. 1066	YPIINPR	88-93 for the protein of SEQ No. 494	2de
SEQ ID No. 1067	YPVVWYSQQVAHHLGAQR	103-120 for the protein of SEQ No. 497	2d
SEQ ID No. 1068	YSNVLAFK	106-113 for the protein of SEQ No. 385	2d
SEQ ID No. 1069	YSPASTFK	68-75 for the proteins of SEQ No. 350, 355, 356, 363, 367, 369, 370, 372, 373, 375, 415, 443, 481, 484, 488, 491; 57-64 for the protein of sequence SEQ ID No. 362	OXA
SEQ ID No. 1070	YSVVPVYQQLAR	141-152 for the protein of SEQ No. 381	2df
SEQ ID No. 1071	YSVVWYSQLTAK	109-120 for the protein of SEQ No. 433	2d
SEQ ID No. 1072	YSVVWYSQQVAHHLGAQR	103-120 for the proteins of SEQ No. 496, 499, 500	2d
SEQ ID No. 1073	YTPASTFK	55-62 for the protein of SEQ No. 433	2d
SEQ ID No. 1074	YTSAFGYGNADVSGEPGK	130-147 for the protein of SEQ No. 433	2d
SEQ ID No. 1075	YVFVSALTGNLGSNLTSSIK	228-247 for the protein of SEQ No. 361; 243-262 for the protein of sequence SEQ ID No. 360	2d
SEQ ID No. 1076	YVFVSALTGSLGSNLTSSIK	243-262 for the protein of SEQ No. 376	2d
SEQ ID No. 1077	YVGHDR	50-55 for the protein of SEQ No. 380	2d
SEQ ID No. 1098	ANQAFLPASTFK	62-73 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 1099	DEHQVFK	88-94 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 1100	DHNLITAMK	108-116 for the proteins of SEQ No. 378, 450, 476	2df
SEQ ID No. 1101	DIATWNR	101-107 for the proteins of SEQ No. 378, 450, 476	2df

SEQ ID No. 1102	IPNSLIALDLGVVK	74-87 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 1103	ISATEQISFLR	164-174 for the proteins of SEQ No. 378, 450, 476	2df
SEQ ID No. 1104	QAMLTEANGDYIIR	193-206 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 1105	QQGFTNNLK	52-60 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df
SEQ ID No. 1106	SQGVVVLWNENK	40-51 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 1107	SWNAHFTEHK	30-39 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 1108	VLALSAVFLVASIIGMPAVAK	3-23 for the proteins of SEQ No. 378, 450, 476, 485	2df
SEQ ID No. 1109	YSVVPVYQEFAR	117-128 for the proteins of SEQ No. 378, 384, 450, 476, 485	2df

In the clinical interest column, the entries 2d, 2de, 2df correspond to the functional subgroups of OXA beta-lactamases which the corresponding peptide makes it possible to detect. Therefore, the detection of a 2df peptide will indicate the presence of a carbapenemase beta-lactamase capable of hydrolysing carbapenems.

The entry 2de will indicate the presence of a beta-lactamase with an extended spectrum (ESBL) capable of hydrolysing penicillins, first-generation cephalosporins such as cephaloridine and cefalotin, and at least one antibiotic from the oxyimino-beta-lactam class such as cefotaxime, ceftazidime or monobactams such as aztreonam.

The entry OXA indicates a common peptide between at least two of the subgroups 2d, 2de and 2df. The corresponding peptide indicates the presence of an OXA beta-lactamase and the presence of a mechanism of resistance at least to penicillins and to first-generation cephalosporins.

The detection of a mechanism of resistance to carbapenems induced by an OXA protein is characterised by the detection of at least one resistance-marking carba peptide chosen from the sequences **SEQ ID No. 510, 511, 512, 513, 514, 520, 521, 522, 523, 525, 527, 530, 532, 537, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 556, 557, 558, 559, 560, 561, 562, 574, 579, 581, 582, 583, 584, 592, 596, 597, 598, 599, 600, 601, 602, 607, 608, 609, 628, 631, 632, 633, 635, 636, 644, 646, 647, 649, 650, 655, 656, 661, 662, 667, 674, 675, 682, 689, 690, 698, 713, 714, 719,**

720, 722, 727, 729, 730, 741, 746, 748, 750, 751, 752, 755, 756, 757, 758, 763, 764, 767, 768, 772, 775, 781, 782, 790, 792, 793, 794, 795, 796, 797, 798, 801, 809, 811, 812, 813, 814, 816, 819, 824, 832, 834, 837, 838, 847, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 862, 868, 869, 870, 874, 875, 876, 877, 879, 880, 881, 882, 894, 895, 898, 902, 903, 904, 906, 907, 908, 911, 912, 913, 914, 915, 919, 920, 922, 923, 927, 929, 937, 938, 939, 945, 946, 948, 949, 950, 951, 954, 956, 957, 959, 962, 964, 967, 969, 971, 972, 974, 975, 979, 980, 985, 988, 990, 993, 994, 995, 996, 997, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1011, 1013, 1015, 1017, 1018, 1019, 1023, 1027, 1030, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1042, 1047, 1048, 1051, 1052, 1057, 1058, 1060, 1070, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109

Certain peptide sequences can be common to several resistance mechanisms. Therefore, the following sequences are identical:

SEQ ID No. 24 and SEQ ID No. 287

In all cases, the sequences above indicate the expression of a mechanism of resistance to penicillins, to cephalosporins, including those of the third generation such as cefotaxime/ceftazidime, to monobactams and to carbapenems.

The method of the invention and its advantages will become apparent from the rest of the present description which presents several non-limiting examples of implementation of said method.

Example 1: Identification of microorganisms from a sample by biochemical profile

1. Culturing of the sample on a culture medium

The optimum culture media and the optimum culture conditions are different according to the species of microorganism. By default, the sample is seeded on different media:

- sheep blood Columbia agar (bioMérieux ref. 43041) for 18 to 24 h at 35°C, in an aerobic or anaerobic atmosphere;
- TSA agar (bioMérieux ref. 43011) for 18 to 24 h at 37°C.

2. Identification of the microorganisms

The identification is performed as follows:

1. Selection of isolated colonies
2. While maintaining the aseptic conditions, transfer of 3.0 mL of aqueous sterile saline solution (0.45-0.50% NaCl, pH 4.5 to 7.0) into a transparent plastic (polystyrene) test tube
3. With the aid of a stirrer or a sterile swab, transfer of a sufficient number of identical colonies into the saline solution tube prepared in step 2, and adjustment of the bacterial suspension between 0.50 and 0.63 McFarland with a calibrated DENSICHEK from VITEK®
4. Positioning of the bacterial suspension tube and of a VITEK® identification card on a VITEK® cartridge
5. Loading of the cartridge into the VITEK® instrument
6. The filling, sealing, incubation and reading operations are automatic
7. Acquisition of a biochemical profile
8. Identification with the VITEK® system performed by comparing to the biochemical profiles of known strains

Example 2: Preparation of a primary urine sample by microorganism enrichment:

The following protocol is performed in 16 steps (steps 5 to 12 are optional and could be omitted if the enriched sample is subsequently treated according to examples 4 and onwards):

1. Centrifuging of 5 mL of contaminated urine, at 2000g for 30 seconds
2. Recovery of the supernatant
3. Centrifuging at 15000g for 5 minutes
4. Elimination of the supernatant
5. Washing of the pellet with 3 mL of distilled water by resuspension
6. Centrifuging at 15000g for 5 minutes
7. Elimination of the supernatant
8. Place the pellet in the presence of solvent (8 acetone volumes for 1 methanol volume) for 1/10 dilution
9. Leave for 1 hour at –20°C

10. Centrifuging at 15000g for 5 minutes
11. Elimination of the supernatant
12. Place the pellet in the presence of solvent (8 acetone volumes for 1 methanol volume) for 1/10 dilution
13. Leave for 1 hour at –20°C
14. Centrifuging at 15000g for 5 minutes
15. Elimination of the supernatant
16. The pellet constitutes the microorganism-enriched sample

Example 3: Identification of microorganisms from a sample by MALDI-TOF

The identification is performed as follows:

1. Transfer, with the aid of a 1 µl oese, of a portion of microorganism colony obtained according to Example 1, or of an enriched sample according to Example 2, and uniform deposition on a plate for MALDI-TOF mass spectrometry
2. Covering the deposit with 1 µl of matrix. The matrix used is a saturated solution of HCCA (alpha-cyano-4-hydroxycinnamic acid) in organic solvent (50% acetonitrile and 2.5% trifluoroacetic acid)
3. Drying at ambient temperature
4. Introducing the plate into the mass spectrometer
5. Acquiring a mass spectrum
6. Comparing the obtained spectrum with the spectra contained in a knowledge base
7. Identification of the microorganism by comparing the obtained peaks with those in the knowledge base

Example 4: Identification of microorganisms from a sample by ESI-TOF

The identification is performed as follows:

1. Sampling of a microorganism colony, obtained according to Example 1, or of an enriched sample according to Example 2, and suspension in 100 µl of demineralised water.
2. Centrifuging at 3000g for 5 minutes.
3. Elimination of the supernatant.

4. Resuspension in 100 µl of demineralised water.
5. Centrifuging at 3000g for 5 minutes.
6. Elimination of the supernatant.
7. Resuspension in 100 µl of an acetonitrile, demineralised water and formic acid mixture (50/50/0.1%).
8. Filtration with a filter with a porosity of 0.45 µm.
9. Injection into a mass spectrometer in single MS mode.
10. Acquisition of a mass spectrum.
11. Comparing the obtained spectrum with the spectra contained in a knowledge base.
12. Identification of the microorganism by referring to reference spectra.

Example 5: Obtaining digested proteins from microorganisms

The following protocol is conventionally performed in 17 steps:

1. Sampling of a microorganism colony, obtained according to Example 1, or of an enriched sample according to Example 2, and suspension in 10 to 100 µl of a 6M guanidine hydrochloride solution, 50 mM Tris-HCl, pH=8.0.
2. Addition of dithiothreitol (DTT) to achieve an end concentration of 5 mM.
3. Reduction for 20 minutes at 95°C in a water bath.
4. Cooling the tubes to ambient temperature.
5. Addition of iodoacetamide to obtain an end concentration of 12.5 mM.
6. Alkylation for 40 minutes at ambient temperature and in the dark.
7. Dilution by a factor of 6 with a 50 mM NH_4HCO_3 solution, pH=8.0 to obtain an end guanidine hydrochloride concentration of 1M.
8. Addition of 1 µg of trypsin.
9. Digestion at 37°C for between 6 hours and one night.
10. Addition of formic acid down to a pH below 4 to stop the reaction.
11. The sample volume is made up to 1 mL with water/0.5% (v/v) formic acid
12. Balancing of the Waters Oasis HLB columns with 1 ml of methanol and then 1 ml of H_2O/ 0.1% (v/v) formic acid
13. Deposition of the sample which runs off by gravity
14. Washing with 1 ml of H_2O/ 0.1% (v/v) formic acid

15. Elution with 1 ml of a mixture of 80% methanol and 20% water/0.1% (v/v) formic acid
16. The eluate is evaporated with a SpeedVac® SPD2010 evaporator (Thermo Electron Corporation, Waltham, Massachusetts, United States of America) over 2 hours, in order to obtain a volume of around 100 µl.
17. The eluate is then taken up in a water/0.5% (v/v) formic acid solution in a quantity sufficient for (QSF) 250 µl

Example 6: Identification of a resistance to NDM-1 beta-lactams:

Samples Sam1 to Sam9 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 1**.

TABLE 1:

Names	Species
Sam1	*K. pneumonia*
Sam2	*C. freundii*
Sam3	*A. baumannii*
Sam4	*A. caviae*
Sam5	*C. braakii*
Sam6	*E. cloacae*
Sam7	*P. rettgeri*
Sam8	*E. coli*
Sam9	*K. pneumonia*

Samples Sam1 to Sam9 correspond to a species able to comprise an NDM-1 resistance mechanism (Enterobacteriaceae, *Pseudomonas* species, *Acinetobacter* species...). The following method is then performed to search for such a mechanism.

Each sample is treated according to Example 5, then a volume of 50 µl of digested proteins is injected and analysed according to the following conditions:

- Dionex Ultimate 3000 chromatographic channel from the Dionex Corporation (Sunnyvale, United States of America).
- Waters BEH130 C18 Column, 2.1 mm inner diameter, 100 mm length, 3.5 µm particle size (Waters, Saint-Quentin En Yvelines, France).
- Solvent A: H_2O + 0.1% formic acid.

- Solvent B: ACN + 0.1% formic acid.

HPLC gradient defined in **Table 2** hereafter:

TABLE 2:

Time (min)	Flow (µl)	Solvent A (%)	Solvent B (%)
0	300	98	2
3	300	98	2
34	300	54.6	45.4
35	300	0	100
55	300	0	100
55.1	300	98	2
74	300	98	2

- The eluate coming from the chromatographic column is directly injected into the ionising source of the QTRAP® 5500 mass spectrometer from Applied Biosystems (Foster City, United States of America).
- The peptides coming from the digestion of the microorganism proteins are analysed by the mass spectrometer in MRM mode. Only the peptides indicated in **TABLE 3** are detected. To this end, the fragment(s) indicated in **TABLE 3** is/are detected.

TABLE 3:

Transition number	Peptide	Charge state of the precursor	Fragment ion	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	AAITHTAR	2	y4 monocharged	5.61	420.74	484.26	24
2	AAITHTAR	2	y5 monocharged	5.61	420.74	585.31	24
3	AAITHTAR	2	y6 monocharged	5.61	420.74	698.39	24
4	AFGAAFPK	2	y6 monocharged	16.03	404.72	590.33	23
5	AFGAAFPK	2	y7 monocharged	16.03	404.72	737.4	23
6	AFGAAFPK	2	y7 dicharged	16.03	404.72	369.2	23
7	ASMIVMSHSAPDSR	2	y7 monocharged	13.65	744.85	769.36	38
8	ASMIVMSHSAPDSR	2	y8 monocharged	13.65	744.85	856.39	38
9	ASMIVMSHSAPDSR	2	y9 monocharged	13.65	744.85	987.43	38
10	FGDLVFR	2	y4 monocharged	19.14	427.23	534.34	24
11	FGDLVFR	2	y5 monocharged	19.14	427.23	649.37	24

12	FGDLVFR	2	y6 monocharged	19.14	427.23	706.39	24
13	MELPNIMHPVAK	2	y10 dicharged	19.09	690.36	560.32	35
14	MELPNIMHPVAK	2	y9 monocharged	19.09	690.36	1006.55	35
15	MELPNIMHPVAK	2	y9 dicharged	19.09	690.36	503.78	35
16	QEINLPVALAVVTHAHQDK	3	y14 dicharged	21.34	695.05	743.41	39
17	QEINLPVALAVVTHAHQDK	3	y7 monocharged	21.34	695.05	836.4	39
18	QEINLPVALAVVTHAHQDK	3	y8 monocharged	21.34	695.05	935.47	39
19	SLGNLGDADTEHYAASAR	2	y14 dicharged	14.64	924.43	738.84	46
20	SLGNLGDADTEHYAASAR	2	y16 dicharged	14.64	924.43	824.37	46
21	SLGNLGDADTEHYAASAR	2	y7 monocharged	14.64	924.43	775.38	46
22	VLVVDTAWTDDQTAQILNWIK	3	y5 monocharged	27.16	810.43	673.4	45
23	VLVVDTAWTDDQTAQILNWIK	3	y6 monocharged	27.16	810.43	786.49	45
24	VLVVDTAWTDDQTAQILNWIK	3	y7 monocharged	27.16	810.43	914.55	45

The precursor peptide charge state, its retention time, the fragment ion type and the transitions, i.e. the $(m/z)_1$ ratio in Q1 and $(m/z)_2$ ratio in Q3 are indicated in **TABLE 3**. The collision energy used to fragment the precursor ion is also indicated in **TABLE 3**.

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	yes
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	50.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	40.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated
Declustering potential (DP):	80.00 V

Entry potential before Q0 (EP):	10.00 V
Collision cell exit potential (CXP):	35 V
Total cycle time:	1.2 sec
Detection window:	90 sec

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. All the transitions having an area greater than or equal to 2500 (arbitrary unit) are considered to be positive and have been labelled "1" in **TABLE 4**. All the transitions having an area less than 2500 are considered to be negative and have been labelled 0 in **TABLE 4**. When no signal peak was observed, the transition has been labelled as negative.

TABLE 4:

Transition number	Sam1	Sam2	Sam3	Sam4	Sam5	Sam6	Sam7	Sam8	Sam9
1	1	1	1	1	1	1	0	1	1
2	1	1	1	1	1	1	1	1	1
3	1	1	0	1	1	1	0	1	1
4	1	1	1	1	1	1	1	1	1
5	1	1	1	1	1	1	1	1	1
6	1	1	0	1	1	1	1	1	1
7	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0
10	1	1	1	1	1	1	1	1	1
11	1	1	1	1	1	1	1	1	1
12	1	1	1	1	1	1	1	1	1
13	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0
16	1	1	0	1	1	0	0	0	1
17	1	1	0	1	1	1	1	0	1
18	1	1	0	1	1	0	1	0	1
19	0	0	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0

The number of positive transitions is then added up and set out in **TABLE 5**:

TABLE 5:

Names	Species	Number of positive transitions
Sam1	*K. pneumoniae*	12
Sam2	*C. freundii*	12
Sam3	*A. baumannii*	7
Sam4	*A. caviae*	12
Sam5	*C. braakii*	12
Sam6	*E. cloacae*	10
Sam7	*P. rettgeri*	9
Sam8	*E. coli*	9
Sam9	*K. pneumoniae*	12

Samples Sam1 to Sam9 comprise more than 6 positive transitions, they therefore contain bacteria which express the NDM-1 protein. The bacteria of Sam1 to Sam9 are therefore resistant to penicillins, to cephalosporins and to carbapenems.

Example 7: Identification of a resistance to KPC beta-lactams:

Samples Sam62 to Sam73 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 6**.

TABLE 6:

Names	Species
Sam62	*K. pneumoniae*
Sam63	*K. pneumoniae*
Sam64	*K. pneumoniae*
Sam65	*K. pneumoniae*
Sam66	*K. pneumoniae*
Sam67	*K. pneumoniae*
Sam68	*K. pneumoniae*
Sam69	*K. pneumoniae*
Sam70	*K. pneumoniae*
Sam71	*K. pneumoniae*
Sam72	*K. pneumoniae*
Sam73	*K. pneumoniae*

Samples Sam62 to Sam73 correspond to a species able to comprise a KPC resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 7** instead of the peptides from **TABLE 3**.

TABLE 7:

Transition number	Peptide	Methionine oxidation	Charge state of the precursor	Fragment ion	Clinical interest
1	AAVPADWAVGDK	no	2	y9 dicharged	2f
2	AAVPADWAVGDK	no	2	y10 dicharged	2f
3	AAVPADWAVGDK	no	2	y9 monocharged	2f
4	APIVLAVYTR	no	2	y7 monocharged	2f
5	APIVLAVYTR	no	2	y5 monocharged	2f
6	APIVLAVYTR	no	2	y6 monocharged	2f
7	AVTESLQK	no	2	y5 monocharged	2f
8	AVTESLQK	no	2	y6 monocharged	2f
9	AVTESLQK	no	2	y4 monocharged	2f
10	ELGGPAGLTAFMR	yes	2	y7 monocharged	2f
11	ELGGPAGLTAFMR	yes	2	y5 monocharged	2f
12	ELGGPAGLTAFMR	yes	2	y9 dicharged	2f
13	ELGGPAGLTAFMR	no	2	y7 monocharged	2f
14	ELGGPAGLTAFMR	no	2	y5 monocharged	2f
15	ELGGPAGLTAFMR	no	2	y9 dicharged	2f
16	FPLCSSFK	no	2	y6 monocharged	2f
17	FPLCSSFK	no	2	y7 monocharged	2f
18	FPLCSSFK	no	2	y5 monocharged	2f
19	GFLAAAVLAR	no	2	y6 monocharged	2f
20	GFLAAAVLAR	no	2	y7 monocharged	2f
21	GFLAAAVLAR	no	2	y5 monocharged	2f
22	GNTTGNHR	no	2	y5 monocharged	2f
23	GNTTGNHR	no	2	y6 monocharged	2f
24	GNTTGNHR	no	2	y4 monocharged	2f
25	LALEGLGVNGQ	no	3	y8 monocharged	2f
26	LALEGLGVNGQ	no	3	y7 monocharged	2f
27	LALEGLGVNGQ	no	3	y6 monocharged	2f
28	LTLGSALAAPQR	no	3	y9 monocharged	2f
29	LTLGSALAAPQR	no	3	y5 monocharged	2f
30	LTLGSALAAPQR	no	3	y6 monocharged	2f
31	NALVPWSPISEK	no	2	y8 monocharged	2f
32	NALVPWSPISEK	no	2	y8 dicharged	2f
33	NALVPWSPISEK	no	2	y5 monocharged	2f
34	QQFVDWLK	no	2	y5 monocharged	2f
35	QQFVDWLK	no	2	y6 monocharged	2f
36	QQFVDWLK	no	2	y4 monocharged	2f
37	SIGDTTFR	no	2	y5 monocharged	2f
38	SIGDTTFR	no	2	y6 monocharged	2f
39	SIGDTTFR	no	2	y4 monocharged	2f
40	SQQQAGLLDTPIR	no	2	y8 monocharged	2f
41	SQQQAGLLDTPIR	no	2	y9 monocharged	2f
42	SQQQAGLLDTPIR	no	2	y10 monocharged	2f
43	WELELNSAIPGDAR	no	2	y5 monocharged	2f
44	WELELNSAIPGDAR	no	2	y8 monocharged	2f

45	WELELNSAIPGDAR	no	2	y9 monocharged	2f

The transitions mentioned in **TABLE 7** are detected by using the parameters set out in **TABLE 8**.

Transition number	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	Positivity threshold
1	16.29	600.31	479.73	31	2000
2	16.29	600.31	529.27	31	2000
3	16.29	600.31	958.46	31	2000
4	19.07	551.83	821.49	29	13000
5	19.07	551.83	609.33	29	13000
6	19.07	551.83	722.42	29	13000
7	10.38	438.25	604.33	24	2000
8	10.38	438.25	705.38	24	2000
9	10.38	438.25	475.29	24	2000
10	18.55	668.34	811.41	34	2000
11	18.55	668.34	641.31	34	2000
12	18.55	668.34	490.26	34	2000
13	21.72	660.34	795.42	34	2000
14	21.72	660.34	625.31	34	2000
15	21.72	660.34	482.26	34	2000
16	17.56	493.24	741.36	27	2000
17	17.56	493.24	838.41	27	2000
18	17.56	493.24	628.28	27	2000
19	20.67	494.8	600.38	27	14000
20	20.67	494.8	671.42	27	14000
21	20.67	494.8	529.35	27	14000
22	1.19	428.7	584.29	24	2000
23	1.19	428.7	685.34	24	2000
24	1.19	428.7	483.24	24	2000
25	18.89	535.8	773.38	42	2000
26	18.89	535.8	644.34	42	2000
27	18.89	535.8	587.31	42	2000
28	17.37	599.35	870.48	42	2000
29	17.37	599.35	542.3	42	2000
30	17.37	599.35	655.39	42	2000
31	20	670.86	943.49	35	2000
32	20	670.86	472.25	35	2000
33	20	670.86	573.32	35	2000
34	20.48	532.28	660.37	28	2000
35	20.48	532.28	807.44	28	2000
36	20.48	532.28	561.3	28	2000
37	13.42	448.73	639.31	25	2000
38	13.42	448.73	696.33	25	2000
39	13.42	448.73	524.28	25	2000
40	17.6	713.89	884.52	36	2000
41	17.6	713.89	955.56	36	2000
42	17.6	713.89	1083.62	36	2000
43	21.1	785.9	515.26	40	2000

44	21.1	785.9	786.41	40	2000
45	21.1	785.9	900.45	40	2000

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the 3 transitions of the same peptide are greater than or equal to the positivity threshold described in **TABLE 8**, the detection of the peptide is considered to be positive and is labelled "1" in **TABLE 9**. When at least one transition comprises an area less than the positivity threshold described in **TABLE 8**, the corresponding peptide is considered non-detected and is labelled "0" in **TABLE 9**.

TABLE 9:

Transition number	Sam62	Sam63	Sam64	Sam65	Sam66	Sam67	Sam68	Sam69	Sam70	Sam71	Sam72	Sam73
1	0	0	0	0	0	0	1	1	1	1	1	1
2	0	0	0	0	0	0	1	1	1	1	1	1
3	0	0	0	0	0	0	1	1	1	1	1	1
4	0	0	0	0	0	0	1	1	1	1	1	1
5	0	0	0	0	0	0	1	1	1	1	1	1
6	0	0	0	0	0	0	1	1	1	1	1	1
7	0	0	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	1	1	1	1	1	1
14	0	0	0	0	0	0	1	1	1	1	1	1
15	0	0	0	0	0	0	1	1	1	1	1	1
16	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	1	1	1	1	1	1
20	0	0	0	0	0	0	1	1	1	1	1	1
21	0	0	0	0	0	0	1	1	1	1	1	1
22	0	0	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	1	1	1	1	1	1
29	0	0	0	0	0	0	1	1	1	1	1	1
30	0	0	0	0	0	0	1	1	1	1	1	1
31	0	0	0	0	0	0	1	1	1	1	1	1
32	0	0	0	0	0	0	1	1	1	1	1	1
33	0	0	0	0	0	0	1	1	1	1	1	1
34	0	0	0	0	0	0	0	0	0	0	0	0

35	0	0	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	1	1	1	1	1	1
38	0	0	0	0	0	0	1	1	1	1	1	1
39	0	0	0	0	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	1	1	1	1	1	1
41	0	0	0	0	0	0	1	1	1	1	1	1
42	0	0	0	0	0	0	1	1	1	1	1	1
43	0	0	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0	0	0
Sum of the transitions	0	0	0	0	0	0	23	23	23	23	23	23

Samples Sam68 to Sam73 comprise at least one transition which is characteristic of KPCs. The bacteria present in samples Sam68 to Sam73 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins, including third-generation cephalosporins such as cefotaxime/ceftazidime, to monobactams and to carbapenems.

Samples Sam62 to Sam67 comprise no transition which is characteristic of KPCs. The bacteria present in samples Sam62 to Sam67 therefore do not express KPC beta-lactamase and may be sensitive to carbapenem antibiotics.

Example 8: Identification of a resistance to NDM-1 or KPC beta-lactams:

The samples corresponding to a species able to comprise an NDM-1 or KPC resistance mechanism can be detected by employing the following method.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 10** instead of the peptides from **TABLE 3**.

TABLE 10:

Proteins	Transition number	Peptide	First-generation fragment ion	Charge state of the precursor	Clinical interest
NDM-1	1	AAITHTAR	y4 monocharged	2	3a
NDM-1	2	AAITHTAR	y5 monocharged	2	3a
NDM-1	3	AAITHTAR	y6 monocharged	2	3a
NDM-1	4	AFGAAFPK	y6 monocharged	2	3a
NDM-1	5	AFGAAFPK	y7 monocharged	2	3a
NDM-1	6	AFGAAFPK	y7 dicharged	2	3a
NDM-1	7	FGDLVFR	y4 monocharged	2	3a
NDM-1	8	FGDLVFR	y5 monocharged	2	3a

NDM-1	9	FGDLVFR	y6 monocharged	2	3a
NDM-1	10	QEINLPVALAVVTHAHQDK	y14 dicharged	3	3a
NDM-1	11	QEINLPVALAVVTHAHQDK	y7 monocharged	3	3a
NDM-1	12	QEINLPVALAVVTHAHQDK	y8 monocharged	3	3a
KPC	13	AAVPADWAVGDK	y9 dicharged	2	2f
KPC	14	AAVPADWAVGDK	y10 dicharged	2	2f
KPC	15	AAVPADWAVGDK	y9 monocharged	2	2f
KPC	16	APIVLAVYTR	y7 monocharged	2	2f
KPC	17	APIVLAVYTR	y5 monocharged	2	2f
KPC	18	APIVLAVYTR	y6 monocharged	2	2f
KPC	19	ELGGPAGLTAFMR	y7 monocharged	2	2f
KPC	20	ELGGPAGLTAFMR	y5 monocharged	2	2f
KPC	21	ELGGPAGLTAFMR	y9 dicharged	2	2f
KPC	22	GFLAAAVLAR	y6 monocharged	2	2f
KPC	23	GFLAAAVLAR	y7 monocharged	2	2f
KPC	24	GFLAAAVLAR	y5 monocharged	2	2f
KPC	25	LTLGSALAAPQR	y9 monocharged	3	2f
KPC	26	LTLGSALAAPQR	y5 monocharged	3	2f
KPC	27	LTLGSALAAPQR	y6 monocharged	3	2f
KPC	28	NALVPWSPISEK	y8 monocharged	2	2f
KPC	29	NALVPWSPISEK	y8 dicharged	2	2f
KPC	30	NALVPWSPISEK	y5 monocharged	2	2f
KPC	31	SQQQAGLLDTPIR	y8 monocharged	2	2f
KPC	32	SQQQAGLLDTPIR	y9 monocharged	2	2f
KPC	33	SQQQAGLLDTPIR	y10 monocharged	2	2f

The entry 2f indicates the presence of a carbapenemase beta-lactamase from subgroup 2f according to the Bush and Jacoby classification [Antimicrob Agents Chemother. 2010 Mar; 54(3):969-76. Epub 2009 Dec 7. Updated functional classification of beta-lactamases.], capable of hydrolysing carbapenems.

The entry 3a indicates the presence of a metallo-beta-lactamase from subgroup 3a according to the Bush and Jacoby classification [9], *supra*, capable of hydrolysing penicillins, cephalosporins and carbapenems.

The transitions mentioned in **TABLE 10** are detected by using the parameters set out in **TABLE 11**.

TABLE 11:

Transition number	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	Positivity threshold
1	5.61	420.74	484.26	24	2500
2	5.61	420.74	585.31	24	2500
3	5.61	420.74	698.39	24	2500
4	16.03	404.72	590.33	23	2500
5	16.03	404.72	737.4	23	2500
6	16.03	404.72	369.2	23	2500
7	19.14	427.23	534.34	24	2500
8	19.14	427.23	649.37	24	2500
9	19.14	427.23	706.39	24	2500
10	21.34	695.05	743.41	39	2500
11	21.34	695.05	836.4	39	2500
12	21.34	695.05	935.47	39	2500
13	16.29	600.31	479.73	31	2000
14	16.29	600.31	529.27	31	2000
15	16.29	600.31	958.46	31	2000
16	19.07	551.83	821.49	29	13000
17	19.07	551.83	609.33	29	13000
18	19.07	551.83	722.42	29	13000
19	21.72	660.34	795.42	34	2000
20	21.72	660.34	625.31	34	2000
21	21.72	660.34	482.26	34	2000
22	20.67	494.8	600.38	27	14000
23	20.67	494.8	671.42	27	14000
24	20.67	494.8	529.35	27	14000
25	17.37	599.35	870.48	42	2000
26	17.37	599.35	542.3	42	2000
27	17.37	599.35	655.39	42	2000
28	20	670.86	943.49	35	2000
29	20	670.86	472.25	35	2000
30	20	670.86	573.32	35	2000
31	17.6	713.89	884.52	36	2000
32	17.6	713.89	955.56	36	2000
33	17.6	713.89	1083.62	36	2000

When the areas of at least two transitions of the same peptide are greater than or equal to the positivity threshold described in **TABLE 11**, the detection of the peptide is considered to be positive. When more than two transitions of the same peptide comprise an area less than the positivity threshold described in **TABLE 11**, the corresponding peptide is considered non-detected.

A sample contains bacteria which express the NDM-1 protein, when at least one peptide corresponding to the NDM-1 resistance mechanism is detected. These bacteria are resistant to penicillins, to cephalosporins and to carbapenems.

A sample contains bacteria which express the KPC protein, when at least one peptide corresponding to the KPC resistance mechanism is detected. These bacteria are resistant to penicillins, to cephalosporins, including third-generation cephalosporins such as cefotaxime/ceftazidime, to monobactams and to carbapenems.

Example 9: Identification of a resistance to IND beta-lactams:

Samples Sam84 to Sam88 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 12**.

TABLE 12:

Names	Species
Sam84	*C. indologenes*
Sam85	*C. indologenes*
Sam86	*C. indologenes*
Sam87	*C. indologenes*
Sam88	*C. indologenes*

Samples Sam84 to Sam88 correspond to a species able to comprise an IND resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 13** instead of the peptides from **TABLE 3**.

TABLE 13:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Declustering potential (eV)	Collision energy (eV)	Collision cell exit potential (eV)	Positivity threshold
1	AATDLGYIK	14.66	476.26	593.37	65.8	26	15	2000
2	AATDLGYIK	14.66	476.26	708.39	65.8	26	15	2000
3	AATDLGYIK	14.66	476.26	809.44	65.8	26	15	2000
4	AGDLSFFNNK	18.08	556.77	522.27	71.7	29.5	15	2000

5	AGDLSFFNNK	18.08	556.77	669.34	71.7	29.5	15	2000
6	AGDLSFFNNK	18.08	556.77	756.37	71.7	29.5	15	2000
7	AGDLSFYNK	14.82	507.75	424.22	68.1	27.3	15	2000
8	AGDLSFYNK	14.84	507.75	571.29	68.1	27.3	15	2000
9	AGDLSFYNK	14.84	507.75	658.32	68.1	27.3	15	2000
10	AGDLSFYNQK	14.91	571.78	552.28	72.8	30.2	15	2000
11	AGDLSFYNQK	14.93	571.78	699.35	72.8	30.2	15	2000
12	AGDLSFYNQK	14.93	571.78	786.38	72.8	30.2	15	2000
13	AQYQSLMDTIK	18.01	649.33	1098.55	78.5	33.6	15	2000
14	AQYQSLMDTIK	18.01	649.33	607.31	78.5	33.6	15	2000
15	AQYQSLMDTIK	18.01	649.33	807.43	78.5	33.6	15	2000
16	ASLVIPGHDEWK	16.84	676.35	434.70	80.4	34.8	15	2000
17	ASLVIPGHDEWK	16.8	676.35	868.40	80.4	34.8	15	2000
18	ASLVIPGHDEWK	16.82	676.35	981.48	80.4	34.8	15	2000
19	ATLIIPGHDDWK	17.47	683.36	427.69	80.9	35.1	15	2000
20	ATLIIPGHDDWK	17.47	683.36	854.38	80.9	35.1	15	2000
21	ATLIIPGHDDWK	17.47	683.36	967.46	80.9	35.1	15	2000
22	ATLIIPGHDEWK	17.54	690.37	1094.56	81.4	35.4	10	2000
23	ATLIIPGHDEWK	17.54	690.37	868.40	81.4	35.4	10	2000
24	ATLIIPGHDEWK	17.54	690.37	981.48	81.4	35.4	10	2000
25	ATSTELIKPGK	11.63	572.83	301.19	72.9	30.2	15	2000
26	ATSTELIKPGK	11.67	572.83	486.79	72.9	30.2	15	2000
27	ATSTELIKPGK	11.67	572.83	655.45	72.9	30.2	15	2000
28	DFVIEPPIK	19.93	529.30	454.30	69.7	28.3	15	2000
29	DFVIEPPIK	19.93	529.30	696.43	69.7	28.3	15	2000
30	DFVIEPPIK	19.93	529.30	795.50	69.7	28.3	15	2000
31	DFVIEPPVKPNLYLYK	22.03	645.69	730.91	78.2	36.3	15	2000
32	DFVIEPPVKPNLYLYK	22.03	645.69	787.45	78.2	36.3	15	2000
33	DFVIEPPVKPNLYLYK	22.08	645.69	836.99	78.2	36.3	15	2000
34	DFVIEQPFGK	19.77	590.31	448.26	74.2	31	15	2000
35	DFVIEQPFGK	19.75	590.31	705.36	74.2	31	15	2000
36	DFVIEQPFGK	19.75	590.31	818.44	74.2	31	15	2000
37	EANLEQWPK	15.53	557.78	430.25	71.8	29.5	15	2000
38	EANLEQWPK	15.55	557.78	558.30	71.8	29.5	15	2000
39	EANLEQWPK	15.55	557.78	687.35	71.8	29.5	15	2000
40	EANVEQWPITIDK	19.5	514.93	343.71	68.7	29.7	10	2000
41	EANVEQWPITIDK	19.5	514.93	686.41	68.7	29.7	10	2000
42	EANVEQWPITIDK	19.48	514.93	872.49	68.7	29.7	10	2000
43	EANVEQWPK	13.84	550.77	430.25	71.3	29.2	15	2000
44	EANVEQWPK	13.86	550.77	558.30	71.3	29.2	15	2000
45	EANVEQWPK	13.86	550.77	687.35	71.3	29.2	15	2000
46	EQYQTLMDTIQK	17.9	749.37	735.37	85.7	38	10	2000
47	EQYQTLMDTIQK	17.9	749.37	848.46	85.7	38	10	2000
48	EQYQTLMDTIQK	17.9	749.37	949.50	85.7	38	10	2000
49	EYSANAVYLTTK	15.26	680.34	1067.57	80.7	34.9	10	2000

50	EYSANAVYLTTK	15.28	680.34	625.36	80.7	34.9	10	2000
51	EYSANAVYLTTK	15.26	680.34	795.46	80.7	34.9	10	2000
52	EYSANSMYLVTK	16.5	703.34	1113.56	82.4	35.9	10	2000
53	EYSANSMYLVTK	16.5	703.34	841.45	82.4	35.9	10	2000
54	EYSANSMYLVTK	16.5	703.34	955.49	82.4	35.9	10	2000
55	EYSANSVYLVTK	16.19	687.35	1081.59	81.2	35.2	10	2000
56	EYSANSVYLVTK	16.14	687.35	623.38	81.2	35.2	10	2000
57	EYSANSVYLVTK	16.12	687.35	923.52	81.2	35.2	10	2000
58	EYSANSVYLVTQK	16.19	501.26	376.22	67.7	29.1	10	2000
59	EYSANSVYLVTQK	16.19	501.26	475.29	67.7	29.1	10	2000
60	EYSANSVYLVTQK	16.21	501.26	751.44	67.7	29.1	10	2000
61	EYSTNALYLVTK	18.83	701.37	1109.62	82.2	35.9	10	2000
62	EYSTNALYLVTK	18.83	701.37	460.31	82.2	35.9	10	2000
63	EYSTNALYLVTK	18.81	701.37	623.38	82.2	35.9	10	2000
64	GGGHVEHTLELLDK	15.6	502.26	730.44	67.7	29.1	10	2000
65	GGGHVEHTLELLDK	15.6	502.26	831.48	67.7	29.1	10	2000
66	GGGHVEHTLELLDK	15.6	502.26	968.54	67.7	29.1	10	2000
67	GGGHVEHTLELLNK	15	501.94	616.37	67.7	29.1	10	2000
68	GGGHVEHTLELLNK	15	501.94	729.45	67.7	29.1	10	2000
69	GGGHVEHTLELLNK	15	501.94	830.50	67.7	29.1	10	2000
70	GGGHVQHTLDLLDK	15.35	745.39	1082.58	85.5	37.8	10	2000
71	GGGHVQHTLDLLDK	15.35	745.39	1181.65	85.5	37.8	10	2000
72	GGGHVQHTLDLLDK	15.35	745.39	488.31	85.5	37.8	10	2000
73	GIPTYATAK	12.63	461.26	376.20	64.7	25.3	15	2000
74	GIPTYATAK	12.63	461.26	654.35	64.7	25.3	15	2000
75	GIPTYATAK	12.63	461.26	751.40	64.7	25.3	15	2000
76	GNDHVK	1.3	335.17	383.24	55.6	19.7	15	2000
77	GNDHVK	1.3	335.17	498.27	55.6	19.7	15	2000
78	GNDHVK	1.3	335.17	612.31	55.6	19.7	15	2000
79	GVVLFDVPWEK	23.79	644.86	559.29	78.1	33.4	15	2000
80	GVVLFDVPWEK	23.82	644.86	658.36	78.1	33.4	15	2000
81	GVVLFDVPWEK	23.82	644.86	920.45	78.1	33.4	15	2000
82	GVVLFDVPWQK	23.32	644.36	558.30	78.1	33.4	15	2000
83	GVVLFDVPWQK	23.32	644.36	772.40	78.1	33.4	15	2000
84	GVVLFDVPWQK	23.32	644.36	919.47	78.1	33.4	15	2000
85	HNLPVIAVFATHSHSDR	17.94	634.33	768.90	77.4	35.7	15	2000
86	HNLPVIAVFATHSHSDR	17.95	634.33	825.44	77.4	35.7	15	2000
87	HNLPVIAVFATHSHSDR	17.93	634.33	882.46	77.4	35.7	15	2000
88	HNLPVVAVFATHSHDDR	17.17	638.99	775.89	77.7	35.9	15	2000
89	HNLPVVAVFATHSHDDR	17.17	638.99	832.43	77.7	35.9	15	2000
90	HNLPVVAVFATHSHDDR	17.17	638.99	889.45	77.7	35.9	15	2000
91	HTLELLDQQK	15.02	612.83	403.23	75.8	32	15	2000
92	HTLELLDQQK	15.02	612.83	518.26	75.8	32	15	2000
93	HTLELLDQQK	15.02	612.83	986.55	75.8	32	15	2000
94	HTLELLNK	14.44	484.28	616.37	66.4	26.3	15	2000

95	HTLELLNK	14.44	484.28	729.45	66.4	26.3	15	2000
96	HTLELLNK	14.44	484.28	830.50	66.4	26.3	15	2000
97	IQYQSLMDTIK	19.41	670.34	1098.55	80	34.5	15	2000
98	IQYQSLMDTIK	19.38	670.34	607.31	80	34.5	15	2000
99	IQYQSLMDTIK	19.41	670.34	807.43	80	34.5	15	2000
100	NLHIYK	11.54	394.23	337.21	59.9	22.3	15	2000
101	NLHIYK	11.54	394.23	423.26	59.9	22.3	15	2000
102	NLHIYK	11.54	394.23	560.32	59.9	22.3	15	2000
103	NLYIYK	14.93	407.23	423.26	60.8	22.9	15	2000
104	NLYIYK	14.91	407.23	586.32	60.8	22.9	15	2000
105	NLYIYK	14.93	407.23	699.41	60.8	22.9	15	2000
106	NNLHIYK	11.29	451.25	423.26	64	24.9	15	2000
107	NNLHIYK	11.29	451.25	560.32	64	24.9	15	2000
108	NNLHIYK	11.27	451.25	673.40	64	24.9	15	2000
109	QLYLYK	15.22	414.24	423.26	61.3	23.2	15	2000
110	QLYLYK	15.2	414.24	586.32	61.3	23.2	15	2000
111	QLYLYK	15.22	414.24	699.41	61.3	23.2	15	2000
112	QWPETMR	14.84	474.22	317.16	65.7	25.9	15	2000
113	QWPETMR	14.75	474.22	407.21	65.7	25.9	15	2000
114	QWPETMR	14.73	474.22	633.30	65.7	25.9	15	2000
115	SFGVFGGK	16.69	399.71	356.20	60.3	22.6	15	2000
116	SFGVFGGK	16.69	399.71	408.22	60.3	22.6	15	2000
117	SFGVFGGK	16.69	399.71	564.31	60.3	22.6	15	2000
118	SIQLLMMSMFLSPLINAQVK	32.4	755.41	441.77	86.2	41.8	15	2000
119	SIQLLMMSMFLSPLINAQVK	32.4	755.41	882.54	86.2	41.8	15	2000
120	SIQLLMMSMFLSPLINAQVK	32.4	755.41	969.57	86.2	41.8	15	2000
121	SNSATDLGYIK	14.71	584.80	593.37	73.7	30.7	15	2000
122	SNSATDLGYIK	14.71	584.80	809.44	73.7	30.7	15	2000
123	SNSATDLGYIK	14.71	584.80	967.51	73.7	30.7	15	2000
124	TATDLGYTGEANVK	13.61	720.35	718.37	83.6	36.7	10	2000
125	TATDLGYTGEANVK	13.61	720.35	881.44	83.6	36.7	10	2000
126	TATDLGYTGEANVK	13.61	720.35	938.46	83.6	36.7	10	2000
127	TFGVFDGK	16.56	435.72	466.23	62.9	24.2	15	2000
128	TFGVFDGK	16.58	435.72	622.32	62.9	24.2	15	2000
129	TFGVFDGK	16.58	435.72	769.39	62.9	24.2	15	2000
130	TFGVFGGK	16.78	406.72	408.22	60.8	22.9	15	2000
131	TFGVFGGK	16.76	406.72	564.31	60.8	22.9	15	2000
132	TFGVFGGK	16.78	406.72	711.38	60.8	22.9	15	2000
133	TGKPYK	1.41	347.20	407.23	56.4	20.3	15	2000
134	TGKPYK	1.41	347.20	535.32	56.4	20.3	15	2000
135	TGKPYK	1.41	347.20	592.35	56.4	20.3	15	2000
136	TGKPYR	1.41	361.20	435.24	57.4	20.9	15	2000

137	TGKPYR	1.41	361.20	563.33	57.4	20.9	15	2000
138	TGKPYR	1.41	361.20	620.35	57.4	20.9	15	2000
139	TGVVLFDVPWEK	24.03	695.37	1033.54	81.8	35.6	10	2000
140	TGVVLFDVPWEK	23.97	695.37	559.29	81.8	35.6	10	2000
141	TGVVLFDVPWEK	23.97	695.37	920.45	81.8	35.6	10	2000
142	TNEFLK	12.85	376.20	407.27	58.5	21.6	15	2000
143	TNEFLK	12.88	376.20	536.31	58.5	21.6	15	2000
144	TNEFLK	12.85	376.20	650.35	58.5	21.6	15	2000
145	TNELLK	11.69	359.21	373.28	57.3	20.8	15	2000
146	TNELLK	11.72	359.21	502.32	57.3	20.8	15	2000
147	TNELLK	11.69	359.21	616.37	57.3	20.8	15	2000
148	TNQFLK	12.3	375.71	407.27	58.5	21.5	15	2000
149	TNQFLK	12.27	375.71	535.32	58.5	21.5	15	2000
150	TNQFLK	12.27	375.71	649.37	58.5	21.5	15	2000
151	TQYQSLMDTIK	18.12	664.33	1098.55	79.5	34.2	15	2000
152	TQYQSLMDTIK	18.1	664.33	607.31	79.5	34.2	15	2000
153	TQYQSLMDTIK	18.12	664.33	807.43	79.5	34.2	15	2000
154	TYATAK	1.9	327.68	319.20	55	19.4	15	2000
155	TYATAK	1.85	327.68	390.24	55	19.4	15	2000
156	TYATAK	1.9	327.68	553.30	55	19.4	15	2000
157	TYATPK	7.79	340.68	345.21	56	20	15	2000
158	TYATPK	7.77	340.68	416.25	56	20	15	2000
159	TYATPK	7.79	340.68	579.31	56	20	15	2000
160	TYATSK	1.45	335.67	335.19	55.6	19.8	15	2000
161	TYATSK	1.45	335.67	406.23	55.6	19.8	15	2000
162	TYATSK	1.47	335.67	569.29	55.6	19.8	15	2000
163	VIPGHDEWK	12.43	540.78	434.70	70.5	28.8	15	2000
164	VIPGHDEWK	12.45	540.78	771.34	70.5	28.8	15	2000
165	VIPGHDEWK	12.43	540.78	868.40	70.5	28.8	15	2000
166	VLDGGCLVK	14.44	480.76	633.34	66.2	26.2	15	2000
167	VLDGGCLVK	14.44	480.76	748.37	66.2	26.2	15	2000
168	VLDGGCLVK	14.46	480.76	861.45	66.2	26.2	15	2000
169	VQYQSLMDTIQK	18.24	727.37	1063.55	84.1	37	10	2000
170	VQYQSLMDTIQK	18.24	727.37	1226.61	84.1	37	10	2000
171	VQYQSLMDTIQK	18.24	727.37	935.49	84.1	37	10	2000
172	YAQATLVIPGHDEWK	18.03	576.63	577.26	73.2	32.8	10	2000
173	YAQATLVIPGHDEWK	18.03	576.63	747.39	73.2	32.8	10	2000
174	YAQATLVIPGHDEWK	18.05	576.63	868.40	73.2	32.8	10	2000
175	YAQATLVIPGHEEWK	17.99	581.30	690.37	73.5	33.1	10	2000
176	YAQATLVIPGHEEWK	17.95	581.30	754.40	73.5	33.1	10	2000
177	YAQATLVIPGHEEWK	17.97	581.30	882.41	73.5	33.1	10	2000
178	YNVLDGGCLVK	17.86	619.32	633.34	76.3	32.2	15	2000
179	YNVLDGGCLVK	17.86	619.32	748.37	76.3	32.2	15	2000
180	YNVLDGGCLVK	17.86	619.32	861.45	76.3	32.2	15	2000
181	YPSTAK	4.3	333.68	319.20	55.4	19.7	15	2000

182	YPSTAK	4.44	333.68	406.23	55.4	19.7	15	2000
183	YPSTAK	4.28	333.68	503.28	55.4	19.7	15	2000
184	YSEAVLIIPGHDEWK	19.76	586.30	753.90	73.9	33.3	15	2000
185	YSEAVLIIPGHDEWK	19.72	586.30	797.42	73.9	33.3	15	2000
186	YSEAVLIIPGHDEWK	19.72	586.30	868.40	73.9	33.3	15	2000

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	no
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	40.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated
Entry potential before Q0 (EP):	10.00 V

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 13**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 14**. When a transition has an area less than the positivity threshold described in **TABLE 13**, the transition is considered non-detected and is labelled "0" in **TABLE 14**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 14:

Transition number	Sam84	Sam85	Sam86	Sam87	Sam88
1	0	1	1	1	1
2	0	0	1	1	0
3	0	0	0	1	0
4	0	0	0	0	0
5	0	0	0	0	0
6	0	0	0	0	0
7	0	0	0	0	0
8	0	0	0	1	0
9	0	0	0	0	0
10	0	1	1	0	1
11	0	0	0	0	0
12	0	0	1	0	0
13	0	0	0	0	0
14	0	0	0	0	0
15	0	0	0	0	0
16	0	0	0	1	0
17	0	0	0	1	0
18	0	1	0	1	1
19	0	0	0	0	0
20	0	0	0	0	0
21	1	1	1	1	0
22	0	0	0	0	0
23	0	0	0	0	0
24	0	0	0	0	0
25	1	1	1	1	1
26	1	1	0	1	1
27	1	1	0	1	1
28	0	1	0	1	1
29	0	1	0	1	1
30	0	1	0	1	1
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	0	0	0	0	0
35	0	0	0	0	0
36	0	0	0	0	0
37	0	0	0	0	0
38	0	0	0	0	0
39	0	0	0	0	0
40	0	0	0	0	0
41	0	0	0	0	0
42	0	0	0	0	0
43	0	0	0	0	0

44	0	0	0	0	0
45	0	0	0	0	0
46	0	0	0	0	0
47	0	0	0	0	0
48	0	0	0	0	0
49	0	0	0	0	0
50	0	0	0	0	0
51	0	0	0	0	0
52	0	0	0	1	0
53	0	0	0	1	0
54	0	0	0	1	0
55	0	0	0	0	0
56	0	0	0	0	0
57	0	0	0	0	0
58	0	0	0	0	0
59	0	0	0	0	0
60	0	0	0	0	0
61	0	0	0	0	0
62	0	0	0	0	0
63	0	0	0	0	0
64	0	0	0	0	0
65	0	0	0	0	0
66	0	0	0	0	0
67	0	0	0	0	0
68	0	0	0	0	0
69	0	0	0	0	0
70	0	0	0	0	0
71	0	0	0	0	0
72	0	0	0	0	0
73	0	0	0	0	0
74	1	0	0	0	0
75	0	0	0	0	0
76	0	0	0	0	0
77	0	0	0	0	0
78	1	0	0	0	0
79	0	0	0	0	0
80	0	0	0	0	0
81	0	0	0	0	0
82	1	0	0	1	0
83	0	0	0	0	0
84	0	0	0	0	0
85	0	0	0	0	0
86	0	0	0	0	0
87	0	0	0	0	0
88	0	0	0	0	0

89	0	0	0	0	0
90	0	0	0	0	0
91	0	0	0	0	0
92	0	0	0	0	0
93	0	0	0	0	0
94	0	0	0	0	0
95	0	0	0	0	0
96	0	0	0	0	0
97	0	0	0	0	0
98	0	0	0	0	0
99	0	0	0	0	0
100	0	0	0	0	0
101	0	0	0	0	0
102	0	0	0	0	0
103	0	0	0	0	0
104	0	0	0	0	0
105	0	0	0	0	0
106	0	0	0	0	0
107	0	0	0	0	0
108	0	0	0	0	0
109	0	0	0	0	0
110	0	0	0	0	0
111	0	0	0	0	0
112	0	0	0	0	0
113	0	0	0	0	0
114	0	0	0	0	0
115	0	0	0	0	0
116	0	0	0	0	0
117	0	0	0	0	0
118	0	0	0	0	0
119	0	0	0	0	0
120	0	0	0	0	0
121	0	0	0	0	0
122	0	0	0	0	0
123	0	0	0	0	0
124	0	0	0	0	0
125	0	0	0	0	0
126	0	0	0	0	0
127	0	0	0	0	0
128	0	0	0	0	0
129	0	0	0	0	0
130	0	0	0	0	0
131	0	0	0	0	0
132	0	0	0	0	0
133	0	1	0	0	1

134	0	1	0	0	1
135	0	1	0	0	1
136	1	0	0	0	0
137	1	0	0	1	0
138	1	0	0	0	1
139	0	0	0	0	0
140	0	0	0	0	0
141	0	0	0	0	0
142	0	0	0	0	0
143	0	0	0	0	0
144	0	0	0	0	0
145	1	0	0	0	0
146	1	0	0	1	0
147	1	0	0	0	0
148	0	0	0	0	0
149	0	0	0	0	0
150	0	0	0	0	0
151	0	0	0	0	0
152	0	0	0	0	0
153	0	0	0	0	0
154	0	0	0	0	0
155	0	0	0	0	0
156	0	0	0	0	0
157	0	0	0	0	0
158	0	0	0	0	0
159	0	0	0	0	0
160	0	0	0	0	0
161	0	0	0	0	0
162	0	0	0	0	0
163	0	0	0	0	0
164	0	0	0	0	0
165	0	0	0	0	0
166	0	0	0	0	0
167	0	0	0	0	0
168	0	0	0	0	0
169	0	0	0	0	0
170	0	0	0	0	0
171	0	0	0	0	0
172	0	0	0	0	0
173	0	0	0	0	0
174	0	0	0	0	0
175	0	1	0	1	1
176	0	1	0	1	1
177	1	1	0	1	1
178	0	0	0	0	0

179	0	0	0	0	0
180	0	0	0	0	0
181	0	0	0	0	0
182	0	0	0	0	0
183	0	0	0	0	0
184	0	0	0	0	0
185	0	0	0	0	0
186	0	0	0	0	0
187	0	0	0	1	0
188	0	0	0	1	0
189	0	1	0	1	0
190	0	0	0	0	0
191	0	0	0	0	0
192	0	0	0	0	0
193	0	0	0	0	0
194	0	0	0	0	0
195	0	0	0	0	0

Samples Sam84 to Sam88 comprise at least one peptide which is characteristic of INDs. The bacteria present in samples Sam84 to Sam88 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins and to carbapenems.

Example 10: Identification of a resistance to GES beta-lactams:

Samples Sam89 and Sam90 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 15**.

TABLE 15:

Names	Species
Sam89	*E. coli*
Sam90	*P. aeruginosa*

Samples Sam89 and Sam90 correspond to a species able to comprise a GES resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 16** instead of the peptides from **TABLE 3**.

TABLE 16:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Declustering potential (eV)	Collision energy (eV)
1	AAEIGVAIVDPQGEIVAGHR	19.11	668.03	695.88	79.8	37.4
2	AAEIGVAIVDPQGEIVAGHR	19.13	668.03	731.39	79.8	37.4
3	AAEIGVAIVDPQGEIVAGHR	19.11	668.03	809.44	79.8	37.4
4	AAQIGVAIVDPQGEIVAGHR	18.76	667.70	695.88	79.8	37.4
5	AAQIGVAIVDPQGEIVAGHR	18.76	667.70	731.39	79.8	37.4
6	AAQIGVAIVDPQGEIVAGHR	18.76	667.70	809.44	79.8	37.4
7	DTTTPIAMAR	14.23	538.77	658.37	70.4	28.7
8	DTTTPIAMAR	14.23	538.77	759.42	70.4	28.7
9	DTTTPIAMAR	14.23	538.77	860.47	70.4	28.7
10	DWVVGEK	14.41	416.71	432.25	61.5	23.3
11	DWVVGEK	14.43	416.71	531.31	61.5	23.3
12	DWVVGEK	14.45	416.71	717.39	61.5	23.3
13	DYAVAVYTTAPK	15.83	649.84	680.36	78.5	33.6
14	DYAVAVYTTAPK	15.83	649.84	779.43	78.5	33.6
15	DYAVAVYTTAPK	15.85	649.84	850.47	78.5	33.6
16	EIGGPAAMTQYFR	20.03	720.85	1198.57	83.7	36.7
17	EIGGPAAMTQYFR	20.03	720.85	845.40	83.7	36.7
18	EIGGPAAMTQYFR	20.03	720.85	916.44	83.7	36.7
19	EPEMGDNTPGDLR	13.53	715.81	557.30	83.3	36.5
20	EPEMGDNTPGDLR	13.53	715.81	772.40	83.3	36.5
21	EPEMGDNTPGDLR	13.53	715.81	944.44	83.3	36.5
22	ESEMSDNTPGDLR	12.72	725.81	557.30	84	36.9
23	ESEMSDNTPGDLR	12.7	725.81	887.42	84	36.9
24	ESEMSDNTPGDLR	12.71	725.81	974.45	84	36.9
25	FAMCSTFK	16.14	496.22	642.29	67.3	26.8
26	FAMCSTFK	16.12	496.22	773.33	67.3	26.8
27	FAMCSTFK	16.12	496.22	844.37	67.3	26.8
28	FIHALLLAGIAHSAYASEK	20.93	671.37	1204.60	80.1	37.6
29	FIHALLLAGIAHSAYASEK	20.92	671.37	807.95	80.1	37.6
30	FIHALLLAGIAHSAYASEK	20.93	671.37	876.48	80.1	37.6
31	FIHALLLAGTAHSAYASEK	18.21	667.36	766.41	79.8	37.4
32	FIHALLLAGTAHSAYASEK	18.21	667.36	801.93	79.8	37.4
33	FIHALLLAGTAHSAYASEK	18.21	667.36	870.46	79.8	37.4
34	FPLAALVFER	24.46	581.84	734.42	73.5	30.6
35	FPLAALVFER	24.46	581.84	805.46	73.5	30.6
36	FPLAALVFER	24.44	581.84	918.54	73.5	30.6
37	IDSGTER	1.66	389.19	462.23	59.5	22.1
38	IDSGTER	1.84	389.19	549.26	59.5	22.1
39	IDSGTER	1.75	389.19	664.29	59.5	22.1

40	IGDSVSR	8.48	367.20	448.25	57.9	21.2
41	IGDSVSR	8.46	367.20	563.28	57.9	21.2
42	IGDSVSR	8.44	367.20	620.30	57.9	21.2
43	LSAVER	9.1	337.70	403.23	55.7	19.9
44	LSAVER	9.08	337.70	474.27	55.7	19.9
45	LSAVER	9.1	337.70	561.30	55.7	19.9
46	LSYGPDMIVEWSPATER	22.31	650.98	573.30	78.6	36.5
47	LSYGPDMIVEWSPATER	22.29	650.98	660.33	78.6	36.5
48	LSYGPDMIVEWSPATER	22.26	650.98	846.41	78.6	36.5
49	LSYGPDMIVK	17.71	561.80	1009.50	72.1	29.7
50	LSYGPDMIVK	17.69	561.80	759.41	72.1	29.7
51	LSYGPDMIVK	17.69	561.80	922.47	72.1	29.7
52	NDIGFFK	17.71	420.72	498.27	61.8	23.5
53	NDIGFFK	17.69	420.72	611.36	61.8	23.5
54	NDIGFFK	17.74	420.72	726.38	61.8	23.5
55	TDLEK	3.66	303.16	389.24	53.2	18.3
56	TDLEK	3.73	303.16	459.21	53.2	18.3
57	TDLEK	3.6	303.16	504.27	53.2	18.3
58	TGACANGAR	1.48	439.20	648.29	63.1	24.3
59	TGACANGAR	1.48	439.20	719.33	63.1	24.3
60	TGACANGAR	1.48	439.20	776.35	63.1	24.3
61	TGTCANGAR	1.48	454.21	648.29	64.2	25
62	TGTCANGAR	1.48	454.21	749.34	64.2	25
63	TGTCANGAR	1.48	454.21	806.36	64.2	25
64	TGTCANGGR	1.48	447.20	474.24	63.7	24.7
65	TGTCANGGR	1.48	447.20	634.27	63.7	24.7
66	TGTCANGGR	1.48	447.20	735.32	63.7	24.7
67	VLYGGALTSTSTHTIER	15.87	602.65	1245.64	75.1	34.1
68	VLYGGALTSTSTHTIER	15.85	602.65	715.87	75.1	34.1
69	VLYGGALTSTSTHTIER	15.87	602.65	797.40	75.1	34.1
70	WLIGNQTGDATLR	18.93	722.88	1032.51	83.8	36.8
71	WLIGNQTGDATLR	19.02	722.88	1145.59	83.8	36.8
72	WLIGNQTGDATLR	18.96	722.88	733.38	83.8	36.8
73	WSPATER	11.37	423.71	476.25	62	23.6
74	WSPATER	11.37	423.71	573.30	62	23.6
75	WSPATER	11.34	423.71	660.33	62	23.6

- The other machine parameters used are as follows:

Scan type: MRM

MRM planned: yes

Polarity: Positive

Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	40.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated
Entry potential before Q0 (EP):	10.00 V
Collision cell exit potential (CXP):	15.00 V

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 16**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 17**. When a transition has an area less than the positivity threshold described in **TABLE 16**, the transition is considered non-detected and is labelled "0" in **TABLE 17**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 17:

Transition number	Sam89	Sam90
1	0	0
2	0	0
3	0	0
4	0	0
5	1	1
6	0	0
7	1	1
8	1	1
9	1	1
10	1	1
11	1	1

12	1	1
13	0	0
14	0	0
15	0	0
16	0	0
17	0	0
18	0	0
19	0	0
20	0	0
21	0	0
22	0	0
23	0	0
24	0	0
25	0	0
26	0	0
27	0	0
28	0	0
29	0	0
30	0	0
31	0	0
32	0	0
33	0	0
34	0	0
35	0	0
36	0	0
37	1	1
38	1	1
39	1	1
40	1	1
41	1	1
42	1	1
43	1	1
44	1	1
45	1	1
46	1	1
47	1	1
48	1	1
49	0	0
50	0	0
51	0	0
52	1	1
53	1	1
54	1	1
55	0	0
56	0	0

57	0	0
58	0	0
59	0	0
60	0	0
61	0	0
62	0	0
63	0	0
64	1	0
65	0	1
66	1	1
67	1	1
68	1	1
69	1	1
70	1	1
71	1	1
72	1	1
73	0	0
74	0	0
75	0	0

Samples Sam89 and Sam90 comprise at least one peptide which is characteristic of the carbapenemase phenotype. The bacteria present in samples Sam89 to Sam90 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins and to carbapenems.

Example 11: Identification of a resistance to SME beta-lactams:

Samples Sam91 to Sam95 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 18**.

TABLE 18:

Names	Species
Sam91	*S. marcescens*
Sam92	*S. marcescens*
Sam93	*S. marcescens*
Sam94	*S. marcescens*
Sam95	*S. marcescens*

Samples Sam91 to Sam95 correspond to a species able to comprise an SME resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 19** instead of the peptides from **TABLE 3**.

TABLE 19:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	positivity threshold
1	AIYQNWLK	18.69	518.29	426.22	25.3	2500
2	AIYQNWLK	18.69	518.29	688.38	25.3	2500
3	AIYQNWLK	18.69	518.29	851.44	25.3	2500
4	APLIVSIYTTR	20.21	617.36	740.39	30.9	2500
5	APLIVSIYTTR	20.21	617.36	839.46	30.9	2500
6	APLIVSIYTTR	20.21	617.36	952.55	30.9	2500
7	ASVPADWVVGDK	17.56	622.32	493.75	31.2	2500
8	ASVPADWVVGDK	17.56	622.32	543.29	31.2	2500
9	ASVPADWVVGDK	17.56	622.32	986.49	31.2	2500
10	AVANSLNK	8.75	408.73	461.27	19	2500
11	AVANSLNK	8.75	408.73	575.32	19	2500
12	AVANSLNK	8.75	408.73	646.35	19	2500
13	DLEYHSPITTK	14.48	435.22	473.75	20.6	2500
14	DLEYHSPITTK	14.48	435.22	538.28	20.6	2500
15	DLEYHSPITTK	14.48	435.22	646.38	20.6	2500
16	DLEYYSPITTK	17.4	665.33	559.35	33.7	2500
17	DLEYYSPITTK	17.4	665.33	646.38	33.7	2500
18	DLEYYSPITTK	17.4	665.33	809.44	33.7	2500
19	DTSTPK	1.45	324.66	345.21	14.2	2500
20	DTSTPK	1.45	324.66	432.25	14.2	2500
21	DTSTPK	1.45	324.66	533.29	14.2	2500
22	FLGGPEGMTK	14.94	518.76	662.32	25.3	2500
23	FLGGPEGMTK	14.94	518.76	719.34	25.3	2500
24	FLGGPEGMTK	14.94	518.76	776.36	25.3	2500
25	GFLAAAVLER	20.49	523.80	587.35	25.6	2500
26	GFLAAAVLER	20.49	523.80	658.39	25.6	2500
27	GFLAAAVLER	20.49	523.80	729.43	25.6	2500
28	GNTTGDAR	6.45	396.19	418.20	18.3	2500
29	GNTTGDAR	6.45	396.19	519.25	18.3	2500
30	GNTTGDAR	6.45	396.19	620.30	18.3	2500
31	IGVFAIDTGSGNTFGYR	21.45	592.30	542.27	25.4	2500
32	IGVFAIDTGSGNTFGYR	21.45	887.94	1174.51	46.3	2500
33	IGVFAIDTGSGNTFGYR	21.45	887.94	958.44	46.3	2500
34	LALGNVLNAK	18.56	506.81	414.75	24.6	2500
35	LALGNVLNAK	18.56	506.81	715.41	24.6	2500
36	LALGNVLNAK	18.56	506.81	828.49	24.6	2500

37	LDINQK	10.3	365.71	389.21	16.6	2500
38	LDINQK	10.3	365.71	502.30	16.6	2500
39	LDINQK	10.3	365.71	617.33	16.6	2500
40	LEEDFDGR	12.51	490.72	609.26	23.7	2500
41	LEEDFDGR	12.51	490.72	738.31	23.7	2500
42	LEEDFDGR	12.51	490.72	867.35	23.7	2500
43	SDAAAK	7.06	281.65	289.19	11.8	2500
44	SDAAAK	7.06	281.65	360.22	11.8	2500
45	SDAAAK	7.06	281.65	475.25	11.8	2500
46	SIGDNEFR	12.81	469.22	565.27	22.5	2500
47	SIGDNEFR	12.81	469.22	680.30	22.5	2500
48	SIGDNEFR	12.81	469.22	737.32	22.5	2500
49	TGSCGAIGTANDYAVIWPK	20.29	660.99	430.25	27.6	2500
50	TGSCGAIGTANDYAVIWPK	20.29	660.99	713.43	27.6	2500
51	TGSCGAIGTANDYAVIWPK	20.29	990.98	430.25	52.2	2500
52	TGSCGAYGTANDYAVIWPK	19.78	1015.97	430.25	53.6	2500
53	TGSCGAYGTANDYAVIWPK	19.78	677.65	642.40	28.1	2500
54	TGSCGAYGTANDYAVIWPK	19.78	677.65	713.43	28.1	2500
55	TIAEASR	6.98	374.20	333.19	17.1	2500
56	TIAEASR	6.98	374.20	462.23	17.1	2500
57	TIAEASR	6.98	374.20	646.35	17.1	2500
58	WELELNTAIPGDK	21.06	495.92	416.21	22.5	2500
59	WELELNTAIPGDK	21.06	743.38	1170.64	38.1	2500
60	WELELNTAIPGDK	21.06	743.38	416.21	38.1	2500

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	yes
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	40.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi

Dynamic filling:	activated
Declustering potential (DP):	100.00 V
Entry potential before Q0 (EP):	10.00 V
Collision cell exit potential (CXP):	15.00 V

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 19**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 20**. When a transition has an area less than the positivity threshold described in **TABLE 19**, the transition is considered non-detected and is labelled "0" in **TABLE 20**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 20:

Transition number	Sam91	Sam92	Sam93	Sam94	Sam95
1	0	1	0	0	0
2	1	1	0	0	1
3	0	1	0	0	0
4	0	0	0	0	0
5	0	0	0	0	0
6	0	0	0	0	0
7	1	1	1	1	1
8	1	1	1	1	1
9	1	1	1	1	1
10	1	1	1	1	1
11	1	1	1	1	1
12	1	1	1	1	1
13	1	1	1	1	1
14	1	1	1	1	1
15	1	1	1	1	1
16	0	0	0	0	0
17	0	0	0	0	0
18	0	0	0	0	0
19	0	0	0	0	0
20	0	0	0	0	0
21	0	0	0	0	0
22	1	1	1	0	1
23	1	1	1	0	1
24	1	1	1	0	1

25	1	1	1	1	1
26	1	1	1	1	1
27	1	1	1	1	1
28	0	0	0	0	0
29	0	0	0	0	0
30	0	0	0	0	0
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	1	1	1	1	1
35	1	1	1	1	1
36	1	1	1	1	1
37	0	0	0	0	0
38	0	0	0	0	0
39	0	0	0	0	0
40	1	1	1	0	1
41	1	1	1	0	1
42	1	1	1	0	1
43	0	0	0	0	0
44	0	0	0	0	0
45	0	0	0	0	0
46	0	0	1	0	0
47	0	0	1	0	0
48	0	0	1	0	0
49	0	0	0	0	0
50	0	0	0	0	0
51	0	0	0	0	0
52	0	0	0	0	0
53	0	0	0	0	0
54	0	0	0	0	0
55	0	0	0	0	0
56	0	0	0	0	0
57	0	0	0	0	0
58	0	0	0	0	0
59	0	0	0	0	0
60	0	0	0	0	0

Samples Sam91 to Sam95 comprise at least one peptide which is characteristic of SMEs. The bacteria present in samples Sam91 to Sam95 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins and to carbapenems.

Example 12: Identification of a resistance to IMP beta-lactams:

The samples corresponding to a species able to comprise an IMP resistance mechanism can be detected by employing the following method.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 21** instead of the peptides from **TABLE 3**.

TABLE 21:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	EVNGWGVVPK	16.02	542.79	742.35	29
2	EVNGWGVVPK	16.02	542.79	856.47	29
3	EVNGWGVVPK	16.02	542.79	955.54	29
4	GSISSHFHSDSTGGIGWLNSR	16.97	551.26	675.36	31
5	GSISSHFHSDSTGGIGWLNSR	16.97	551.26	732.38	31
6	GSISSHFHSDSTGGIGWLNSR	16.97	734.68	959.51	41
7	HGLVILVNTDAYLIDTPFTAK	24.53	767.75	892.48	42
8	HGLVILVNTDAYLIDTPFTAK	24.53	767.75	1005.56	42
9	HGLVILVNTDAYLIDTPFTAK	24.53	767.75	1133.63	42
10	HGLVVLVNNDAYLIDTPFTNK	22.75	781.75	822.4	43
11	HGLVVLVNNDAYLIDTPFTNK	22.75	781.75	935.48	43
12	HGLVVLVNNDAYLIDTPFTNK	22.75	781.75	1132.61	43
13	HGLVVLVNTDAYLIDTPFTAK	23.91	763.08	779.39	42
14	HGLVVLVNTDAYLIDTPFTAK	23.91	763.08	892.48	42
15	HGLVVLVNTDAYLIDTPFTAK	23.91	763.08	1119.62	42
16	HGLVVLVNTEAYLIDTPFTAK	24.53	767.75	779.39	42
17	HGLVVLVNTEAYLIDTPFTAK	24.53	767.75	892.48	42
18	HGLVVLVNTEAYLIDTPFTAK	24.53	767.75	1133.63	42
19	IEVFYPGPGHTQDNVVVWLPK	22.25	599.57	642.4	33
20	IEVFYPGPGHTQDNVVVWLPK	22.25	599.57	741.47	33
21	IEVFYPGPGHTQDNVVVWLPK	22.25	799.09	872.46	44
22	ILMEK	11.28	317.19	407.2	19
23	ILMEK	11.28	317.19	487.26	19
24	ILMEK	11.28	317.19	520.28	19
25	ILMSK	10.48	296.18	365.19	18
26	ILMSK	10.48	296.18	445.25	18
27	ILMSK	10.48	296.18	478.27	18
28	LDEGVYVHTSFK	15.03	465.57	482.26	27
29	LDEGVYVHTSFK	15.03	465.57	619.32	27
30	LDEGVYVHTSFK	15.03	465.57	881.45	27
31	LEEGVYVHTSYEEVK	14.55	594.62	855.41	34
32	LEEGVYVHTSYEEVK	14.55	594.62	992.47	34
33	LEEGVYVHTSYEEVK	14.55	891.43	992.47	44
34	LLISK	12.19	287.2	347.23	18

35	LLISK	12.19	287.2	427.29	18
36	LLISK	12.19	287.2	460.31	18
37	LLMSK	11.18	296.18	365.19	18
38	LLMSK	11.18	296.18	445.25	18
39	LLMSK	11.18	296.18	478.27	18
40	LLVSK	10.48	280.19	333.21	17
41	LLVSK	10.48	280.19	413.28	17
42	LLVSK	10.48	280.19	446.3	17
43	LPDLK	12.56	293.18	375.22	18
44	LPDLK	12.56	293.18	439.26	18
45	LPDLK	12.56	293.18	472.28	18
46	LVVSGHSETGDATHLK	11.41	413.47	569.34	24
47	LVVSGHSETGDATHLK	11.41	550.95	719.85	32
48	LVVSGHSETGDATHLK	11.41	550.95	1058.51	32
49	NSFDGVSYWLAK	20.75	693.84	767.41	36
50	NSFDGVSYWLAK	20.75	693.84	1038.53	36
51	NSFDGVSYWLAK	20.75	693.84	1185.59	36

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the three transitions of the same peptide are greater than or equal to 2500, the detection of the peptide is considered to be positive and is labelled "1". When at least one transition comprises an area less than 2500, the corresponding peptide is considered non-detected and is labelled "0".

Example 13: Identification of a resistance to KPC beta-lactams:

The samples corresponding to a species able to comprise a KPC resistance mechanism can be detected by employing the following method.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 22** instead of the peptides from **TABLE 3**.

TABLE 22:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	NALVR	8.14	286.68	387.27	18
2	NALVR	8.14	286.68	398.24	18
3	NALVR	8.14	286.68	458.31	18
4	TGTC[CAM]GAYGTANDYAVVWPTGR	18.76	739.67	1169.45	41
5	TGTC[CAM]GAYGTANDYAVVWPTGR	18.76	1109.01	1163.58	54
6	TGTC[CAM]GAYGTANDYAVVWPTGR	18.76	1109.01	1169.45	54
7	WELELNSAIPSDAR	20.43	534.27	545.27	31

8	WELELNSAIPSDAR	20.43	800.9	930.46	40
9	WELELNSAIPSDAR	20.43	800.9	1043.55	40
10	WELEMNSAIPGDAR	19.35	794.87	900.45	40
11	WELEMNSAIPGDAR	19.35	794.87	1031.49	40
12	WELEMNSAIPGDAR	19.35	794.87	1074.49	40

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the three transitions of the same peptide are greater than or equal to 2500, the detection of the peptide is considered to be positive and is labelled "1". When at least one transition comprises an area less than 2500, the corresponding peptide is considered non-detected and is labelled "0".

Example 14: Identification of a resistance to NDM beta-lactams:

The samples corresponding to a species able to comprise an NDM resistance mechanism can be detected by employing the following method.
Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 23** instead of the peptides from **TABLE 3**.

TABLE 23:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	VLLVDTAWTDDQTAQILNWIK	27.87	815.1	914.55	45
2	VLLVDTAWTDDQTAQILNWIK	27.86	815.1	985.58	45
3	VLLVDTAWTDDQTAQILNWIK	27.85	815.1	1086.63	45

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the three transitions of the same peptide are greater than or equal to 2500, the detection of the peptide is considered to be positive and is labelled "1". When at least one transition comprises an area less than 2500, the corresponding peptide is considered non-detected and is labelled "0".

Example 15: Identification of a resistance to VIM beta-lactams:

The samples corresponding to a species able to comprise a VIM resistance mechanism can be detected by employing the following method.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 24** instead of the peptides from **TABLE 3**.

TABLE 24:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	LANEIPTHSLEGLSSSGDAVR	16.72	718.37	778.37	40
2	LANEIPTHSLEGLSSSGDAVR	16.72	718.37	948.47	40
3	LANEIPTHSLEGLSSSGDAVR	16.72	718.37	1077.52	40

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the three transitions of the same peptide are greater than or equal to 2500, the detection of the peptide is considered to be positive and is labelled "1". When at least one transition comprises an area less than 2500, the corresponding peptide is considered non-detected and is labelled "0".

Example 16: Identification of a resistance to OXA beta-lactams:

The samples corresponding to a species able to comprise an OXA resistance mechanism can be detected by employing the following method.

Each sample is treated according to Example 5, then analysed according to Example 6 by detecting the peptides from **TABLE 25** instead of the peptides from **TABLE 3**.

TABLE 25:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)
1	AAAYELAENLFEAGQADGWR	24.48	728.01	1249.6	40
2	AAAYELAENLFEAGQADGWR	24.48	1091.51	1193.58	53
3	AAAYELAENLFEAGQADGWR	24.48	1091.51	1249.6	53
4	AAEGFIPASTFK	17.74	619.82	763.43	32
5	AAEGFIPASTFK	17.74	619.82	910.5	32
6	AAEGFIPASTFK	17.74	619.82	967.52	32
7	ADGQVVAFALNMQMK	21.27	811.91	982.48	41
8	ADGQVVAFALNMQMK	21.29	811.91	1053.52	41
9	ADGQVVAFALNMQMK	21.27	811.91	1152.59	41
10	ADINEIFK	17.3	475.25	650.35	26
11	ADINEIFK	17.3	475.25	763.43	26
12	ADINEIFK	17.3	475.25	878.46	26
13	ADWGK	6.9	288.64	390.21	18
14	ADWGK	6.91	288.64	430.17	18

15	ADWGK	6.89	288.64	505.24	18
16	AEGAIVISDER	13.52	387.2	419.19	23
17	AEGAIVISDER	13.53	387.2	506.22	23
18	AEGAIVISDER	13.52	387.2	619.3	23
19	AFALNLDIDK	20.16	560.31	717.38	30
20	AFALNLDIDK	20.16	560.31	830.46	30
21	AFALNLDIDK	20.16	560.31	901.5	30
22	AFAPMSTFK	16.96	500.25	710.35	27
23	AFAPMSTFK	16.96	500.25	781.39	27
24	AFAPMSTFK	16.96	500.25	928.46	27
25	AFGYGNADVSGDPGQNNGLDR	15.12	708.65	873.42	39
26	AFGYGNADVSGDPGQNNGLDR	15.12	708.65	970.47	39
27	AFGYGNADVSGDPGQNNGLDR	15.12	708.65	1154.47	39
28	AFTMTK	11.32	349.68	480.25	20
29	AFTMTK	11.33	349.68	552.25	20
30	AFTMTK	11.33	349.68	627.32	20
31	AGDDIALR	12.23	415.72	587.35	23
32	AGDDIALR	12.23	415.72	702.38	23
33	AGDDIALR	12.23	415.72	759.4	23
34	AGHVYAFALNIDMPR	20.63	558.95	631.32	32
35	AGHVYAFALNIDMPR	20.63	558.95	745.37	32
36	AGHVYAFALNIDMPR	20.63	558.95	817.4	32
37	AGLWR	13.44	301.67	361.2	18
38	AGLWR	13.44	301.67	474.28	18
39	AGLWR	13.44	301.67	531.3	18
40	AHTEYVPASTFK	13.18	450.89	553.3	27
41	AHTEYVPASTFK	13.18	450.89	602.26	27
42	AHTEYVPASTFK	13.18	450.89	650.35	27
43	AIIPWDGKPR	15.84	384.89	428.23	23
44	AIIPWDGKPR	15.84	384.89	457.29	23
45	AIIPWDGKPR	15.84	384.89	572.32	23
46	AISDITITR	14.8	495.28	603.38	27
47	AISDITITR	14.8	495.28	718.41	27
48	AISDITITR	14.8	495.28	805.44	27
49	ALGQDR	11.25	330.18	475.23	20
50	ALGQDR	11.25	330.18	485.24	20
51	ALGQDR	11.25	330.18	588.31	20
52	ALQAK	1.86	265.67	346.21	17
53	ALQAK	1.87	265.67	384.22	17
54	ALQAK	1.87	265.67	459.29	17
55	AMETFSPASTFK	17.06	658.81	737.38	34
56	AMETFSPASTFK	17.05	658.81	985.5	34
57	AMETFSPASTFK	17.06	658.81	1114.54	34
58	AMLFLQER	18.48	504.27	545.3	27
59	AMLFLQER	18.48	504.27	692.37	27

60	AMLFLQER	18.48	504.27	805.46	27
61	AMLVFDPVR	19.87	524.29	732.4	28
62	AMLVFDPVR	19.87	524.29	845.49	28
63	AMLVFDPVR	19.87	524.29	976.53	28
64	AMTLLESGPGWELHGK	19.32	575.96	923.47	33
65	AMTLLESGPGWELHGK	19.32	575.96	980.49	33
66	AMTLLESGPGWELHGK	19.32	575.96	1067.53	33
67	ANLHITLHGK	12.18	368.55	403.24	22
68	ANLHITLHGK	12.18	368.55	555.32	22
69	ANLHITLHGK	12.18	368.55	668.41	22
70	ANQLIVK	11.87	393.25	600.41	22
71	ANQLIVK	11.86	393.25	639.38	22
72	ANQLIVK	11.86	393.25	714.45	22
73	ANTEYVPASTFK	14.54	664.33	912.48	34
74	ANTEYVPASTFK	14.54	664.33	1041.53	34
75	ANTEYVPASTFK	14.54	664.33	1142.57	34
76	ANVSR	9.57	273.65	361.22	17
77	ANVSR	9.57	273.65	372.19	17
78	ANVSR	9.57	273.65	475.26	17
79	APIGWFIGWATR	25.58	687.87	850.46	35
80	APIGWFIGWATR	25.58	687.87	1093.56	35
81	APIGWFIGWATR	25.58	687.87	1206.64	35
82	APLGWFIGWATHEER	24.69	590.63	742.35	34
83	APLGWFIGWATHEER	24.69	590.63	985.45	34
84	APLGWFIGWATHEER	24.69	590.63	1098.53	34
85	AQDEVQSMLFIEEK	20.15	833.9	996.51	42
86	AQDEVQSMLFIEEK	20.14	833.9	1124.57	42
87	AQDEVQSMLFIEEK	20.15	833.9	1223.63	42
88	AQGVIVLWNENK	18.95	685.87	902.47	35
89	AQGVIVLWNENK	18.95	685.87	1015.56	35
90	AQGVIVLWNENK	18.95	685.87	1171.65	35
91	ASAIAVYQDLAR	18.05	639.35	765.39	33
92	ASAIAVYQDLAR	18.05	639.35	864.46	33
93	ASAIAVYQDLAR	18.05	639.35	935.49	33
94	ASAILVYQDLAR	19.08	660.37	765.39	34
95	ASAILVYQDLAR	19.08	660.37	864.46	34
96	ASAILVYQDLAR	19.08	660.37	977.54	34
97	ASAIPVYQDLAR	17.45	652.35	765.39	34
98	ASAIPVYQDLAR	17.45	652.35	864.46	34
99	ASAIPVYQDLAR	17.45	652.35	961.51	34
100	ASAIPVYQDLPR	17.59	665.36	791.4	34
101	ASAIPVYQDLPR	17.59	665.36	890.47	34
102	ASAIPVYQDLPR	17.6	665.36	987.53	34
103	ASAIQVYQDLAR	18.37	667.86	765.39	34
104	ASAIQVYQDLAR	18.37	667.86	864.46	34

105	ASAIQVYQDLAR	18.37	667.86	992.52	34
106	ASAISVYQDLAR	17.93	647.34	765.39	33
107	ASAISVYQDLAR	17.93	647.34	864.46	33
108	ASAISVYQDLAR	17.93	647.34	951.49	33
109	ASALPVYQDLAR	17.77	652.35	864.46	34
110	ASALPVYQDLAR	17.77	652.35	961.51	34
111	ASALPVYQDLAR	17.77	652.35	1074.59	34
112	ASAMPVYQDLAR	16.64	661.33	765.39	34
113	ASAMPVYQDLAR	16.64	661.33	864.46	34
114	ASAMPVYQDLAR	16.64	661.33	961.51	34
115	ASAVPVYQDLAR	16.29	645.35	765.39	33
116	ASAVPVYQDLAR	16.29	645.35	864.46	33
117	ASAVPVYQDLAR	16.29	645.35	961.51	33
118	ASIEYVPASTFK	16.7	656.84	749.42	34
119	ASIEYVPASTFK	16.7	656.84	912.48	34
120	ASIEYVPASTFK	16.7	656.84	1041.53	34
121	ASNVPVYQELAR	18.48	673.86	779.4	35
122	ASNVPVYQELAR	18.48	673.86	878.47	35
123	ASNVPVYQELAR	18.48	673.86	975.53	35
124	ASPASTFK	10.29	404.71	553.3	23
125	ASPASTFK	10.29	404.71	650.35	23
126	ASPASTFK	10.28	404.71	737.38	23
127	ASTAYIPASTFK	15.69	628.83	763.43	33
128	ASTAYIPASTFK	15.69	628.83	926.5	33
129	ASTAYIPASTFK	15.69	628.83	997.54	33
130	ASTEYVPASTFK	14.59	650.82	749.42	34
131	ASTEYVPASTFK	14.59	650.82	912.48	34
132	ASTEYVPASTFK	14.6	650.82	1041.53	34
133	ASTTEVFK	11.78	441.73	623.34	24
134	ASTTEVFK	11.78	441.73	724.39	24
135	ASTTEVFK	11.78	441.73	811.42	24
136	ATSTEIFK	13.15	448.74	637.36	25
137	ATSTEIFK	13.15	448.74	724.39	25
138	ATSTEIFK	13.15	448.74	825.44	25
139	ATTNEIFK	13.21	462.25	650.35	25
140	ATTNEIFK	13.21	462.25	751.4	25
141	ATTNEIFK	13.21	462.25	852.45	25
142	ATTTAVFK	11.9	419.74	464.29	23
143	ATTTAVFK	11.9	419.74	565.33	23
144	ATTTAVFK	11.9	419.74	666.38	23
145	ATTTEIFK	13.64	455.75	637.36	25
146	ATTTEIFK	13.65	455.75	738.4	25
147	ATTTEIFK	13.65	455.75	839.45	25
148	ATTTEVFK	11.98	448.74	623.34	25
149	ATTTEVFK	11.98	448.74	724.39	25

150	ATTTEVFK	11.98	448.74	825.44	25
151	AVSDITILEQTDNYTLHGK	19.19	706.7	974.49	39
152	AVSDITILEQTDNYTLHGK	19.19	706.7	1048.51	39
153	AVSDITILEQTDNYTLHGK	19.18	706.7	1176.56	39
154	AVSDITILEQTYNYTLHGK	22.29	722.71	995.49	40
155	AVSDITILEQTYNYTLHGK	22.29	722.71	998.5	40
156	AVSDITILEQTYNYTLHGK	22.28	722.71	1224.6	40
157	AVVPHFEAGDWDVQGK	17.81	585.62	743.34	33
158	AVVPHFEAGDWDVQGK	17.81	585.62	792.88	33
159	AVVPHFEAGDWDVQGK	17.81	585.62	904.42	33
160	AWEHDMSLR	13.99	572.76	758.36	30
161	AWEHDMSLR	13.99	572.76	887.4	30
162	AWEHDMSLR	13.99	572.76	1073.48	30
163	AWIGSSLQISPLEQLEFLGK	26.98	739.4	963.51	41
164	AWIGSSLQISPLEQLEFLGK	26.99	739.4	1173.65	41
165	AWIGSSLQISPLEQLEFLGK	26.98	1108.6	1173.65	54
166	DAFLK	12.42	297.17	407.27	18
167	DAFLK	12.43	297.17	447.22	18
168	DAFLK	12.42	297.17	478.3	18
169	DDFILHGK	13.99	472.75	714.43	26
170	DDFILHGK	13.99	472.75	798.38	26
171	DDFILHGK	13.99	472.75	829.46	26
172	DDVLK	8.62	295.16	359.27	18
173	DDVLK	8.63	295.16	443.21	18
174	DDVLK	8.62	295.16	474.29	18
175	DEFHVFR	15.39	475.23	705.38	26
176	DEFHVFR	15.39	475.23	775.34	26
177	DEFHVFR	15.39	475.23	834.43	26
178	DEFQIFR	19.02	477.74	520.2	26
179	DEFQIFR	19.02	477.74	563.33	26
180	DEFQIFR	19.02	477.74	710.4	26
181	DEFQVFR	17.29	470.73	549.31	26
182	DEFQVFR	17.28	470.73	619.27	26
183	DEFQVFR	17.29	470.73	696.38	26
184	DELVR	9.33	316.17	387.27	19
185	DELVR	9.35	316.17	457.23	19
186	DELVR	9.33	316.17	516.31	19
187	DFDYGNQDFSGDK	14.72	754.3	967.41	38
188	DFDYGNQDFSGDK	14.72	754.3	1130.47	38
189	DFDYGNQDFSGDK	14.72	754.3	1245.5	38
190	DFTLGEAMQASTVPVYQELAR	24.19	776.05	975.53	43
191	DFTLGEAMQASTVPVYQELAR	24.19	776.05	1074.59	43
192	DFTLGEAMQASTVPVYQELAR	24.19	1163.57	1175.64	56
193	DHDLITAMK	14.23	522.26	563.32	28
194	DHDLITAMK	14.23	522.26	695.34	28

195	DHDLITAMK	14.23	522.26	791.43	28
196	DIAAWNR	13.63	423.22	546.28	24
197	DIAAWNR	13.63	423.22	617.32	24
198	DIAAWNR	13.62	423.22	730.4	24
199	DILYIQELAGGWK	24.49	753.4	888.46	38
200	DILYIQELAGGWK	24.48	753.4	1001.54	38
201	DILYIQELAGGWK	24.49	753.4	1164.6	38
202	DITILEK	15.9	416.24	603.37	23
203	DITILEK	15.91	416.24	685.38	23
204	DITILEK	15.91	416.24	716.46	23
205	DLLSAK	12.45	323.69	429.23	19
206	DLLSAK	12.44	323.69	500.27	19
207	DLLSAK	12.45	323.69	531.35	19
208	DLMITEAGR	15.07	503.26	533.27	27
209	DLMITEAGR	15.07	503.26	646.35	27
210	DLMITEAGR	15.07	503.26	777.39	27
211	DLMIVEAGR	16.68	502.27	531.29	27
212	DLMIVEAGR	16.68	502.27	644.37	27
213	DLMIVEAGR	16.68	502.27	775.41	27
214	DLMIVEAK	16.23	459.75	473.24	25
215	DLMIVEAK	16.23	459.75	559.34	25
216	DLMIVEAK	16.23	459.75	690.39	25
217	DLSGNPGK	6.69	394.2	472.25	22
218	DLSGNPGK	6.69	394.2	559.28	22
219	DLSGNPGK	6.7	394.2	672.37	22
220	DLSLR	12.37	302.18	375.24	18
221	DLSLR	12.35	302.18	429.23	18
222	DLSLR	12.36	302.18	488.32	18
223	DLTLR	12.48	309.18	389.25	19
224	DLTLR	12.47	309.18	443.25	19
225	DLTLR	12.47	309.18	502.33	19
226	DMTLGDAIK	15.97	482.24	503.28	26
227	DMTLGDAIK	15.97	482.24	616.37	26
228	DMTLGDAIK	15.97	482.24	717.41	26
229	DMTLGDAMALSAVPVYQELAR	25.76	751.04	975.53	42
230	DMTLGDAMALSAVPVYQELAR	25.76	1126.06	1145.63	55
231	DMTLGDAMALSAVPVYQELAR	25.75	1126.06	1232.66	55
232	DMTLGDAMK	14.46	491.22	634.32	27
233	DMTLGDAMK	14.46	491.22	735.37	27
234	DMTLGDAMK	14.46	491.22	866.41	27
235	DMTLGEAMALSAVPVYQDLAR	25.92	751.04	961.51	42
236	DMTLGEAMALSAVPVYQDLAR	25.92	1126.06	1131.62	55
237	DMTLGEAMALSAVPVYQDLAR	25.92	1126.06	1218.65	55
238	DMTLGEAMALSAVPVYQELAR	26.48	755.71	779.4	42
239	DMTLGEAMALSAVPVYQELAR	26.48	755.71	975.53	42

240	DMTLGEAMALSAVPVYQELAR	26.47	1133.07	1232.66	55
241	DMTLGEAMK	15.09	498.23	535.25	27
242	DMTLGEAMK	15.09	498.23	648.34	27
243	DMTLGEAMK	15.09	498.23	749.39	27
244	DMTLGQAMQASAVPVYQELAR	23.29	760.38	779.4	42
245	DMTLGQAMQASAVPVYQELAR	23.29	760.38	975.53	42
246	DMTLGQAMQASAVPVYQELAR	23.29	760.38	976.42	42
247	DQDLR	2.54	323.66	403.23	19
248	DQDLR	2.55	323.66	472.2	19
249	DQDLR	2.55	323.66	531.29	19
250	DQQIGWFVGWASKPGK	21.64	601.98	830.45	34
251	DQQIGWFVGWASKPGK	21.64	902.46	929.52	45
252	DQQIGWFVGWASKPGK	21.64	902.46	1076.59	45
253	DQQVQVYGNDLNR	13.59	774.87	851.4	39
254	DQQVQVYGNDLNR	13.58	774.87	950.47	39
255	DQQVQVYGNDLNR	13.59	774.87	1078.53	39
256	DQTLESAFK	15.21	519.76	581.29	28
257	DQTLESAFK	15.21	519.76	694.38	28
258	DQTLESAFK	15.21	519.76	795.42	28
259	DSIVWYSQELTR	19.61	748.87	896.45	38
260	DSIVWYSQELTR	19.61	748.87	1082.53	38
261	DSIVWYSQELTR	19.61	748.87	1181.59	38
262	DSIVWYSQQLTR	19.1	748.38	895.46	38
263	DSIVWYSQQLTR	19.11	748.38	1081.54	38
264	DSIVWYSQQLTR	19.1	748.38	1180.61	38
265	DSNLR	1.77	302.66	402.25	18
266	DSNLR	1.77	302.66	430.19	18
267	DSNLR	1.77	302.66	489.28	18
268	DSYIAWGGEAWK	19.67	691.82	833.39	35
269	DSYIAWGGEAWK	19.67	691.82	904.43	35
270	DSYIAWGGEAWK	19.66	691.82	1017.52	35
271	DTLNPEWPYK	17.3	631.81	819.4	33
272	DTLNPEWPYK	17.3	631.81	933.45	33
273	DTLNPEWPYK	17.3	631.81	1046.53	33
274	DVDEVFYK	15.62	507.74	685.36	27
275	DVDEVFYK	15.62	507.74	800.38	27
276	DVDEVFYK	15.62	507.74	899.45	27
277	DWILR	17.44	351.7	415.2	20
278	DWILR	17.44	351.7	528.28	20
279	DWILR	17.44	351.7	587.37	20
280	EAFLR	12.51	318.18	435.27	19
281	EAFLR	12.51	318.18	461.24	19
282	EAFLR	12.51	318.18	506.31	19
283	EAIVR	7.84	294.18	387.27	18
284	EAIVR	7.84	294.18	413.24	18

285	EAIVR	7.84	294.18	458.31	18
286	EAIVTEATPEYIVHSK	16.43	596.31	746.42	34
287	EAIVTEATPEYIVHSK	16.43	596.31	972.51	34
288	EAIVTEATPEYIVHSK	16.42	596.31	1073.56	34
289	EALVTEAAPEYLVHSK	17.3	586.31	875.46	33
290	EALVTEAAPEYLVHSK	17.3	586.31	972.51	33
291	EALVTEAAPEYLVHSK	17.3	586.31	1114.59	33
292	EALVTEAPEYLVHSK	17.58	562.63	637.32	32
293	EALVTEAPEYLVHSK	17.58	562.63	972.51	32
294	EALVTEAPEYLVHSK	17.58	562.63	1043.55	32
295	EEIVR	8.41	323.18	387.27	19
296	EEIVR	8.4	323.18	471.24	19
297	EEIVR	8.4	323.18	516.31	19
298	EEVLAALPAQLK	19.48	641.37	740.47	33
299	EEVLAALPAQLK	19.47	641.37	811.5	33
300	EEVLAALPAQLK	19.47	641.37	924.59	33
301	EFSAEAVNGVFVLC[CAM]K	21.1	835.42	936.5	42
302	EFSAEAVNGVFVLC[CAM]K	21.1	835.42	1106.6	42
303	EFSAEAVNGVFVLC[CAM]K	21.1	835.42	1235.65	42
304	EFSSESVHGVFVLC[CAM]K	18.26	575.62	666.36	33
305	EFSSESVHGVFVLC[CAM]K	18.26	575.62	822.45	33
306	EFSSESVHGVFVLC[CAM]K	18.26	575.62	959.51	33
307	EGMSGSIR	9.88	418.7	432.26	23
308	EGMSGSIR	9.88	418.7	519.29	23
309	EGMSGSIR	9.88	418.7	707.35	23
310	EGMTGSIR	10.63	425.71	432.26	24
311	EGMTGSIR	10.63	425.71	533.3	24
312	EGMTGSIR	10.63	425.71	664.34	24
313	EIAVWNR	14.78	444.24	475.24	25
314	EIAVWNR	14.77	444.24	574.31	25
315	EIAVWNR	14.77	444.24	645.35	25
316	EIAYK	8.46	312.17	381.21	19
317	EIAYK	8.46	312.17	477.23	19
318	EIAYK	8.46	312.17	494.3	19
319	EIFER	11.7	347.18	451.23	20
320	EIFER	11.7	347.18	519.24	20
321	EIFER	11.7	347.18	564.31	20
322	EIFYHYR	13.31	514.25	785.37	28
323	EIFYHYR	13.31	514.25	853.39	28
324	EIFYHYR	13.32	514.25	898.46	28
325	EIGDDK	1.99	338.66	434.19	20
326	EIGDDK	1.99	338.66	530.21	20
327	EIGDDK	1.99	338.66	547.27	20
328	EIGDGK	1.76	309.66	376.18	19
329	EIGDGK	1.75	309.66	472.2	19

330	EIGDGK	1.75	309.66	489.27	19
331	EIGEDK	2.32	345.67	448.2	20
332	EIGEDK	2.33	345.67	544.22	20
333	EIGEDK	2.33	345.67	561.29	20
334	EIGEDNAR	10.05	452.21	604.27	25
335	EIGEDNAR	10.05	452.21	661.29	25
336	EIGEDNAR	10.06	452.21	774.37	25
337	EIGENK	1.86	345.18	447.22	20
338	EIGENK	1.86	345.18	543.24	20
339	EIGENK	1.86	345.18	560.3	20
340	EIGSEIDK	11.04	445.73	591.3	25
341	EIGSEIDK	11.04	445.73	648.32	25
342	EIGSEIDK	11.04	445.73	761.4	25
343	EMIYLK	15.11	398.72	536.34	23
344	EMIYLK	15.11	398.72	650.32	23
345	EMIYLK	15.11	398.72	667.38	23
346	EMLYVER	14.12	470.23	566.29	26
347	EMLYVER	14.12	470.23	679.38	26
348	EMLYVER	14.12	470.23	810.42	26
349	ENIEK	11.07	316.67	389.24	19
350	ENIEK	11.07	316.67	486.22	19
351	ENIEK	11.07	316.67	503.28	19
352	ENQLIVK	12.15	422.25	472.35	24
353	ENQLIVK	12.15	422.25	600.41	24
354	ENQLIVK	12.15	422.25	714.45	24
355	EQAILLFR	19.88	495.29	548.36	27
356	EQAILLFR	19.88	495.29	661.44	27
357	EQAILLFR	19.88	495.29	732.48	27
358	EQIQFLLR	19.45	523.8	548.36	28
359	EQIQFLLR	19.45	523.8	676.41	28
360	EQIQFLLR	19.45	523.8	789.5	28
361	EQLAFDPQVQQQVK	16.43	829.43	954.54	41
362	EQLAFDPQVQQQVK	16.42	829.43	1069.56	41
363	EQLAFDPQVQQQVK	16.42	829.43	1216.63	41
364	EQVDFVQR	13.09	510.76	549.31	27
365	EQVDFVQR	13.09	510.76	664.34	27
366	EQVDFVQR	13.09	510.76	763.41	27
367	EVGEIR	9.35	351.69	474.27	20
368	EVGEIR	9.35	351.69	528.27	20
369	EVGEIR	9.35	351.69	573.34	20
370	EVGEVR	6.91	344.68	460.25	20
371	EVGEVR	6.91	344.68	514.25	20
372	EVGEVR	6.91	344.68	559.32	20
373	EYLPASTFK	15.41	528.27	553.3	28
374	EYLPASTFK	15.41	528.27	650.35	28

375	EYLPASTFK	15.41	528.27	763.43	28
376	EYLPVSTFK	17.16	542.29	581.33	29
377	EYLPVSTFK	17.16	542.29	678.38	29
378	EYLPVSTFK	17.16	542.29	791.47	29
379	EYNTSGTFVFYDGK	18.2	814.37	1033.5	41
380	EYNTSGTFVFYDGK	18.2	814.37	1120.53	41
381	EYNTSGTFVFYDGK	18.2	814.37	1221.58	41
382	EYVPASTFK	13.89	521.27	553.3	28
383	EYVPASTFK	13.89	521.27	650.35	28
384	EYVPASTFK	13.89	521.27	749.42	28
385	FAPESTFK	13.67	463.73	482.26	25
386	FAPESTFK	13.67	463.73	611.3	25
387	FAPESTFK	13.67	463.73	708.36	25
388	FAQYAK	9.39	364.19	509.27	21
389	FAQYAK	9.39	364.19	580.31	21
390	FAQYAK	9.39	364.19	581.27	21
391	FDYGNR	10.1	386.17	509.25	22
392	FDYGNR	10.1	386.17	597.23	22
393	FDYGNR	10.09	386.17	624.27	22
394	FEDLYK	13.52	407.7	423.26	23
395	FEDLYK	13.52	407.7	538.29	23
396	FEDLYK	13.52	407.7	667.33	23
397	FEDTFHISNQK	14.33	455.89	476.25	27
398	FEDTFHISNQK	14.33	455.89	589.33	27
399	FEDTFHISNQK	14.33	455.89	726.39	27
400	FEDTFHTSNQQHEK	10.66	583.26	870.41	33
401	FEDTFHTSNQQHEK	10.66	583.26	971.45	33
402	FEDTFHTSNQQHEK	10.66	583.26	1108.51	33
403	FEYGNQDVSGDSGK	11.95	751.82	764.34	38
404	FEYGNQDVSGDSGK	11.95	751.82	1063.47	38
405	FEYGNQDVSGDSGK	11.95	751.82	1226.53	38
406	FFSDFQAK	16	495.24	608.3	27
407	FFSDFQAK	16	495.24	695.34	27
408	FFSDFQAK	16	495.24	842.4	27
409	FFSDLQAEGAIVIADER	20.44	627.65	1143.6	35
410	FFSDLQAEGAIVIADER	20.43	940.97	1143.6	46
411	FFSDLQAEGAIVIADER	20.44	940.97	1179.57	46
412	FFSDLR	15.38	392.7	490.26	22
413	FFSDLR	15.38	392.7	610.29	22
414	FFSDLR	15.38	392.7	637.33	22
415	FFSEFQAK	16.13	502.25	622.32	27
416	FFSEFQAK	16.13	502.25	709.35	27
417	FFSEFQAK	16.13	502.25	856.42	27
418	FGLEGQLR	15.8	460.25	473.28	25
419	FGLEGQLR	15.8	460.25	602.33	25

420	FGLEGQLR	15.8	460.25	772.43	25
421	FLESLYLNNLPASK	20.75	804.94	856.49	40
422	FLESLYLNNLPASK	20.75	804.94	1019.55	40
423	FLESLYLNNLPASK	20.75	804.94	1219.67	40
424	FLLEGQLR	18.06	488.28	602.33	26
425	FLLEGQLR	18.06	488.28	715.41	26
426	FLLEGQLR	18.06	488.28	828.49	26
427	FQQYVDR	11.19	478.24	552.28	26
428	FQQYVDR	11.19	478.24	680.34	26
429	FQQYVDR	11.19	478.24	808.39	26
430	FSDYVQR	11.83	457.72	565.31	25
431	FSDYVQR	11.83	457.72	680.34	25
432	FSDYVQR	11.83	457.72	767.37	25
433	FSTASTFK	12.71	444.73	553.3	25
434	FSTASTFK	12.7	444.73	654.35	25
435	FSTASTFK	12.7	444.73	741.38	25
436	FSWDGK	14.32	370.17	505.24	21
437	FSWDGK	14.32	370.17	592.27	21
438	FSWDGK	14.32	370.17	593.24	21
439	FSYGNQNISGGIDK	14.61	750.36	803.43	38
440	FSYGNQNISGGIDK	14.61	750.36	1045.53	38
441	FSYGNQNISGGIDK	14.61	750.36	1102.55	38
442	FSYGNQNISGGTDK	12.74	744.34	791.39	38
443	FSYGNQNISGGTDK	12.74	744.34	1033.49	38
444	FSYGNQNISGGTDK	12.74	744.34	1090.51	38
445	FSYGSQNISGGIDK	14.74	736.85	803.43	37
446	FSYGSQNISGGIDK	14.74	736.85	1075.54	37
447	FSYGSQNISGGIDK	14.75	736.85	1238.6	37
448	FTEYVK	11.81	393.71	538.29	22
449	FTEYVK	11.81	393.71	639.33	22
450	FTEYVK	11.81	393.71	640.3	22
451	FVPASTYK	11.76	456.74	498.26	25
452	FVPASTYK	11.76	456.74	569.29	25
453	FVPASTYK	11.77	456.74	666.35	25
454	FVYDLAQGQLPFKPEVQQQVK	20.48	821.44	955.52	45
455	FVYDLAQGQLPFKPEVQQQVK	20.48	821.44	1108.59	45
456	FVYDLAQGQLPFKPEVQQQVK	20.49	821.44	1109.07	45
457	FWLEDQLR	20.39	553.79	660.33	29
458	FWLEDQLR	20.39	553.79	773.42	29
459	FWLEDQLR	20.38	553.79	959.49	29
460	FWLEGPLK	20.63	495.28	543.31	27
461	FWLEGPLK	20.63	495.28	656.4	27
462	FWLEGPLK	20.63	495.28	842.48	27
463	FWLEGQLR	19.49	524.78	602.33	28
464	FWLEGQLR	19.49	524.78	715.41	28

465	FWLEGQLR	19.48	524.78	901.49	28
466	FYPASSFK	14.74	473.74	636.34	26
467	FYPASSFK	14.74	473.74	799.4	26
468	FYPASSFK	14.74	473.74	800.36	26
469	FYPASTFK	14.98	480.74	553.3	26
470	FYPASTFK	14.99	480.74	650.35	26
471	FYPASTFK	14.98	480.74	813.41	26
472	GAIQVSAVPVFQQIAR	21.6	842.48	958.55	42
473	GAIQVSAVPVFQQIAR	21.6	842.48	1057.62	42
474	GAIQVSAVPVFQQIAR	21.59	842.48	1128.65	42
475	GAIQVSAVPVFQQITR	21.52	857.49	988.56	43
476	GAIQVSAVPVFQQITR	21.51	857.49	1087.63	43
477	GAIQVSAVPVFQQITR	21.52	857.49	1158.66	43
478	GELPVSEDALEMTK	18.1	759.87	936.43	38
479	GELPVSEDALEMTK	18.11	759.87	1023.47	38
480	GELPVSEDALEMTK	18.11	759.87	1122.53	38
481	GISSSVR	8.65	353.2	448.25	21
482	GISSSVR	8.65	353.2	535.28	21
483	GISSSVR	8.67	353.2	648.37	21
484	GNQTLVFAR	14.83	503.28	605.38	27
485	GNQTLVFAR	14.83	503.28	706.42	27
486	GNQTLVFAR	14.83	503.28	834.48	27
487	GPLEISAFEEAR	18.95	659.84	809.38	34
488	GPLEISAFEEAR	18.94	659.84	922.46	34
489	GPLEISAFEEAR	18.94	659.84	1051.51	34
490	GPLTITPIQEVK	18.14	648.38	814.47	34
491	GPLTITPIQEVK	18.15	648.38	927.55	34
492	GPLTITPIQEVK	18.14	648.38	1028.6	34
493	GSLLLWDQK	19.61	530.3	576.28	28
494	GSLLLWDQK	19.61	530.3	689.36	28
495	GSLLLWDQK	19.61	530.3	802.45	28
496	GTFVLYDVQR	17.93	599.32	680.34	31
497	GTFVLYDVQR	17.93	599.32	793.42	31
498	GTFVLYDVQR	17.93	599.32	892.49	31
499	GTIVVADER	11.82	480.26	490.23	26
500	GTIVVADER	11.82	480.26	589.29	26
501	GTIVVADER	11.82	480.26	688.36	26
502	GTIVVLDAR	15.77	472.28	573.34	26
503	GTIVVLDAR	15.77	472.28	672.4	26
504	GTIVVLDAR	15.77	472.28	785.49	26
505	GTIVVVDER	13.6	494.28	518.26	27
506	GTIVVVDER	13.6	494.28	617.33	27
507	GTIVVVDER	13.6	494.28	716.39	27
508	GTLPFSAR	14.96	424.73	577.31	24
509	GTLPFSAR	14.96	424.73	690.39	24

510	GTLPFSAR	14.97	424.73	791.44	24
511	HIADSK	11.91	335.68	420.21	20
512	HIADSK	11.9	335.68	524.25	20
513	HIADSK	11.91	335.68	533.29	20
514	HNGTDGAWIISSLR	19.36	509.6	575.35	29
515	HNGTDGAWIISSLR	19.35	509.6	653.26	29
516	HNGTDGAWIISSLR	19.36	509.6	688.44	29
517	HTLSVFDQER	14.25	411.21	432.22	25
518	HTLSVFDQER	14.25	411.21	547.25	25
519	HTLSVFDQER	14.25	411.21	694.32	25
520	HVTFASFR	14.36	322.17	338.18	20
521	HVTFASFR	14.36	322.17	409.22	20
522	HVTFASFR	14.36	322.17	485.25	20
523	IAISLMGYDAGFLR	23.93	763.91	898.44	39
524	IAISLMGYDAGFLR	23.93	763.91	1029.48	39
525	IAISLMGYDAGFLR	23.94	763.91	1229.6	39
526	IALSLMGFDSGILK	24.91	732.91	836.45	37
527	IALSLMGFDSGILK	24.91	732.91	967.49	37
528	IALSLMGFDSGILK	24.91	732.91	1167.61	37
529	IANALIGLENHK	15.95	431.58	697.36	26
530	IANALIGLENHK	15.95	646.87	697.36	33
531	IANALIGLENHK	15.95	646.87	810.45	33
532	IDTFWLDNSLK	21.79	676.35	689.38	35
533	IDTFWLDNSLK	21.79	676.35	875.46	35
534	IDTFWLDNSLK	21.79	676.35	1123.58	35
535	IDYYNLDR	14.85	536.26	680.34	29
536	IDYYNLDR	14.85	536.26	843.4	29
537	IDYYNLDR	14.85	536.26	958.43	29
538	IFNALIALDSGVIK	24.74	737.44	802.47	37
539	IFNALIALDSGVIK	24.74	737.44	915.55	37
540	IFNALIALDSGVIK	24.74	737.44	1028.64	37
541	IFNSLLALDSGALDNER	22.76	924.48	976.43	46
542	IFNSLLALDSGALDNER	22.77	924.48	1089.52	46
543	IFNSLLALDSGALDNER	22.76	924.48	1160.55	46
544	IFNTLIGLENGIVK	23.29	765.95	829.48	39
545	IFNTLIGLENGIVK	23.3	765.95	942.56	39
546	IFNTLIGLENGIVK	23.3	765.95	1055.65	39
547	IGLDLMQK	17.7	459.26	634.32	25
548	IGLDLMQK	17.7	459.26	747.41	25
549	IGLDLMQK	17.7	459.26	804.43	25
550	IGLEK	8.54	280.18	389.24	17
551	IGLEK	8.55	280.18	413.24	17
552	IGLEK	8.54	280.18	446.26	17
553	IGLELMQQEVQR	18.73	722.38	787.41	37
554	IGLELMQQEVQR	18.73	722.38	918.45	37

555	IGLELMQQEVQR	18.73	722.38	1031.53	37
556	IGLELMSK	17.52	445.75	478.27	25
557	IGLELMSK	17.52	445.75	720.4	25
558	IGLELMSK	17.52	445.75	777.42	25
559	IGLELMSNEVK	18.73	616.83	707.34	32
560	IGLELMSNEVK	18.73	616.83	820.42	32
561	IGLELMSNEVK	18.73	616.83	949.47	32
562	IGLER	10.96	294.18	304.16	18
563	IGLER	10.96	294.18	417.25	18
564	IGLER	10.96	294.18	474.27	18
565	IGLNK	9.59	272.68	374.24	17
566	IGLNK	9.59	272.68	398.24	17
567	IGLNK	9.59	272.68	431.26	17
568	IGLNLMQK	17.1	458.77	633.34	25
569	IGLNLMQK	17.09	458.77	746.42	25
570	IGLNLMQK	17.11	458.77	803.44	25
571	IGPSLMQSELQR	17.02	679.86	760.39	35
572	IGPSLMQSELQR	17.02	679.86	891.44	35
573	IGPSLMQSELQR	17.02	679.86	1188.6	35
574	IGYGNMQIGTEVDQFWLK	24.31	700.35	935.5	39
575	IGYGNMQIGTEVDQFWLK	24.32	1050.02	1164.54	51
576	IGYGNMQIGTEVDQFWLK	24.3	1050.02	1222.61	51
577	IINHNLPVK	11.88	349.88	456.32	21
578	IINHNLPVK	11.88	349.88	570.36	21
579	IINHNLPVK	11.88	349.88	592.32	21
580	IINHNLPVR	12.04	359.22	598.37	22
581	IINHNLPVR	12.04	538.32	598.37	29
582	IINHNLPVR	12.04	538.32	849.47	29
583	ILFQQGTQQAC[CAM]AER	14.51	550.61	606.27	32
584	ILFQQGTQQAC[CAM]AER	14.51	825.41	1020.45	41
585	ILFQQGTQQAC[CAM]AER	14.51	825.41	1148.51	41
586	ILNNWFK	18.98	467.76	594.3	26
587	ILNNWFK	18.98	467.76	708.35	26
588	ILNNWFK	18.97	467.76	821.43	26
589	ILNTLISLEEK	19.98	636.87	718.4	33
590	ILNTLISLEEK	19.98	636.87	1046.57	33
591	ILNTLISLEEK	19.98	636.87	1159.66	33
592	INIVK	11.43	293.7	359.27	18
593	INIVK	11.43	293.7	440.29	18
594	INIVK	11.43	293.7	473.31	18
595	INLYGNALSR	16.05	560.81	617.34	30
596	INLYGNALSR	16.05	560.81	780.4	30
597	INLYGNALSR	16.05	560.81	893.48	30
598	IPFSLNLEMK	21.68	596.33	834.44	31
599	IPFSLNLEMK	21.67	596.33	981.51	31

600	IPFSLNLEMK	21.67	596.33	1078.56	31
601	IPHTLFALDADAVR	20	513.62	531.29	30
602	IPHTLFALDADAVR	20	513.62	646.32	30
603	IPHTLFALDADAVR	20	769.92	1191.64	39
604	IPHTLFALDAGAAR	18.58	726.9	744.4	37
605	IPHTLFALDAGAAR	18.58	726.9	891.47	37
606	IPHTLFALDAGAAR	18.58	726.9	1004.55	37
607	IPHTLFALDAGAVR	19.72	494.28	588.31	29
608	IPHTLFALDAGAVR	19.71	494.28	780.44	29
609	IPHTLFALDAGAVR	19.72	740.92	1133.63	38
610	IPNAIIGLETGVIK	21.75	719.44	816.48	37
611	IPNAIIGLETGVIK	21.75	719.44	929.57	37
612	IPNAIIGLETGVIK	21.75	719.44	1227.73	37
613	IPNALIGLETGAIK	20.96	705.42	788.45	36
614	IPNALIGLETGAIK	20.96	705.42	901.54	36
615	IPNALIGLETGAIK	20.96	705.42	1014.62	36
616	IPNSLIAFDTGAVR	20.24	737.41	765.39	37
617	IPNSLIAFDTGAVR	20.24	737.41	836.43	37
618	IPNSLIAFDTGAVR	20.24	737.41	949.51	37
619	IPSAIIGLETGVIK	21.66	705.93	816.48	36
620	IPSAIIGLETGVIK	21.67	705.93	929.57	36
621	IPSAIIGLETGVIK	21.66	705.93	1200.72	36
622	ISAFNQVK	13.02	453.76	488.28	25
623	ISAFNQVK	13.02	453.76	706.39	25
624	ISAFNQVK	13.02	453.76	793.42	25
625	ISAHEQILFLR	18.28	442.92	548.36	26
626	ISAHEQILFLR	18.28	442.92	789.5	26
627	ISAHEQILFLR	18.28	663.88	918.54	34
628	ISAMEQTR	9.84	468.23	664.31	26
629	ISAMEQTR	9.84	468.23	735.35	26
630	ISAMEQTR	9.84	468.23	822.38	26
631	ISAMEQVK	11.65	453.24	634.32	25
632	ISAMEQVK	11.65	453.24	705.36	25
633	ISAMEQVK	11.65	453.24	792.39	25
634	ISATEQVAFLR	17.7	412.23	435.27	25
635	ISATEQVAFLR	17.71	412.23	506.31	25
636	ISATEQVAFLR	17.7	412.23	605.38	25
637	ISATQQIAFLR	18.58	624.36	747.45	32
638	ISATQQIAFLR	18.58	624.36	1047.59	32
639	ISATQQIAFLR	18.58	624.36	1134.63	32
640	ISAVNQVEFLESLFLNK	28.77	976.03	988.51	48
641	ISAVNQVEFLESLFLNK	28.77	976.03	1110.62	48
642	ISAVNQVEFLESLFLNK	28.77	976.03	1239.66	48
643	ISAVNQVK	10.32	429.76	488.28	24
644	ISAVNQVK	10.32	429.76	658.39	24

645	ISAVNQVK	10.32	429.76	745.42	24
646	ISPEEQIQFLR	18.87	680.37	933.52	35
647	ISPEEQIQFLR	18.87	680.37	1062.56	35
648	ISPEEQIQFLR	18.87	680.37	1159.61	35
649	ISPEEQVR	10.49	479.25	531.29	26
650	ISPEEQVR	10.49	479.25	660.33	26
651	ISPEEQVR	10.49	479.25	757.38	26
652	ISPEGQVR	9.86	443.24	459.27	25
653	ISPEGQVR	9.86	443.24	588.31	25
654	ISPEGQVR	9.86	443.24	685.36	25
655	ISPLEQLAFLR	24.02	643.88	876.49	33
656	ISPLEQLAFLR	24.01	643.88	989.58	33
657	ISPLEQLAFLR	24.02	643.88	1086.63	33
658	ITAFQQVDFLR	21.11	669.36	777.43	34
659	ITAFQQVDFLR	21.12	669.36	905.48	34
660	ITAFQQVDFLR	21.12	669.36	1123.59	34
661	ITPIQEVNFADDFANNR	21.25	655.32	736.34	37
662	ITPIQEVNFADDFANNR	21.25	655.32	851.36	37
663	ITPIQEVNFADDFANNR	21.25	655.32	922.4	37
664	ITPIQEVNFADDLANNR	20.95	643.99	817.38	36
665	ITPIQEVNFADDLANNR	20.95	965.49	1149.53	47
666	ITPIQEVNFADDLANNR	20.96	965.49	1248.6	47
667	ITPQQEAQFAYK	14.52	712.36	856.42	36
668	ITPQQEAQFAYK	14.52	712.36	984.48	36
669	ITPQQEAQFAYK	14.52	712.36	1209.59	36
670	ITPQQEAQFTYK	14.33	485.25	558.29	28
671	ITPQQEAQFTYK	14.33	727.37	1014.49	37
672	ITPQQEAQFTYK	14.33	727.37	1239.6	37
673	ITPVQEVNFADDLAHNR	18.98	646.99	840.4	36
674	ITPVQEVNFADDLAHNR	18.98	646.99	862.92	36
675	ITPVQEVNFADDLAHNR	18.98	646.99	911.43	36
676	IVAFALK	17.21	381.25	478.3	22
677	IVAFALK	17.22	381.25	549.34	22
678	IVAFALK	17.21	381.25	648.41	22
679	IVAFALNMEMR	17.95	647.84	864.41	34
680	IVAFALNMEMR	17.95	647.84	1011.48	34
681	IVAFALNMEMR	17.97	647.84	1082.51	34
682	IVESTTLADGTVVHGK	13.69	542.96	697.4	31
683	IVESTTLADGTVVHGK	13.69	542.96	812.43	31
684	IVESTTLADGTVVHGK	13.68	542.96	883.46	31
685	IYNSLIGLNEK	17.37	632.35	673.39	33
686	IYNSLIGLNEK	17.37	632.35	786.47	33
687	IYNSLIGLNEK	17.37	632.35	987.55	33
688	KPDIGWWVGWIER	24.47	547.96	660.35	31
689	KPDIGWWVGWIER	24.47	547.96	883.45	31

690	KPDIGWWVGWIER	24.46	821.43	1188.59	41
691	LAC[CAM]ATNNLAR	11.22	552.28	688.37	29
692	LAC[CAM]ATNNLAR	11.22	552.28	759.41	29
693	LAC[CAM]ATNNLAR	11.22	552.28	919.44	29
694	LAQGELPFPAPVQSTVR	19.84	905.5	954.54	45
695	LAQGELPFPAPVQSTVR	19.84	905.5	1101.61	45
696	LAQGELPFPAPVQSTVR	19.84	905.5	1198.66	45
697	LAQNELPYPIEIQK	19.09	828.45	929.47	41
698	LAQNELPYPIEIQK	19.09	828.45	987.55	41
699	LAQNELPYPIEIQK	19.08	828.45	1100.64	41
700	LAQNELQYPIEIQK	17.98	843.96	890.5	42
701	LAQNELQYPIEIQK	17.98	843.96	1018.56	42
702	LAQNELQYPIEIQK	17.98	843.96	1131.64	42
703	LDFGNK	11.75	347.18	465.25	20
704	LDFGNK	11.74	347.18	547.25	20
705	LDFGNK	11.75	347.18	580.27	20
706	LDGSLNR	9.48	387.71	402.25	22
707	LDGSLNR	9.48	387.71	546.3	22
708	LDGSLNR	9.48	387.71	661.33	22
709	LEILQQALAELGLYPK	29.81	900.02	1003.58	45
710	LEILQQALAELGLYPK	29.81	900.02	1074.62	45
711	LEILQQALAELGLYPK	29.81	900.02	1202.68	45
712	LENQEQVK	7.6	494.26	631.34	27
713	LENQEQVK	7.59	494.26	745.38	27
714	LENQEQVK	7.59	494.26	874.43	27
715	LETQEEVEK	9.88	552.77	633.31	29
716	LETQEEVEK	9.88	552.77	862.42	29
717	LETQEEVEK	9.88	552.77	991.46	29
718	LETQEEVK	9.5	488.25	504.27	26
719	LETQEEVK	9.49	488.25	733.37	26
720	LETQEEVK	9.49	488.25	862.42	26
721	LFAAEGVK	13.53	417.74	503.28	23
722	LFAAEGVK	13.53	417.74	574.32	23
723	LFAAEGVK	13.53	417.74	721.39	23
724	LFESAGVK	12.99	425.74	461.27	24
725	LFESAGVK	12.99	425.74	590.31	24
726	LFESAGVK	12.99	425.74	737.38	24
727	LFGAAGVK	13.94	381.73	445.28	22
728	LFGAAGVK	13.94	381.73	502.3	22
729	LFGAAGVK	13.94	381.73	649.37	22
730	LGVDR	8.51	280.16	290.15	17
731	LGVDR	8.51	280.16	389.21	17
732	LGVDR	8.5	280.16	446.24	17
733	LLNLLSQSK	17.97	508.31	562.32	27
734	LLNLLSQSK	17.97	508.31	789.45	27

735	LLNLLSQSK	17.97	508.31	902.53	27
736	LLQDER	9.34	387.21	547.25	22
737	LLQDER	9.31	387.21	599.3	22
738	LLQDER	9.34	387.21	660.33	22
739	LLVQDGDC[CAM]GR	11.92	566.77	679.25	30
740	LLVQDGDC[CAM]GR	11.92	566.77	807.3	30
741	LLVQDGDC[CAM]GR	11.92	566.77	906.37	30
742	LNEVGYGNR	10.74	511.26	566.27	27
743	LNEVGYGNR	10.74	511.26	665.34	27
744	LNEVGYGNR	10.73	511.26	794.38	27
745	LNYGNADPSTK	10.76	590.29	732.35	31
746	LNYGNADPSTK	10.76	590.29	789.37	31
747	LNYGNADPSTK	10.76	590.29	952.44	31
748	LNYGNK	7.21	354.69	481.24	21
749	LNYGNK	7.24	354.69	562.26	21
750	LNYGNK	7.22	354.69	595.28	21
751	LPASK	1.93	258.16	305.18	16
752	LPASK	1.93	258.16	369.21	16
753	LPASK	1.93	258.16	402.23	16
754	LPHTLFALDADAVR	19.98	769.92	977.51	39
755	LPHTLFALDADAVR	19.98	769.92	1090.59	39
756	LPHTLFALDADAVR	19.98	769.92	1191.64	39
757	LPHTLFALDAGAVR	19.7	740.92	919.5	38
758	LPHTLFALDAGAVR	19.67	740.92	1032.58	38
759	LPHTLFALDAGAVR	19.7	740.92	1133.63	38
760	LPLAIMGFDSGILQSPK	25.08	893.99	944.5	44
761	LPLAIMGFDSGILQSPK	25.08	893.99	1091.57	44
762	LPLAIMGFDSGILQSPK	25.08	893.99	1148.59	44
763	LPLAIMGYDADILLDATTPR	27.86	720.39	773.42	40
764	LPLAIMGYDADILLDATTPR	27.87	720.39	886.5	40
765	LPLAIMGYDADILLDATTPR	27.87	720.39	1160.57	40
766	LPSSLIALETGAVR	20.6	713.92	816.46	36
767	LPSSLIALETGAVR	20.6	713.92	929.54	36
768	LPSSLIALETGAVR	20.6	713.92	1216.69	36
769	LPVSAQTLQYTANILK	21.84	880.5	950.53	44
770	LPVSAQTLQYTANILK	21.84	880.5	1063.61	44
771	LPVSAQTLQYTANILK	21.85	880.5	1164.66	44
772	LPVSER	9.57	350.7	490.26	20
773	LPVSER	9.57	350.7	526.29	20
774	LPVSER	9.57	350.7	587.31	20
775	LPVSPTAVDMTER	16.21	708.36	1019.48	36
776	LPVSPTAVDMTER	16.21	708.36	1106.51	36
777	LPVSPTAVDMTER	16.21	708.36	1205.58	36
778	LSASK	10.72	253.15	305.18	16
779	LSASK	10.71	253.15	359.19	16

780	LSASK	10.71	253.15	392.21	16
781	LSAVPIYQEVAR	17.96	673.38	765.39	35
782	LSAVPIYQEVAR	17.96	673.38	975.53	35
783	LSAVPIYQEVAR	17.95	673.38	1074.59	35
784	LSAVPVYQELAR	18.45	449.25	616.34	26
785	LSAVPVYQELAR	18.44	673.38	779.4	35
786	LSAVPVYQELAR	18.44	673.38	975.53	35
787	LSC[CAM]TLVIDEASGDLLHR	20.38	633.66	797.43	36
788	LSC[CAM]TLVIDEASGDLLHR	20.38	633.66	868.46	36
789	LSC[CAM]TLVIDEASGDLLHR	20.38	633.66	1112.53	36
790	LSLQHGWFIGWIEK	23.95	571.98	632.34	33
791	LSLQHGWFIGWIEK	23.95	571.98	892.49	33
792	LSLQHGWFIGWIEK	23.95	571.98	969.49	33
793	LSQNSLPFSQEAMNSVK	18.64	627.31	1140.54	35
794	LSQNSLPFSQEAMNSVK	18.63	940.46	1140.54	46
795	LSQNSLPFSQEAMNSVK	18.64	940.46	1237.59	46
796	LSVNPK	9.8	329.2	457.28	19
797	LSVNPK	9.79	329.2	511.29	19
798	LSVNPK	9.8	329.2	544.31	19
799	LTVGAR	9.51	308.69	402.25	19
800	LTVGAR	9.51	308.69	442.27	19
801	LTVGAR	9.51	308.69	503.29	19
802	LYGFALNIDMPGGEADIGK	23.35	661	843.42	37
803	LYGFALNIDMPGGEADIGK	23.35	990.99	1089.49	49
804	LYGFALNIDMPGGEADIGK	23.35	990.99	1202.57	49
805	LYHNELPFR	15.29	396.88	414.21	24
806	LYHNELPFR	15.29	396.88	419.24	24
807	LYHNELPFR	15.29	396.88	657.3	24
808	LYHNK	8.54	337.68	414.21	20
809	LYHNK	8.53	337.68	528.26	20
810	LYHNK	8.53	337.68	561.28	20
811	LYQNDLPFR	17.2	583.3	761.39	31
812	LYQNDLPFR	17.2	583.3	889.45	31
813	LYQNDLPFR	17.2	583.3	1052.52	31
814	MDDLFK	15.5	384.68	522.29	22
815	MDDLFK	15.5	384.68	622.25	22
816	MDDLFK	15.5	384.68	637.32	22
817	MEDLHK	6.66	386.69	512.28	22
818	MEDLHK	6.65	386.69	626.26	22
819	MEDLHK	6.66	386.69	641.33	22
820	MLIALIGLENHK	21.33	451.26	527.26	27
821	MLIALIGLENHK	21.33	451.26	697.36	27
822	MLIALIGLENHK	21.33	451.26	810.45	27
823	MLLIK	15.81	309.21	373.28	19
824	MLLIK	15.81	309.21	471.3	19

825	MLLIK	15.81	309.21	486.36	19
826	MLNALIGLEHHK	16.89	459.26	550.27	27
827	MLNALIGLEHHK	16.89	459.26	720.38	27
828	MLNALIGLEHHK	16.89	459.26	833.46	27
829	MLNALIGLENHK	18.39	451.58	697.36	27
830	MLNALIGLENHK	18.38	676.87	697.36	35
831	MLNALIGLENHK	18.39	676.87	810.45	35
832	MLNALIGLENQK	19.71	672.37	688.36	35
833	MLNALIGLENQK	19.71	672.37	801.45	35
834	MLNALIGLENQK	19.71	672.37	914.53	35
835	MLNALIGLEYHK	19.6	701.38	746.38	36
836	MLNALIGLEYHK	19.6	701.38	859.47	36
837	MLNALIGLEYHK	19.6	701.38	1157.63	36
838	MLNALIGLQHGK	17.5	432.25	582.34	26
839	MLNALIGLQHGK	17.5	432.25	639.36	26
840	MLNALIGLQHGK	17.5	432.25	752.44	26
841	MLNALISLEHHK	17.2	352.2	359.17	21
842	MLNALISLEHHK	17.21	469.26	750.39	27
843	MLNALISLEHHK	17.2	469.26	863.47	27
844	MQAYVDAFDYGNR	17.56	775.34	957.41	39
845	MQAYVDAFDYGNR	17.56	775.34	1056.47	39
846	MQAYVDAFDYGNR	17.56	775.34	1219.54	39
847	MQEGLNK	8.68	410.21	560.3	23
848	MQEGLNK	8.66	410.21	673.3	23
849	MQEGLNK	8.68	410.21	688.36	23
850	MSPASTYK	9.49	442.71	569.29	24
851	MSPASTYK	9.49	442.71	666.35	24
852	MSPASTYK	9.49	442.71	753.38	24
853	NEHDPVLPYR	13.09	413.88	435.24	25
854	NEHDPVLPYR	13.09	620.31	744.44	32
855	NEHDPVLPYR	13.09	620.31	859.47	32
856	NEHQIFK	9.91	458.24	509.21	25
857	NEHQIFK	9.91	458.24	622.29	25
858	NEHQIFK	9.91	458.24	672.38	25
859	NEHQVFK	7.74	451.23	658.37	25
860	NEHQVFK	7.74	451.23	755.35	25
861	NEHQVFK	7.74	451.23	787.41	25
862	NEITYK	9.35	384.2	524.31	22
863	NEITYK	9.35	384.2	621.29	22
864	NEITYK	9.35	384.2	653.35	22
865	NELLMK	13.08	374.21	504.32	21
866	NELLMK	13.09	374.21	601.3	21
867	NELLMK	13.09	374.21	633.36	21
868	NELPFR	14.39	388.21	419.24	22
869	NELPFR	14.39	388.21	532.32	22

870	NELPFR	14.4	388.21	661.37	22
871	NISSYGNNLVR	14.36	618.82	835.44	32
872	NISSYGNNLVR	14.36	618.82	922.47	32
873	NISSYGNNLVR	14.36	618.82	1009.51	32
874	NISTYGNNLTR	13.1	626.82	674.36	33
875	NISTYGNNLTR	13.09	626.82	837.42	33
876	NISTYGNNLTR	13.1	626.82	1025.5	33
877	NLFNEVHTTGVLVIR	20.69	571.32	757.49	33
878	NLFNEVHTTGVLVIR	20.7	571.32	858.54	33
879	NLFNEVHTTGVLVIR	20.7	571.32	995.6	33
880	NLSTYGNALAR	14.34	590.31	764.4	31
881	NLSTYGNALAR	14.35	590.31	865.45	31
882	NLSTYGNALAR	14.35	590.31	952.48	31
883	NMENLELFGK	19.08	597.79	820.46	31
884	NMENLELFGK	19.08	597.79	949.5	31
885	NMENLELFGK	19.08	597.79	1080.54	31
886	NMLLLEENNGYK	16.71	719.36	853.37	37
887	NMLLLEENNGYK	16.69	719.36	966.45	37
888	NMLLLEENNGYK	16.68	719.36	1079.54	37
889	NMLLLEESNGYK	18.12	705.85	939.44	36
890	NMLLLEESNGYK	18.13	705.85	1052.53	36
891	NMLLLEESNGYK	18.11	705.85	1165.61	36
892	NMLLLEK	16.99	430.75	502.32	24
893	NMLLLEK	16.98	430.75	615.41	24
894	NMLLLEK	16.98	430.75	746.45	24
895	NMTLGDAMK	14.42	490.73	521.24	27
896	NMTLGDAMK	14.42	490.73	634.32	27
897	NMTLGDAMK	14.42	490.73	735.37	27
898	NNGLTEAWLESSLK	20.61	781.4	862.47	39
899	NNGLTEAWLESSLK	20.6	781.4	933.5	39
900	NNGLTEAWLESSLK	20.62	781.4	1163.59	39
901	NQLPFK	13.49	373.71	391.23	21
902	NQLPFK	13.49	373.71	504.32	21
903	NQLPFK	13.49	373.71	632.38	21
904	NQLPFQVEHQR	14.33	698.36	796.41	36
905	NQLPFQVEHQR	14.33	698.36	1040.53	36
906	NQLPFQVEHQR	14.33	698.36	1153.61	36
907	NSAIENTIDNMYLQDLENSTK	22.77	805.04	934.45	44
908	NSAIENTIDNMYLQDLENSTK	22.77	805.04	1047.53	44
909	NSAIENTIDNMYLQDLENSTK	22.77	805.04	1210.6	44
910	NSAIENTIENMYLQDLDNSTK	23.13	805.04	920.43	44
911	NSAIENTIENMYLQDLDNSTK	23.13	805.04	1033.52	44
912	NSAIENTIENMYLQDLDNSTK	23.14	805.04	1196.58	44
913	NSAIENTIENMYLQDLENSTK	23.7	809.72	934.45	44
914	NSAIENTIENMYLQDLENSTK	23.7	809.72	1047.53	44

915	NSAIENTIENMYLQDLENSTK	23.7	809.72	1217.55	44
916	NSAVWVYELFAK	24.66	713.87	869.48	36
917	NSAVWVYELFAK	24.66	713.87	1055.56	36
918	NSAVWVYELFAK	24.65	713.87	1154.62	36
919	NSQVPAYK	9.78	453.74	478.27	25
920	NSQVPAYK	9.78	453.74	577.33	25
921	NSQVPAYK	9.78	453.74	705.39	25
922	NSTVWIYELFAK	25.64	735.88	883.49	37
923	NSTVWIYELFAK	25.64	735.88	1069.57	37
924	NSTVWIYELFAK	25.64	735.88	1168.64	37
925	NSTVWVYELFAK	24.42	728.88	770.41	37
926	NSTVWVYELFAK	24.43	728.88	869.48	37
927	NSTVWVYELFAK	24.42	728.88	1055.56	37
928	NSTVWVYQLFAK	23.9	728.39	769.42	37
929	NSTVWVYQLFAK	23.91	728.39	1054.57	37
930	NSTVWVYQLFAK	23.91	728.39	1153.64	37
931	NTSGALVIQTDK	13.34	623.84	816.48	32
932	NTSGALVIQTDK	13.34	623.84	944.54	32
933	NTSGALVIQTDK	13.34	623.84	1031.57	32
934	NTSGVLVIQTDK	14.9	637.85	816.48	33
935	NTSGVLVIQTDK	14.9	637.85	972.57	33
936	NTSGVLVIQTDK	14.91	637.85	1059.6	33
937	NVDEMFYYYDGSK	18.86	815.84	895.38	41
938	NVDEMFYYYDGSK	18.86	815.84	1042.45	41
939	NVDEMFYYYDGSK	18.85	815.84	1173.49	41
940	NWILR	16.3	351.21	414.21	20
941	NWILR	16.29	351.21	527.3	20
942	NWILR	16.3	351.21	587.37	20
943	NWNAAMDLR	16.54	545.76	605.31	29
944	NWNAAMDLR	16.55	545.76	676.34	29
945	NWNAAMDLR	16.54	545.76	790.39	29
946	NYVDAFHYGNQDISGDK	15.76	648.29	933.43	36
947	NYVDAFHYGNQDISGDK	15.77	648.29	1096.49	36
948	NYVDAFHYGNQDISGDK	15.76	971.93	1233.55	48
949	QADHAILVFDQAR	16.58	495.26	523.23	29
950	QADHAILVFDQAR	16.61	495.26	636.31	29
951	QADHAILVFDQAR	16.58	495.26	735.38	29
952	QAEHALLVFGQER	16.86	499.93	636.31	29
953	QAEHALLVFGQER	16.85	499.93	735.38	29
954	QAEHALLVFGQER	16.87	499.93	763.41	29
955	QAITK	11	280.67	361.24	17
956	QAITK	11	280.67	414.23	17
957	QAITK	11.01	280.67	432.28	17
958	QAMLTEANSDYIIR	18.26	812.9	951.49	41
959	QAMLTEANSDYIIR	18.25	812.9	1080.53	41

960	QAMLTEANSDYIIR	18.26	812.9	1181.58	41
961	QEVQFVSALAR	17.69	624.34	763.45	32
962	QEVQFVSALAR	17.68	624.34	891.5	32
963	QEVQFVSALAR	17.68	624.34	990.57	32
964	QFASIK	11.66	347.2	434.2	20
965	QFASIK	11.66	347.2	547.29	20
966	QFASIK	11.68	347.2	565.33	20
967	QGMPGSIR	11.4	423.22	529.31	24
968	QGMPGSIR	11.43	423.22	660.35	24
969	QGMPGSIR	11.4	423.22	717.37	24
970	QGMSGSIR	9.44	418.21	519.29	23
971	QGMSGSIR	9.45	418.21	650.33	23
972	QGMSGSIR	9.44	418.21	707.35	23
973	QGQTQQSYGNDLAR	11.16	783.37	895.43	39
974	QGQTQQSYGNDLAR	11.17	783.37	1023.49	39
975	QGQTQQSYGNDLAR	11.16	783.37	1151.54	39
976	QIDYGNADPSTIK	13.41	711.35	845.44	36
977	QIDYGNADPSTIK	13.42	711.35	902.46	36
978	QIDYGNADPSTIK	13.42	711.35	1065.52	36
979	QIDYGNVDPSTIK	15.08	725.36	873.47	37
980	QIDYGNVDPSTIK	15.07	725.36	930.49	37
981	QIDYGNVDPSTIK	15.07	725.36	1093.55	37
982	QIGQAR	2.3	336.69	431.24	20
983	QIGQAR	2.33	336.69	498.27	20
984	QIGQAR	2.32	336.69	544.32	20
985	QIMLIEQTPAFTLR	24.42	830.96	933.52	42
986	QIMLIEQTPAFTLR	24.42	830.96	1062.56	42
987	QIMLIEQTPAFTLR	24.42	830.96	1175.64	42
988	QLGSAIDQFWLR	22.67	717.38	864.44	37
989	QLGSAIDQFWLR	22.68	717.38	977.52	37
990	QLGSAIDQFWLR	22.67	717.38	1192.61	37
991	QLPVK	9.57	292.69	343.23	18
992	QLPVK	9.58	292.69	438.27	18
993	QLPVK	9.57	292.69	456.32	18
994	QLSLDVLDK	18.63	515.79	589.32	28
995	QLSLDVLDK	18.62	515.79	789.44	28
996	QLSLDVLDK	18.63	515.79	902.52	28
997	QLVYAR	11.04	375.22	508.29	22
998	QLVYAR	11.04	375.22	575.32	22
999	QLVYAR	11.04	375.22	621.37	22
1000	QMMLTEASTDYIIR	19.82	836.41	867.46	42
1001	QMMLTEASTDYIIR	19.82	836.41	1067.54	42
1002	QMMLTEASTDYIIR	19.82	836.41	1168.58	42
1003	QMSIVEATPDYVLHGK	18.77	894.45	1029.54	44
1004	QMSIVEATPDYVLHGK	18.77	894.45	1100.57	44

1005	QMSIVEATPDYVLHGK	18.77	894.45	1229.62	44
1006	QTLVFAR	14.65	417.75	492.29	23
1007	QTLVFAR	14.65	417.75	605.38	23
1008	QTLVFAR	14.65	417.75	706.42	23
1009	QVVFAR	12.06	360.21	492.29	21
1010	QVVFAR	12.04	360.21	545.31	21
1011	QVVFAR	12.06	360.21	591.36	21
1012	SADEVLPYGGKPQR	12.96	506.26	642.37	29
1013	SADEVLPYGGKPQR	12.96	506.26	805.43	29
1014	SADEVLPYGGKPQR	12.96	506.26	902.48	29
1015	SC[CAM]ATNDLAR	9.37	504.23	689.36	27
1016	SC[CAM]ATNDLAR	9.37	504.23	760.39	27
1017	SC[CAM]ATNDLAR	9.37	504.23	920.43	27
1018	SC[CAM]ATNNLAR	8.66	503.74	688.37	27
1019	SC[CAM]ATNNLAR	8.66	503.74	759.41	27
1020	SC[CAM]ATNNLAR	8.67	503.74	919.44	27
1021	SDIPGGSK	7.63	380.7	558.32	22
1022	SDIPGGSK	7.63	380.7	614.28	22
1023	SDIPGGSK	7.63	380.7	673.35	22
1024	SDWGK	5.75	296.64	390.21	18
1025	SDWGK	5.75	296.64	446.17	18
1026	SDWGK	5.75	296.64	505.24	18
1027	SEDNFHISSQQHEK	10.36	422.19	541.27	24
1028	SEDNFHISSQQHEK	10.36	422.19	730.28	24
1029	SEDNFHISSQQHEK	10.36	422.19	756.36	24
1030	SEMPASIR	12.02	445.72	674.37	25
1031	SEMPASIR	12.02	445.72	716.33	25
1032	SEMPASIR	12.02	445.72	803.41	25
1033	SEMPASTR	8.2	439.71	662.33	24
1034	SEMPASTR	8.19	439.71	704.29	24
1035	SEMPASTR	8.19	439.71	791.37	24
1036	SFAAHNQDQDLR	10.35	467.89	531.29	27
1037	SFAAHNQDQDLR	10.35	467.89	871.37	27
1038	SFAAHNQDQDLR	10.35	467.89	888.42	27
1039	SFAGHNK	9.4	380.69	455.24	22
1040	SFAGHNK	9.4	380.69	526.27	22
1041	SFAGHNK	9.38	380.69	673.34	22
1042	SFAGHNQDQDLR	10.18	694.32	888.42	36
1043	SFAGHNQDQDLR	10.18	694.32	1025.48	36
1044	SFAGHNQDQDLR	10.18	694.32	1082.5	36
1045	SFAGHNQDQNLR	9.8	462.89	530.3	27
1046	SFAGHNQDQNLR	9.8	462.89	773.39	27
1047	SFAGHNQDQNLR	9.8	462.89	887.43	27
1048	SFLESWAK	18.27	484.25	491.26	26
1049	SFLESWAK	18.27	484.25	620.3	26

1050	SFLESWAK	18.27	484.25	733.39	26
1051	SFTAWEK	14.44	434.71	462.23	24
1052	SFTAWEK	14.44	434.71	533.27	24
1053	SFTAWEK	14.44	434.71	634.32	24
1054	SFTTWEK	14.1	449.72	462.23	25
1055	SFTTWEK	14.1	449.72	563.28	25
1056	SFTTWEK	14.1	449.72	664.33	25
1057	SGSGWLR	13.25	381.7	531.3	22
1058	SGSGWLR	13.25	381.7	618.34	22
1059	SGSGWLR	13.25	381.7	675.36	22
1060	SGWGMAVDPQVGWYVGFVEK	24.65	738.02	841.45	41
1061	SGWGMAVDPQVGWYVGFVEK	24.65	738.02	1029.45	41
1062	SGWGMAVDPQVGWYVGFVEK	24.68	1106.53	1128.51	54
1063	SGWGMDVSPQVGWLTGWVEK	26.32	1110.03	1144.51	54
1064	SGWGMDVSPQVGWLTGWVEK	26.32	1110.03	1174.63	54
1065	SGWGMDVSPQVGWLTGWVEK	26.32	1110.03	1201.53	54
1066	SGWGMDVTPQVGWLTGWVEK	26.61	745.03	832.46	41
1067	SGWGMDVTPQVGWLTGWVEK	26.61	745.03	1018.54	41
1068	SGWGMDVTPQVGWLTGWVEK	26.61	745.03	1075.56	41
1069	SIHPASTFK	10.74	494.27	650.35	27
1070	SIHPASTFK	10.73	494.27	787.41	27
1071	SIHPASTFK	10.73	494.27	900.49	27
1072	SISTK	10.41	268.16	335.19	17
1073	SISTK	10.42	268.16	389.2	17
1074	SISTK	10.42	268.16	448.28	17
1075	SLGLSNNLSR	14.23	530.79	690.35	28
1076	SLGLSNNLSR	14.23	530.79	803.44	28
1077	SLGLSNNLSR	14.23	530.79	860.46	28
1078	SLSMSGK	9.31	355.18	509.24	21
1079	SLSMSGK	9.32	355.18	563.25	21
1080	SLSMSGK	9.32	355.18	622.32	21
1081	SMLFIEEK	17.82	498.76	518.28	27
1082	SMLFIEEK	17.82	498.76	665.35	27
1083	SMLFIEEK	17.82	498.76	778.43	27
1084	SNGLTHSWLGSSLK	16.78	743.89	877.48	38
1085	SNGLTHSWLGSSLK	16.78	743.89	1014.54	38
1086	SNGLTHSWLGSSLK	16.78	743.89	1115.58	38
1087	SPTWELKPEYNPSPR	16.02	600.97	733.36	34
1088	SPTWELKPEYNPSPR	16.02	600.97	808.91	34
1089	SPTWELKPEYNPSPR	16.02	600.97	959.46	34
1090	SQDIVR	8.4	359.2	502.3	21
1091	SQDIVR	8.38	359.2	543.28	21
1092	SQDIVR	8.4	359.2	630.36	21
1093	SQQKPTDPTIWLK	16.6	514.62	660.41	30
1094	SQQKPTDPTIWLK	16.6	514.62	757.46	30

1095	SQQKPTDPTIWLK	16.6	514.62	785.38	30
1096	SQVGWLTGWVEQPDGK	22.27	893.94	1015.5	44
1097	SQVGWLTGWVEQPDGK	22.28	893.94	1116.53	44
1098	SQVGWLTGWVEQPDGK	22.28	893.94	1229.62	44
1099	SSSNSC[CAM]TTNNAAR	16.84	685.29	907.41	35
1100	SSSNSC[CAM]TTNNAAR	16.85	685.29	994.44	35
1101	SSSNSC[CAM]TTNNAAR	16.84	685.29	1108.48	35
1102	SVYGELR	12.65	412.22	417.25	23
1103	SVYGELR	12.65	412.22	474.27	23
1104	SVYGELR	12.65	412.22	637.33	23
1105	SWILR	16.33	337.7	401.29	20
1106	SWILR	16.32	337.7	500.29	20
1107	SWILR	16.33	337.7	587.37	20
1108	SYLEK	9.09	320.17	389.24	19
1109	SYLEK	9.09	320.17	493.23	19
1110	SYLEK	9.1	320.17	552.3	19
1111	TAYIPASTFK	15.43	549.8	650.35	29
1112	TAYIPASTFK	15.43	549.8	763.43	29
1113	TAYIPASTFK	15.43	549.8	926.5	29
1114	TDDLFK	13.48	369.69	407.27	21
1115	TDDLFK	13.48	369.69	522.29	21
1116	TDDLFK	13.48	369.69	637.32	21
1117	TDINEIFK	17.44	490.26	650.35	27
1118	TDINEIFK	17.44	490.26	763.43	27
1119	TDINEIFK	17.44	490.26	878.46	27
1120	TFIHNDPR	18.92	500.25	751.38	27
1121	TFIHNDPR	18.92	500.25	825.39	27
1122	TFIHNDPR	18.92	500.25	898.45	27
1123	TGAGFTANR	9.64	447.72	461.25	25
1124	TGAGFTANR	9.64	447.72	665.34	25
1125	TGAGFTANR	9.64	447.72	793.4	25
1126	TGFNDGQK	7.5	433.7	561.26	24
1127	TGFNDGQK	7.5	433.7	708.33	24
1128	TGFNDGQK	7.5	433.7	765.35	24
1129	TGLADSK	9.7	346.18	533.29	20
1130	TGLADSK	9.67	346.18	545.26	20
1131	TGLADSK	9.7	346.18	590.31	20
1132	TGLDLMQK	15.32	453.24	634.32	25
1133	TGLDLMQK	15.32	453.24	747.41	25
1134	TGLDLMQK	15.32	453.24	804.43	25
1135	TGLELMQK	15.03	460.25	648.34	25
1136	TGLELMQK	15.03	460.25	761.42	25
1137	TGLELMQK	15.03	460.25	818.44	25
1138	TGMGYPK	10.28	377.18	464.25	22
1139	TGMGYPK	10.28	377.18	595.29	22

1140	TGMGYPK	10.28	377.18	652.31	22
1141	TGNGR	0.8	252.63	330.14	16
1142	TGNGR	0.8	252.63	346.18	16
1143	TGNGR	0.81	252.63	403.2	16
1144	TGTGSFIDAR	13.35	512.76	708.37	28
1145	TGTGSFIDAR	13.35	512.76	765.39	28
1146	TGTGSFIDAR	13.35	512.76	866.44	28
1147	TGTGSLSDAK	8.32	468.74	620.32	26
1148	TGTGSLSDAK	8.32	468.74	677.35	26
1149	TGTGSLSDAK	8.32	468.74	778.39	26
1150	TGVATEYQPEIGWWAGWVER	25.49	779.04	903.45	43
1151	TGVATEYQPEIGWWAGWVER	25.5	779.04	1146.55	43
1152	TGVATEYQPEIGWWAGWVER	25.52	1168.06	1189.57	56
1153	TGVSYPLLADGTR	17.4	675.36	842.47	35
1154	TGVSYPLLADGTR	17.41	675.36	1005.54	35
1155	TGVSYPLLADGTR	17.4	675.36	1092.57	35
1156	TGWAMDIK	16.71	461.23	577.3	25
1157	TGWAMDIK	16.71	461.23	763.38	25
1158	TGWAMDIK	16.72	461.23	820.4	25
1159	TGWATR	9.71	346.18	517.24	20
1160	TGWATR	9.69	346.18	533.28	20
1161	TGWATR	9.69	346.18	590.3	20
1162	TGWC[CAM]FDC[CAM]TPELGWWVGWVK	28.39	795.36	960.51	44
1163	TGWC[CAM]FDC[CAM]TPELGWWVGWVK	28.39	795.36	1017.53	44
1164	TGWC[CAM]FDC[CAM]TPELGWWVGWVK	28.38	795.36	1028.36	44
1165	TGWEGR	9.1	353.17	531.22	21
1166	TGWEGR	9.09	353.17	547.26	21
1167	TGWEGR	9.09	353.17	604.28	21
1168	TGWFVDK	16.08	426.72	694.36	24
1169	TGWFVDK	16.1	426.72	706.32	24
1170	TGWFVDK	16.08	426.72	751.38	24
1171	TGYDTK	2.09	342.66	526.25	20
1172	TGYDTK	2.09	342.66	538.21	20
1173	TGYDTK	2.08	342.66	583.27	20
1174	TGYGVR	8.09	326.67	478.23	19
1175	TGYGVR	8.1	326.67	494.27	19
1176	TGYGVR	8.1	326.67	551.29	19
1177	TGYSAR	2.24	327.66	480.21	19
1178	TGYSAR	2.24	327.66	496.25	19
1179	TGYSAR	2.24	327.66	553.27	19
1180	TGYSTR	2.08	342.67	510.22	20
1181	TGYSTR	2.08	342.67	526.26	20
1182	TGYSTR	2.08	342.67	583.28	20
1183	THESSNWGK	5.36	523.24	678.32	28
1184	THESSNWGK	5.37	523.24	807.36	28

1185	THESSNWGK	5.37	523.24	944.42	28
1186	TIC[CAM]TAIADAGTGK	14.35	639.82	732.39	33
1187	TIC[CAM]TAIADAGTGK	14.35	639.82	904.47	33
1188	TIC[CAM]TAIADAGTGK	14.35	639.82	1064.5	33
1189	TIGGAPDAYWVDDSLQISAR	21.22	712.35	1004.5	40
1190	TIGGAPDAYWVDDSLQISAR	21.22	712.35	1103.57	40
1191	TIGGAPDAYWVDDSLQISAR	21.21	1068.02	1103.57	52
1192	TLPFSASSYETLR	18.73	736.37	855.42	37
1193	TLPFSASSYETLR	18.73	736.37	1013.49	37
1194	TLPFSASSYETLR	18.73	736.37	1160.56	37
1195	TLPFSPK	15	395.23	478.27	22
1196	TLPFSPK	15	395.23	575.32	22
1197	TLPFSPK	15	395.23	688.4	22
1198	TLPFSQEVQDEVQSILFIEEK	28.55	827.09	891.52	45
1199	TLPFSQEVQDEVQSILFIEEK	28.56	827.09	978.55	45
1200	TLPFSQEVQDEVQSILFIEEK	28.56	827.09	1106.61	45
1201	TLPFSQEVQDEVQSMLFIEEK	27.7	833.08	996.51	46
1202	TLPFSQEVQDEVQSMLFIEEK	27.69	833.08	1124.57	46
1203	TLPFSQEVQDEVQSMLFIEEK	27.7	833.08	1223.63	46
1204	TLQNGWFEGFIISK	24.12	820.43	940.51	41
1205	TLQNGWFEGFIISK	24.11	820.43	1126.59	41
1206	TLQNGWFEGFIISK	24.11	820.43	1183.61	41
1207	TMQEYLNK	12.6	513.75	666.35	28
1208	TMQEYLNK	12.6	513.75	794.4	28
1209	TMQEYLNK	12.6	513.75	925.44	28
1210	TQTYQAYDAAR	11.2	644.3	666.32	33
1211	TQTYQAYDAAR	11.2	644.3	957.44	33
1212	TQTYQAYDAAR	11.2	644.3	1058.49	33
1213	TTDPTIWEK	14.39	545.77	676.37	29
1214	TTDPTIWEK	14.39	545.77	773.42	29
1215	TTDPTIWEK	14.39	545.77	888.45	29
1216	TTTTEVFK	12.06	463.75	522.29	25
1217	TTTTEVFK	12.06	463.75	623.34	25
1218	TTTTEVFK	12.06	463.75	724.39	25
1219	TWASNDFSR	13.73	542.25	638.29	29
1220	TWASNDFSR	13.73	542.25	725.32	29
1221	TWASNDFSR	13.73	542.25	796.36	29
1222	TWDMVQR	14.28	468.22	648.31	26
1223	TWDMVQR	14.28	468.22	761.33	26
1224	TWDMVQR	14.28	468.22	834.39	26
1225	TYVVDPAR	12.15	460.75	557.3	25
1226	TYVVDPAR	12.14	460.75	656.37	25
1227	TYVVDPAR	12.15	460.75	819.44	25
1228	VAFSLNIEMK	20.65	576.31	747.41	30
1229	VAFSLNIEMK	20.65	576.31	834.44	30

1230	VAFSLNIEMK	20.65	576.31	981.51	30
1231	VANSLIGLSTGAVR	17.97	679.39	760.43	35
1232	VANSLIGLSTGAVR	17.97	679.39	873.52	35
1233	VANSLIGLSTGAVR	17.97	679.39	986.6	35
1234	VELGK	7.74	273.17	342.2	17
1235	VELGK	7.75	273.17	399.22	17
1236	VELGK	7.74	273.17	446.26	17
1237	VFLDSWAK	18.2	483.26	606.29	26
1238	VFLDSWAK	18.2	483.26	719.37	26
1239	VFLDSWAK	18.2	483.26	866.44	26
1240	VFLESWAK	18.11	490.27	620.3	27
1241	VFLESWAK	18.11	490.27	733.39	27
1242	VFLESWAK	18.11	490.27	880.46	27
1243	VFLSSWAQDMNLSSAIK	23.66	948.98	978.49	47
1244	VFLSSWAQDMNLSSAIK	23.66	948.98	1106.55	47
1245	VFLSSWAQDMNLSSAIK	23.66	948.98	1177.59	47
1246	VGFER	10.32	304.16	433.21	18
1247	VGFER	10.32	304.16	451.23	18
1248	VGFER	10.32	304.16	508.25	18
1249	VILVFDQVR	19.69	544.83	664.34	29
1250	VILVFDQVR	19.69	544.83	763.41	29
1251	VILVFDQVR	19.69	544.83	876.49	29
1252	VMAAMVR	12.3	389.21	476.26	22
1253	VMAAMVR	12.3	389.21	547.3	22
1254	VMAAMVR	12.3	389.21	678.34	22
1255	VPLAVMGYDAGILVDAHNPR	21.61	703.37	709.34	39
1256	VPLAVMGYDAGILVDAHNPR	21.61	703.37	808.41	39
1257	VPLAVMGYDAGILVDAHNPR	21.61	703.37	921.49	39
1258	VQDEVQSMLFIEEK	20.48	847.92	996.51	42
1259	VQDEVQSMLFIEEK	20.48	847.92	1124.57	42
1260	VQDEVQSMLFIEEK	20.47	847.92	1223.63	42
1261	VQDGVQSMLFIEEK	20.26	811.91	996.51	41
1262	VQDGVQSMLFIEEK	20.27	811.91	1124.57	41
1263	VQDGVQSMLFIEEK	20.25	811.91	1223.63	41
1264	VSC[CAM]LPC[CAM]YQVVSHK	14.32	526.26	569.34	30
1265	VSC[CAM]LPC[CAM]YQVVSHK	14.32	526.26	860.46	30
1266	VSC[CAM]LPC[CAM]YQVVSHK	14.31	526.26	1020.49	30
1267	VSC[CAM]VWC[CAM]YQALAR	18.41	756.86	881.43	38
1268	VSC[CAM]VWC[CAM]YQALAR	18.41	756.86	1067.51	38
1269	VSC[CAM]VWC[CAM]YQALAR	18.41	756.86	1166.58	38
1270	VSDVC[CAM]SEVTAEGWQEVR	17.33	650.97	774.39	37
1271	VSDVC[CAM]SEVTAEGWQEVR	17.34	975.95	1075.52	48
1272	VSDVC[CAM]SEVTAEGWQEVR	17.34	975.95	1174.59	48
1273	VSEVEGWQIHGK	13.92	456.9	582.34	27
1274	VSEVEGWQIHGK	13.92	456.9	768.42	27

1275	VSEVEGWQIHGK	13.92	456.9	825.44	27
1276	VSFSLNIEMK	20.65	584.31	834.44	31
1277	VSFSLNIEMK	20.64	584.31	981.51	31
1278	VSFSLNIEMK	20.65	584.31	1068.54	31
1279	VSPC[CAM]SSFK	11.04	456.22	468.25	25
1280	VSPC[CAM]SSFK	11.04	456.22	628.28	25
1281	VSPC[CAM]SSFK	11.04	456.22	725.33	25
1282	VSQVPAYK	10.68	446.25	478.27	25
1283	VSQVPAYK	10.68	446.25	577.33	25
1284	VSQVPAYK	10.68	446.25	705.39	25
1285	VVFAR	11.17	296.18	393.22	18
1286	VVFAR	11.17	296.18	417.25	18
1287	VVFAR	11.17	296.18	492.29	18
1288	WDGAK	4.9	288.64	302.11	18
1289	WDGAK	4.9	288.64	390.2	18
1290	WDGAK	4.9	288.64	430.17	18
1291	WDGHIYDFPDWNR	20.52	574.25	590.27	33
1292	WDGHIYDFPDWNR	20.52	574.25	687.32	33
1293	WDGHIYDFPDWNR	20.52	574.25	887.37	33
1294	WDGIK	12.03	309.67	359.13	19
1295	WDGIK	12.03	309.67	432.25	19
1296	WDGIK	12.03	309.67	472.22	19
1297	WDGKPR	6.36	379.7	457.29	22
1298	WDGKPR	6.35	379.7	572.32	22
1299	WDGKPR	6.36	379.7	584.28	22
1300	WDGQTR	7.41	381.68	461.25	22
1301	WDGQTR	7.41	381.68	576.27	22
1302	WDGQTR	7.41	381.68	588.24	22
1303	WDGVK	10.1	302.66	359.13	18
1304	WDGVK	10.1	302.66	418.23	18
1305	WDGVK	10.1	302.66	458.2	18
1306	WDGVNR	10.39	373.68	445.25	21
1307	WDGVNR	10.39	373.68	560.28	21
1308	WDGVNR	10.42	373.68	572.25	21
1309	YAQAK	12.58	290.66	363.17	18
1310	YAQAK	12.58	290.66	417.25	18
1311	YAQAK	12.58	290.66	434.2	18
1312	YFSDFNAK	14.21	496.23	681.32	27
1313	YFSDFNAK	14.21	496.23	828.39	27
1314	YFSDFNAK	14.21	496.23	828.39	27
1315	YGTHLDR	8.51	431.21	641.34	24
1316	YGTHLDR	8.52	431.21	687.31	24
1317	YGTHLDR	8.51	431.21	698.36	24
1318	YLDELVK	15.52	440.24	488.31	24
1319	YLDELVK	15.53	440.24	603.33	24

1320	YLDELVK	15.52	440.24	716.42	24
1321	YLMITEAGR	15.86	527.27	533.27	28
1322	YLMITEAGR	15.86	527.27	646.35	28
1323	YLMITEAGR	15.86	527.27	777.39	28
1324	YLNLFSYGNANIGGGIDK	22.16	639.32	773.42	36
1325	YLNLFSYGNANIGGGIDK	22.16	958.48	1015.52	47
1326	YLNLFSYGNANIGGGIDK	22.16	958.48	1178.58	47
1327	YPVVWYSQQVAHHLGAQR	18.11	535.53	544.32	30
1328	YPVVWYSQQVAHHLGAQR	18.11	535.53	681.38	30
1329	YPVVWYSQQVAHHLGAQR	18.11	535.53	889.48	30
1330	YSNVLAFK	16.44	471.26	478.3	26
1331	YSNVLAFK	16.44	471.26	691.41	26
1332	YSNVLAFK	16.44	471.26	778.45	26
1333	YSPASTFK	12.22	450.73	553.3	25
1334	YSPASTFK	12.22	450.73	650.35	25
1335	YSPASTFK	12.22	450.73	737.38	25
1336	YSVVPVYQQLAR	18.42	711.89	778.42	36
1337	YSVVPVYQQLAR	18.42	711.89	974.54	36
1338	YSVVPVYQQLAR	18.43	711.89	1073.61	36
1339	YSVVWYSQLTAK	19.75	722.88	810.44	37
1340	YSVVWYSQLTAK	19.76	722.88	996.51	37
1341	YSVVWYSQLTAK	19.76	722.88	1095.58	37
1342	YSVVWYSQQVAHHLGAQR	18.61	533.02	544.32	30
1343	YSVVWYSQQVAHHLGAQR	18.61	533.02	681.38	30
1344	YSVVWYSQQVAHHLGAQR	18.61	533.02	889.48	30
1345	YTPASTFK	11.95	305.49	553.3	19
1346	YTPASTFK	11.98	457.73	553.3	25
1347	YTPASTFK	11.98	457.73	650.35	25
1348	YTSAFGYGNADVSGEPGK	15.03	607.28	673.35	34
1349	YTSAFGYGNADVSGEPGK	15.02	607.28	788.38	34
1350	YTSAFGYGNADVSGEPGK	15.02	910.41	1030.48	45
1351	YVFVSALTGNLGSNLTSSIK	23.66	691.04	906.49	39
1352	YVFVSALTGNLGSNLTSSIK	23.66	1036.06	1165.63	51
1353	YVFVSALTGNLGSNLTSSIK	23.67	1036.06	1190.64	51
1354	YVFVSALTGSLGSNLTSSIK	24.04	682.04	906.49	38
1355	YVFVSALTGSLGSNLTSSIK	24.04	1022.55	1106.61	50
1356	YVFVSALTGSLGSNLTSSIK	24.04	1022.55	1163.63	50

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the three transitions of the same peptide are greater than or equal to 2500, the detection of the peptide is considered to be positive and is labelled “1”. When at least one transition comprises an area less than 2500, the corresponding peptide is considered non-detected and is labelled “0”.

Example 17: Identification of a resistance to IMP beta-lactams:

Samples Sam145 to Sam154 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 26.**

TABLE 26:

Names	Species
Sam145	*A. baumannii*
Sam146	*A. baumannii*
Sam147	*E. coli*
Sam148	*K. pneumoniae*
Sam149	*K. pneumoniae*
Sam150	*P. aeruginosa*
Sam151	*P. aeruginosa*
Sam152	*P. aeruginosa*
Sam153	*P. aeruginosa*
Sam154	*P. putida*

Samples Sam145 to Sam154 correspond to a species able to comprise an IMP resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 27** instead of the peptides from **TABLE 3**.

TABLE 27:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	Positivity threshold
1	DTENLVNWFVER	24.3	761.37	550.3	39.1	2000
2	DTENLVNWFVER	24.3	761.37	850.42	39.1	2000
3	DTENLVNWFVER	24.3	761.37	949.49	39.1	2000
4	GDASLMK	10.6	361.18	391.24	16.3	2000
5	GDASLMK	10.6	361.18	478.27	16.3	2000
6	GDASLMK	10.6	361.18	549.31	16.3	2000
7	GFNESK	2	341.16	312.65	15.2	2000
8	GFNESK	2	341.16	363.19	15.2	2000
9	GFNESK	2	341.16	477.23	15.2	2000
10	GLNESK	1.1	324.17	363.19	14.2	2000
11	GLNESK	1.1	324.17	477.23	14.2	2000
12	GLNESK	1.1	324.17	590.31	14.2	2000
13	GLNESR	2.2	338.18	309.66	15	2000

14	GLNESR	2.2	338.18	391.19	15	2000
15	GLNESR	2.1	338.18	505.24	15	2000
16	GVYVHTSFEEVK	15.1	465.57	488.74	21.5	2000
17	GVYVHTSFEEVK	15.1	465.57	538.28	21.5	2000
18	GVYVHTSFEEVK	15.1	465.57	619.81	21.5	2000
19	GWGVVTK	14.3	373.71	345.2	17	2000
20	GWGVVTK	14.3	373.71	347.23	17	2000
21	GWGVVTK	14.3	373.71	503.32	17	2000
22	GWSVVTK	14.2	388.72	347.23	17.9	2000
23	GWSVVTK	14.2	388.72	446.3	17.9	2000
24	GWSVVTK	14.2	388.72	533.33	17.9	2000
25	HGLVVLVK	15.4	432.79	557.4	20.4	2000
26	HGLVVLVK	15.5	432.79	670.49	20.4	2000
27	HGLVVLVK	15.4	432.79	727.51	20.4	2000
28	HSFNGVSYSLIK	17	451.24	460.31	21.1	2000
29	HSFNGVSYSLIK	17	451.24	623.38	21.1	2000
30	HSFNGVSYSLIK	17	451.24	710.41	21.1	2000
31	LEEGVYVHTSFEEVK	16.9	589.29	697.85	25.4	2000
32	LEEGVYVHTSFEEVK	16.9	589.29	762.37	25.4	2000
33	LEEGVYVHTSFEEVK	16.9	589.29	826.89	25.4	2000
34	LFVLCVCFLCSITAAGAR	19.5	686.68	659.38	28.4	2000
35	LFVLCVCFLCSITAAGAR	19.6	686.68	906.45	28.4	2000
36	LFVLCVCFLCSITAAGAR	19.5	1029.52	374.22	54.4	2000
37	LFVLCVCFLCSITAAGAR	19.5	1029.52	659.38	54.4	2000
38	LTLEQAVK	15.2	451.27	574.32	21.5	2000
39	LTLEQAVK	15.2	451.27	687.4	21.5	2000
40	LTLEQAVK	15.2	451.27	788.45	21.5	2000
41	LTWEQAVK	16.3	487.77	574.32	23.5	2000
42	LTWEQAVK	16.3	487.77	760.4	23.5	2000
43	LTWEQAVK	16.3	487.77	861.45	23.5	2000
44	LTWEQTVK	15.4	502.77	395.71	24.4	2000
45	LTWEQTVK	15.4	502.77	604.33	24.4	2000
46	LTWEQTVK	15.4	502.77	790.41	24.4	2000
47	LVAWFVGR	21.3	474.28	478.28	22.8	2000
48	LVAWFVGR	21.3	474.28	664.36	22.8	2000
49	LVAWFVGR	21.3	474.28	735.39	22.8	2000
50	LVNWFIEHGYR	20.1	478.58	611.29	21.9	2000
51	LVNWFIEHGYR	20.1	478.58	660.83	21.9	2000
52	LVNWFIEHGYR	20.1	478.58	661.31	21.9	2000
53	LVNWFVER	20.9	531.79	550.3	26	2000
54	LVNWFVER	20.9	531.79	736.38	26	2000
55	LVNWFVER	20.9	531.79	850.42	26	2000
56	LVTWFVER	20.6	525.29	550.3	25.7	2000
57	LVTWFVER	20.6	525.29	736.38	25.7	2000
58	LVTWFVER	20.6	525.29	837.43	25.7	2000

59	LVVPGHSEVGDASLLK	17.6	540.97	655.34	23.9	2000
60	LVVPGHSEVGDASLLK	17.6	540.97	704.88	23.9	2000
61	LVVPGHSEVGDASLLK	17.6	810.95	655.34	42	2000
62	LVVPSHSDIGDASLLK	18	550.97	670.35	24.2	2000
63	LVVPSHSDIGDASLLK	18	550.97	719.88	24.2	2000
64	LVVPSHSDIGDASLLK	18	825.96	670.35	42.8	2000
65	LVVPSHSDIGDSSLLK	17.7	556.31	678.34	24.3	2000
66	LVVPSHSDIGDSSLLK	17.7	556.31	719.39	24.3	2000
67	LVVPSHSDIGDSSLLK	17.7	556.31	727.88	24.3	2000
68	LVVPSHSDVGDASLLK	17.5	546.3	663.34	24	2000
69	LVVPSHSDVGDASLLK	17.5	546.3	712.87	24	2000
70	LVVPSHSDVGDASLLK	17.5	818.95	663.34	42.4	2000
71	LVVPSHSEAGDASLLK	16.1	541.63	656.33	23.9	2000
72	LVVPSHSEAGDASLLK	16.1	541.63	705.87	23.9	2000
73	LVVPSHSEAGDASLLK	16.1	541.63	755.4	23.9	2000
74	LVVPSHSEVGDASLLK	17.5	550.97	670.35	24.2	2000
75	LVVPSHSEVGDASLLK	17.5	550.97	719.88	24.2	2000
76	LVVPSHSEVGDASLLK	17.5	825.96	670.35	42.8	2000
77	LVVSGHSEIGNASLLK	16.8	541.97	656.85	23.9	2000
78	LVVSGHSEIGNASLLK	16.8	541.97	706.38	23.9	2000
79	LVVSGHSEIGNASLLK	16.8	541.97	755.92	23.9	2000
80	LVVSSHSDIGDVSLLK	18.9	556.98	679.35	24.3	2000
81	LVVSSHSDIGDVSLLK	18.9	556.98	728.89	24.3	2000
82	LVVSSHSDIGDVSLLK	18.9	556.98	778.42	24.3	2000
83	LVVSSHSEIGDASLLK	17.6	552.31	672.34	24.2	2000
84	LVVSSHSEIGDASLLK	17.6	552.31	721.88	24.2	2000
85	LVVSSHSEIGDASLLK	17.6	552.31	771.41	24.2	2000
86	LVVSSHSEIGNASLLQR	16.8	604	416.26	25.8	2000
87	LVVSSHSEIGNASLLQR	16.8	604	616.38	25.8	2000
88	LVVSSHSEIGNASLLQR	16.8	604	799.42	25.8	2000
89	LVVSSHSEK	8.1	329.18	387.19	17.3	2000
90	LVVSSHSEK	8.1	329.18	587.28	17.3	2000
91	LVVSSHSEK	8.1	493.27	773.38	23.9	2000
92	LVVSSHSETGNASLLK	14.7	547.97	665.83	24.1	2000
93	LVVSSHSETGNASLLK	14.7	547.97	715.37	24.1	2000
94	LVVSSHSETGNASLLK	14.7	547.97	764.9	24.1	2000
95	NDAYLIDTPITAK	18.8	717.88	745.41	36.7	2000
96	NDAYLIDTPITAK	18.8	717.88	858.49	36.7	2000
97	NDAYLIDTPITAK	18.8	717.88	971.58	36.7	2000
98	NSFGGVNYWLVK	21.4	692.36	822.45	35.2	2000
99	NSFGGVNYWLVK	21.4	692.36	1035.56	35.2	2000
100	NSFGGVNYWLVK	21.4	692.36	1182.63	35.2	2000
101	NSFSGASYWLVK	20.8	679.84	795.44	34.5	2000
102	NSFSGASYWLVK	20.8	679.84	923.5	34.5	2000
103	NSFSGASYWLVK	20.8	679.84	1010.53	34.5	2000

104	NSFSGGSYWLVNNK	18.8	786.88	375.2	40.6	2000
105	NSFSGGSYWLVNNK	18.8	786.88	474.27	40.6	2000
106	NSFSGGSYWLVNNK	18.8	786.88	1224.6	40.6	2000
107	NSFSGVSYWLLK	23.6	700.86	809.46	35.7	2000
108	NSFSGVSYWLLK	23.6	700.86	1052.58	35.7	2000
109	NSFSGVSYWLLK	23.6	700.86	1199.65	35.7	2000
110	NSFSGVSYWLVK	22.3	693.86	795.44	35.3	2000
111	NSFSGVSYWLVK	22.3	693.86	951.53	35.3	2000
112	NSFSGVSYWLVK	22.3	693.86	1038.56	35.3	2000
113	SIPTYASELTNELLK	23.8	560.3	717.41	24.5	2000
114	SIPTYASELTNELLK	23.8	560.3	739.89	24.5	2000
115	SIPTYASELTNELLK	23.8	839.95	739.89	43.6	2000
116	TLEQAVK	10.5	394.73	445.28	18.2	2000
117	TLEQAVK	10.5	394.73	574.32	18.2	2000
118	TLEQAVK	10.5	394.73	687.4	18.2	2000
119	TWEQALK	15.1	438.24	459.29	20.7	2000
120	TWEQALK	15.1	438.24	588.34	20.7	2000
121	TWEQALK	15.1	438.24	774.41	20.7	2000
122	TWEQAVK	12.8	431.23	445.28	20.3	2000
123	TWEQAVK	12.8	431.23	574.32	20.3	2000
124	TWEQAVK	12.8	431.23	760.4	20.3	2000
125	VQATNSFSGVNYWLVK	22.1	604.98	708.41	25.8	2000
126	VQATNSFSGVNYWLVK	22.1	604.98	822.45	25.8	2000
127	VQATNSFSGVNYWLVK	22.1	906.97	1212.64	47.4	2000
128	VQATNSFSGVSYSLIK	19.9	567.63	710.41	24.7	2000
129	VQATNSFSGVSYSLIK	19.9	567.63	953.53	24.7	2000
130	VQATNSFSGVSYSLIK	19.9	850.95	710.41	44.2	2000
131	VQATNSFSGVSYWLVK	22.5	595.98	708.41	25.6	2000
132	VQATNSFSGVSYWLVK	22.5	595.98	795.44	25.6	2000
133	VQATNSFSGVSYWLVK	22.5	893.46	1038.56	46.7	2000
134	YSFSEVSYWLVK	23.8	754.38	795.44	38.7	2000
135	YSFSEVSYWLVK	23.8	754.38	894.51	38.7	2000
136	YSFSEVSYWLVK	23.8	754.38	1110.58	38.7	2000
137	YSFSGVSYWLVK	23.4	718.37	795.44	36.7	2000
138	YSFSGVSYWLVK	23.4	718.37	951.53	36.7	2000
139	YSFSGVSYWLVK	23.4	718.37	1185.63	36.7	2000

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	yes
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution

Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	50.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated
Declustering potential (DP):	100.00 V
Entry potential before Q0 (EP):	6.00 V
Collision cell exit potential (CXP):	15 V
Total cycle time:	1 sec
Detection window:	120 sec

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 27**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 28**. When a transition has an area less than the positivity threshold described in **TABLE 27**, the transition is considered non-detected and is labelled "0" in **TABLE 28**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 28:

Transition number	Sam145	Sam146	Sam147	Sam148	Sam149	Sam150	Sam151	Sam152	Sam153	Sam154
1	0	0	1	0	0	0	0	0	0	0
2	0	0	1	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	1	0
5	0	0	0	0	0	0	0	0	1	0
6	0	0	0	0	0	0	0	0	1	0
7	0	0	0	0	0	0	0	0	0	0

8	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0
10	1	1	0	0	0	0	0	0	0	0
11	1	1	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	1	1	0	1	0
18	0	0	0	0	0	0	0	0	0	0
19	0	1	0	0	0	0	0	0	0	0
20	0	0	0	0	0	1	0	1	1	0
21	0	0	0	0	0	0	0	1	0	0
22	0	0	0	0	1	0	0	0	0	0
23	0	0	1	1	1	0	0	0	1	0
24	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0	0	0
33	1	0	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0	0	0	0
38	0	1	1	1	0	0	0	1	0	0
39	0	1	1	1	0	0	0	1	0	0
40	0	1	1	1	0	0	0	1	0	0
41	0	0	1	0	0	0	0	0	0	1
42	0	0	0	0	0	0	0	0	0	1
43	0	0	0	0	0	0	0	0	0	1
44	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	1
49	0	0	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0
52	0	0	0	0	0	1	0	0	0	0

53	1	0	0	0	1	1	0	0	1	0
54	1	0	1	0	0	1	0	0	1	0
55	1	1	1	0	1	1	0	0	1	0
56	0	1	1	1	1	0	1	1	0	0
57	0	1	1	1	1	0	1	1	0	0
58	0	1	1	1	1	0	1	1	0	0
59	0	0	0	0	0	1	1	0	0	0
60	0	0	0	0	0	1	1	0	0	0
61	0	0	0	0	0	1	1	0	0	0
62	0	0	0	1	0	0	1	1	0	0
63	0	0	0	1	0	0	1	1	0	0
64	0	0	0	1	0	0	1	1	0	0
65	0	0	0	0	0	1	1	1	1	0
66	0	0	0	0	0	0	0	0	0	0
67	0	0	0	0	0	0	0	0	0	0
68	0	0	0	0	0	0	0	0	0	0
69	0	0	0	0	0	0	0	0	0	0
70	0	1	0	0	0	0	0	0	0	0
71	1	1	1	0	0	0	0	0	0	0
72	0	1	1	0	0	0	0	0	0	0
73	0	1	1	0	0	0	0	0	0	0
74	0	0	0	1	0	0	1	1	0	0
75	0	0	0	1	0	0	1	1	0	0
76	0	0	0	1	0	0	1	1	0	0
77	0	0	0	0	0	0	0	0	0	1
78	0	0	0	0	0	0	0	0	0	1
79	0	1	1	0	0	0	0	0	0	1
80	0	0	0	0	0	0	0	0	0	0
81	0	0	0	0	0	0	0	0	0	0
82	0	1	0	0	0	0	0	0	0	0
83	1	0	0	0	1	1	0	0	0	1
84	1	0	0	0	1	1	0	0	1	0
85	1	0	1	1	1	1	1	1	1	0
86	0	0	1	0	0	0	0	0	0	0
87	0	0	1	0	0	0	0	0	0	0
88	0	0	0	0	0	0	0	0	0	0
89	0	0	0	0	0	0	0	0	0	0
90	0	0	0	0	0	0	0	0	1	0
91	0	0	0	0	0	0	0	0	1	0
92	1	0	0	0	0	0	0	0	0	0
93	0	0	0	0	0	0	0	0	0	0
94	0	0	0	0	0	0	0	0	0	0
95	0	1	0	0	0	0	0	0	0	0
96	0	0	0	0	0	0	0	0	0	0
97	0	0	0	0	0	0	0	0	0	0

98	0	1	1	0	0	0	0	0	0	0
99	0	1	1	0	0	0	0	0	0	0
100	0	1	1	1	0	0	0	0	0	0
101	0	0	0	0	0	0	0	0	0	0
102	0	0	0	0	0	0	0	0	0	0
103	0	0	0	0	0	0	1	1	0	0
104	0	0	0	1	0	0	0	0	0	0
105	0	0	0	1	1	0	0	0	0	0
106	0	0	0	0	0	0	0	0	0	0
107	0	0	0	0	0	0	0	0	0	0
108	0	0	0	0	0	0	0	0	0	0
109	0	0	0	0	0	0	0	0	0	0
110	1	1	0	0	0	0	0	0	0	0
111	1	1	0	0	0	0	0	0	1	0
112	1	0	0	0	0	0	0	0	0	0
113	0	0	0	1	0	0	0	0	0	0
114	0	0	0	1	0	0	0	1	0	0
115	0	0	0	1	0	0	0	0	0	0
116	0	1	0	1	0	0	1	0	0	0
117	0	1	1	1	0	0	1	0	0	0
118	0	1	0	1	0	0	1	0	0	0
119	0	0	0	0	0	0	0	0	1	0
120	0	0	0	0	0	0	0	0	1	0
121	0	0	0	0	0	0	0	0	1	0
122	1	0	0	0	1	1	0	0	0	0
123	1	0	0	0	1	1	0	0	0	0
124	1	0	0	0	1	1	0	0	0	0
125	0	0	0	0	0	0	0	0	0	0
126	0	0	0	0	0	0	0	1	0	0
127	0	0	0	1	1	0	0	0	0	0
128	0	0	0	0	0	0	0	0	0	1
129	0	0	0	0	0	0	0	0	0	0
130	0	0	0	0	0	0	0	0	0	0
131	0	0	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0
133	0	0	0	0	0	0	0	0	0	0
134	0	0	0	0	0	0	0	0	0	0
135	0	0	0	0	0	0	1	0	0	0
136	0	0	0	0	0	0	0	0	0	0
137	1	0	0	0	0	0	0	0	0	0
138	0	0	0	0	0	0	0	0	0	0
139	0	0	0	0	0	0	0	0	0	0

Samples Sam145 to Sam154 comprise at least one peptide which is characteristic of IMPs. The bacteria present in samples Sam145 to Sam154 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins and to carbapenems.

Example 18: identification of a resistance to OXA-48 beta-lactams:

Samples Sam155 to Sam164 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 29.**

TABLE 29:

Names	Species
Sam155	*K. pneumoniae*
Sam156	*K. pneumoniae*
Sam157	*K. pneumoniae*
Sam158	*E. cloacae*
Sam159	*E. cloacae*
Sam160	*K. pneumoniae*
Sam161	*K. pneumoniae*
Sam162	*K. pneumoniae*
Sam163	*K. pneumoniae*
Sam164	*K. pneumoniae*

Samples Sam155 to Sam164 correspond to a species able to comprise an OXA-48 resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 30** instead of the peptides from **TABLE 3**.

TABLE 30:

Transition number	Peptide	Charge state of the precursor	Fragment ion	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	Positivity threshold
1	ANQAFLPASTFK	2	y6 monocharged	18.09	647.84	650.35	32.7	2000
2	ANQAFLPASTFK	2	y7 monocharged	18.11	647.84	763.44	32.7	2000
3	ANQAFLPASTFK	2	y8 monocharged	18.09	647.84	910.5	32.7	2000
4	DEHQVFK	3	y5 dicharged	9.89	301.48	329.69	16.4	2000
5	DEHQVFK	2	y4 monocharged	9.89	451.72	521.31	21.5	2000

6	DEHQVFK	2	y5 monocharged	9.91	451.72	658.37	21.5	2000
7	DHNLITAMK	3	y3 monocharged	14.57	348.18	349.19	17.9	2000
8	DHNLITAMK	3	y4 monocharged	14.57	348.18	450.24	17.9	2000
9	DHNLITAMK	2	y7 monocharged	14.57	521.77	790.45	25.5	2000
10	DIATWNR	2	y3 monocharged	13.79	438.22	475.24	20.7	2000
11	DIATWNR	2	y4 monocharged	13.79	438.22	576.29	20.7	2000
12	DIATWNR	2	y5 monocharged	13.79	438.22	647.33	20.7	2000
13	IPNSLIALDLGVVK	3	y6 monocharged	23.68	484.63	630.38	22.1	2000
14	IPNSLIALDLGVVK	2	y13 dicharged	23.68	726.45	669.9	37.1	2000
15	IPNSLIALDLGVVK	2	y8 monocharged	23.68	726.45	814.5	37.1	2000
16	ISATEQISFLR	2	y4 monocharged	19.17	632.85	522.3	31.8	2000
17	ISATEQISFLR	2	y5 monocharged	19.17	632.85	635.39	31.8	2000
18	ISATEQISFLR	2	y6 monocharged	19.17	632.85	763.45	31.8	2000
19	QAMLTEANGDYIIR	3	y4 monocharged	18.36	532.27	564.35	23.6	2000
20	QAMLTEANGDYIIR	3	y6 monocharged	18.36	532.27	736.4	23.6	2000
21	QAMLTEANGDYIIR	2	y10 monocharged	18.36	797.9	1151.57	41.2	2000
22	QQGFTNNLK	2	y4 monocharged	12.58	525.27	488.28	25.7	2000
23	QQGFTNNLK	2	y5 monocharged	12.58	525.27	589.33	25.7	2000
24	QQGFTNNLK	2	y7 monocharged	12.58	525.27	793.42	25.7	2000
25	SQGVVVLWNENK	2	y5 monocharged	18.54	686.87	690.32	34.9	2000
26	SQGVVVLWNENK	2	y6 monocharged	18.54	686.87	803.41	34.9	2000
27	SQGVVVLWNENK	2	y7 monocharged	18.52	686.87	902.47	34.9	2000
28	SWNAHFTEHK	3	y8 dicharged	12.23	419.53	492.24	20.1	2000
29	SWNAHFTEHK	3	y9 dicharged	12.23	419.53	585.28	20.1	2000
30	SWNAHFTEHK	3	y5 monocharged	12.23	419.53	661.33	20.1	2000
31	VLALSAVFLVASIIGMPAVAK	3	y6 monocharged	34.92	690.75	616.35	28.5	2000
32	VLALSAVFLVASIIGMPAVAK	3	y7 monocharged	34.94	690.75	673.37	28.5	2000
33	VLALSAVFLVASIIGMPAVAK	3	y8 monocharged	34.94	690.75	786.45	28.5	2000
34	YSVVPVYQEFAR	3	y5 monocharged	20.05	486.59	650.33	22.2	2000
35	YSVVPVYQEFAR	2	y8 dicharged	20.07	729.38	505.26	37.3	2000
36	YSVVPVYQEFAR	2	y8 monocharged	20.07	729.38	1009.51	37.3	2000

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	no
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s

Curtain gas:	40.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated
Declustering potential (DP):	100.00 V
Entry potential before Q0 (EP):	6.00 V
Collision cell exit potential (CXP):	15 V
Total cycle time:	1.1 sec

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 30**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 31**. When a transition has an area less than the positivity threshold described in **TABLE 30**, the transition is considered non-detected and is labelled "0" in **TABLE 31**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 31:

Transition number	Sam155	Sam156	Sam157	Sam158	Sam159	Sam160	Sam161	Sam162	Sam163	Sam164
1	0	1	1	0	1	1	1	1	1	0
2	0	1	1	0	1	1	1	0	1	0
3	0	1	0	0	0	1	1	0	0	0
4	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0
7	0	1	0	0	0	1	1	0	0	0
8	0	1	1	1	0	1	1	0	1	0
9	1	1	1	1	1	1	1	1	1	0
10	0	0	0	0	0	0	0	0	0	0
11	0	0	0	1	1	0	0	0	0	0
12	0	0	0	0	0	0	0	1	0	0
13	0	1	1	1	1	1	1	1	1	0
14	0	1	1	1	1	1	1	1	1	1

15	0	1	1	1	1	1	1	1	1	0
16	1	1	1	1	1	1	1	1	1	1
17	1	1	1	1	1	1	1	1	1	1
18	1	1	1	1	1	1	1	1	1	1
19	1	1	1	1	1	1	1	1	1	1
20	1	1	1	1	1	1	1	1	1	0
21	1	1	1	1	1	1	1	1	1	1
22	1	1	1	1	1	1	1	1	1	0
23	1	1	1	1	1	1	1	1	1	1
24	1	1	1	1	1	1	1	1	1	0
25	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0
28	1	1	1	1	1	1	1	1	1	1
29	1	1	1	1	1	1	1	1	1	1
30	1	1	1	1	1	1	1	1	1	0
31	1	0	0	0	1	0	0	0	0	0
32	1	1	1	1	1	1	1	1	1	0
33	1	1	0	1	1	1	1	1	1	0
34	0	1	1	0	1	1	1	0	1	0
35	0	1	1	0	1	1	1	0	1	0
36	0	1	1	0	1	1	1	0	1	0

Samples Sam155 to Sam164 comprise at least one peptide which is characteristic of the OXA-48 group. The bacteria present in samples Sam155 to Sam164 therefore express a beta-lactamase which confers on them a resistance to penicillins, to first-generation and second-generation cephalosporins (but not to broad-spectrum cephalosporins), and to carbapenems.

Example 19: Identification of a resistance to VIM beta-lactams:

Samples Sam165 to Sam170 are identified according to one of the methods described in examples 1, 3 or 4. The identification of the species is set out in **TABLE 32.**

TABLE 32

Names	Species
Sam165	*P. aeruginosa*
Sam166	*E. coli*
Sam167	*A. baumannii complex*
Sam168	*A. junii*
Sam169	*E. coli*

Sam170	*K. pneumoniae ssp pneumoniae*

Samples Sam165 to Sam170 correspond to a species able to comprise a VIM resistance mechanism. The following method is then performed to detect such a mechanism.

Each sample is treated according to Example 5, then analysed according to Example 6 unless otherwise stated in the rest of the example, by detecting the peptides from **TABLE 33** instead of the peptides from **TABLE 3**.

TABLE 33:

Transition number	Peptide	Retention time (minutes)	(m/z) filtered in Q1	(m/z) filtered in Q3	Collision energy (eV)	Positivity threshold
1	AAGVATYASPSAR	12.3	611.32	588.31	30.6	2500
2	AAGVATYASPSAR	12.3	611.32	852.42	30.6	2500
3	AAGVATYASPSAR	12.3	611.32	923.46	30.6	2500
4	AAGVATYASPSIR	14.5	632.34	630.36	31.8	2500
5	AAGVATYASPSIR	14.5	632.34	894.47	31.8	2500
6	AAGVATYASPSIR	14.5	632.34	965.51	31.8	2500
7	AAGVATYASPSTR	12	626.32	618.32	31.4	2500
8	AAGVATYASPSTR	12	626.32	882.43	31.4	2500
9	AAGVATYASPSTR	12	626.32	953.47	31.4	2500
10	AAGVATYTSPLTR	15.7	654.35	674.38	33	2500
11	AAGVATYTSPLTR	15.7	654.35	938.49	33	2500
12	AAGVATYTSPLTR	15.7	654.35	1009.53	33	2500
13	AGVATYASPSTR	11.8	590.8	547.28	29.4	2500
14	AGVATYASPSTR	11.8	590.8	618.32	29.4	2500
15	AGVATYASPSTR	11.8	590.8	781.38	29.4	2500
16	ALSSSGDVVR	11.3	495.76	632.34	24	2500
17	ALSSSGDVVR	11.3	495.76	719.37	24	2500
18	ALSSSGDVVR	11.3	495.76	806.4	24	2500
19	AVSTHFHDDR	9.2	395.52	413.68	19.3	2500
20	AVSTHFHDDR	9.2	395.52	507.72	19.3	2500
21	AVSTHFHDDR	9.2	395.52	689.3	19.3	2500
22	DADELLLIDTAWGAK	24.3	544.28	748.36	24	2500
23	DADELLLIDTAWGAK	24.3	815.92	544.31	42.2	2500
24	DADELLLIDTAWGAK	24.3	815.92	748.36	42.2	2500
25	DADELLLIDTAWGAK	24.3	815.92	861.45	42.2	2500
26	DGDELLLIDTAWGAK	24	539.61	748.36	23.8	2500
27	DGDELLLIDTAWGAK	24	808.91	748.36	41.8	2500
28	DGDELLLIDTAWGAK	24	808.91	861.45	41.8	2500
29	DGDELLLIDTAWGTK	24.1	549.61	778.37	24.1	2500
30	DGDELLLIDTAWGTK	24.1	823.92	778.37	42.7	2500

31	DGDELLLIDTAWGTK	24.1	823.92	891.46	42.7	2500
32	ESAGNVADANLAEWPATIK	20.2	652.99	529.33	27.3	2500
33	ESAGNVADANLAEWPATIK	20.2	652.99	715.41	27.3	2500
34	ESAGNVADANLAEWPATIK	20.2	978.99	529.33	51.5	2500
35	GEYPTVSEIPVGEVR	18.4	544.61	656.37	24	2500
36	GEYPTVSEIPVGEVR	18.4	816.42	641.85	42.3	2500
37	GEYPTVSEIPVGEVR	18.4	816.42	656.37	42.3	2500
38	HTTNVVK	1.3	399.73	345.25	18.5	2500
39	HTTNVVK	1.3	399.73	560.34	18.5	2500
40	HTTNVVK	1.3	399.73	661.39	18.5	2500
41	IGDGVWSHIATQK	17	471.25	563.8	21.7	2500
42	IGDGVWSHIATQK	17	471.25	621.32	21.7	2500
43	IGDGVWSHIATQK	17	471.25	649.83	21.7	2500
44	LGDTVYSSNGLIVR	17.9	747.4	387.27	38.3	2500
45	LGDTVYSSNGLIVR	17.9	747.4	845.48	38.3	2500
46	LGDTVYSSNGLIVR	17.9	747.4	1008.55	38.3	2500
47	LYQIADGVWSHIATK	20.8	567.97	592.81	24.7	2500
48	LYQIADGVWSHIATK	20.8	567.97	649.35	24.7	2500
49	LYQIADGVWSHIATK	20.8	567.97	713.38	24.7	2500
50	LYQIADGVWSHIATR	21	577.31	606.81	25	2500
51	LYQIADGVWSHIATR	21	577.31	663.35	25	2500
52	LYQIADGVWSHIATR	21	577.31	727.38	25	2500
53	NTAALLAEIEK	19.8	586.83	589.32	29.2	2500
54	NTAALLAEIEK	19.8	586.83	702.4	29.2	2500
55	NTAALLAEIEK	19.8	586.83	886.52	29.2	2500
56	NTVALLAEIEK	21.2	600.85	589.32	30	2500
57	NTVALLAEIEK	21.2	600.85	702.4	30	2500
58	NTVALLAEIEK	21.2	600.85	886.52	30	2500
59	QIGLPVTR	15.6	442.27	472.29	20.9	2500
60	QIGLPVTR	15.6	442.27	642.39	20.9	2500
61	QIGLPVTR	15.6	442.27	755.48	20.9	2500
62	QLAEAAGNEVPAHSLK	13.8	545.62	597.32	24	2500
63	QLAEAAGNEVPAHSLK	13.8	545.62	652.38	24	2500
64	QLAEAAGNEVPAHSLK	13.8	545.62	697.36	24	2500
65	SFDGAVYPSNGLIVR	19.2	797.92	559.32	41.2	2500
66	SFDGAVYPSNGLIVR	19.2	797.92	855.51	41.2	2500
67	SFDGAVYPSNGLIVR	19.2	797.92	1018.57	41.2	2500
68	SISTHFHDDR	10.6	405.52	413.68	19.7	2500
69	SISTHFHDDR	10.6	405.52	507.72	19.7	2500
70	SISTHFHDDR	10.6	405.52	689.3	19.7	2500
71	SVSTHFHDDR	9.2	400.85	413.68	19.5	2500
72	SVSTHFHDDR	9.2	400.85	507.72	19.5	2500
73	SVSTHFHDDR	9.2	400.85	689.3	19.5	2500
74	TSAGNVADADLAEWPGSVER	19.2	682.32	322.67	28.2	2500
75	TSAGNVADADLAEWPGSVER	19.2	682.32	644.34	28.2	2500

76	TSAGNVADADLAEWPGSVER	19.2	682.32	830.42	28.2	2500
77	TSAGNVADADLAEWPGSVER	19.2	1022.98	644.34	54	2500
78	TSAGNVADADLAEWPTSIER	20.7	701.67	351.69	28.8	2500
79	TSAGNVADADLAEWPTSIER	20.7	701.67	702.38	28.8	2500
80	TSAGNVADADLAEWPTSIER	20.7	701.67	888.46	28.8	2500
81	TSAGNVADADLAEWPTSIER	20.7	1052	702.38	55.7	2500
82	TSAGNVADADLAEWPTSVER	19.6	697	344.69	28.7	2500
83	TSAGNVADADLAEWPTSVER	19.6	697	688.36	28.7	2500
84	TSAGNVADADLAEWPTSVER	19.6	697	874.44	28.7	2500
85	TSAGNVADADLAEWPTSVER	19.6	1045	688.36	55.3	2500
86	VGGVDALR	12.8	393.73	474.27	18.2	2500
87	VGGVDALR	12.8	393.73	630.36	18.2	2500
88	VGGVDALR	12.8	393.73	687.38	18.2	2500
89	VGGVDVLR	14.8	407.74	502.3	19	2500
90	VGGVDVLR	14.8	407.74	658.39	19	2500
91	VGGVDVLR	14.8	407.74	715.41	19	2500
92	VLFGGCAVHEASR	15.1	468.24	522.24	21.6	5100
93	VLFGGCAVHEASR	15.1	468.24	595.77	21.6	5100
94	VLFGGCAVHEASR	15.1	468.24	599.29	21.6	5100
95	VLYGGCAVHELSR	15.3	487.58	543.26	22.2	2500
96	VLYGGCAVHELSR	15.3	487.58	624.79	22.2	2500
97	VLYGGCAVHELSR	15.3	487.58	641.34	22.2	2500

- The other machine parameters used are as follows:

Scan type:	MRM
MRM planned:	yes
Polarity:	Positive
Ionising source:	Turbo V™ (Applied BioSystems)
Q1 setting:	Filtering with unit resolution
Q3 setting:	Filtering with unit resolution
Inter-scan pause:	5.00 msec
Scanning speed:	10 Da/s
Curtain gas:	50.00 psi
Cone voltage:	5500.00 V
Source temperature:	500.00°C
Nebulising gas:	50.00 psi
Heating gas:	50.00 psi
Collision gas which induces dissociation:	9.00 psi
Dynamic filling:	activated

Declustering potential (DP):	100.00 V
Entry potential before Q0 (EP):	6.00 V
Collision cell exit potential (CXP):	15 V
Total cycle time:	0.04 sec
Detection window:	120 sec

The areas obtained for each of the transitions and for each of the microorganisms studied were measured. When the areas of the transitions are greater than or equal to the positivity threshold described in **TABLE 33**, the detection of the transition is considered to be positive and is labelled "1" in **TABLE 34**. When a transition has an area less than the positivity threshold described in **TABLE 33**, the transition is considered non-detected and is labelled "0" in **TABLE 34**.

For a given peptide, when at least 3 transitions are labelled "1", the peptide is considered as being detected.

TABLE 34:

Transition number	Sam165	Sam166	Sam167	Sam168	Sam169	Sam170
1	0	0	0	0	0	0
2	0	0	0	0	0	0
3	0	0	0	0	0	0
4	0	0	0	0	0	0
5	0	0	0	0	0	0
6	0	0	0	0	0	0
7	0	0	0	0	0	1
8	0	0	0	0	0	1
9	0	0	0	0	0	1
10	0	0	0	0	0	0
11	0	0	0	0	0	0
12	0	0	0	0	0	0
13	0	0	0	0	0	1
14	0	0	0	0	0	1
15	0	0	0	0	0	1
16	0	0	0	0	0	0
17	0	0	0	0	0	0
18	0	0	0	0	0	0
19	1	1	1	1	1	1
20	1	1	1	1	1	1

21	1	1	1	1	1	1
22	0	0	0	0	0	0
23	0	0	0	0	0	0
24	0	0	0	0	0	0
25	0	0	0	0	0	0
26	0	0	0	0	0	0
27	0	0	0	0	0	0
28	0	0	0	0	0	0
29	0	0	0	0	0	0
30	0	0	0	0	0	0
31	0	0	0	0	0	0
32	0	0	0	0	0	0
33	0	0	0	0	0	0
34	0	0	0	0	0	0
35	0	0	0	0	0	0
36	0	0	0	0	0	0
37	0	0	0	0	0	0
38	0	0	0	0	0	0
39	0	0	0	0	0	0
40	0	0	0	0	0	0
41	0	0	0	0	0	0
42	0	0	0	0	0	0
43	0	0	0	0	0	0
44	0	0	0	0	0	0
45	0	0	0	0	0	0
46	0	0	0	0	0	0
47	0	0	0	0	0	0
48	0	0	0	0	0	0
49	0	0	0	0	0	0
50	0	0	0	0	0	0
51	0	0	0	0	0	0
52	0	0	0	0	0	0
53	0	0	0	0	0	0
54	0	0	0	0	0	0
55	0	0	0	0	0	0
56	0	0	0	0	0	0
57	0	0	0	0	0	0
58	0	0	0	0	0	0
59	0	0	0	0	0	0
60	0	0	0	0	0	0
61	0	0	0	0	0	0
62	0	0	0	0	0	0
63	0	0	0	0	0	0
64	0	0	0	0	0	0
65	0	0	0	0	0	0

66	0	0	0	0	0	0
67	0	0	0	0	0	0
68	0	0	0	0	0	0
69	0	0	0	0	0	0
70	0	0	0	0	0	0
71	0	0	0	0	0	0
72	0	0	0	0	0	0
73	0	0	0	0	0	0
74	0	0	0	0	0	0
75	0	0	0	0	0	0
76	0	0	0	0	0	0
77	0	0	0	0	0	0
78	1	0	1	0	0	0
79	1	0	1	0	0	0
80	1	0	1	0	0	0
81	1	0	1	0	0	0
82	0	0	0	1	1	0
83	0	0	0	1	1	0
84	0	0	0	1	1	0
85	0	0	0	1	1	0
86	0	0	0	0	0	0
87	0	0	0	0	0	0
88	0	0	0	0	0	0
89	1	1	1	1	1	1
90	1	1	1	1	1	1
91	1	1	1	1	1	1
92	0	0	0	0	0	0
93	0	0	0	0	0	0
94	0	0	0	0	0	0
95	0	0	0	0	1	1
96	0	0	0	0	1	1
97	0	0	0	0	1	1

Samples Sam165 to Sam170 comprise at least one peptide which is characteristic of VIMs. The bacteria present in samples Sam165 to Sam170 therefore express a beta-lactamase which confers on them a resistance to penicillins, to cephalosporins and to carbapenems.

The detection methods described in examples 6 to 11 are particularly advantageous because they make it possible to assay a large number of peptides and at the same

time to detect the presence of one or more resistance mechanisms induced by one or more carbapenemases.

Furthermore, the detection is performed in a short time, less than one hour. In fact, only the part of the gradient between 3 and 34 minutes is useful to the analysis. Furthermore, the retention times of the assayed peptides are all below 34 minutes.

In addition, the detection methods described in examples 6 to 11 are more advantageous than the molecular biology methods because they detect the product of the expression of the genes, and not the genes themselves. The detection of a resistance may not have any clinical meaning if this gene is not expressed, or it if is expressed too weakly to lead to an effective resistance. The detection of a peptide characterising a protein characteristic of a resistance mechanism does not have this disadvantage.

Surprisingly, the above examples show that it is possible to attain by mass spectrometry the sensitivity necessary for the specific detection of the existence of a mechanism of resistance to at least one antimicrobial of a microorganism contained in a sample, without employing an amplification method as is usually the case when molecular biology methods are used.

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5

CLAIMS

1. A method of detecting at least one carbapenem resistance marker in a sample, the method comprising: subjecting the sample to MS/MS spectrometry in MRM mode, and detecting whether at least one of the carbapenem resistance marker is present in the sample, wherein the at least one carbapenem resistance marker comprises a KPC peptide of SEQ ID NO: 20-33, 1094, 1096, or 1097.

2. The method of claim 1, wherein the at least one carbapenem resistance marker comprises a KPC peptide of SEQ ID NO: 20, 21, 23, 25, 28, 29, 31, or 32.

3. The method of claim 1 or 2, wherein at least one of the carbapenem resistance markers are from a microorganism in the sample.

4. The method of any one of claims 1 to 3, further comprising, before performing MS/MS spectrometry in MRM mode, digesting proteins in the sample to produce peptides.

5. The method of claim 4, wherein the digestion is performed by an enzyme.

6. The method of claim 5, wherein the enzyme is trypsin.

7. The method of any one of claims 1 to 6, wherein the carbapenem resistance markers further comprise proteins or peptides of NDM, GES, IMP, IND, SME, VIM, OXA type, or any combination thereof.

8. The method of claim 7, wherein the carbapenem resistance markers comprise one or more NDM peptides of SEQ ID NO: 2-9 or 1083.

9. The method of claim 8, wherein the carbapenem resistance markers comprise one or more NDM peptides of SEQ ID NO: 2, 3, 5, or 7.

10. The method of any one of claims 7 to 9, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 51, 52, 54-58, 61-75, or 77-79.

11. The method of claim 10, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 51, 61, 64, 70, 73, 74, or 79.

12. The method of claim 10, wherein the carbapenem resistance markers comprise one or more GES peptides of SEQ ID NO: 54, 55, 66, 67, 68, 69, 71, 77, or 78.

13. The method of any one of claims 7 to 12, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 106, 108-130, 133-173, or 175-180.

14. The method of claim 13, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 106, 108, 109, 110, 112, 113, 115, 116, 117, 118, 121, 124, 126, 127, 128, 129, 130, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 175, 176, 177, 179, or 180.

15. The method of claim 13, wherein the carbapenem resistance markers comprise one or more IMP peptides of SEQ ID NO: 109, 143, 144, 148, 149, 150, 151, 154, 155, 156, 159, 165, 169, 170, 171, 172, or 173.

16. The method of any one of claims 7 to 15, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188-197, 200, 201, or 203-262.

17. The method of claim 16, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188, 189, 190, 191, 192, 193, 194, 195, 197, 201, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 215, 216, 218, 219, 220, 221, 222, 225, 226, 227, 228, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243,

244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, or 262.

18. The method of claim 16, wherein the carbapenem resistance markers comprise one or more IND peptides of SEQ ID NO: 188, 193, 207, 242, 243, 246, 256, or 260.

19. The method of any one of claims 7 to 18, wherein the carbapenem resistance markers comprise one or more SME peptides of SEQ ID NO: 266-281 or 283-287.

20. The method of claim 19, wherein the carbapenem resistance markers comprise one or more SME peptides of SEQ ID NO: 266, 268, 269, 270, 273, 274, 277, 279, or 281.

21. The method of any one of claims 7 to 20, wherein the carbapenem resistance markers comprise one or more VIM peptides of SEQ ID NO: 314-318, or 320-346.

22. The method of claim 21, wherein the carbapenem resistance markers comprise one or more VIM peptides of SEQ ID NO: 316, 318, 321, 341, 342, 344, or 346.

23. The method of any one of claims 7 to 22, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 509-523, 525-572, 574-604, 606-618, 620-696, 698-1077, or 1098-1109.

24. The method of claim 23, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 509, 510, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 525, 526, 528, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 571, 572, 574, 575, 576, 577, 578, 580, 581, 583, 584, 586, 587, 588, 589, 590, 591, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 604, 606, 607, 609, 611, 612, 613, 614, 615, 616, 618, 620, 622, 623, 624, 625, 626, 627, 632, 633, 635, 636, 637, 638, 639, 640, 641, 642, 643, 645, 648, 649, 651, 652, 653, 654, 655, 656, 659, 660, 664, 665, 666, 667, 669, 670, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 696, 698, 699, 700, 701, 702, 703, 706, 707, 710, 714, 717, 719,

720, 722, 725, 726, 727, 728, 729, 732, 735, 736, 737, 738, 740, 741, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 759, 760, 762, 763, 766, 767, 768, 769, 770, 771, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 785, 786, 787, 788, 789, 790, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 803, 804, 805, 806, 807, 809, 810, 811, 812, 813, 814, 815, 818, 821, 822, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 840, 841, 842, 844, 845, 846, 847, 848, 849, 850, 851, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 865, 866, 867, 868, 869, 871, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 912, 913, 914, 918, 920, 921, 922, 923, 928, 930, 932, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 953, 954, 955, 956, 958, 961, 962, 963, 964, 967, 968, 970, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 988, 990, 992, 993, 994, 995, 996, 997, 998, 1000, 1001, 1003, 1004, 1005, 1008, 1009, 1011, 1012, 1013, 1014, 1015, 1018, 1019, 1020, 1022, 1024, 1025, 1026, 1027, 1028, 1030, 1031, 1034, 1036, 1041, 1042, 1044, 1045, 1046, 1048, 1049, 1050, 1052, 1053, 1054, 1058, 1059, 1060, 1062, 1063, 1064, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, or 1109.

25. The method of claim 24, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 510, 512, 513, 514, 520, 521, 522, 523, 525, 530, 532, 537, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 556, 557, 558, 559, 560, 561, 562, 574, 581, 582, 583, 584, 596, 597, 598, 599, 600, 601, 602, 607, 609, 632, 633, 635, 636, 649, 655, 656, 667, 674, 675, 689, 690, 698, 714, 719, 720, 722, 727, 729, 741, 746, 748, 750, 751, 752, 755, 756, 757, 763, 767, 768, 772, 775, 781, 782, 790, 792, 793, 794, 795, 796, 797, 798, 801, 809, 811, 812, 813, 814, 824, 832, 834, 837, 838, 847, 851, 853, 854, 855, 856, 857, 858, 859, 860, 862, 868, 869, 870, 874, 875, 876, 877, 879, 880, 881, 882, 894, 895, 898, 902, 903, 904, 906, 907, 908, 912, 913, 914, 920, 922, 923, 937, 938, 939, 945, 946, 948, 949, 950, 951, 954, 956, 962, 964, 967, 969, 971, 972, 974, 975, 979, 980, 985, 988, 990, 993, 994, 995, 996, 997, 1000, 1001, 1003, 1004, 1005, 1011, 1013, 1015, 1018, 1019, 1027, 1030, 1034, 1035, 1036, 1042, 1048, 1052, 1058, 1060, 1070, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, or 1109.

26. The method of claim 24, wherein the carbapenem resistance markers comprise one or more OXA peptides of SEQ ID NO: 1098, 1100, 1102, 1103, 1104, 1105, 1107, 1108, or 1109.