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(54) **Title:** STREM1 MARKER PANELS FOR EARLY DETECTION OF SEPSIS

(57) **Abstract:** The present invention concerns the field of diagnostics. Specifically, it relates to a method for assessing a subject with suspected infection comprising the steps of determining the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1, determining the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6, comparing the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers, and assessing said subject based on the comparison and/or the calculation. The invention also relates to the use of a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM- 1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6 or a detection agent specifically binding to said first biomarker and a detection agent specifically binding to said second biomarker for assessing a subject with suspected infection. Moreover, the invention further relates to a computer-implemented method for assessing a subject with suspected infection and a device and a kit for assessing a subject with suspected infection.

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sTREM1 marker panels for early detection of sepsis

The present invention concerns the field of diagnostics. Specifically, it relates to a method for assessing a subject with suspected infection comprising the steps of determining the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1, determining the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6, comparing the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers, and assessing said subject based on the comparison and/or the calculation. The invention also relates to the use of a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6 or a detection agent specifically binding to said first biomarker and a detection agent specifically binding to said second biomarker for assessing a subject with suspected infection. Moreover, the invention further relates to a computer-implemented method for assessing a subject with suspected infection and a device and a kit for assessing a subject with suspected infection.

Infection, in particular, infection occurring in patients having more severe signs and symptoms thereof such as those presenting in emergency units, may sometimes develop to more life threatening medical conditions including systemic inflammatory response syndrome (SIRS) and sepsis.

According to the sepsis-3 definition, sepsis is defined as a life threatening organ dysfunction caused by a dysregulated host response to infection. As it develops rapidly, early recognition is important for sepsis patient management and start of correct therapeutic measures including appropriate antibiotic therapy within the first hour of admission, and start of resuscitation with intravenous fluids and vasoactive drugs (surviving sepsis campaign guidelines 2016). Delay for every hour, incrementally increases morbidity and mortality.

Diagnosis of sepsis is based on clinical signs and symptoms that are non-specific and can be easily missed. Thus, patients are frequently misdiagnosed and the severity of disease is often underestimated. There is no gold standard for diagnosis of sepsis in general and in the emergency department in particular so far. In high income countries c-reactive protein (CRP), Procalcitonin (PCT) and white blood cell (WBC) count are often used in emergency units for detection of patients with bloodstream infection at risk for development of sepsis, together with lactate for detection of septic shock. In low income countries, diagnosis is mostly based on clinical signs and symptoms and in some instances SIRS and SOFA criteria. However, in the most current guidelines, besides lactate, no biomarker has been listed to diagnose sepsis (with the exception of clinical chemistry, BGE and hematology components of the SOFA score). PCT has only been recommended to potentially deescalate antibiotic therapy, however, with moderate evidence. Limitations of PCT in sepsis diagnosis are mainly the moderate sensitivity and specificity.

WO 2007/009071 discloses method of diagnosing an inflammatory response in a test subject based on sFlt-1. The disclosed method further comprises analyzing the level of at least one of VEGF, PlGF, TNF-α, IL-6, D-dimer, P-selectin, ICAM-I. VCAM-I, Cox-2, or PAI-I.

EP 2 174 143 B1 discloses an *in vitro* method for prognosis for a patient having a primary disease not being an infection, the method comprising determining the level of procalcitonin.

A multitude of markers have been suggested to be useful for detection or diagnosis of sepsis. These include, amongst many others, PCT, Presepsin, GDF-15, sFLT, inflammatory markers like CRP or interleukins, or markers specific of organ failure (see, e.g., Spanuth, 2014, Comparison of sCD14-ST (presepsin) with eight biomarkers for mortality prediction in patients admitted with acute heart failure, 2014 AACC Annual Meeting Abstracts. B-331; van Engelen, 2018, Crit Care Clin 34(1): 139-152.)

WO2015/031996 describes biomarkers for early determination of a critical or life threatening response to illness and/or treatment response.

However, there is still a need for biomarkers, which allow for a reliable and early assessment of patients exhibiting signs and symptoms of infection.

The present invention, therefore, provides means and methods complying with these needs.

The present invention relates to a method for assessing a subject with suspected infection comprising the steps of:

(a) determining the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;

(b) determining the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;

(c) comparing the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and

(d) assessing said subject based on the comparison and/or the calculation made in step (c).

It is to be understood that as used in the specification and in the claims, “a” or “an” can mean one or more, depending upon the context in which it is used. Thus, for example, reference to “an” item can mean that at least one item can be utilized.

As used in the following, the terms “have”, “comprise” or “include” or any arbitrary grammatical variations thereof are used in a non-exclusive way. Thus, these terms may both refer to a situation in which, besides the feature introduced by these terms, no further features are present in the entity described in this context and to a situation in which one or more further features are present. As an example, the expressions “A has B”, “A comprises B” and “A includes B” may both refer to a situation in which, besides B, no other element is present in A (i.e. a situation in which A solely and exclusively consists of B) and to a situation in which, besides B, one or more further elements are present in entity A, such as element C, elements C and D or even further elements. The term “comprising” also encompasses embodiments where only the items referred to are present, i.e. it has a limiting meaning in the sense of “consisting of”.

Further, as used in the following, the terms "particularly", "more particularly", “typically”, and “more typically” or similar terms are used in conjunction with additional / alternative features, without restricting alternative possibilities. Thus, features introduced by these terms are additional / alternative features and are not intended to restrict the scope of the claims in any way. The invention may, as the skilled person will recognize, be performed by using alternative features. Similarly, features introduced by "in an embodiment of the invention" or similar expressions are intended to be additional / alternative features, without any restriction regarding alternative embodiments of the invention, without any

restrictions regarding the scope of the invention and without any restriction regarding the possibility of combining the features introduced in such way with other additional / alternative or non-additional / alternative features of the invention.

Further, it will be understood that the term “at least one” as used herein means that one or more of the items referred to following the term may be used in accordance with the invention. For example, if the term indicates that at least one sampling unit shall be used this may be under-stood as one sampling unit or more than one sampling units, i.e. two, three, four, five or any other number. Depending on the item the term refers to, the skilled person understands as to what upper limit the term may refer, if any.

The term “about” as used herein means that with respect to any number recited after said term an interval accuracy exists within in which a technical effect can be achieved. Accordingly, about as referred to herein, preferably, refers to the precise numerical value or a range around said precise numerical value of ±20 %, preferably ±15 %, more preferably ±10 %, or even more preferably ±5 %.

Furthermore, the terms "first", "second", "third" and the like in the description and in the claims are used for distinguishing between similar elements and not necessarily for describing a sequential or chronological order.

The method of the present invention may consist of the aforementioned step or may comprise additional steps, such as steps for further evaluation of the assessment obtained in step (d), steps recommending therapeutic measures such as treatments, or the like. Moreover, it may comprise steps prior to step (a) such as steps relating to sample pre-treatments. However, preferably, it is envisaged that the above-mentioned method is an ex vivo method which does not require any steps being practiced on the human or animal body. Moreover, the method may be assisted by automation. Typically, the determination of the biomarkers may be supported by robotic equipment while the comparison and assessment may be supported by data processing equipment such as computers.

The term “assessing” as used herein refers to assessing whether a subject suffers from sepsis, is at risk of suffering from sepsis, exhibits a medical condition which deteriorates with respect to the overall health condition or with respect to sepsis or signs and symptoms accompanying sepsis and/or infection. Accordingly, assessing as used herein includes diagnosing sepsis, predicting the risk for developing sepsis, and/or predicting any deterioration of the health condition of the subject, in particular, with respect to signs and symptoms accompanying sepsis and/or infection. Typically, the assessment referred to in

accordance with the present invention is the assessment of the risk of developing sepsis (and thus the prediction of the risk of developing sepsis. Alternatively, the assessment is the prediction of the risk that the subject's (health) condition will deteriorate. Moreover, it will be understood that if the risk of developing sepsis or risk of the deterioration of the health condition is predicted, typically, the prediction is made within a predictive window. More typically, said predictive window is about 8 h, about 10 h, about 12 h, about 16 h, about 20 h, about 24 h, about 48 h, in particular at least about 48h, preferably, after the sample has been obtained. Further, the risk of developing sepsis within 24 or 48 hours, preferably after the test sample has been obtained, may be predicted.

In some embodiments, the risk of developing sepsis within 24 hours is predicted.
In some embodiments, the risk of developing sepsis within 48 hours is predicted. The period of 48 hours was analyzed in the Examples section.

In yet another embodiment, the assessment is the prediction of the risk that the subject's (health) condition will deteriorate in the future, or not. The term "deterioration of the condition" of a subject who is suspected to suffer from an infection and/or who is suffering from an infection is well understood by the skilled person. The term typically relates to deterioration of the condition which may ultimately lead to further medication or other intervention.

Preferably, the condition of the subject deteriorates, if the subject's disease severity increases, if the subject's antibiotic therapy is intensified, if the subject is admitted to the ICU or to another unit for higher level of care, if the subject requires emergency surgery, if the subject dies in the hospital, if the subject dies within 30 days of admission, if the subject is re-hospitalized within 30 days of discharge, if the subject experiences organ dysfunction or failure, as measured e.g. with the SOFA score, and/or if the subject requires organ support.

The skilled person understands when the condition of a subject does not deteriorate. Typically, the condition of the subject does not deteriorate, if the subject does not have the outcomes mentioned in the previous paragraph.

In an embodiment, the condition of the subject deteriorates, if the subject has one or more of the following outcomes: if the subject admitted to the ICU, if the subject dies in the hospital, if the subject dies within 30 days of admission, and/or if the subject is re-hospitalized within 30 days of discharge.

In an embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the risk that subject's antibiotic therapy is intensified.

In an embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the risk of a subject to be admitted to ICU. Thus, it is assessed whether the subject is at risk of being admitted to the ICU, or not.

In another embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the subject's risk of death in hospital. Thus, it is assessed whether the subject is at risk of death in hospital, or not.

In yet another embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the subject's risk of death within 30 days of admission. Thus, it is assessed whether the subject is at risk of death within 30 days of admission to the hospital, or not.

In yet another embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the subject's risk of re-hospitalization within 30 days of discharge. Thus, it is assessed whether the subject is at risk of re-hospitalization within 30 days of discharge, or not.

In yet another embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the risk that the subject experiences organ dysfunction or failure. Organ dysfunction and failure can be e.g. assessed via the SOFA score. Accordingly, the present invention further is directed to the prediction of the risk that the SOFA score of the subject will increase, or not (after the test sample has been obtained). An increase of the SOFA score (such as by at least one, at least two, at least three, or at least four points etc.) is considered as a deterioration of the condition. In contrast, the condition typically does not deteriorate, if the SOFA score does not increase (provided that the subject does not have the highest SOFA score). The predictive window may be a predictive window as described above for the prediction of the risk to develop sepsis.

The sequential organ failure assessment (SOFA) is a validated score, combining clinical assessment and laboratory measures, that quantitatively describes organ dysfunction/failure. Dysfunction of respiration, coagulation, the liver, the cardiovascular system, the central nervous system and the kidney are scored individually, and are summed up to the SOFA score, which ranges from 0 to 24. Preferably, the SOFA score is

determined as described in Vincent 1996 (Vincent et al. Intensive Care Med. 1996 Jul;22(7):707-10. doi: 10.1007/BF01709751. PMID: 8844239.).

In yet another embodiment, the prediction of the risk that the condition of the subject will deteriorate is the prediction of the risk that the subject requires organ support, such as the prediction of the risk that the subject requires vasoactive therapy, hemodynamic support (such as fluid therapy), oxygen supply (e.g. by ventilation or by extracorporeal membrane oxygenation), and/or renal replacement therapy. The predictive window may be a predictive window as described above for the prediction of the risk to develop sepsis, for example 24 or 48 hours after the sample has been obtained.

In an embodiment, the term "assessment" refers to the diagnosis of sepsis. Thus, it is diagnosed whether a subject with suspected infection suffers from sepsis, or not. Preferably, the assessment refers to the early detection of sepsis.

As will be understood by those skilled in the art, the assessment made in accordance with the present invention, although preferred to be, may usually not be correct for 100% of the investigated subjects. The term, typically, requires that a statistically significant portion of subjects can be correctly assessed. Whether a portion is statistically significant can be determined without further ado by the person skilled in the art using various well known statistic evaluation tools, e.g., determination of confidence intervals, p-value determination, Student´s t-test, Mann-Whitney test, etc.. Details may be found in Dowdy and Wearden, Statistics for Research, John Wiley & Sons, New York 1983. Typically envisaged confidence intervals are at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%. The p-values are, typically, 0.2, 0.1, 0.05.

The term "subject" as used herein refers to an animal, preferably a mammal and, more typically to a human. The subject to be investigated by the method of the present invention shall be a subject having suspected infection. The term "suspected infection" as used herein means that the subject shall exhibit clinical parameters, signs and/or symptoms of infection. Thus, the subject according to the invention is, typically, a subject that suffers from an infection or is suspected to suffer from an infection. Typically, the subject is a subject presenting at the emergency department.

Advantageously, the sample has been obtained at presentation. Preferably, the sample has been obtained at presentation at the emergency department. However, the sample may be also obtained at presentation at the primary care physician.

The term "sample" as used herein refers to any sample that under physiological conditions comprises the first, second and/or third biomarkers referred to herein. More typically, the sample is a body fluid sample, e.g. a blood sample or sample derived therefrom, a urine sample, a saliva sample a lymphatic fluid sample or the like. Most typically, said sample is a blood sample or a sample derived therefrom. Accordingly, the sample may be a blood, serum or plasma sample.

Blood samples, typically, include capillary, venous or arterial blood samples.

In an embodiment, the sample is an interstitial fluid sample.

The term "sepsis" is well-known in the art. As used herein, the term refers a life-threatening organ dysfunction caused by a dysregulated host response to infection. A definition for sepsis, for example, can be found in Singer et al. (Sepsis-3 The Third International Consensus Definitions for Sepsis and Septic Shock. JAMA 2016; 315:801-819) which herewith is incorporated by reference with respect to the entire disclosure content. Preferably, the term "sepsis" refers to sepsis according to the Sepsis-3 definition as disclosed in Singer et al. (loc. cit.).

Typically, the subject to be tested shall be suspected to suffer from an infection. The term "infection" is well understood by the skilled person. As used herein, the term "infection" preferably refers to an invasion of the subject's body tissues by a disease-causing microorganism, its multiplication, and the reaction of subject's tissues to the microorganism. In an embodiment, the infection is a bacterial infection. Thus, the subject shall be suspected to suffer from bacterial infection.

As set forth elsewhere herein, the present invention allows for the early identification of patients at risk. In an embodiment of the prediction as set forth herein, the subject to be tested thus does not suffer from sepsis at the time at which the sample is obtained. In particularly preferred embodiment, the subject to be tested does not suffer from septic shock, preferably, at the time at which the sample is obtained. The term "septic shock" is defined in Singer et al. (loc. cit.). Thus, a subject suffers from septic shock if the following criteria are met.

- Sepsis, i.e. suspected/documented infection AND change in total SOFA score $\geq$2 points consequent to the infection
- AND persisting hypotension requiring vasopressors to maintain MAP $\geq$65 mm Hg and having a serum lactate level >2 mmol/L (18mg/dL) despite adequate volume resuscitation

Further, it is envisaged that subject to be tested may or may not suffer from infection with SARS-CoV-2.

The term "determining" as used herein refers to qualitative and quantitative determination of the biomarkers referred to in accordance with the present invention, i.e. the term encompasses the determination of the presence or absence or the determination of the absolute or relative amount of said biomarkers.

The term "amount" as used herein refers to the absolute amount of a compound referred to herein, the relative amount or concentration of the said compound as well as any value or parameter which correlates thereto or can be derived therefrom. Such values or parameters comprise intensity signal values from all specific physical or chemical properties obtained from the said compounds by direct measurements, e.g., intensity values in mass spectra or NMR spectra. Moreover, encompassed are all values or parameters which are obtained by indirect measurements specified elsewhere in this description, e.g., response levels determined from biological read out systems in response to the compounds or intensity signals obtained from specifically bound ligands. It is to be understood that values correlating to the aforementioned amounts or parameters can also be obtained by all standard mathematical operations. In the biomarker is an enzyme, such as Alanine aminotransferase (ALAT) or Aspartate aminotransferase (AST or ASAT), the term "amount" may also encompass the activity of the enzyme.

Determining the amount in the method of the present invention may be carried out by any technique which allows for detecting the presence or absence or the amount of said second molecule upon its release from the first molecule. Suitable techniques depend on the molecular nature and the properties of the biomarkers and are discussed elsewhere herein in more detail.

Typically, the amount of a biomarker as referred to in accordance with the present invention can be determined by immunoassays using sandwich, competition, or other assay formats. Said assays will develop a signal which is indicative for the presence or absence or the amount of a biomarker. Further suitable methods comprise measuring a physical or chemical property specific for the biomarker such as its precise molecular mass or NMR spectrum. Said methods comprise, preferably, biosensors, optical devices coupled to immunoassays, biochips, analytical devices such as mass- spectrometers, NMR-analysers, surface plasmon resonance measurement equipment or chromatography devices. Further, methods include micro-plate ELISA-based methods, fully-automated or robotic

immunoassays (available, e.g., from Roche). Suitable measurement methods according the present invention may also include precipitation (particularly immunoprecipitation), electrochemiluminescence (electro-generated chemiluminescence), RIA (radioimmunoassay), ELISA (enzyme-linked immunosorbent assay), electrochemiluminescence sandwich immunoassays (ECLIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA), turbidimetry, nephelometry, latex-enhanced turbidimetry or nephelometry, or solid phase immune tests. Further methods known in the art such as gel electrophoresis, 2D gel electrophoresis, SDS polyacrylamid gel electrophoresis (SDS-PAGE) or Western Blotting. More typically, techniques particular envisaged for determining the biomarkers referred to herein are described in the accompanying Examples, below.

The biomarkers to be determined in accordance with the present invention are well-known in the art. Moreover, methods for the determination of the amount of the biomarkers are known. For example, the biomarkers can be measured as described in the Examples section (see Example 1). Some of the tested biomarkers are enzymes (ALAT and ASAT). The amount of these biomarkers can be also determined by determining the activity of said enzymes in the sample.

sTREM-1 or soluble TREM1 (or STREM1) is the soluble form of TREM-1 (Triggering Receptor Expressed on Myeloid Cells-1). Thus, the term refers to non-cell bound forms of TREM-1. TREM-1 is an immune receptor known to be expressed on neutrophils and monocytes/macrophages. It is a recently discovered member of the immunoglobulin superfamily which is involved in the innate immune response. TREM-1 is an about 30 kD monomeric protein synthesized as a 234 amino acid precursor with a signal peptide of 16 amino acids, an extracellular domain of 184 amino acid, a transmembrane domain of 29 amino acids and a short cytoplasmic domain of 5 amino acids. During infections, receptor expression is change and sTREM-1 is released. sTREM-1 (17 kDa) is, thus, soluble form of TREM-1 shed from the membrane of activated phagocytes, Typically, the term "sTREM-1" encompasses all naturally occurring cleaved or released forms which have at least the extracellular portion of TREM-1.

Interleukin-6 (abbreviated as IL-6) is an interleukin is secreted by T cells and macrophages to stimulate immune response, e.g. during infection and after trauma, especially burns or other tissue damage leading to inflammation. It acts as both a pro-inflammatory and anti-inflammatory cytokine. In humans, it is encoded by the IL6 gene. The sequence of human IL-6 can be assessed via GenBank (see NM_000600.3 for the polynucleotide sequence, and NP_000591.1 for the amino acid sequence). IL-6 signals through a cell-surface type I

cytokine receptor complex consisting of the ligand-binding IL-6Rα chain (CD126), and the signal-transducing component gp130 (also called CD130). CD130 is the common signal transducer for several cytokines including leukemia inhibitory factor (LIF), ciliary neurotropic factor, oncostatin M, IL-11 and cardiotrophin-1, and is almost ubiquitously expressed in most tissues. In contrast, the expression of CD126 is restricted to certain tissues. As IL-6 interacts with its receptor, it triggers the gp130 and IL-6R proteins to form a complex, thus activating the receptor. These complexes bring together the intracellular regions of gp130 to initiate a signal transduction cascade through certain transcription factors, Janus kinases (JAKs) and Signal Transducers and Activators of Transcription.

The marker "creatinine" is well known in the art. In muscle metabolism, creatinine is synthesized endogeneously from creatine and creatine phosphate. Under conditions of normal renal function, creatinine is excreted by glomerular filtration. Creatinine determinations are performed for the diagnosis and monitoring of acute and chronic renal disease as well as for the monitoring of renal dialysis. Creatinine concentrations in urine can be used as reference values for the excretion of certain analytes (albumin, α-amylase). Creatinine can be determined as described by Popper et al., (Popper H et al. Biochem Z 1937;291:354), Seelig and Wüst (Seelig HP, Wüst H. Ärztl Labor 1969;15:34) or Bartels (Bartels H et al. Clin Chim Acta 1972;37:193). For example, sodium hydroxide and picric acid are added to the sample to start the formation of creatinine-picric acid complex. In alkaline solution, creatinine forms a yellow-orange complex with picrate. The color intensity is directly proportion-al to the creatinine concentration and can be measured photometrically.

The biomarker endothelial cell specific molecule 1 (abbreviated ESM-1) is well known in the art. The biomarker is frequently also referred to as endocan. ESM-1 is a secreted protein which is mainly expressed in the endothelial cells in human lung and kidney tissues. Public domain data suggest expression also in thyroid, lung and kidney, but also in heart tissue, see. e.g. the entry for ESM-1 in the Protein Atlas database (Uhlén M. et al., Science 2015;347(6220): 1260419). The expression of this gene is regulated by cytokines. ESM-1 is a proteoglycan composed of a 20 kDa mature polypeptide and a 30 kDa O-linked glycan chain (Bechard D et al., J Biol Chem 2001;276(51):48341-48349). In a preferred embodiment of the present invention, the amount of the human ESM-1 polypeptide is determined in a sample from the subject. The sequence of the human ESM-1 polypeptide is well known in the art (see e.g. Lassale P. et al., J. Biol. Chem. 1996;271:20458-20464 and can be e.g. assessed via Uniprot database, see entry Q9NQ30 (ESM1_HUMAN). Two isoforms of ESM-1 are produced by alternative splicing, isoform 1 (having the Uniprot identifier Q9NQ30-1) and isoform 2 (having the Uniprot identifier Q9NQ30-2). Isoform 1

has length of 184 amino acids. In isoform 2, amino acids 101 to 150 of isoform 1 are missing. Amino acids 1 to 19 form the signal peptide (which might be cleaved off).

In a preferred embodiment, the amount of isoform 1 of the ESM-1 polypeptide is determined, i.e. isoform 1 having a sequence as shown under UniProt accession number Q9NQ30-1.

In another preferred embodiment, the amount of isoform 2 of the ESM-1 polypeptide is determined, i.e. isoform 2 having a sequence as shown under UniProt accession number Q9NQ30-2.

In another preferred embodiment, the amount of isoform-1 and isoform 2 of the ESM-1 polypeptide is determined, i.e. total ESM-1.

The marker "bilirubin" is well known in the art. Bilirubin is a member of the class of biladienes that is a linear tetrapyrrole with the dipyrrole units being of both exovinyl and endovinyl type. A product of heme degradation, it is produced in the reticuloendothelial system by the reduction of biliverdin and transported to the liver as a complex with serum albumin. It has a role as an antioxidant. Bilirubin measurements are performed routinely in most medical laboratories and can be measured by a variety of methods (such as by the method as described in the Examples section).

The term "cardiac Troponin" typically refers to human cardiac Troponin T or cardiac Troponin I. The term, however, also compasses variants of the aforementioned specific Troponins, i.e., preferably, of Troponin I, and more preferably, of Troponin T. Such variants have at least the same essential biological and immunological properties as the specific cardiac Troponins. In particular, they share the same essential biological and immunological properties if they are detectable by the same specific assays referred to in this specification, e.g., by ELISA Assays using polyclonal or monoclonal antibodies specifically recognizing the said cardiac Troponins. Moreover, it is to be understood that a variant as referred to in accordance with the present invention shall have an amino acid sequence which differs due to at least one amino acid substitution, deletion and/or addition wherein the amino acid sequence of the variant is still, preferably, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 92%, at least about 95%, at least about 97%, at 10 least about 98%, or at least about 99% identical with the amino sequence of the specific Troponin. Variants may be allelic variants or any other species specific homologs, paralogs, or orthologs. Moreover, the variants referred to herein include fragments of the specific cardiac

Troponins or the aforementioned types of variants as long as these fragments have the essential immunological and biological properties as referred to above. Preferably, the cardiac troponin variants have immunological properties (i.e. epitope composition) comparable to those of human troponin T or troponin I. Thus, the variants shall be recognizable by the aforementioned means or ligands used for determination of the concentration of the cardiac troponins. Thus, the variants shall be recognizable by the aforementioned means or ligands used for determination of the concentration of the cardiac troponins. Such fragments may be, e.g., degradation products of the Troponins. Further included are variants which differ due to posttranslational modi-fications such as phosphorylation or myristylation. Preferably the biological property of troponin I and its variant is the ability to inhibit actomyosin ATPase or to inhibit angiogenesis in vivo and in vitro, which may e.g. be detected based on the assay described by Moses et al. 1999 PNAS USA 96 (6): 2645-2650). Preferably the biological property of troponin T and its variant is the ability to form a complex with troponin C and I, to bind calcium ions or to bind to tropomyosin, preferably if present as a complex of troponin C, I and T or a complex formed by troponin C, troponin I and a variant of troponin T. Troponin T or Troponin I can be determined by immunoassays, e.g., ELISAs, that are well known in the art and commercially available. Particularly preferred in accordance with the present invention is the determination of Troponin T with high sensitivity using, e.g. a commercially available hs-cTn assay.

Alanine aminotransferase (ALAT) catalyzes the transamination of L-alanine to α-ketoglutarate (α-KG), forming L-glutamate and pyruvate. The pyruvate formed is reduced to lactate by lactate dehydrogenase (LDH) with simultaneous oxidation of reduced nicotinamide-adenine dinucleotide (NADH). The change in absorbance is directly proportional to the alanine aminotransferase activity and can be, e.g., measured using a bichromatic (340, 700 nm) rate technique.

Aspartate aminotransferase (AST or ASAT) catalyzes the transamination from L-aspartate to α-ketoglutarate, forming L-glutamate and oxalacetate. The oxalacetate formed is reduced to malate by malate dehydrogenase (MDH) with simultaneous oxidation of reduced nicotinamide adenine dinucleotide (NADH). The change in absorbance with time due to the conversion of NADH to NAD is directly proportional to the AST activity and can be e.g. measured using a bichromatic (340, 700 nm) rate technique.

The biomarker "Haptoglobin" (abbreviated as HAPT) is well-known in the art. In humans, the protein is encoded by the HP gene. Haptoglobin captures, and combines with free plasma hemoglobin to allow hepatic recycling of heme iron and to prevent kidney damage.

Haptoglobin also acts as an antioxidant, has antibacterial activity, and plays a role in modulating many aspects of the acute phase response. Information on the sequence of the human Haptoglobin polypeptide can be accessed via Uniprot(See UniProtKB - P00738 (HPT_HUMAN)).

As used herein, the term "BNP-type peptide", preferably, comprises pre-proBNP, proBNP, NT-proBNP, and BNP. More preferably, the BNP-type peptide is NT-proBNP or BNP. Most preferably, the BNP-type peptide is NT-proBNP. The pre-pro peptide (134 amino acids in the case of pre-proBNP) comprises a short signal peptide, which is enzymatically cleaved off to release the pro peptide (108 amino acids in the case of proBNP). The pro peptide is further cleaved into an N-terminal pro peptide (NT-pro peptide, 76 amino acids in case of NT-proBNP) and the active hormone (32 amino acids in the case of BNP). Preferably, BNP-type peptides according to the present invention are NT-proBNP, BNP, and variants thereof. BNP (brain natriuretic peptide) is the active hormone and has a shorter half-life than the respective inactive counterpart NT-proBNP.

The biomarker Calprotectin (also referred to as S100A8/A9, calgranulin A and B, alarmins, CLP) is well known in the art. It is a small calcium and zinc-binding heterodimer, derived from neutrophils and macrophages that often associates with its main receptor, TLR4 (Toll-like receptor 4) via a non-covalent bond to mediate downstream signaling with active involvement in inflammation (Bresnick A.R. S100 proteins as therapeutic targets. Biophys. Rev. 2018;10:1617–1629. doi: 10.1007/s12551-018-0471-y).

The biomarker Angiopoietin-2 (abbreviated "Ang-2", frequently also referred to as ANGPT2) is well known in the art. It is a naturally occurring antagonist for both Ang-1 and TIE2 (see e.g. Maisonpierre et al., Science 277 (1997) 55-60). The protein can induce tyrosine phosphorylation of TEK/TIE2 in the absence of ANG-1. In the absence of angiogenic inducers, such as VEGF, ANG2-mediated loosening of cell-matrix contacts may induce endothelial cell apoptosis with consequent vascular regression. In concert with VEGF, it may facilitate endothelial cell migration and proliferation, thus serving as a permissive angiogenic signal. The sequence of human Angiopoietin is well known in the art. Uniprot lists three isoforms of Angiopoietin-2: Isoform 1 (Uniprot identifier: O15123-1), Isoform 2 (identifier: O15123-2) and Isoform 3 (O15123-3). In a preferred embodiment, the total amount of Angiopoietin-2 is determined. The total amount is preferably the sum of the amounts of complexed and free Angiopoietin-2.

The biomarker Heparin Binding Protein (abbreviated HBP) is also known as Cationic Antimicrobial Protein of 37kDa (CAP37) or azurocidin. It is a 37kDa glycoprotein

synthesised in neutrophils. Furthermore it is known that it is neutrophil granule-derived antibacterial and monocyte- and fibroblast-specific chemotactic glycoprotein which heparin. HBP belongs to the serine protease superfamily. However, it is inactive as a protease. The amino acid sequence of human HBP can be accessed via UniProt (see UniProtKB - P20160 (CAP7_HUMAN)).

In the method according to the present invention, a third biomarker may be determined. In particular, in step (b) of the method of the invention

(i) if the amount of Aspartate aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;

(ii) if the amount of a cardiac Troponin is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;

(iii) if the amount of ESM-1 is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, HBP or Creatinine as a third biomarker;

(iv) if the amount of HBP is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker; or

(v) if the amount of Alanine aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker, or

(vi) if the amount of a HBP is determined as the second biomarker, the method will further comprise determining the amount of Alanine aminotransferase or IL6 as a third biomarker.

Thus, the present invention concerns the determination of at least two biomarkers (i.e. a first and second biomarker as referred to herein), or of at least three biomarkers (i.e. a first, second and third biomarker as referred to herein).

The first biomarker is sTREM1. The second biomarker shall be selected from Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6.

In an embodiment, the second biomarker is a cardiac Troponin, such as cardiac Troponin T or I, preferably Troponin T.
In an alternative embodiment, the second biomarker is Bilirubing.
In an alternative embodiment, the second biomarker is ESM-1.
In an alternative embodiment, the second biomarker is HBP.
In an alternative embodiment, the second biomarker is Alanine aminotransferase..
In an alternative embodiment, the second biomarker is IL6.

Further, a third marker may be determined as described elsewhere herein.

It is to be understood that that the invention is not limited to the above markers. Rather, the invention may encompass the determination of additional markers.

The term "reference" as used herein refers to an amount or value which allows for allocation of a subject into either the group of subjects suffering from a disease or condition or being at risk for developing it or the group of subjects which do not suffer from said disease or condition or which are not at risk for developing it. Such a reference can be a threshold amount which separates these groups from each other. Accordingly, the reference shall be an amount or score which allows for allocation of a subject into a group of subjects suffering from a disease or condition or being at risk for developing it, or not. For example, the reference shall be an amount or score which allows for allocation of a subject into a group of subjects being at risk of developing sepsis, or not being at risk of developing sequence (within a predictive window as set forth above, such as within about 48 hours).

A suitable threshold amount separating the two groups can be calculated without further ado by the statistical tests referred to herein elsewhere based on amounts of biomarkers from either a subject or group of subjects known to suffer from a disease or condition or being at risk for developing it or a subject or group of subjects known not to suffer from a disease or condition or being at risk for developing it. The reference amount applicable for an individual subject may vary depending on various physiological parameters such as age, gender, or subpopulation.

Typically, said references are references for each biomarker derived from at least one subject known to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being at risk for developing sepsis, while amounts for each of the

biomarkers being different from the corresponding references are indicative for a subject being not at risk for developing sepsis.

Also typically, said references are references for each biomarker derived from at least one subject known not to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being not at risk for developing sepsis, while amounts for each of the biomarkers being different from the corresponding references are indicative for a subject being at risk for developing sepsis.

The term "at least one subject" refers to one subject or more than one subject, such as at least 10, 50, 100, 200, or 1000 subjects.

In an embodiment, amounts of the biomarkers larger than the references for said biomarkers are indicative for a subject being at risk (e.g. of developing sepsis as described elsewhere herein). Further, amounts of the biomarkers lower than the references for said biomarkers are indicative for a subject not being at risk (with the exception of Haptoglobin: For Haptoglobin, an amount of the biomarker lower than the reference for said biomarker is indicative for a subject being at risk, whereas an amount of the biomarker larger than the reference for said biomarker is indicative for a subject not being at risk).

Reference amounts can, in principle, be calculated for a cohort of subjects based on the average or mean values for a given parameter such as biomarker amount by applying standard statistically methods. In particular, accuracy of a test such as a method aiming to diagnose an event, or not, is best described by its receiver-operating characteristics (ROC) (see especially Zweig 1993, Clin. Chem. 39:561-577). The ROC graph is a plot of all of the sensitivity/specificity pairs resulting from continuously varying the decision threshold over the entire range of data observed. The clinical performance of a diagnostic method depends on its accuracy, i.e. its ability to correctly allocate subjects to a certain prognosis or diagnosis. The ROC plot indicates the overlap between the two distributions by plotting the sensitivity versus 1-specificity for the complete range of thresholds suitable for making a distinction. On the y-axis is sensitivity, or the true-positive fraction, which is defined as the ratio of number of true-positive test results to the product of number of true-positive and number of false-negative test results. This has also been referred to as positivity in the presence of a disease or condition. It is calculated solely from the affected subgroup. On the x-axis is the false-positive fraction, or 1-specificity, which is defined as the ratio of number of false-positive results to the product of number of true-negative and number of false-positive results. It is an index of specificity and is calculated entirely from the

unaffected subgroup. Because the true- and false-positive fractions are calculated entirely separately, by using the test results from two different subgroups, the ROC plot is independent of the prevalence of the event in the cohort. Each point on the ROC plot represents a sensitivity/-specificity pair corresponding to a particular decision threshold. A test with perfect discrimination (no overlap in the two distributions of results) has an ROC plot that passes through the upper left corner, where the true-positive fraction is 1.0, or 100% (perfect sensitivity), and the false-positive fraction is 0 (perfect specificity). The theoretical plot for a test with no discrimination (identical distributions of results for the two groups) is a 45° diagonal line from the lower left corner to the upper right corner. Most plots fall in between these two extremes. If the ROC plot falls completely below the 45° diagonal, this is easily remedied by reversing the criterion for "positivity" from "greater than" to "less than" or vice versa. Qualitatively, the closer the plot is to the upper left corner, the higher the overall accuracy of the test. Dependent on a desired confidence interval, a threshold can be derived from the ROC curve allowing for the diagnosis or prediction for a given event with a proper balance of sensitivity and specificity, respectively. Accordingly, the reference to be used for the aforementioned method of the present invention, i.e. a threshold which allows to discriminate between subjects being at risk and not being at risk can be generated, usually, by establishing a ROC for said cohort as described above and deriving a threshold amount therefrom. Dependent on a desired sensitivity and specificity for a diagnostic method, the ROC plot allows deriving suitable thresholds. It will be understood that an optimal sensitivity is desired for excluding a subject for being at increased risk (i.e. a rule out) whereas an optimal specificity is envisaged for a subject to be assessed as being at an increased risk (i.e. a rule in).

Step c) of the method of the present invention comprises comparing the amounts of the biomarkers (i.e. the first biomarker, the second biomarker and optionally the third biomarker) to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers.

Thus, the amount of the first biomarker, the second biomarker and optionally the third biomarker, respectively, may be compared to a reference for the first biomarker, a reference for the second biomarker and optionally a reference for the third biomarker.

Alternatively, a score may be calculated based on the amounts the biomarkers, i.e. based on the amounts of the first biomarker, the second biomarker and, optionally the third biomarker. Said score shall allow for assessing the subject with suspected infection, such as for predicting the risk of developing sepsis. Optionally, said score may be compared to a suitable reference score.

The term "comparing" as used herein encompasses comparing the determined amount for a biomarker as referred to herein to a reference. It is to be understood that comparing as used herein refers to any kind of comparison made between the value for the amount with the reference. However, it is to be understood that, preferably, identical types of values are compared with each other, e.g., if an absolute amount is determined and to be compared in the method of the invention, the reference shall also be an absolute amount, if a relative amount is determined and to be compared in the method of the invention, the reference shall also be a relative amount, etc.. Alternatively, the term "comparing" as used herein encompasses comparing a calculated score with a suitable reference core. The comparison may be carried out manually or computer assisted. The value of the amount and the reference can be, e.g., compared to each other and the said comparison can be automatically carried out by a computer program executing an algorithm for the comparison. The computer program carrying out the said evaluation will provide the desired assessment in a suitable output format.

As set forth above, it is also envisaged to calculate a score (in particular a single score) based on the amounts of the first and second biomarker, or the first, second or third biomarker, i.e. a single score, and to compare this score to a reference score. Preferably, the score is based on the amounts of the first and second biomarker in the sample from the test subject, and, if the amount of the third biomarker is determined, on the amounts of first, second and third biomarker in the sample from the test subject.

The calculated score combines information on the amounts of the at least two or three biomarkers. Moreover, in the score, the biomarkers are, preferably, weighted in accordance with their contribution to the establishment of the assessment. Thus, the values for the individual markers are typically weighted and the weighted values are used for calculating the score. Suitable coefficients (weights) can be determined by the skilled person without further ado. A score can also be calculated from a decision tree or a set (ensemble) of decision trees that has been trained on at least two biomarkers. Based on the combination of biomarkers applied in the method of the invention, the weight of an individual biomarker as well as the structure of decision trees may be different.

The score can be regarded as a classifier parameter for assessing a subject as set forth herein. In particular, it enables the person who provides the assessment based on a single score. The reference score is preferably a value, in particular a cut-off value which allows for assessing a subject with suspected infection as set forth herein.. Preferably, the reference is a single value. Thus, the person does not have to interpret the entire information on the amounts of the individual biomarkers. Using a scoring system as

described herein, advantageously, values of different dimensions or units for the biomarkers may be used since the values will be mathematically transformed into the score. Accordingly, e.g. values for absolute concentrations may be combined in a score with peak area ratios. The reference score to be applied may be elected based on the desired sensitivity or the desired specificity. How to elect a suitable reference score is well known in the art.

Advantageously, it has been found in the studies underlying the present invention that a combination of a first biomarker with a second and, preferably, a third biomarker allows for a reliable and early assessment of patients exhibiting signs and symptoms of infection. In the studies, patients presenting at emergency departments being medical (non-surgical) emergencies were investigated. To this end, patients were subdivided into those that are suffering from sepsis with a high probability and those suspected to suffer from infection without sepsis. The amount of various biomarkers has been determined and the biomarkers were analyzed and mathematically combined via logic regression analysis. The area under the receiver operating characteristic (AUC) was used to evaluate biomarker performance. The AUC values are the mathematical integer of a function f(x) within the interval [a][b]. AUC was also investigated for biomarker pairs and triplets. Biomarker combinations which together showed improved AUC over the best single biomarker AUC were identified. The results are described in the accompanying Examples, below.

In particular, if these patients are presenting in, e.g., emergency units, an early assessment of the risk for developing severe complications such as sepsis, SIRS or general deterioration of their overall health condition is decisive to start therapeutic measures including drug administration, physical or other therapeutic interventions and/or hospitalization. These therapeutic measures, in particular, may include, e.g., rapid administration of broad spectrum antibiotics, fluid resuscitation, vasoactive drug therapy, mechanical ventilation, other organ support (e.g., continuous hemofiltration, extracorporeal membrane oxygenation). Also encompassed as therapeutic measures is triage to higher level of care (e.g. intensive care unit, intermediate care unit). If there is no risk for severe complication, patients could be discharged home and managed in the outpatient setting or admitted to the hospital at a low level of care (e.g. general ward). Thanks to the present invention, life- threatening developments can be prevented since patients can be assessed by biomarker determination at an early stage. The biomarker pairs and triplets identified in the studies underling the present invention are a reliable basis for medical decisions and the assessment can be performed in a time- and cost-effective manner.

Thus, the methods of the present invention may further comprise recommending or initiating a suitable therapeutic measure. Typically, said suitable therapeutic measure is

selected from the medical guidelines or recommendations for management of sepsis such as International Guidelines for Management of Sepsis and Septic Shock (Intensive Care Med, 2017). For example, the therapeutic measure may be treatment of sepsis or further diagnostic investigation or other aspects of care deemed necessary by the practitioners.

In an embodiment, the therapeutic measure to be recommended or initiated if a patient has been assessed to be at risk is selected from

- administration of empiric broad spectrum therapy with at least one or more broad spectrum antibiotics, such as a cephalosporine, a beta-lactam/beta-lactamase inhibitor (e.g. piperacillin), or a carbapenem, typically depending on the organisms that are considered likely pathogens and antibiotic susceptibilities
- fluid resuscitation
- administration of one or more vasopressors, such as administration of norepinephrine, and
- administration of one or more corticosteroids, such as administration of hydrocortisone

The definitions given herein above, apply mutatis mutandis to the following.

The present invention also relates to a computer-implemented method for assessing a subject with suspected infection comprising the steps of:

(a) receiving a value for the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;

(b) receiving a value for the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;

(c) comparing the values for the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and

(d) assessing said subject based on the comparison and/or the calculation made in step (c).

The term “computer-implemented” as used herein means that the method is carried out in an automated fashion on a data processing unit which is, typically, comprised in a computer or similar data processing device. The data processing unit shall receive values for the amount of the biomarkers. Such values can be the amounts, relative amounts or any other calculated value reflecting the amount as described elsewhere herein in detail.

Accordingly, it is to be understood that the aforementioned method does not require the determination of amounts for the biomarkers but rather uses values for already predetermined amounts.

Typically, in step (b) of said method

(i) if the value for the amount of Aspartate aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;

(ii) if the value for the amount of a cardiac Troponin is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;

(iii) if the value for the amount of ESM-1 is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, sTREM-1, HBP or Creatinine as a third biomarker;

(iv) if the value for the amount of Bilirubin is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker; or

(v) if the value for the amount of Alanine aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker,

(vi) if the value for the amount of HBP is received as the second biomarker, the method will further comprise receiving a value for the amount of Alanine aminotransferase or IL6 as a third biomarker.

The present invention also, in principle, contemplates a computer program, computer program product or computer readable storage medium having tangibly embedded said computer program, wherein the computer program comprises instructions which, when run on a data processing device or computer, carry out the method of the present invention as specified above. Specifically, the present disclosure further encompasses:

- a computer or computer network comprising at least one processor, wherein the processor is adapted to perform the method according to one of the embodiments described in this description,
- a computer loadable data structure that is adapted to perform the method according to one of the embodiments described in this description while the data structure is being executed on a computer,

- a computer script, wherein the computer program is adapted to perform the method according to one of the embodiments described in this description while the program is being executed on a computer,
- a computer program comprising program means for performing the method according to one of the embodiments described in this description while the computer program is being executed on a computer or on a computer network,
- a computer program comprising program means according to the preceding embodiment, wherein the program means are stored on a storage medium readable to a computer,
- a storage medium, wherein a data structure is stored on the storage medium and wherein the data structure is adapted to perform the method according to one of the embodiments described in this description after having been loaded into a main and/or working storage of a computer or of a computer network,
- a computer program product having program code means, wherein the program code means can be stored or are stored on a storage medium, for performing the method according to one of the embodiments described in this description, if the program code means are executed on a computer or on a computer network,
- a data stream signal, typically encrypted, comprising a data for parameters as defined herein elsewhere, and
- a data stream signal, typically encrypted, comprising the assessment provided by the methods of the present invention.

The present invention relates to a device for assessing a subject with suspected infection comprising:

(a) a measuring unit for determining the amount of a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6 in a sample of the subject, said measuring unit comprising a detection system for the first biomarker and the second biomarker; and

(b) an evaluation unit operably linked to the measuring unit comprising a database with stored references for the first biomarker and the second biomarker, preferably, as specified above and a data processor comprising instructions for carrying out a comparison of the amount of the first biomarker and the second biomarker to references and/or for carrying out a calculation of a score for assessing the subject with suspected infection based on the amounts of the biomarkers, preferably, as specified above and

for assessing said subject based on the comparison, said evaluation unit being capable of automatically receiving values for the amounts of the biomarkers from the measuring unit.

The term "device" as used herein relates to a system comprising the aforementioned units operatively linked to each other as to allow the determination of the amounts of biomarkers and evaluation thereof according to the method of the invention such that an assessment can be provided.

The analyzing unit, typically, comprises at least one reaction zone having a biomarker detection agent for the first and second biomarker and, preferably also the third biomarker, in immobilized form on a solid support or carrier which is to be contacted to the sample. Moreover, in the reaction zone, it is possible to apply conditions which allow for the specific binding of the detection agent(s) to the biomarkers comprised in the sample.

The reaction zone may either allow directly for sample application or it may be connected to a loading zone where the sample is applied. In the latter case, the sample can be actively or passively transported via the connection between the loading zone and the reaction zone to the reaction zone. Moreover, the reaction zone shall be also connected to a detector. The connection shall be such that the detector can detect the binding of the biomarkers to their detection agents. Suitable connections depend on the techniques used for measuring the presence or amount of the biomarkers. For example, for optical detection, transmission of light may be required between the detector and the reaction zone while for electrochemical determination a fluidal connection may be required, e.g., between the reaction zone and an electrode.

The detector shall be adapted to detect determination of the amount of the biomarkers. The determined amount can be subsequently transmitted to the evaluation unit. Said evaluation unit comprises a data processing element, such as a computer, with an implemented algorithm for determining the amount present in the sample.

The processing unit as referred to in accordance with the method of the present invention, typically, comprises a Central Processing Unit (CPU) and/or one or more Graphics Processing Units (GPUs) and/or one or more Application Specific Integrated Circuits (ASICs) and/or one or more Tensor Processing Units (TPUs) and/or one or more field-programmable gate arrays (FPGAs) or the like. A data processing element may be a general purpose computer or a portable computing device, for example. It should also be understood that multiple computing devices may be used together, such as over a network

or other methods of transferring data, for performing one or more steps of the methods disclosed herein. Exemplary computing devices include desktop computers, laptop computers, personal data assistants ("PDA"), cellular devices, smart or mobile devices, tablet computers, servers, and the like. In general, a data processing element comprises a processor capable of executing a plurality of instructions (such as a program of software).

The evaluation unit, typically comprises or has access to a memory. A memory is a computer readable medium and may comprise a single storage device or multiple storage devices, located either locally with the computing device or accessible to the computing device across a network, for example. Computer-readable media may be any available media that can be accessed by the computing device and includes both volatile and non-volatile media. Further, computer readable-media may be one or both of removable and non-removable media. By way of example, and not limitation, computer-readable media may comprise computer storage media. Exemplary computer storage media includes, but is not limited to, RAM, ROM, EEPROM, flash memory or any other memory technology, CD-ROM, Digital Versatile Disk (DVD) or other optical disk storage, magnetic cassettes, magnetic tape, magnetic disk storage or other magnetic storage devices, or any other medium which can be used for storing a plurality of instructions capable of being accessed by the computing device and executed by the processor of the computing device.

According to embodiments of the instant disclosure, software may include instructions which, when executed by a processor of the computing device, may perform one or more steps of the methods disclosed herein. Some of the instructions may be adapted to produce signals that control operation of other machines and thus may operate through those control signals to transform materials far removed from the computer itself. These descriptions and representations are the means used by those skilled in the art of data processing, for example, to most effectively convey the substance of their work to others skilled in the art.

The plurality of instructions may also comprise an algorithm which is generally conceived to be a self-consistent sequence of steps leading to a desired result. These steps are those requiring physical manipulations of physical quantities. Usually, though not necessarily, these quantities take the form of electrical or magnetic pulses or signals capable of being stored, transferred, transformed, combined, compared, and otherwise manipulated. It proves convenient at times, principally for reasons of common usage, to refer to these signals as values, characters, display data, numbers, or the like as a reference to the physical items or manifestations in which such signals are embodied or expressed. It should be borne in mind, however, that all of these and similar terms are to be associated

with the appropriate physical quantities and are merely used here as convenient labels applied to these quantities.

The evaluation unit may also comprise or has access to an output device. Exemplary output devices include fax machines, displays, printers, and files, for example. According to some embodiments of the present disclosure, a computing device may perform one or more steps of a method disclosed herein, and thereafter provide an output, via an output device, relating to a result, indication, ratio or other factor of the method.

Typically, said measuring unit determines and comprises a detection system for a third biomarker and wherein said database comprises stored a reference for a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;
(iv) if Bilirubin is the second biomarker, Creatinine;
(v) if Alanine aminotransferase is the second biomarker, Creatinine, or
(vi) if HBP is the second biomarker, Alanine aminotransferase or IL6.

More typically, said detection system comprises at least one detection agent being capable of specifically detecting each of the biomarkers.

The present invention further contemplates a device for assessing a subject with suspected infection comprising an evaluation unit comprising a database with stored references for a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6 and a data processor comprising instructions for carrying out a comparison of the amount of the first biomarker and the second biomarker to references, preferably, as specified above and for assessing said subject based on the comparison, said evaluation unit being capable of receiving values for the amounts of the biomarkers determined in a sample of the subject.

Typically, said database comprises a stored reference for a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;

(iv) if Billirubin is the second biomarker, Creatinine;

(v) if Alanine aminotransferase is the second biomarker, Creatinine, or

(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

The present invention, in principle, also relates to the use of a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6 or a detection agent specifically binding to said first biomarker and a detection agent specifically binding to said second biomarker for assessing a subject with suspected infection.

The term "detection agent" as used herein, typically, refers to any agent which specifically binds to a biomarker, i.e. an agent which does not cross-react with other components present in the sample. Typically, a detection agent specifically binding a biomarker as referred to herein may be an antibody, an antibody fragment or derivative, an aptamer, a ligand for the biomarker, a receptor for the biomarker, an enzyme known to bind and/or convert the biomarker, or a small molecule known to specifically bind to the biomarker. For example, antibodies as referred to herein as detection agents include both polyclonal and monoclonal antibodies, as well as fragments thereof, such as Fv, Fab and F(ab)2 fragments that are capable of binding antigen or hapten. The present invention also includes single chain antibodies and humanized hybrid antibodies wherein amino acid sequences of a non-human donor antibody exhibiting a desired antigen-specificity are combined with sequences of a human acceptor antibody. The donor sequences will usually include at least the antigen-binding amino acid residues of the donor but may comprise other structurally and/or functionally relevant amino acid residues of the donor antibody as well. Such hybrids can be prepared by several methods well known in the art. Aptamer detection agents, e.g., may be nucleic acid or peptide aptamers. Methods to prepare such aptamers are well-known in the art. For example, random mutations can be introduced into the nucleic acids or peptides being the basis for aptamers. These derivatives can then be tested for binding according to screening procedures known in the art, e.g. phage display. Specific binding of a detection agent means that it should not bind substantially to, i.e. cross-react with, another peptide, polypeptide or substance present in the sample to be

analyzed. Preferably, the specifically bound biomarker should be bound with at least 3 times higher, more preferably at least 10 times higher and even more preferably at least 50 times higher affinity than any other components of the sample. Non-specific binding may be tolerable, if it can still be distinguished and measured unequivocally, e.g. according to its size on a Western Blot, or by its relatively higher abundance in the sample.

The detection agent may be fused or linked permanently or reversibly to a detectable label. Suitable labels are well known to the skilled artisan. Suitable detectable labels are any labels detectable by an appropriate detection method. Typical labels include gold particles, latex beads, acridan ester, luminol, ruthenium, enzymatically active labels, radioactive labels, magnetic labels ("e.g. magnetic beads", including paramagnetic and superparamagnetic labels), and fluorescent labels. Enzymatically active labels include e.g. horseradish peroxidase, alkaline phosphatase, beta-Galactosidase, Luciferase, and derivatives thereof. Suitable substrates for detection include di-amino-benzidine (DAB), 3,3'-5,5'-tetramethylbenzidine, NBT-BCIP (4-nitro blue tetrazolium chloride and 5-bromo-4-chloro-3-indolyl-phosphate, available as ready-made stock solution from Roche Diagnostics), CDP-Star™ (Amersham Biosciences), ECF™ (Amersham Biosciences). A suitable enzyme-substrate combination may result in a colored reaction product, fluorescence or chemoluminescence, which can be measured according to methods known in the art (e.g. using a light-sensitive film or a suitable camera system). As for measuring the enyzmatic reaction, the criteria given above apply analogously. Typical fluorescent labels include fluorescent proteins (such as GFP and its derivatives), Cy3, Cy5, Texas Red, Fluorescein, and the Alexa dyes (e.g. Alexa 568). Further fluorescent labels are available e.g. from Molecular Probes (Oregon). Also the use of quantum dots as fluorescent labels is contemplated. Typical radioactive labels include 35S, 125I, 32P, 33P and the like. A radioactive label can be detected by any method known and appropriate, e.g. a light-sensitive film or a phosphor imager. Suitable labels may also be or comprise tags, such as biotin, digoxygenin, His-Tag, Glutathion-S-Transferase, FLAG, GFP, myc-tag, influenza A virus haemagglutinin (HA), maltose binding protein, and the like.

Preferred detection agents for biomarkers such as AST, ALT and creatinine are e.g. described in the Examples (see e.g. Example 1).

If the biomarker is an enzyme, such as AST or ALT, the detection agent may be the substrate of the enzyme, or any agent that is used for the detection (see Examples)

In an embodiment, the detection agent for ALT (ALAT) is e.g. L-alanine.
In an embodiment, the detection agent for AST (ASAT) is e.g. L-aspartate.

A detection agent for Creatinine is e.g. creatininase, or any agent that is used for the detection (see Examples).
Detection agents for Bilirubin a, e.g. sodium nitrite and sulfanilic acid, or any agent that is used for the detection (see Examples).

The determination of a biomarker as set forth herein may comprise mass spectrometry (MS) which is carried out after the separation step (e.g. by LC or HPLC). Mass spectrometry as used herein encompasses all techniques which allow for the determination of the molecular weight (i.e. the mass) or a mass variable corresponding to a compound, i.e. a biomarker, to be determined in accordance with the present invention. Preferably, mass spectrometry as used herein relates to GC-MS, LC-MS, direct infusion mass spectrometry, FT-ICR-MS, CE-MS, HPLC-MS, quadrupole mass spectrometry, any sequentially coupled mass spectrometry such as MS-MS or MS-MS-MS, ICP-MS, Py-MS, TOF or any combined approaches using the aforementioned techniques. How to apply these techniques is well known to the per-son skilled in the art. Moreover, suitable devices are commercially available. More preferably, mass spectrometry as used herein relates to LC-MS and/or HPLC-MS, i.e. to mass spectrometry being operatively linked to a prior liquid chromatography separation step. Preferably, the mass spectrometry is tandem mass spectrometry (also known as MS/MS). Tandem mass spectrometry, also known as MS/MS involves two or more mass spectrometry step, with a fragmentation occurring in between the stages. In tandem mass spectrometry two mass spectrometers in a series connected by a collision cell. The mass spectrometers are coupled to the chromatographic device. The sample that has been separated by a chromatography is sorted and weighed in the first mass spectrometer, then fragmented by an inert gas in the collision cell, and a piece or pieces sorted and weighed in the second mass spectrometer. The fragments are sorted and weighed in the second mass spectrometer. Identification by MS/MS is more accurate.

In an embodiment, mass spectrometry as used herein encompasses quadrupole MS. Most preferably, said quadrupole MS is carried out as follows: a) selection of a mass/charge quotient (m/z) of an ion created by ionisation in a first analytical quadrupole of the mass spectrometer, b) frag-mentation of the ion selected in step a) by applying an acceleration voltage in an additional subsequent quadrupole which is filled with a collision gas and acts as a collision chamber, c) selection of a mass/charge quotient of an ion created by the fragmentation process in step b) in an additional subsequent quadrupole, whereby steps a) to c) of the method are carried out at least once and analysis of the mass/charge quotient of all the ions present in the mixture of substances as a result of the ionisation process, whereby the quadrupole is filled with collision gas but no acceleration voltage is applied

during the analysis. Details on said most preferred mass spectrometry to be used in accordance with the present invention can be found in WO2003/073464.

More preferably, said mass spectrometry is liquid chromatography (LC) MS such high performance liquid chromatography (HPLC) MS, in particular HPLC-MS/MS. Liquid chromatography as used herein refers to all techniques which allow for separation of compounds (i.e. metabolites) in liquid or supercritical phase.

For mass spectrometry, the analytes in the sample are ionized in order to generate charged molecules or molecule fragments. Afterwards, the mass-to-charge of the ionized analyte, in particular of the ionized biomarkers, or fragments thereof is measured. Prior to the ionization, the sample may be subjected to cleavage with a protease, e.g. with trypsin. The protease cleaves the protein biomarkers into smaller fragments.

Thus, the mass spectrometry step preferably comprises an ionization step in which the biomarkers to be determined are ionized. Of course, other compounds present in the sample/elulate are ionizied as well. Ionization of the biomarkers can be carried out by any method deemed appropriate, in particular by electron impact ionization, fast atom bombardment, electrospray ionization (ESI), atmospheric pressure chemical ionization (APCI), matrix assisted laser desorption ionization (MALDI).

In a preferred embodiment, the ionization step (for mass spectrometry) is carried out by electrospray ionization (ESI). Accordingly, the mass spectrometry is preferably ESI-MS (or if tandem MS is carried out: ESI-MS/MS). Electrospray is a soft ionization method which results in the formation of ions without breaking any chemical bonds.

More typically, a third biomarker or an detection agent specifically binding to said third biomarker is used in addition, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Billirubin or Procalcitonin;
(iv) if Billirubin is the second biomarker, Creatinine;
(v) if sTREM-1 is the second biomarker, Creatinine, or
(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

The present invention also relates to a kit for assessing a subject with suspected infection comprising a detection agent specifically binding to a first biomarker being STREM1 and a detection agent specifically binding to a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6.

The term "kit" as used herein refers to a collection of the aforementioned components, typically, provided in separate or within a single container. The container also typically comprises instructions for carrying out the method of the present invention. These instructions may be in the form of a manual or may be provided by a computer program code which is capable of carrying out or supports the determination of the biomarkers referred to in the methods of the present invention when implemented on a computer or a data processing device. The computer program code may be provided on a data storage medium or device such as an optical storage medium (e.g., a Compact Disc) or directly on a computer or data processing device or may be provided in a download format such as a link to an accessible server or cloud. Moreover, the kit may, usually, comprise standards for reference amounts of biomarkers for calibration purposes as described elsewhere herein in detail. The kit according to the present invention may also comprise further components which are necessary for carrying out the method of the invention such as solvents, buffers, washing solutions and/or reagents required for detection of the released second molecule. Further, it may comprise the device of the invention either in parts or in its entirety.

More typically, said kit further comprises a detection agent specifically binding a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;
(iv) if Billirubin is the second biomarker, Creatinine;
(v) if Alanine aminotransferase is the second biomarker, Creatinine, or
(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

It is to be understood that the definitions and explanations of the terms made above apply accordingly for all embodiments described in this specification and the accompanying

claims. The following embodiments are particular embodiments envisaged according to the present invention:

1. A method for assessing a subject with suspected infection comprising the steps of:
   (a) determining the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;
   (b) determining the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;
   (c) comparing the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and
   (d) assessing said subject based on the comparison and/or the calculation made in step (c).

2. The method of embodiment 1, wherein in step (b)
   (i) if the amount of Aspartate aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;
   (ii) if the amount of a cardiac Troponin is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;
   (iii) if the amount of ESM-1 is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, HBP or Creatinine as a third biomarker;
   (iv) if the amount of HBP is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker; or
   (v) if the amount of Alanine aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker, or

(vi) if the amount of a HBP is determined as the second biomarker, the method will further comprise determining the amount of Alanine aminotransferase or IL6 as a third biomarker.

3. The method of embodiment 1 or 2, wherein the subject is a subject presenting at the emergency department.

4. The method of any one of embodiments 1 to 3, wherein the assessment is the assessment of the risk of developing sepsis and/or the assessment of the risk that the subject's condition of the subject will deteriorate.

5. The method of any one of embodiments 1 to 4, wherein said references are references for each biomarker derived from at least one subject known to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being at risk for developing sepsis while amounts for each of the biomarkers being different from the corresponding references are indicative for a subject being not at risk for developing sepsis.

6. The method of any one of embodiments 1 to 4, wherein said references are references for each biomarker derived from at least one subject known not to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being not at risk for developing sepsis while amounts for each of the biomarkers being different from the corresponding references are indicative for a subject being at risk for developing sepsis.

7. The method of any one of embodiments 1 to 6, wherein said subject suffers from an infection or is suspected to suffer from an infection.

8. The method of any one of embodiments 1 to 7, wherein said sample is a blood sample or a sample derived therefrom.

9. The method of any one of embodiments 1 to 8, wherein said subject is a human.

10. A computer-implemented method for assessing a subject with suspected infection comprising the steps of:

(a) receiving a value for the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;

(b) receiving a value for the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;

(c) comparing the values for the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and

(d) assessing said subject based on the comparison and/or the calculation made in step (c).

11. The method of embodiment 10, wherein in step (b)

(i) if the value for the amount of Aspartate aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;

(ii) if the value for the amount of a cardiac Troponin is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;

(iii) if the value for the amount of ESM-1 is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, sTREM-1, HBP or Creatinine as a third biomarker;

(iv) if the value for the amount of Bilirubin is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker; or

(v) if the value for the amount of Alanine aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker,

(vi) if the value for the amount of HBP is received as the second biomarker, the method will further comprise receiving a value for the amount of Alanine aminotransferase or IL6 as a third biomarker.

12. A device for assessing a subject with suspected infection comprising:

(a) a measuring unit for determining the amount of a first biomarker being STREM1 and a second biomarker selected from the group consisting of:

Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6 in a sample of the subject, said measuring unit comprising a detection system for the first biomarker and the second biomarker; and

(b) an evaluation unit operably linked to the measuring unit comprising a database with stored references for the first biomarker and the second biomarker, preferably, as specified in any one of embodiments 1 to 9 and a data processor comprising instructions for carrying out a comparison of the amount of the first biomarker and the second biomarker to references and/or for carrying out a calculation of a score for assessing the subject with suspected infection based on the amounts of the biomarkers, preferably, as specified in any one of embodiments 1 to 9 and for assessing said subject based on the comparison, said evaluation unit being capable of automatically receiving values for the amounts of the biomarkers from the measuring unit.

13. The device of embodiment 12, wherein said measuring unit determines and comprises a detection system for a third biomarker and wherein said database comprises stored a reference for a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;

(iv) if Bilirubin is the second biomarker, Creatinine;

(v) if Alanine aminotransferase is the second biomarker, Creatinine, or

(vi) if HBP is the second biomarker, Alanine aminotransferase or IL6.

14. The device of embodiment 12 or 13, wherein said detection system comprises at least one detection agent being capable of specifically detecting each of the biomarkers.

15. A device for assessing a subject with suspected infection comprising an evaluation unit comprising a database with stored references for a first biomarker being STREM1 and a second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6 and a data processor comprising instructions

for carrying out a comparison of the amount of the first biomarker and the second biomarker to references, preferably, as specified in any one of embodiments 1 to 11 and for assessing said subject based on the comparison, said evaluation unit being capable of receiving values for the amounts of the biomarkers determined in a sample of the subject.

16. The device of embodiment 15, wherein said database comprises a stored reference for a third biomarker, said third biomarker being
(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;
(iv) if Billirubin is the second biomarker, Creatinine;
(v) if Alanine aminotransferase is the second biomarker, Creatinine, or
(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

17. Use of a first biomarker being STREM1 and a second biomarker selected from the group consisting of Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6 or an detection agent specifically binding to said first biomarker and an detection agent specifically binding to said second biomarker for assessing a subject with suspected infection.

18. The use of embodiment 17, wherein a third biomarker or an detection agent specifically binding to said third biomarker is used in addition, said third biomarker being
(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Billirubin or Procalcitonin;
(iv) if Billirubin is the second biomarker, Creatinine;
(v) if sTREM-1 is the second biomarker, Creatinine, or
(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

19. A kit for assessing a subject with suspected infection comprising an detection agent specifically binding to a first biomarker being STREM1 and an detection agent specifically binding to a second biomarker selected from the group consisting of Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6.

20. The kit of embodiment 19, wherein said kit further comprises an detection agent specifically binding a third biomarker, said third biomarker being
(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;
(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);
(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;
(iv) if Billirubin is the second biomarker, Creatinine;
(v) if Alanine aminotransferase is the second biomarker, Creatinine, or
(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

21, The method, device, use or kit of any one of the preceding embodiments, wherein the assessment is the assessment of the risk of developing sepsis.

22. The method, device, use or kit of any one of the preceding embodiments, wherein risk of developing sepsis within 48 hours is predicted.

All references cited throughout this specification are herewith incorporated with respect to the disclosure content specifically referred to above as well as in their entireties.

Example 1: Determination of biomarkers

The Elecsys® Electro- ChemiLuminescence (ECL) technology and assay method is briefly described below. The concentration of NT-proBNP was determined by a cobas e801 analyzer. Detection with a cobas e801 analyzer is based on the Elecsys® Electro-ChemiLuminescence (ECL) technology. In brief, biotin-labelled and ruthenium-labelled antibodies are combined with the respective amount of undiluted sample and incubated on the analyzer. Subsequently, streptavidin-coated magnetic microparticles are added and incubated on the instrument in order to facilitate binding of the biotin-labelled immunological complexes. After this incubation step the reaction mixture is transferred into the measuring cell where the beads are magnetically captured on the surface of an

electrode. ProCell M Buffer containing tripropylamine (TPA) for the subsequent ECL the reaction is then introduced into the measuring cell in order to separate bound immunoassay complexes from the free remaining particles. Induction of voltage between the working and the counter electrode then initiates the reaction leading to emission of photons by the ruthenium complexes as well as TPA. The resulting electrochemiluminescent signal is recorded by a photomultiplier and converted into numeric values indicating concentration level of the respective analyte.

TNTHS or cTNThs (cardiac troponin T) was measured with a commercial ECLIA assay for high-sensitivity-cTroponinT, a sandwich-immunoassay which was developed for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds cTnThs. 50 µL were used from each serum sample and measured undiluted on a cobas e801 analyzer (Roche Diagnostics, Germany).

PBNP or NTpBNP (N-terminal prohormone of brain natriuretic peptide) was measured with a commercial ECLIA assay for NTproBNP, a sandwich-immunoassay which was developed for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds NTproBNP. 15 µL were used from each serum sample and measured undiluted on a cobas e801 analyzer (Roche Diagnostics, Germany).

IL6 (Interleukin 6) was measured with a commercial ECLIA assay for Interleukin-6, a sandwich-immunoassay which was developed for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds IL-6. 30 µL were used from each serum sample and measured undiluted on a cobas e801 analyzer (Roche Diagnostics, Germany).

ESM1 (Endothelial cell-specific molecule 1) was measured with a robust prototype ECLIA assay for ESM-1, a sandwich-immunoassay which was developed in-house for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds ESM-1. 20 µL were used from each serum sample and measured undiluted on a cobas e601 analyzer (Roche Diagnostics, Germany).

STREM1 or sTREM-1 (Soluble triggering receptor expressed on myeloid cells 1) was measured with a robust prototype ECLIA assay for sTREM-1, a sandwich-immunoassay

which was developed in-house for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds sTREM-1. 50 µL were used from each serum sample and measured undiluted on a cobas e601 analyzer (Roche Diagnostics, Germany).

ANG2 or Ang-2 (Angiopoietin-2) was measured with a robust prototype ECLIA assay for Angiopoietin-2, a sandwich-immunoassay which was developed in-house for the cobas Elecsys® ECLIA platform (ECLIA Assay from Roche Diagnostics, Germany). The assay comprises a biotinylated and a ruthenylated monoclonal antibody that specifically binds Ang-2. 20 µL were used from each serum sample and measured undiluted on a cobas e601 analyzer (Roche Diagnostics, Germany).

CREP2 (Creatinine): This enzymatic method is based on the conversion of creatinine with the aid of creatininase, creatinase, and sarcosine oxidase to glycine, formaldehyde and hydrogen peroxide. Catalyzed by peroxidase the liberated hydrogen peroxide reacts with 4-aminophenazone and HTIB a) to form a quinone imine chromogen. The color intensity of the quinone imine chromogen formed is directly proportional to the creatinine concentration in the reaction mixture. Assay from Roche Diagnostics (Germany). 1,7 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

KL6 (Sialylated carbohydrate antigen KL-6): Sialylated carbohydrate antigen KL-6 (KL-6) in samples agglutinates with mouse KL-6 monoclonal antibody coated latex through the antigen-antibody reaction. The change in absorbance caused by this agglutination is measured to determine the KL-6 level. Reagents were from Sekisui Medical Co. (Japan). 2.5 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

LDHI2 (Lactate dehydrogenase): UV assay Lactate dehydrogenase catalyzes the conversion of L-lactate to pyruvate; NAD is reduced to NADH in the process. L-Lactate + NAD + LDH Pyruvate + NADH + H + The initial rate of the NADH formation is directly proportional to the catalytic LDH activity. It is determined by photometrically measuring the increase in absorbance. . Assay from Roche Diagnostics (Germany). 2.2 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

AT.pc (Antithrombin percentage): Kinetic colorimetric test. This test works according to the Antithrombin (AT) Heparin Cofactor assay principle. Heparin and a predefined amount

of thrombin are added to the sample in excess. All free antithrombin present binds to thrombin to form an inactive complex. Non-inhibited thrombin liberates p-nitroaniline from the chromogenic substrate MeOCO-Gly-Pro-Arg-pNA. The remaining amount of thrombin is inversely proportional to the antithrombin content of the sample and therefore the increase in absorbance at a wavelength of 415 nm can be used to calculate the antithrombin activity. Assay from Roche Diagnostics (Germany). 1 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

HAPT2 (Haptoglobin): An Immunoturbidimetric assay for human haptoglobin that forms a precipitate with a specific antiserum which is determined turbidimetric. 3,9 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

HBP (Heparin Binding Protein): The determination of HBP is based on a turbidimetric reaction which occurs between circulating HBP and avian monospecific polyclonal antibodies bound to chloromethyl microparticles at optimal pH conditions in the presence of polyethylene glycol polymer (PEG). The magnitude of the change is proportional to the quantity of HBP in the test sample. Reagents from Axis-Shield Diagnostics Ltd. (Scotland). 10 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

Calprotectin: The Gentian (Norway) Calprotectin Immunoassay is a Particle-Enhanced Turbidimetric Immunoassay (PETIA) for in vitro diagnostic testing of calprotectin in human plasma and serum samples. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

BILI (Bilirubin): Diazotized sulfanilic acid is formed by combining sodium nitrite and sulfanilic acid at low pH. Bilirubin (unconjugated) in the sample is solubilized by dilution in a mixture of caffeine/benzoate/acetate/EDTA. Upon addition of the diazotized sulfanilic acid, the solubilized bilirubin including conjugated bilirubins (mono and diglucoronides) and the delta form2 (biliprotein-bilirubin covalently bound to albumin) is converted to diazo-bilirubin, a red chromophore representing the total bilirubin which absorbs at 540 nm and is measured using a bichromatic (540, 700 nm) endpoint technique. A sample blank correction is used.

CREAJ2 (Creatinine): This kinetic colorimetric assay is based on the Jaffé method. In alkaline solution, creatinine forms a yellow-orange complex with picrate. The rate of dye formation is proportional to the creatinine concentration in the specimen. The assay uses "rate-blanking" to minimize interference by bilirubin. Assay from Roche Diagnostics (Germany). 7,5µL of Plasma were use for the determination. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

CREP2 (Creatinine): This enzymatic method is based on the conversion of creatinine with the aid of creatininase, creatinase, and sarcosine oxidase to glycine, formaldehyde and hydrogen peroxide. Catalyzed by peroxidase the liberated hydrogen peroxide reacts with 4-aminophenazone and HTIB a) to form a quinone imine chromogen. The color intensity of the quinone imine chromogen formed is directly proportional to the creatinine concentration in the reaction mixture. Assay from Roche Diagnostics (Germany). 1,7 µL of Plasma were analyzed. Samples were measured on a cobas c 501 analyzer (Roche Diagnostics, Germany).

ALAT (Alanine aminotransferase): Alanine aminotransferase catalyzes the transamination of L-alanine to α-ketoglutarate (α-KG), forming L-glutamate and pyruvate. The pyruvate formed is reduced to lactate by lactate dehydrogenase (LDH) with simultaneous oxidation of reduced nicotinamide-adenine dinucleotide (NADH). The change in absorbance is directly proportional to the alanine aminotransferase activity and is measured using a bichromatic (340, 700 nm) rate technique.

ASAT (Aspartate aminotransferase): Aspartate aminotransferase (AST) catalyzes the transamination from L-aspartate to α-ketoglutarate, forming L-glutamate and oxalacetate. The oxalacetate formed is reduced to malate by malate dehydrogenase (MDH) with simultaneous oxidation of reduced nicotinamide adenine dinucleotide (NADH). The change in absorbance with time due to the conversion of NADH to NAD is directly proportional to the AST activity and is measured using a bichromatic (340, 700 nm) rate technique.

Example 2: Analysis of the patients from the TRIAGE Study

TRIAGE Study, Kantonsspital Aarau, Switzerland, Emergency Department. (Schuetz 2013, BMC emergency medicine, 13(1), 12).

All consecutive patients seeking emergency department (ED) care for medical emergencies were included at ED admission. From a total of 4000 patients, a subset of patients with suspected infection at admission was selected and classified into a highly probable sepsis case group or infection control group according to:

- Case (N=64): Highly probable sepsis cases with deterioration/higher severity within 48h of ED presentation if they have been admitted to the ICU or meet the criteria of Rhee 2017, "Incidence and Trends of Sepsis in US Hospitals Using Clinical vs Claims Data, 2009-2014." JAMA 318(13): 1241-1249.

- Control (N=207): Patients with suspected infection but no sepsis within 48h of ED presentation.

Markers were mathematically combined via logistic regression and the "area under the receiver operating characteristic" (AUC) was used as a general measure for marker performance.

Combinations of marker pairs (bivariate marker combinations) having improved AUCs over the single markers by at least one percentage point are shown in Table 1.

Table 1: Bivariate marker combinations with their joint performance (AUC.bi), the univariate performance of the first marker (AUC.1) and the second marker (AUC.2), along with the performance improvement of the bivariate marker over the best single marker (Impr.AUC).

Marker	AUC.bi	AUC.1	AUC.2	Impr.AUC
STREM1 + ASAT	0.8370	0.7696	0.6939	0.0674
STREM1 + TNTHS	0.8344	0.7696	0.7967	0.0378
STREM1 + ESM1	0.8276	0.7696	0.7280	0.0580
STREM1 + HBP	0.8260	0.7696	0.5094	0.0564
STREM1 + ALAT	0.8113	0.7696	0.6004	0.0417
STREM1 + BILI	0.8080	0.7696	0.6829	0.0385
STREM1 + IL6	0.8075	0.7696	0.7328	0.0379

Combinations of marker triplets (trivariate marker combinations) having improved AUCs over the bivariate marker pairs as well as all three single markers by at least one percentage point are shown in Table 2.

Table 2: Trivariate marker combinations with their joint performance (AUC.tri), the bivariate performance of the first two markers as listed in Table 1 (AUC.bi), the univariate performance of the first marker (AUC.1), the second marker (AUC.2) and the third marker

(AUC.3), along with the performance improvement of the trivariate marker over the bivariate marker (Impr.AUC).

Marker	AUC.tri	AUC.bi	AUC.1	AUC.2	AUC.3	Impr.AUC
STREM1 + ASAT + BILI	0.8548	0.8370	0.7696	0.6939	0.6829	0.0178
STREM1 + ASAT + IL6	0.8614	0.8370	0.7696	0.6939	0.7328	0.0244
STREM1 + ASAT + PBNP	0.8588	0.8370	0.7696	0.6939	0.7549	0.0219
STREM1 + ASAT + TNTHS	0.8724	0.8370	0.7696	0.6939	0.7967	0.0354
STREM1 + ASAT + ANG2	0.8480	0.8370	0.7696	0.6939	0.7445	0.0110
STREM1 + ASAT + ESM1	0.8703	0.8370	0.7696	0.6939	0.7280	0.0333
STREM1 + ASAT + LDHI2	0.8482	0.8370	0.7696	0.6939	0.5740	0.0112
STREM1 + ASAT + HAPT2	0.8507	0.8370	0.7696	0.6939	0.5641	0.0138
STREM1 + ASAT + HBP	0.8692	0.8370	0.7696	0.6939	0.5094	0.0322
STREM1 + ASAT + Calprotectin	0.8497	0.8370	0.7696	0.6939	0.5801	0.0127
STREM1 + ASAT + CREP2	0.8621	0.8370	0.7696	0.6939	0.7903	0.0251
STREM1 + ASAT + CREJ2	0.8558	0.8370	0.7696	0.6939	0.7915	0.0189
STREM1 + TNTHS + BILI	0.8635	0.8344	0.7696	0.7967	0.6829	0.0291
STREM1 + TNTHS + ALAT	0.8594	0.8344	0.7696	0.7967	0.6004	0.0250
STREM1 + TNTHS + IL6	0.8503	0.8344	0.7696	0.7967	0.7328	0.0158
STREM1 + TNTHS + ESM1	0.8569	0.8344	0.7696	0.7967	0.7280	0.0224
STREM1 + TNTHS + HAPT2	0.8506	0.8344	0.7696	0.7967	0.5641	0.0162
STREM1 + TNTHS + HBP	0.8542	0.8344	0.7696	0.7967	0.5094	0.0197
STREM1 + ESM1 + BILI	0.8499	0.8276	0.7696	0.7280	0.6829	0.0223
STREM1 + ESM1 + ALAT	0.8580	0.8276	0.7696	0.7280	0.6004	0.0304
STREM1 + ESM1 + HBP	0.8690	0.8276	0.7696	0.7280	0.5094	0.0414
STREM1 + ESM1 + CREP2	0.8476	0.8276	0.7696	0.7280	0.7903	0.0200
STREM1 + HBP + BILI	0.8522	0.8260	0.7696	0.5094	0.6829	0.0262
STREM1 + HBP + ALAT	0.8510	0.8260	0.7696	0.5094	0.6004	0.0250
STREM1 + HBP + IL6	0.8489	0.8260	0.7696	0.5094	0.7328	0.0229
STREM1 + ALAT + CREP2	0.8525	0.8113	0.7696	0.6004	0.7903	0.0413
STREM1 + BILI + CREP2	0.8519	0.8080	0.7696	0.6829	0.7903	0.0438

Examples of bivariate combinations of markers not having improved over the single markers are shown in Table 3.

Table 3: Bivariate marker combinations with their joint performance (AUC.bi), the univariate performance of the first marker (AUC.1) and the second marker (AUC.2), along with the performance improvement of the bivariate marker over the best single marker (Impr.AUC).

Marker	AUC.bi	AUC.1	AUC.2	Impr.AUC
STREM1 + KL6	0.7546	0.7696	0.5569	-0.0149
STREM1 + NGAL	0.7565	0.7696	0.7344	-0.0130
STREM1 + AT.pc	0.7680	0.7696	0.5692	-0.0016

Claims

1. A method for assessing a subject with suspected infection comprising the steps of:
   (a) determining the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;
   (b) determining the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;
   (c) comparing the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and
   (d) assessing said subject based on the comparison and/or the calculation made in step (c).

2. The method of claim 1, wherein in step (b)
   (i) if the amount of Aspartate aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;
   (ii) if the amount of a cardiac Troponin is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;
   (iii) if the amount of ESM-1 is determined as the second biomarker, the method will further comprise determining the amount of Bilirubin, Alanine aminotransferase, HBP or Creatinine as a third biomarker;
   (iv) if the amount of HBP is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker; or
   (v) if the amount of Alanine aminotransferase is determined as the second biomarker, the method will further comprise determining the amount of Creatinine as a third biomarker, or

(vi) if the amount of a HBP is determined as the second biomarker, the method will further comprise determining the amount of Alanine aminotransferase or IL6 as a third biomarker.

3. The method of claim 1 or 2, wherein the subject is a subject presenting at the emergency department.

4. The method of any one of claims 1 to 3, wherein the assessment is the assessment of the risk of developing sepsis and/or the assessment of the risk that the subject's condition of the subject will deteriorate.

5. The method of any one of claims 1 to 4, wherein said references are references for each biomarker derived from at least one subject known to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being at risk for developing sepsis while amounts for each of the biomarkers being different from the corresponding references are indicative for a subject being not at risk for developing sepsis,
and/or
wherein said references are references for each biomarker derived from at least one subject known not to be at risk for developing sepsis, preferably wherein amounts for each of the biomarkers being essentially identical or similar to the corresponding references are indicative for a subject being not at risk for developing sepsis while amounts for each of the biomarkers being different from the corresponding references are indicative for a subject being at risk for developing sepsis.

6. The method of any one of claims 1 to 5, wherein said subject suffers from an infection or is suspected to suffer from an infection.

7. The method of any one of claims 1 to 6, wherein said sample is a blood sample or a sample derived therefrom, such as a serum or plasma sample, and/or wherein said subject is a human.

8. A computer-implemented method for assessing a subject with suspected infection comprising the steps of:

(a) receiving a value for the amount of a first biomarker in a sample of the subject, said first biomarker being STREM1;

(b) receiving a value for the amount of a second biomarker in a sample of the subject, wherein said second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, Alanine aminotransferase, and IL6;

(c) comparing the values for the amounts of the biomarkers to references for said biomarkers and/or calculating a score for assessing the subject with suspected infection based on the amounts of the biomarkers; and

(d) assessing said subject based on the comparison and/or the calculation made in step (c)

wherein optionally in step (b)

(i) if the value for the amount of Aspartate aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine as a third biomarker;

(ii) if the value for the amount of a cardiac Troponin is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, Alanine aminotransferase, IL6, ESM-1, HBP or HAPT (Haptoglobin) as a third biomarker;

(iii) if the value for the amount of ESM-1 is received as the second biomarker, the method will further comprise receiving a value for the amount of Bilirubin, sTREM-1, HBP or Creatinine as a third biomarker;

(iv) if the value for the amount of Bilirubin is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker; or

(v) if the value for the amount of Alanine aminotransferase is received as the second biomarker, the method will further comprise receiving a value for the amount of Creatinine as a third biomarker,

(vi) if the value for the amount of HBP is received as the second biomarker, the method will further comprise receiving a value for the amount of Alanine aminotransferase or IL6 as a third biomarker.

9. A device for assessing a subject with suspected infection comprising:

(a) a measuring unit for determining the amount of a first biomarker being STREM1 and a second biomarker selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6 in a sample of the subject,

said measuring unit comprising a detection system for the first biomarker and the second biomarker; and

(b) an evaluation unit operably linked to the measuring unit comprising a database with stored references for the first biomarker and the second biomarker, preferably, as specified in any one of claims 1 to 7 and a data processor comprising instructions for carrying out a comparison of the amount of the first biomarker and the second biomarker to references and/or for carrying out a calculation of a score for assessing the subject with suspected infection based on the amounts of the biomarkers, preferably, as specified in any one of claims 1 to 7 and for assessing said subject based on the comparison, said evaluation unit being capable of automatically receiving values for the amounts of the biomarkers from the measuring unit.

10. The device of claim 9, wherein said measuring unit determines and comprises a detection system for a third biomarker and wherein said database comprises stored a reference for a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;

(iv) if Bilirubin is the second biomarker, Creatinine;

(v) if Alanine aminotransferase is the second biomarker, Creatinine, or

(vi) if HBP is the second biomarker, Alanine aminotransferase or IL6.

11. The device of claim 9 or 10, wherein said detection system comprises at least one detection agent being capable of specifically detecting each of the biomarkers.

12. A device for assessing a subject with suspected infection comprising an evaluation unit comprising a database with stored references for a first biomarker being STREM1 and a second biomarker is selected from the group consisting of: Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6 and a data processor comprising instructions for carrying out a comparison of the amount of the first biomarker and the second biomarker to references, preferably, as specified in any one of claims 1 to 8 and for assessing said subject based on the comparison, said evaluation unit being capable

of receiving values for the amounts of the biomarkers determined in a sample of the subject,

wherein optionally said database comprises a stored reference for a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;

(iv) if Billirubin is the second biomarker, Creatinine;

(v) if Alanine aminotransferase is the second biomarker, Creatinine, or

(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

13. Use of a i) first biomarker being STREM1 and a second biomarker selected from the group consisting of Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6, or ii) an detection agent specifically binding to said first biomarker and an detection agent specifically binding to said second biomarker for assessing a subject with suspected infection.

14. The use of claim 13, wherein a third biomarker or an detection agent specifically binding to said third biomarker is used in addition, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Billirubin or Procalcitonin;

(iv) if Billirubin is the second biomarker, Creatinine;

(v) if sTREM-1 is the second biomarker, Creatinine, or

(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

15. A kit for assessing a subject with suspected infection comprising an detection agent specifically binding to a first biomarker being STREM1 and an detection agent specifically binding to a second biomarker selected from the group consisting of Aspartate aminotransferase, Bilirubin, ESM-1, HBP (Heparin-binding protein), a cardiac Troponin, sTREM-1, and IL6,

wherein optionally said kit further comprises an detection agent specifically binding a third biomarker, said third biomarker being

(i) if Aspartate aminotransferase is the second biomarker, Bilirubin, IL6, a BNP-type peptide, a cardiac Troponin, Ang2, ESM-1, Lactate dehydrogenase, HBP, HAPT (Haptoglobin), Calprotectin or Creatinine;

(ii) if a cardiac Troponin is the second biomarker, Bilirubin, sTREM-1, IL6, ESM-1, HBP or HAPT (Haptoglobin);

(iii) if ESM-1 is the second biomarker, Bilirubin, sTREM-1, HBP or Creatinine;

(iv) if Billirubin is the second biomarker, Creatinine;

(v) if Alanine aminotransferase is the second biomarker, Creatinine, or

(vi) if a HBP is the second biomarker, Alanine aminotransferase or IL6.

16. The method, device, use or kit of any one of the preceding claims, wherein the assessment is the assessment of the risk of developing sepsis.

17. The method, device, use or kit of any one of the preceding claims, wherein the risk of developing sepsis within 48 hours is predicted.