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(54) BIOMARKER FOR OSTEOARTHRITIS AND USE THEREOF

(57) The invention relates to the identification of a biomarker whose abundance in biological sample is changed in subjects with osteoarthritis and/or other ageing-related diseases. The biomarker has applications in the diagnosis of osteoarthritis and/or other ageing-related diseases, in determining the prognosis for an individual diagnosed with osteoarthritis and/or other ageing-related diseases, and in monitoring the efficacy of treatment for osteoarthritis and/or other ageing-related diseases.

Figure 1A

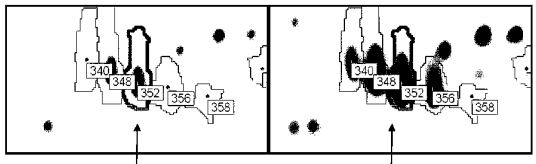
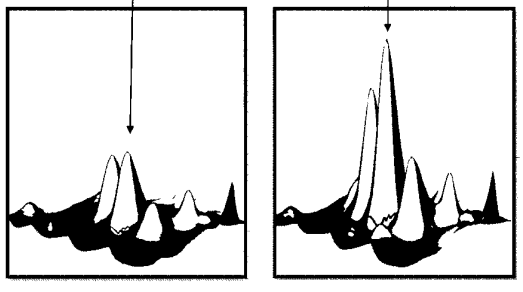


Figure 1B



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Description

[0001] The present invention relates to a biomarker for osteoarthritis and/or other ageing-related diseases. In particular, the invention relates to a method of diagnosing osteoarthritis, and/or other ageing-related diseases, by determining the level of a biomarker in a biological sample. The invention also relates to the use of a biomarker found in biological sample to monitor the efficacy of a treatment for osteoarthritis, and/or other ageing-related diseases, and to determine the prognosis for an individual diagnosed with osteoarthritis, and/or other ageing-related diseases.

[0002] Osteoarthritis is a progressive disorder characterized by destruction of articular cartilage and by subchondral bone and synovial changes. Currently the diagnosis of osteoarthritis is based on clinical and radiographic changes which occur late during disease progression. More specifically, diagnosis is based on cartilage integrity, which as articular cartilage is invisible on radiographs must be assessed indirectly from the spacing between subchondral bone ends in a joint. This method does not allow detection of early structural damage, and is cumbersome to use in daily practice.

[0003] Biochemical markers of bone, synovium or cartilage turnover have been proposed as potential tools for the diagnosis, prognosis and treatment monitoring of osteoarthritis (Garnero, P., et al., Ann Rheum Dis, 2001. 60(6): p. 619-26; Bruyere, O., et al., J Rheumatol, 2003. 30(5): p. 1043-50; and Wu, J., et al., Arthritis Rheum, 2007. 56(11): p. 3675-84). More specifically, Wu et al. (Arthritis Rheum, 2007. 56(11): p. 3675-84) describe potential molecular mediators and biomarkers of osteoarthritis in cartilage tissue. The method of Wu et al uses articular cartilage, obtained by an invasive procedure which provides only a limited amount of tissue. The method is therefore costly, time consuming and unsuitable for routine diagnostic testing, or for monitoring disease progression, or for determining the therapeutic effect of a treatment.

[0004] There therefore remains a need for a simple, rapid and effective method for the diagnosis of osteoarthritis and/or other ageing-related diseases, and/or to monitor the efficacy of treatments for osteoarthritis and/or other ageing-related diseases, and/or to determine the prognosis for a patient diagnosed with osteoarthritis and/or other ageing-related diseases.

[0005] The present invention provides a method for (i) diagnosing osteoarthritis and/or another ageing-related disease, (ii) determining the prognosis for a patient with osteoarthritis and/or another ageing-related disease, and (iii) monitoring the efficacy of a treatment for osteoarthritis and/or another ageing-related disease, using readily available biological samples and allow for rapid and cost effective use.

[0006] Reference herein to "other ageing-related diseases" or "another ageing related disease" is intended to refer to one or more diseases related to ageing which may include one or more of osteoporosis, macular degeneration and other degenerative diseases.

[0007] According to one aspect, the present invention provides a method of determining the osteoarthritis status of a subject, and/or the status of another ageing-related disease in a subject, comprising the steps of:

(i) determining the concentration in a biological sample of a free fragment comprising the same or substantially the same amino acid sequence as Seq ID no:1 or a fragment thereof;
(ii) comparing the free fragment concentration determined in step (i) with one or more reference values.

[0008] Reference herein to "free fragment" is intended to refer to a polypeptide, a peptide or otherwise released from mammalian fibulin-3 molecule by an oxidative or enzymatic processing. A free fragment is different from the native protein by its structure and configuration and may undergo modification such as phosphorylation, glycosylation or any other post-traductional modification resulting of a pathological mechanism. The free fragment according to the invention contributes to the identification of the pathologic status of osteoarthritis or osteoporotic patient.

[0009] According to another aspect, the present invention provides a method of diagnosing osteoarthritis and/or another ageing-related disease in a subject, comprising the steps of:

(i) determining the concentration in the sample of a free fragment comprising the same or substantially the same amino acid sequence as Seq ID no:1 or a fragment thereof;
(ii) comparing the free fragment concentration determined in step (ii) with one or more reference values.

[0010] According to yet another aspect, the present invention provides a method of determining the prognosis for a subject with osteoarthritis and/or another ageing-related disease, comprising the steps of:

(i) determining the concentration in the sample of a free fragment comprising the same or substantially the same amino acid sequence as Seq ID no:1 or a fragment thereof;
(ii) comparing the free fragment levels determined in step (i) with one or more reference values.

[0011] According to a further aspect, the present invention provides a method of determining the efficacy of a treatment

for osteoarthritis and/or another ageing-related disease in a subject, comprising the steps of:

(i) determining the concentration in a biological sample of a free fragment comprising the same or substantially the same amino acid sequence as Seq ID no:1 or a fragment thereof;
(ii) administering a treatment for osteoarthritis and/or another ageing related disease to the subject;
(iii) determining after treatment the concentration in another biological sample of a free fragment comprising the same or substantially the same amino acid sequence as Seq ID no:1 or a fragment thereof;
(iv) comparing the free fragment concentrations determined in step (i) and step (iii) with one another, and optionally with one or more reference values.

[0012] Preferably, in any method of the invention, the concentration of a free fragment with the same sequence as the sequence of Seq ID no: 1 is determined. Alternatively, the concentration of a free fragment with a sequence substantially the same as the sequence of Seq ID no: 1 may be determined.

[0013] Alternatively, the concentration of a peptide fragment having a sequence the same, or substantially the same, as part of the sequence of Seq ID no: 1 may be determined. The peptide fragment may have a sequence the same or substantially the same as one end of the sequence of Seq ID no: 1. Alternatively, the peptide fragment may have a sequence the same or substantially the same as an internal part, that is, not including either end, of the sequence of Seq ID No: 1. Preferably the peptide fragment is at least 5, preferably at least 10, preferably at least 20, more preferably at least 30 or more amino acids long.

[0014] Preferably if the concentration of a fragment having a sequence the same, or substantially the same, as part of the sequence of Seq ID no: 1 is determined, the fragment represents an epitope within the sequence of Seq ID no: 1.

[0015] An epitope is a binding site of an antibody on an antigen. In a peptide antigen, generally a linear epitope will be at least about 7 amino acids in length, and may be at least 8, at least 9, at least 10, at least 11, at least 12, at least 14, at least 16, at least 18, at least 20, at least 22, at least 24, or at least 30 or more amino acid residues in length. However, antibodies may also recognise conformational determinants formed by non-contiguous residues on an antigen, and an epitope can therefore require a larger fragment of the antigen to be present for binding, e. g. a domain.

[0016] Reference herein to "a sequence substantially the same as" all or part of the sequence of Seq ID no: 1, refers to a free fragment with a sequence which has at least 80%, preferably at least 90%, more preferably at least 95% or 98%, sequence identity with all or part of the sequence of Seq ID No:1. Preferably the peptide has a sequence the same or substantially the same as at least about 5, 10, 15, 20, 25, 30, 35, 40, 45 or more consecutive amino acids of the sequence of Seq ID No: 1. Preferably, the free fragment has a sequence the same, or substantially the same, as the entire sequence of Seq ID No: 1.

[0017] Homology or sequence identity of two or more amino acid sequences can be measured by using a homology scoring algorithm NCBI BLAST (National Center for Biotechnology Information Basic Local Alignment Search Tool). Alternatively, the UWGCC Package provides the BESTFIT program which can be used to calculate sequence identity between two or more sequences (e.g. used on its default setting) (Devereux et al (1984) Nucleic Acids Research 12 p387-395).

[0018] The sequence of Seq ID no:1 represents a fragment of the fibulin-3 protein. The fragment may be a degradation product of fibulin-3.

[0019] In any method of the invention the free fragment comprising a sequence the same or substantially the same as the sequence of Seq ID no: 1 or a part thereof is preferably differentially present in the sample from a subject with osteoarthritis or another ageing-related disease compared to a normal subject.

[0020] A free fragment comprising the same or substantially the same sequence as Seq ID no:1 or a fragment thereof, which is measured in step (i) and/or step (iv) in any method of the invention, is also referred to herein as the biomarker or the biomarker peptide.

[0021] Reference to the "osteoarthritis status" or to the "status of an ageing-related disease" refers to any distinguishable manifestation of osteoarthritis or an ageing-related disease, including diseased and non-diseased. For example, osteoarthritis status includes, without limitation, the presence or absence of osteoarthritis in a subject, the risk of a subject developing osteoarthritis, the stage of the disease, the progression of the disease, and the effectiveness or response of a subject to a treatment for osteoarthritis.

[0022] Any method of the invention may be used in conjunction with the assessment of clinical symptoms and/or imaging results and/or the concentration of one or more other biomarkers.

[0023] Preferably all methods of the invention are carried out *in vitro*.

[0024] The biological sample may comprise urine, whole blood, blood serum, blood plasma, synovium, sweat, cerebrospinal fluid, mucous, saliva, lymph, bronchial aspirate, milk and the like. Preferably the biological sample is urine.

[0025] Biological sample, such as urine, have the advantage of being abundant and easily accessible.

[0026] A further advantage of using a biological sample, compared to a tissue such as cartilage, is that the progression of osteoarthritis or another ageing-related disease, and/or the therapeutic effect of a treatment, may be monitored by

taking and testing samples as often as necessary without the need for invasive procedures.

[0027] The concentration of the biomarker peptide in a sample may be determined by any suitable assay. A suitable assay may include one or more of the following methods, an enzyme assay, an immunoassay, mass spectrometry, HPLC, electrophoresis or an antibody microarray, or any combination thereof. If an immunoassay is used it may be an enzyme linked immunoassay (ELISA), a sandwich assay, a competitive assay, a radioimmunoassay, a Western Blot, an immunoassay using a biosensor, an immunoprecipitation assay, an agglutination assay, a turbidity assay or a nephlelometric assay. If mass spectrometry is used it may be Matrix Assisted Laser Desorption/Ionization Time-of-Flight (MALDI-TOF) Mass Spectrometry.

[0028] Preferably the concentration of the biomarker peptide is determined using an immunoassay which uses one or more antibodies directed to the specific biomarker peptide to determine the concentration of the biomarker peptide in the sample.

[0029] If one or more antibodies are used to determine the concentration of a biomarker peptide in a sample the one or more antibodies may be synthetic, monoclonal, polyclonal, oligoclonal, bispecific, chimeric and/or humanised.

[0030] One or more of the antibodies used may comprise a tag or a label. The tag or label may be selected from the group comprising a radioactive, a fluorescent, a chemiluminescent, a dye, an enzyme, or a histidine tag or label, or any other suitable label or tag known in the art.

[0031] Preferably the reference value, to which the determined concentration of the biomarker peptide is compared, is the concentration of the same peptide in one or more "normal" subjects that do not have any detectable osteoarthritis and/or other ageing-related disease, or any clinical symptoms of osteoarthritis and/or other ageing-related disease, and have so called "normal values" of the biomarker peptide.

[0032] Alternatively, the reference value may be a previous value for the biomarker peptide obtained from a specific subject. This kind of reference value may be used if the method is to be used to monitor progression of osteoarthritis and/or another ageing-related disease, or to monitor the response of a subject to a particular treatment.

[0033] When the determined concentration of the biomarker is compared with a reference value, an increase or a decrease in the concentration of the biomarker may be indicative of the osteoarthritis status, and/or the status of another ageing-related disease, in the subject.

[0034] More specifically an increase or a decrease in the concentration of the biomarker may be indicative, or diagnostic, of osteoarthritis in the subject. An increase in the concentration of the biomarker, preferably of a free fragment with the sequence of Seq ID no:1, in a sample may be diagnostic of osteoarthritis.

[0035] Preferably an at least about 2 fold or more increase in the concentration of a free fragment with the sequence of Seq ID no:1, or with a sequence substantially the same as Seq ID no:1, or a fragment thereof, in a sample from a subject compared to a reference sample from a normal subject is diagnostic of osteoarthritis.

[0036] The method of the invention may also be used to monitor osteoarthritis progression, and/or the progression of another ageing-related disease, in a subject. Furthermore, the method of the invention may be used to monitor the efficacy of a treatment for osteoarthritis, and/or another ageing-related disease, following administration of the treatment to a subject. Efficacy of a treatment may be monitored by analysing samples taken from a subject at various time points following initiation of the treatment. By monitoring changes in the concentration of the biomarker peptide over time and comparing these concentrations to normal and/or reference values, efficacy of the treatment may be determined. In this case, reference concentrations may include the concentration of the biomarker peptide in the subject when a sample was first taken and analysed, or the concentration of the biomarker peptide in the subject when a sample was last taken, or both.

[0037] The subject in any method of the invention may be mammal, and is preferably a human, but may alternatively be a monkey, ape, dog, cow, gallus or rodent.

[0038] According to another aspect of the invention there is provided a kit for use in determining the osteoarthritis status, or the status of another ageing-related disease, in a subject, wherein the kit comprises at least one agent for determining the concentration of a free fragment comprising the same or substantially the same amino acid sequence as the sequence of Seq ID No:1, or a part thereof, in a biological sample.

[0039] The kit may be used to diagnose osteoarthritis and/or another ageing-related disease in a subject. The kit may alternatively be used to monitor disease progression or the efficacy of a treatment administered to a subject with osteoarthritis and/or another ageing-related disease.

[0040] The agent may be an enzyme, an antibody, a protein probe, a metabolite or any other suitable composition.

[0041] The agent for determining the concentration of the free fragment is preferably labelled. The kit may also comprise means for detecting the label.

[0042] The kit may comprise one or more capture agents for capturing the free fragment comprising the same or substantially the same amino acid sequence as the sequence of Seq ID No:1, or a part thereof, in a biological sample. The capture agent may be one or more antibodies. The capture agent may be an antibody according to an aspect of the invention.

[0043] The kit may comprise two antibodies for use in a sandwich assay to determine the concentration of a free

fragment comprising the same or substantially the same amino acid sequence as the sequence of Seq ID No:1, or a part thereof. Preferably the kit comprises two antibodies, each directed to a different epitope on the free fragment comprising the same or substantially the same amino acid sequence as the sequence of Seq ID No: 1, or a part thereof. One antibody is preferably the capture antibody, and the other antibody is preferably a detection antibody and may be labelled to allow its detection.

[0044] The capture agent may be attached to a solid support. The solid support may be a chip, a microtitre plate, a bead or a resin.

[0045] The kit may comprise instructions for suitable operational parameters in the form of a label or separate insert. The instructions may inform a user about how to collect the sample, and/or how to wash the capture agent.

[0046] The kit may comprise samples of the biomarker peptide to be detected. The samples of the biomarker peptide may be used as a standard for calibration and comparison. The kit may also comprise instructions to compare the concentration of the biomarker peptide detected in a sample with a calibration sample or chart. The kit may also include instructions indicating what concentration of the biomarker peptide is diagnostic of osteoarthritis and/or another ageing-related disease.

[0047] According to a yet further aspect, the invention provides the use of the determination of the concentration of the biomarker peptide in a sample of biological sample as a means of assessing the osteoarthritis status in a subject or as a means of assessing the status of another ageing-related disease in a subject.

[0048] According to a yet further aspect, the present invention provides the use of a biological sample, such as urine, as a source of at least one biomarker for use in determining the prognosis of osteoarthritis progression and/or another ageing-related disease, and/or for diagnosing osteoarthritis and/or another ageing-related disease, and/or for monitoring the effect of a treatment for osteoarthritis and/or another ageing-related disease.

[0049] According to another aspect the invention provides a free fragment which comprises the same, or substantially the same, amino acid sequence as the amino acid sequence of Seq ID NO: 1, or a part thereof, or its amide, or a salt thereof

[0050] Preferably the free fragment of the invention has a sequence the same as that of Seq ID No:1.

[0051] According to a further aspect, the invention provides a polynucleotide encoding a free fragment according to the invention. Preferably, the polynucleotide is a DNA molecule.

[0052] According to a yet further aspect the invention provides a recombinant vector, which comprises a polynucleotide of the invention.

[0053] According to another aspect the invention provides a transformant, which is transformed with the recombinant vector of the invention.

[0054] In a further aspect, the invention provides the use of a free fragment according to the invention in the manufacture of an antibody.

[0055] It a yet further aspect, the invention provides an antibody specific for a free fragment according to the invention. In particular, the invention provides an antibody specific for a free fragment having the sequence of Seq ID No: 1.

[0056] An antibody according to the invention may be synthetic, monoclonal, polyclonal, oligoclonal, bispecific, chimeric or humanised. The antibody may be complete or a fragment thereof, such as, Fv, Fab and $F(ab)_2$ fragments. Methods of generating antibodies are well known in the art, and may include immunisation of suitable animals, such as, a rabbit, mouse, sheep or goat, with the peptide of interest (or an immunogenic fragment thereof) or recombinant techniques.

[0057] The skilled man will appreciate that preferred features of any one embodiment and/or aspect of the invention may be applied to all other embodiments and/or aspects of the invention.

[0058] Embodiments of the invention will now be described merely by way of examples with reference to the accompanying figures in which:

Figure 1A - shows an enlargement of a portion of a 2D-DIGE map from osteoarthritis (OA) subjects (right) and non-osteoarthritis (NO) subjects (left).

Figure 1B - shows a representation of spot volume variation between OA subjects (right) and NO subjects (left).

Figure 2 - shows a graphic view of fibulin-3 abundance modification based on the spot volume increase shown in Figure 1B.

Figure 3A - shows the result of a mass spectrometry analysis of tryptic fragments of the peptide of fibulin-3 recovered from spot 352 detailed in Figures 1A, Figure 1B and Figure 2.

Figure 3B - shows the sequence of human fibulin-3 containing the fragments shown in Figure 3A.

Figure 4 - shows the modular domain structure of the fibulin proteins.

Figure 5 - shows the protein sequence of SEQ ID No. 1.

Figure 6 - shows the protein sequence of SEQ ID No. 2.

Figure 7A - shows an enlargement of a portion of a 2D-DIGE map from osteoarthritis (OA) subjects (Cy3, left) and osteoporosis (OP) subjects (Cy5, right).

Figure 7B - shows a graphic view of fibulin-3 abundance modification based on the spot volume increase shown in Figure 7A.

Figure 8 - shows an enhanced portion of 2D-DIGE gel obtained from proteins extracted from patients with severe osteoarthritis (OA), patients with osteoporosis (OP) and controls younger than 30 years (CTRL).

[0059] 2D-DIGE (two dimensional difference gel electrophoresis - Marouga et al, (2005) Anal Bioanal Chem 382(3): 669-78) methodology is a powerful tool for investigating protein expression profiles in multiple sets of samples.

[0060] In the examples, 2D-DIGE was used to study the protein expression profiles in urine samples from subjects with serious osteoarthritis or osteoporosis and from healthy young subjects. Proteins in the samples to be compared were labelled with either Cy3 or Cy5 CyDye DIGE Fluors. The Cy2 CyDye DIGE Fluor was used to label a pooled sample comprising equal amounts of each of the samples within the study, and this used as an internal standard. The use of this internal standard ensured that all proteins present in the samples were represented, assisting both inter- and intra-gel matching.

MATERIALS AND METHODS

Urine samples preparation

[0061] Urine samples were collected from 10 women undergoing hip replacement surgery due to severe osteoarthritis. Control samples were obtained from 5 healthy women (25.6 $\pm$ 2.6 years) without articular degeneration. The urine samples were concentrated 100x by ultracentrifugation on Amicon Ultra-15 (Millipore, USA). Proteins were purified by precipitation using PlusOne 2D Clean-up kit (GE Healthcare, Sweden). Albumin depletion from urine samples was performed using affinity columns according to the Montage Albumin Deplete Kit (Millipore, USA) manual utilisation.

Labelling of proteins with Cy3 and Cy5 dyes

[0062] In all experiments, the purified proteins were labelled on lysine residues with Cy3 or Cy5 CyDye DIGE Fluors. The samples were minimal labelled which means that the ratio of dye to protein used was such that each protein molecule was labelled with only one dye molecule. Three gels were made as shown in Table 1. Proteins from different samples were labelled with Cy3 or Cy5 and loaded on the same gel. On the first and second gels, proteins from normal (NO) samples were labelled with Cy3 CyDye DIGE Fluor whereas protein from osteoarthritis (OA) samples were labelled with Cy5 CyDye DIGE Fluor. Conversely, on the third gel, proteins from NO samples were labelled with Cy5 CyDye DIGE Fluor and proteins from OA samples were labelled with Cy3 CyDye DIGE Fluor. An internal standard (MIX) comprising equal amounts of NO and OA samples was labelled with Cy2 CyDye DIGE Fluor and loaded on each gel.

Table 1

	Gel 1	Gel 2	Gel 3
Cy3	NO	NO	OA
Cy5	OA	OA	NO
Cy2	MIX	MIX	MIX

Two-dimensional electrophoresis

[0063] Protein samples (37.5 μg) labelled with Cy3, Cy5 or Cy2 DIGE Fluor were separated by 2D electrophoresis using an IEF (ioselectric focusing) buffer (8 M urea, 2% CHAPS, 0.5% immobilized pH gradient [IPG] buffer, 1% DTT, and trace of bromophenol blue) which was loaded into an immobiline DryStrip (pH 3-10 NL, 24 cm) (GE Healthcare, Sweden). The first dimension isoelectric focusing was performed for 70,000 Vhr using a Protean IEF Cell (Biorad) at

20°C. Next, the gels were equilibrated for 12 minutes in equilibration buffer I (375 mM Tris-Cl [pH 8.8], 6 M urea, 20% glycerol, 2% SDS, and 130 mM DTT) and II (375mM Tris-Cl [pH 8.8], 6 M urea, 20% glycerol, 2% SDS, and 135mM IAA). The second dimension was run according to the Ettan DALTsix Electrophoresis Unit operating manual (GE Healthcare, Sweden). A 12.5% SDS-polyacrylamide slab gel (24 cm) was used for the second-dimension gel electrophoresis. The IPG strips were placed on the surface of the second-dimension gel. The gels were then placed in SDS electrophoresis buffer (25 mM Tris base, 192 mM glycine, 0.1% SDS) and run overnight at 1.5 W per gel.

[0064] Gels were scanned while still between two low-fluorescence glass plates using a Typhoon 9400 fluorescent scanner and saved in .gel format using ImageQuant software (GE Healthcare, Sweden). The excitation wavelengths for Cy3 and Cy5 are 550 nm and 645 nm, and the emission wavelengths are 570 nm and 670 nm for Cy3 and Cy5, respectively. The excitation/emission wavelength of Cy2 is around 489/505 nm. Image analysis was performed on DeCyder™ software (GE Healthcare, Sweden). Interesting spots with differential fluorescent intensity between Cy3 and Cy5 were picked out the gel, after post-staining with Coomassie Blue, in order to allow protein identification.

[0065] DeCyder 2D v6.5 software (GE Healthcare, Sweden) was used for the simultaneous comparison of abundance changes across sample groups. The DeCyder differential in-gel analysis (DIA) module generated ratios for each protein "spot" by comparing Cy3 and Cy5 signals to the Cy2 control signal. The DeCyder biological variation analysis module matched all protein spot maps from the gels and normalized the DIA-generated Cy3:Cy2 and Cy5:Cy2 ratios relative to the Cy2 signals for each resolved feature separately. This enabled the calculation of average abundance changes across all three samples within each test group, and the application of univariate statistical analyses (Student's t-test, ANOVA).

Proteins identification

[0066] Protein spots were cut out of the polyacrylamide gel and washed twice for 5 minutes with an ammonium hydrogenocarbonate (50 mM)-acetonitrile mix (1:1). Gel spots were incubated in dithiothreitol (10 mM), NH_4HCO_3 (50 mM), for 40 min in a 56°C water bath. Proteins in the gel spots were alkylated for 1h in the dark with iodoacetamide (55 mM) in NH_4HCO_3 (50 mM). The gel spots were then washed twice with an ammonium hydrogenocarbonate (50 mM)-acetonitrile mix (1:1), dehydrated with acetonitrile, and then dried for 15 minutes at room temperature. The gel spots were then rehydrated for 10 minutes on ice with modified trypsin (10 ng/μl) in NH_4HCO_3 (25 mM) and then incubated overnight at 37°C. Hydrolysis of peptides was stopped in TFA (1%)-ACN (5%) solution. The gel spots were then sonicated twice for 1 minute in order to release protein fragments out of the isolated gel spots. Protein fragments in solution were freeze-dried. The identity of proteins was determined by tandem mass spectrometry (MS-MS spectrometry). The Mowse score (Pappin et al (1993) Curr Biol Jun 1;3(6):327-32) gave the fidelity of identification.

Results

[0067] Proteins isolated from the urine samples and labelled with Cy3 or Cy5 were separated by two-dimensional electrophoresis. The first separation was performed with an isoelectric focusing range of pH 3-10 NL and a load of 37.5 μg of protein. 372 spots of proteins were matched between all gels. Spots with a modification of intensity between OA and NO with a ratio superior to 1.5 (t-test: $p < 0.05$) were selected for protein identification using mass spectrometry. Table 2 shows the results of analysis of these spots, and details the size of the spot, the Mowse score (which is -10 log (P) where P is the probability that the observed match is a random event), the abundance ratio, the name of the protein identified in the spot and the accession number for the identified protein in the Swiss Prot database.

TABLE 2

Spot n°	Sequence coverage (%)	Mowse score	Abundance ratio (OA/NO)	Protein description	Swiss-Prot Accession
40	9	390	1.83	Poly-Ig receptor (PIGR)	P01833
43	5	159	1.6	Poly-Ig receptor (PIGR)	P01833
75	10	340	-1.68	Transferrin	P02787
219	11 6	334 55	-1.7	Kininogen-1 precursor Alpha 1 anti-trypsin (A1AT)	P01042 P01009
222	15 7	349 99	-1.64	Kininogen-1 precursor A1AT	P01042 P01009
223	13 16	405 311	-1.89	Kininogen-1 precursor A1AT	P01042 P01009

(continued)

Spot n°	Sequence coverage (%)	Mowse score	Abundance ratio (OA/NO)	Protein description	Swiss-Prot Accession
226	18 6	334 219	-1.73	A1AT Kininogen-1 precursor	P01009 P01042
262	13 6	368 61	-1.91	Kininogen-1 precursor A1AT	P01042 P01009
267	10	304	-1.98	Kininogen-1 precursor	P01042
269	5	143	-1.83	Kininogen-1 precursor	P01042
343		189	4.18	Beta-actine	
348	21	192	2	Zn-α-2-glycoprotein precursor	P25311
349	8	195	-2.44	Serpin B3	P29508
351	6	115	-5.84	Serpin B1	P30740
352	5	130 73	2.2	Fibulin-3 Apoptosis-inducing factor 2 (two proteins identified in the same spot)	Q12805 Q9BRQ8
356	8 2	110 45	2.01	Zn-α-2-glycoprotein precursor FIBULIN3	P25311 Q12805
386	10	197	1.54	GP36b	Q12907
398	5	187	2.28	AMBP protein precursor	P02760
485	8	289	-2.3	Mannan-binding lectin serine protease 2 precursor	000187 E.C 3.4.21.104

[0068] As can be seen from Table 2, various proteins with significant changes in concentration in samples from osteoarthritis compared to samples from normal subjects were identified. Some of the proteins identified are known to be implicated in the inflammatory process, for example, the kininogen precursor or alpha-1-antitrypsin. This observation coincides with the pathology of osteoarthritis.

[0069] A significant increase in the concentration of a specific fibulin-3 fragment was observed in osteoarthritis subjects compared to normal subject, as shown in Table 2 and Figures 1A and 1B. In Figure 1A there is shown an enlargement of the area around spot 352 (indicated by one side of the double headed arrow) on the 2D-DIGE map of proteins extracted from urine from osteoarthritis subjects (right) compared to normal subjects (left). Spot 352 was shown by mass spectrometry to contain a fibulin-3 fragment. In Figure 1B the same spot (spot 352) is represented by volume variation of the spot (indicated by the other head of the double headed arrow, equivalent to the spot of Figure 1A) between samples from OA subjects (right) and NO subjects (left). A graphic view of the abundance modification based on the spot 352 volume increase is also shown in Figure 2.

[0070] Tryptic fragments from spot 352 were identified by mass spectrometry analysis as shown in Figure 3A. These fragments were identified as being fragments from the protein fibulin-3, as shown in Figure 3B. Figure 3B shows the protein sequence derived by the translation of the mRNA of human fibulin-3 and in bold the specific sequence identified by mass spectrometry. Each tryptic fragment studied was given a score which is - 10 log (P), where P is the probability that the observed match is a random event. Individual ion scores > 50 indicate identity or extensive homology. In the case of Figure 3A the tryptic peptides scored 58 and 72 respectively indicating extensive homology.

[0071] In addition to the experiments comparing OA and NO subjects, further studies were undertaken to compare OA and osteoporosis (OP) subjects. In these studies urine samples obtained from four women with serious osteoporosis. Three gels were made, as shown in Table 3, to compare the OA and OP subjects. Proteins from different samples were labelled with Cy3 or Cy5 CyDye DIGE Fluor and loaded on gels as indicated in Table 3. An internal standard (MIX) comprising equal amounts of OA and OP samples was labelled with Cy2 CyDye DIGE Fluor and loaded on each gel. The first separation was performed with an isoelectric focusing range of pH 4-7 and a load of 37.5 μg of protein.

Table 3

	Gel 1	Gel 2	Gel 3
Cy3	OA	OA	OP

(continued)

	Gel 1	Gel 2	Gel 3
Cy5	OP	OP	OA
Cy2	MIX	MIX	MIX

[0072] Analysis of the gels shows that the spot containing the fibulin-3 fragment (as described with reference to Figures 3A and 3B) shows a decrease of abundance in OP samples compared to OA samples with a ratio of 6.72. These results are illustrated in Figures 7A and 7B.

[0073] In a second experiment, proteins extracted from urine of osteoarthritic (OA) and control (NO) populations used in the initial experiment (described with reference to Figures 1 to 6) and from the urine of osteoporotic patients (OP) (described with reference to Figures 7A and 7B) were compared. Five gels were made as shown in Table 4. Proteins from different samples were labelled with Cy3 or Cy5 and loaded on the same gel. An internal standard (MIX) comprising equal amounts of NO, OA and OP samples was labelled with Cy2 CyDye DIGE Fluor and loaded on each gel. The first separation was performed with an isoelectric focusing range of pH 4-7 and a load of 37.5 μg of protein.

Table 4

	Gel 1	Gel 2	Gel 3	Gel4	Gel5
Cy3	OA	OP	NO	NO	OA
Cy5	OP	OA	OA	OP	NO
Cy2	MIX	MIX	MIX	MIX	MIX

[0074] Analysis of the five gels showed that spots containing the fragment of fibulin-3 (as described with reference to Figures 3A and 3B) show an abundance modification with a ratio comprised between 4-8 for OA/NO comparison and 4-12 for OP/OA comparison, depending on the spot containing the fragment. Indeed, we have identified five different forms of the fibulin-3 which differently discriminate osteoarthritic and osteoporotic patients as illustrated in figure 8.

[0075] The appearance of several spots containing fragments of fibulin-3 suggests that the protein is present in various forms in the urinary proteome. The sequence could be modified specifically by phosphorylation, glycosylation or other post-traductional modifications resulting of a pathophysiological mechanism. All the identified forms are increased in OA samples compared to OP and NO samples. However, some forms appear to be more increased regarding the spot observed and could be more concerned by the pathologic process. Selected fragment discriminates patients with osteoarthritis from those with osteoporosis. This could not be identified by a person skilled in the art.

[0076] This data shows that the increased abundance of the fragment of fibulin-3 is a specific event occurring in osteoarthritic disease. Furthermore, a decrease in the level of this protein is seen in samples from subjects with osteoporosis samples compared to those from subjects with osteoarthritis. Note that different ratios were found between multiple experiments because the internal standard was changed for each of them.

[0077] In figure 8, Proteins were separated on a linear pH gradient (pH 4-7) IPG strip, followed by a 12.5% SDS-PAGE. Selected spots (▭) contain fragments of fibulin-3 identified by mass spectrometry. Modified ratio of fibulin-3 content is annotated under the corresponding spot.

[0078] Fibulins are a family of five extracellular matrix proteins characterized by modular domain structures as depicted in Figure 4. The general fibulins modular domain structure comprises tandem arrays of epidermal growth factor-like (EGF-like) modules (domain II, represented by circles) and a C-terminal fibulin-type module (domain III, represented by rectangles). Some of the EGF-like modules possess a consensus motif for calcium binding (cbEGF-like module represented by circles with black dots). Fibulin-1 and fibulin-2 comprise anaphylatoxin-like modules (domain I, represented by diamonds). Domain N, which is unique to fibulin-2, can be subdivided into a Cys-rich segment (Na) and a Cys-free segment (Nb). Fibulin-3, fibulin-4, and fibulin-5 have a modified cbEGF-like module at their N-terminus. This modified cbEGF-like module has an extra Cys^5 -Cys^6 loop at the beginning of the module and a long linker region between Cys^2-Cys^4 and Cys^5 -Cys^6 loops. The residues between Cys^4 and Cys^5 are shown in parentheses. Four different alternative splice variants are reported for human fibulin-1, shown as variants A-D, and the numbers in parentheses indicate residues of domain III.

[0079] Fibulin-1 (703 AA; 77.2 kDa) and Fibulin-2 (1184 AA; 126.5 kDa) are localized in basement membranes, elastic fibers, and other connective tissue structures. Fibulin-4 (443 AA; 49.4 kDa) was identified through its sequence homology to fibulin-1, fibulin-2, and fibulin-3 and independently as a protein interacting with a mutant form of the tumor suppressor protein p53. Fibulin-5 (48 AA; 50.2 kDa) was first characterized as a gene strongly expressed in large blood vessels

during embryonic development and highly up-regulated upon vascular injury.

[0080] Fibulin-3 is also known as EFEMP1 protein and has SWISS-PROT accession number Q12805. Fibulin-3 is a protein comprising 493 amino acids and has a molecular weight of about 54.6 kDa. Fibulin-3 was originally identified by subtractive cDNA cloning from a Werner syndrome fibroblast library and shown to be expressed at increased levels in serum-deprived fibroblasts. As with all other fibulins, fibulin-3 is present in blood vessels of different sizes and is capable of inhibiting vessel development and angiogenesis both *in vitro* and *in vivo.* Fibulin-3 is expressed in cartilage and bone structures during development and may play a role in the skeletal system. Fibulin-3 is known to be intimately associated with TIMP-3, an inhibitor of metalloproteinase involved in the pathogenesis of osteoarthritis (Klenotic et al., J Biol Chem, 2004. 279(29): p. 30469-73; Sahebjam et al., Arthritis Rheum, 2007. 56(3): p. 905-9; Kevorkian et al., Arthritis Rheum, 2004. 50(1): p. 131-41). The results presented herein show that the fibulin-3 fragment described with reference to Seq ID No: 1, Figure 3B and Figure 5 is present in an increased amount in biological sample , such as urine, of subjects with osteoarthritis. The data also shows that a decreased level of the fibulin-3 fragment may be diagnostic of osteoporosis as well as osteoarthritis. Thus, peptides having the sequence of Seq ID No: 1, or substantially the sequence of Seq ID No: 1, or a part thereof, may be used as biomarkers for osteoarthritis, osteoporosis and/or other ageing-related diseases.

SEQUENCE LISTING

<110> UNIVERSITE DE LIEGE

<120> BIOMARKER FOR OSTEOARTHRITIS AND/OR OTHER AGEING-RELATED DISEASES, AND USE THEREOF

<130> 2007-28

<160> 2

<170> PatentIn version 3.3

<210> 1
<211> 57
<212> PRT
<213> Homo sapiens

<400> 1

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20 25 30

Asn Pro Cys Gln Asp Pro Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val
35 40 45

Cys Pro Val Ser Asn Ala Met Cys Arg
50 55

<210> 2
<211> 493
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<400> 2

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1 5 10 15

Ser Gln Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly
20 25 30

Tyr Glu Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys
35 40 45

Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His
50 55 60

Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn
65 70 75 80

```
Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly
                85                  90                  95

Ala Thr Thr Gly Val Val Ala Ala Ser Ser Met Ala Thr Ser Gly Val
            100                 105                 110

Leu Pro Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro
        115                 120                 125

Glu Met Gln Thr Gly Arg Asn Asn Phe Val Ile Arg Arg Asn Pro Ala
    130                 135                 140

Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser His Arg Ile Gln Cys Ala
145                 150                 155                 160

Ala Gly Tyr Glu Gln Ser Glu His Asn Val Cys Gln Asp Ile Asp Glu
                165                 170                 175

Cys Thr Ala Gly Thr His Asn Cys Arg Ala Asp Gln Val Cys Ile Asn
            180                 185                 190

Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro Pro Gly Tyr Gln Lys Arg
        195                 200                 205

Gly Glu Gln Cys Val Asp Ile Asp Glu Cys Thr Ile Pro Pro Tyr Cys
    210                 215                 220

His Gln Arg Cys Val Asn Thr Pro Gly Ser Phe Tyr Cys Gln Cys Ser
225                 230                 235                 240

Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr Thr Cys Val Asp Ile Asn
                245                 250                 255

Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln Gln Cys Tyr Asn Ile Leu
            260                 265                 270

Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly Tyr Glu Leu Ser Ser Asp
        275                 280                 285

Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys Arg Thr Ser Ser Tyr Leu
    290                 295                 300

Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly Lys Phe Ser Cys Met Cys
305                 310                 315                 320

Pro Gln Gly Tyr Gln Val Val Arg Ser Arg Thr Cys Gln Asp Ile Asn
                325                 330                 335
```

```
Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu Asp Glu Met Cys Trp Asn
            340                 345                 350

Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg Asn Pro Cys Gln Asp Pro
        355                 360                 365

Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val Cys Pro Val Ser Asn Ala
    370                 375                 380

Met Cys Arg Glu Leu Pro Gln Ser Ile Val Tyr Lys Tyr Met Ser Ile
385                 390                 395                 400

Arg Ser Asp Arg Ser Val Pro Ser Asp Ile Phe Gln Ile Gln Ala Thr
                405                 410                 415

Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe Arg Ile Lys Ser Gly Asn
            420                 425                 430

Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr Ser Pro Val Ser Ala Met
        435                 440                 445

Leu Val Leu Val Lys Ser Leu Ser Gly Pro Arg Glu His Ile Val Asp
    450                 455                 460

Leu Glu Met Leu Thr Val Ser Ser Ile Gly Thr Phe Arg Thr Ser Ser
465                 470                 475                 480

Val Leu Arg Leu Thr Ile Ile Val Gly Pro Phe Ser Phe
                485                 490
```

Claims

1. A method of diagnosing osteoarthritis and/or another ageing-related disease in a subject, comprising the steps of:

   (i) determining the concentration in a biological sample of a peptide fragment consisting of an amino acid sequence of first through fifteen and/or forty seventh through fifty seventh amino acids of Seq ID no:1;
   (ii) comparing the peptide fragment concentration determined in step (i) with one or more reference value;

   wherein an increase in the concentration of the peptide fragment compared to the reference values is diagnostic of osteoarthritis and/or another ageing-related disease.

2. A method of determining the prognosis for a subject with osteoarthritis and/or another ageing-related disease, comprising the steps of:

   (i) determining the concentration in a biological sample of a peptide fragment consisting of an amino acid sequence of first through fifteen and/or forty seventh through fifty seventh amino acids of Seq ID no:1;
   (iii) comparing the peptide fragment concentration determined in step (i) with one or more reference values ;

   wherein an increase in the concentration of the peptide fragment compared to the reference values is prognostic of osteoarthritis and/or another ageing-related disease.

3. The method of any preceding claim wherein the biological sample is selected from the group comprising urine, whole blood, blood serum, blood plasma, synovium, sweat, cerebrospinal fluid, mucous, saliva, lymph, bronchial aspirates and milk.

4. The method of any preceding claim wherein the concentration of the peptide fragment is determined by using mass spectrometry or an immunoassay.

5. The method of any preceding claim wherein the reference value is the concentration of the peptide fragment in one or more normal subjects.

6. A kit for use in diagnosing osteoarthritis and/or another ageing-related disease in a subject or in determining the prognosis for a subject with osteoarthritis and/or another ageing-related disease, said kit comprising at least one agent for determining the concentration of a peptide fragment consisting of an amino acid sequence of first through fifteen and/or forty seventh through fifty seventh amino acids of Seq ID no:1, in a biological sample.

7. The kit according to claim 6 wherein the agent is selected from the group comprising an enzyme, an antibody, a protein probe, a metabolite or any other suitable composition.

8. The kit according to claim 6 or 7 wherein the agent comprises two antibodies directed to different epitopes on the peptide fragment.

9. The kit according to claim 8 for use in determining the concentration of the peptide fragment by using a sandwich immunoassay.

10. An isolated peptide fragment consisting of an amino acid sequence of first through fifteen and/or forty seventh through fifty seventh amino acids of Seq ID no:1, or its amide, or a salt thereof.

11. A polynucleotide encoding a peptide fragment according to claim 10.

12. A recombinant vector comprising a polynucleotide according to claim 11.

13. A transformant transformed with a recombinant vector according to claim 12.

14. Use of a peptide fragment according to claim 10 in the manufacture of an antibody.

15. An antibody specific for a peptide fragment according to claim 10.

Figure 1A

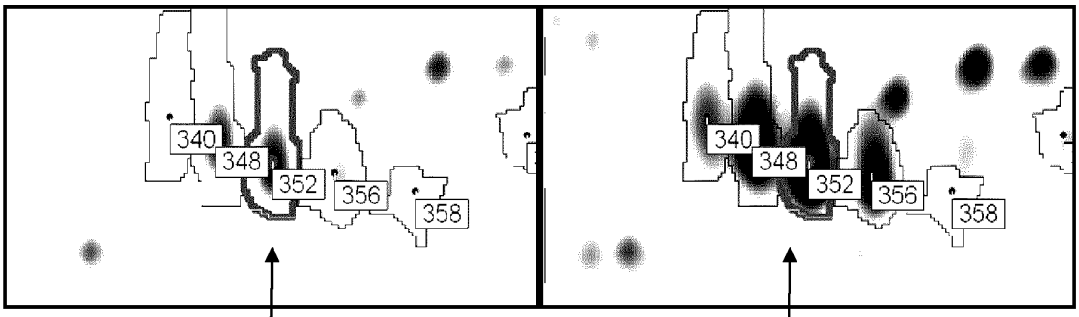


Figure 1B

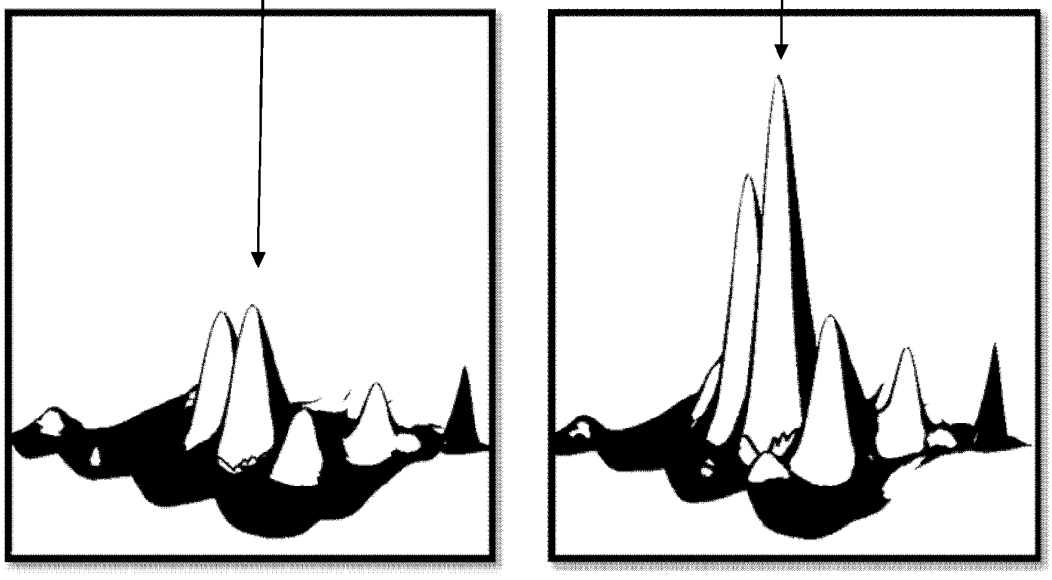
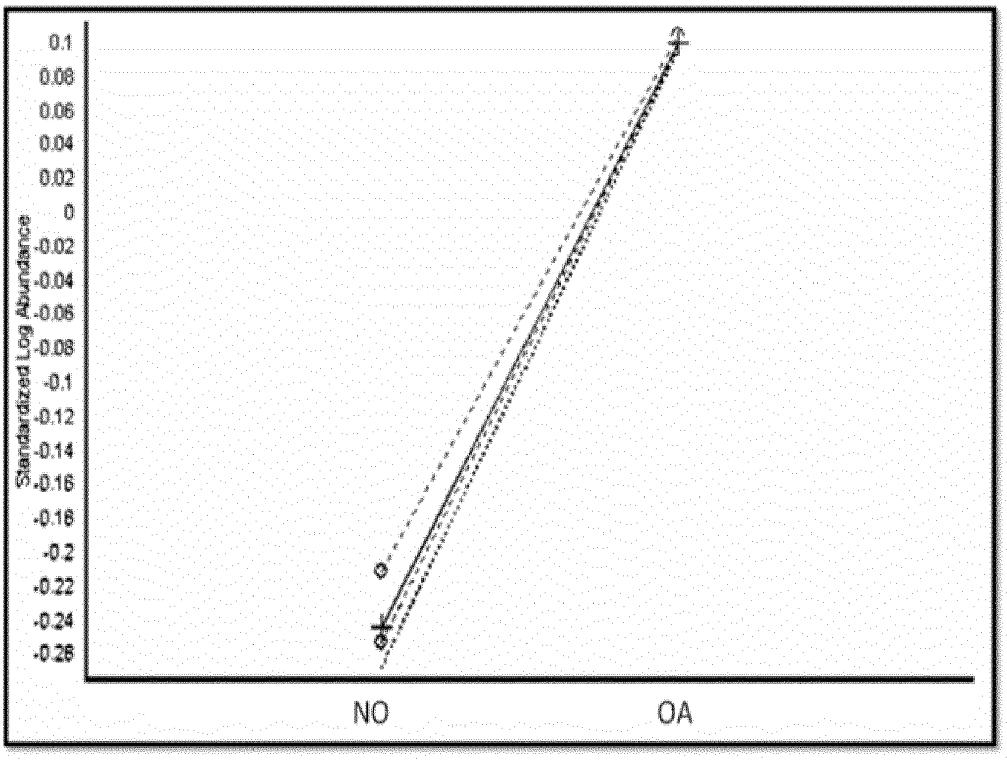


Figure 2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-0.26
NO
OA

Figure 3A

FBLN3_HUMAN **Mass:** 54604 **Score:** 130 **Queries matched:** 2

EGF-containing fibulin-like extracellular matrix protein 1 precursor (Fibulin-3) (FIBL-3)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
149	685.33	1368.64	1368.54	0.09	0	58	0.00027	1	R.CVCPVSNAMCR.E
444	965.32	1928.63	1928.73	-0.10	0	72	4.2e-06	1	R.TCQDINECETTNECR.E

Figure 3B

```
       10         20         30         40         50         60
MLKALFLTML TLALVKSQDT EETITYTQCT DGYEWDPVRQ QCKDIDECDI VPDACKGGMK

       70         80         90        100        110        120
CVNHYGGYLC LPKTAQIIVN NEQPQQETQP AEGTSGATTG VVAASSMATS GVLPGGGFVA

      130        140        150        160        170        180
SAAAVAGPEM QTGRNNFVIR RNPADPQRIP SNPSHRIQCA AGYEQSEHNV CQDIDECTAG

      190        200        210        220        230        240
THNCRADQVC INLRGSFACQ CPPGYQKRGE QCVDIDECTI PPYCHQRCVN TPGSFYCQCS

      250        260        270        280        290        300
PGFQLAANNY TCVDINECDA SNQCAQQCYN ILGSFICQCN QGYELSSDRL NCEDIDECRT

      310        320        330        340        350        360
SSYLCQYQCV NEPGKFSCMC PQGYQVVRSR TCQDINECET TNECREDEMC WNYHGGFRCY

      370        380        390        400        410        420
PRNPCQDPYI LTPENRCVCP VSNAMCRELP QSIVYKYMSI RSDRSVPSDI FQIQATTIYA

      430        440        450        460        470        480
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      490
VLRLTIIVGP FSF
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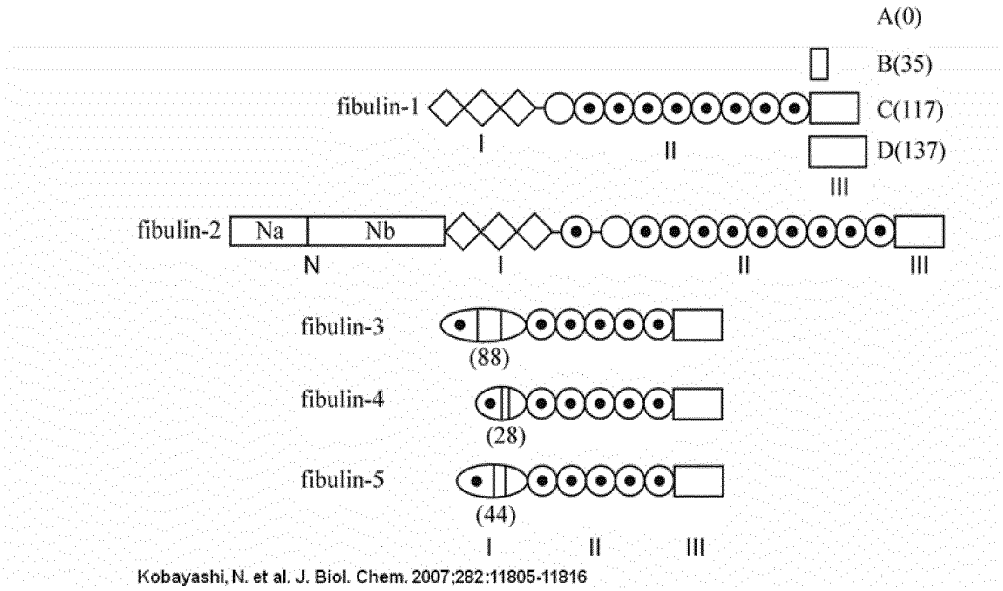
Figure 4



Kobayashi, N. et al. J. Biol. Chem. 2007;282:11805-11816

Figure 5

TCQDINECETTNECREDEMCWNYHGGFRCYPRNPCQDPYILTPENRC
VCPVSNAMCR

Figure 6

MLKALFLTMLTLALVKSQDTEETITYTQCTDGYEWDPVRQQCKDIDE
CDIVPDACKGGMKCVNHYGGYLCLPKTAQIIVNNEQPQQETQPAEGT
SGATTGVVAASSMATSGVLPGGGFVASAAAVAGPEMQTGRNNFVIRR
NPADPQRIPSNPSHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQV
CINLRGSFACQCPPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYC
QCSPGFQLAANNYTCVDINECDASNQCAQQCYNILGSFICQCNQGYEL
SSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQVVRSRTC
QDINECETTNECREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC
PVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIK
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SSVLRLTIIVGPFSF

Figure 7A

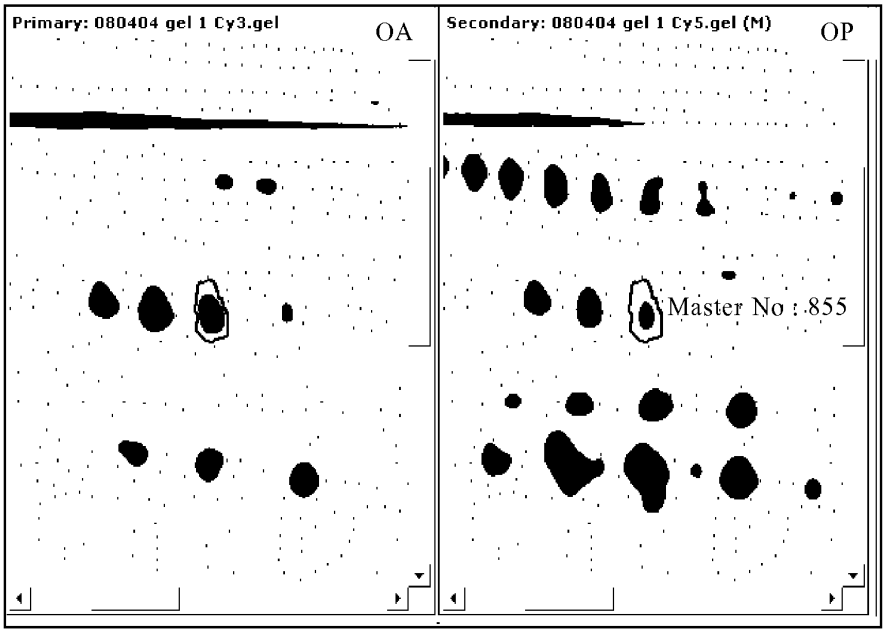


Figure 7B

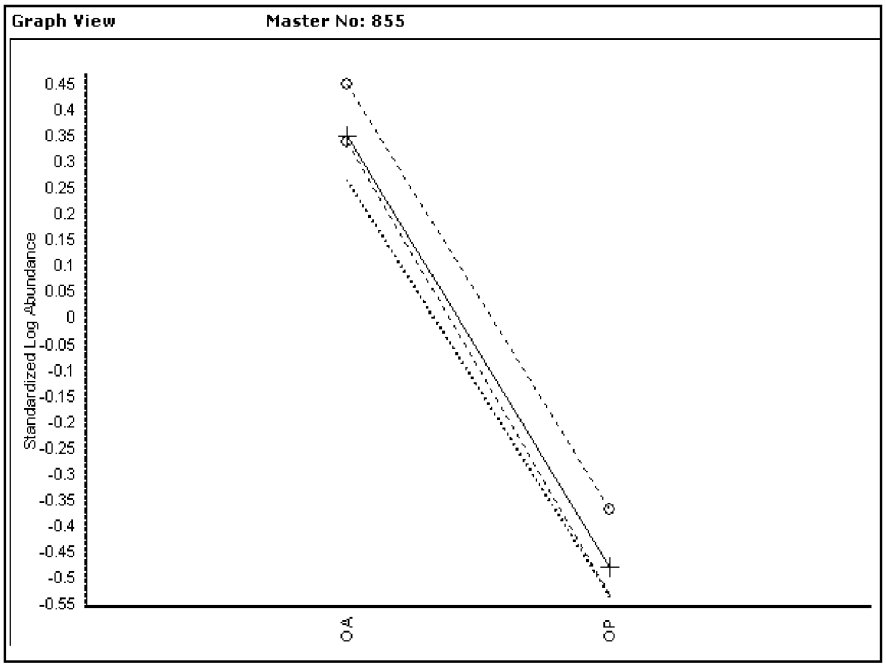
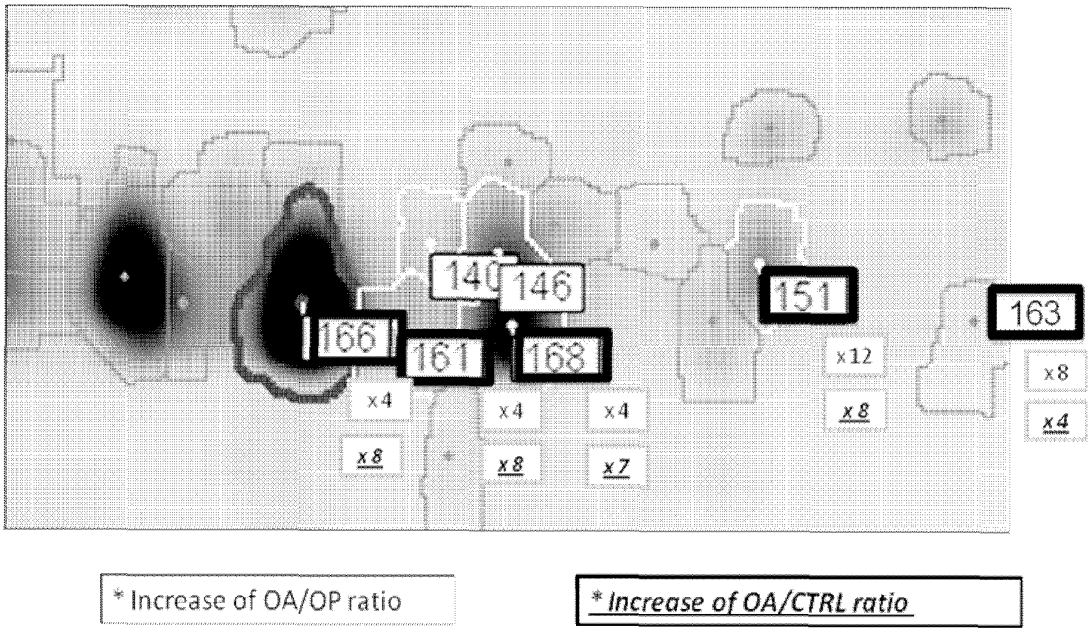


Figure 8


140
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163
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x4
x4
x12
x8
x8
x8
x7
x8
x4
* Increase of OA/OP ratio
* Increase of OA/CTRL ratio

Europäisches Patentamt
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EUROPEAN SEARCH REPORT

Application Number
EP 15 18 0470

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	WO 2008/012362 A2 (OXFORD GENOME SCIENCES UK LTD [GB]; ROHLFF CHRISTIAN [GB]) 31 January 2008 (2008-01-31) * page 100, paragraph 4; table 1; sequences 56,351 *	6-15	INV. G01N33/68 C07K16/44
X	WO 2006/006477 A (SHIONOGI & CO [JP]; MIE UNIVERSITY [JP]; UCHIDA ATSUMASA [JP]; MATSUMI) 19 January 2006 (2006-01-19) * claims 1,2,12,16,17; sequence 13 *	1,3-5	
X	-& IDE N ET AL: "Detecting or screening bone or joint disease, involves comparing expression level of gene encoding antioncogene candidate 1 protein, of test sample with control sample", WPI/THOMSON,, vol. 2006, no. 11, 19 January 2006 (2006-01-19), XP002494472,	1-3, 8-12,17	
X	LANE NANCY E ET AL: "Wnt signaling antagonists are potential prognostic biomarkers for the progression of radiographic hip osteoarthritis in elderly Caucasian women", ARTHRITIS & RHEUMATISM, WILEY, US, vol. 56, no. 10, 1 October 2007 (2007-10-01), pages 3319-3325, XP002530290, ISSN: 0004-3591, DOI: 10.1002/ART.22867 * the whole document *	2-5	TECHNICAL FIELDS SEARCHED (IPC) G01N
A	EP 1 764 413 A (LOCOMOGENE INC [JP]) 21 March 2007 (2007-03-21) * claims 16,22; sequence 2 *	1-15	

-/--

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
The Hague	13 October 2015	Wiesner, Martina

CATEGORY OF CITED DOCUMENTS

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EUROPEAN SEARCH REPORT

Application Number
EP 15 18 0470

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
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A	WO 03/063689 A (QUARK BIOTECH INC [US]; SHIONOGI & CO [JP]; SEGEV ORIT [IL]; FEINSTEIN) 7 August 2003 (2003-08-07) * claim 33 *	1-15	
A	WO 2006/138646 A (BRIGHAM & WOMENS HOSPITAL [US]; MILLETT PETER J [US]; SARRACINO DAVID) 28 December 2006 (2006-12-28) * claims 1,6,7 *	1-15	
A	WU JIANG ET AL: "Comparative proteomic characterization of articular cartilage tissue from normal donors and patients with osteoarthritis.", ARTHRITIS AND RHEUMATISM NOV 2007, vol. 56, no. 11, November 2007 (2007-11), pages 3675-3684, XP002492862, ISSN: 0004-3591 * page 3676, right-hand column, paragraph 3; figure 5; table 1 * * page 3682, right-hand column, paragraph 3 *	1-15	
	-/--		TECHNICAL FIELDS SEARCHED (IPC)

The present search report has been drawn up for all claims

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EUROPEAN SEARCH REPORT

Application Number
EP 15 18 0470

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
A	MARSHALL ET AL: "Blood-based biomarkers for detecting mild osteoarthritis in the human knee", OSTEOARTHRITIS AND CARTILAGE, BAILLIERE TINDALL, LONDON, GB, vol. 13, no. 10, 1 October 2005 (2005-10-01), pages 861-871, XP005094311, ISSN: 1063-4584 * tables supplementary4,IV *	1-15	
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			TECHNICAL FIELDS SEARCHED (IPC)

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
The Hague	13 October 2015	Wiesner, Martina

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13-10-2015

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