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(71) Applicant *(for all designated States except US)*: **GALAPAGOS GENOMICS N.V.** [BE/BE]; Generaal De Wittelaan L11 A3, B-2800 Mechelen (BE).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BRYS, Reginald** [BE/BE]; Nijvelsebaan 206, B-3060 Korbeek-Dijle (BE). **VANDEGHINSTE, Nick** [BE/BE]; Hermansstraat 3 bus 14, B-2570 Duffel (BE). **TOMME, Peter, Herwig, Maria** [BE/BE]; Vogelmarkt 33, B-9000 Gent (BE).

(74) Agent: **HOOIVELD, Arjen J.W.**; Arnold & Siedsma, Sweelinckplein 1, NL-2514 GK The Hague (NL).

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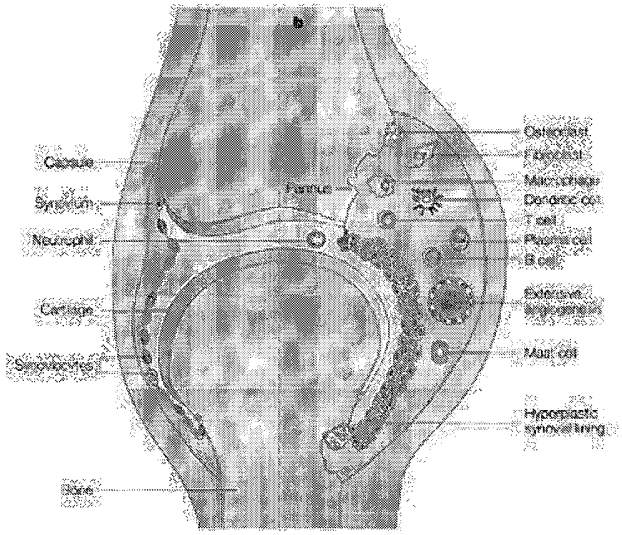
(54) **Title:** METHODS FOR IDENTIFICATION, AND COMPOUNDS USEFUL FOR THE TREATMENT OF DEGENERATIVE & INFLAMMATORY DISEASES

Schematic view of a normal joint and its changes in rheumatoid arthritis
(From Smolen and Steiner, 2003).



(57) **Abstract:** The present invention relates to in vivo and in vitro methods, agents and compound screening assays for inhibiting extra-cellular matrix degradation, including joint degenerative inhibiting and/or anti-inflammatory pharmaceutical compositions, and the use thereof in treating and/or preventing a disease involving extra-cellular matrix degradation in a subject.

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METHODS FOR IDENTIFICATION, AND COMPOUNDS USEFUL FOR THE TREATMENT OF DEGENERATIVE & INFLAMMATORY DISEASES

Field of Invention

The present invention relates to a methods for identifying compounds, and expression-inhibition agents, capable of inhibiting the expression of proteins involved in the pathway resulting in the degradation of extra-cellular matrix (ECM), which inhibition is useful in the prevention and treatment of joint degeneration and diseases involving such degradation and/or inflammation.

Diseases involving the degradation of extra-cellular matrix include, but are not limited to, psoriatic arthritis, juvenile arthritis, early arthritis, reactive arthritis, osteoarthritis, ankylosing spondylitis. osteoporosis, muskulo skeletal diseases like tendinitis and periodontal disease, cancer metastasis, airway diseases (COPD, asthma), renal and liver fibrosis, cardio-vascular diseases like atherosclerosis and heart failure, and neurological diseases like neuroinflammation and multiple sclerosis. Diseases involving primarily joint degeneration include, but are not limited to, psoriatic arthritis, juvenile arthritis, early arthritis, reactive arthritis, osteoarthritis, ankylosing spondylitis.

Rheumatoid arthritis (RA) is a chronic joint degenerative disease, characterized by inflammation and destruction of the joint structures. When the disease is unchecked, it leads to substantial disability and pain due to loss of joint functionality and even premature death. The aim of an RA therapy, therefore, is not to slow down the disease but to attain remission in order to stop the joint destruction. Besides the severity of the disease outcome, the high prevalence of RA (~ 0.8% of the adults are affected worldwide) means a high socio-economic impact. (For reviews on RA, we refer to Smolen and Steiner (2003); Lee and Weinblatt (2001); Choy and Panayi (2001); O'Dell (2004) and Firestein (2003)).

Although it is widely accepted that RA is an auto-immune disease, there is no consensus concerning the precise mechanisms driving the 'initiation stage' of the disease. What is known is that the initial trigger(s) does mediate, in a predisposed host, a cascade of events that leads to the activation of various cell types (B-cells, T-cells, macrophages, fibroblasts, endothelial cells, dendritic cells and others). Concomitantly, an increased production of various cytokines is observed in the joints and tissues surrounding the joint (e.g. TNF-α , IL-6, IL-1, IL-15, IL-18 and others). When the disease progresses, the cellular activation and cytokine production cascade becomes self-perpetuating. At this early stage, the destruction of joint structures is already very clear at this early stage. Thirty percent of the patients have radiographic evidence of bony erosions at the time of diagnosis and this proportion increases to 60 percent after two years.

Histologic analysis of the joints of RA patients clearly evidences the mechanisms involved in the RA-associated degradative processes. The synovium is a cell layer, composed of a sublining and a lining region that separates the joint capsule from the synovial cavity. The inflamed synovium is central to the pathophysiology of RA. Histological differences in the synovium between normal and RA patients are indicated in Figure 1: A. The synovial joint is composed of two adjacent bony ends each covered with a layer of cartilage, separated by a joint space and surrounded by the synovial membrane and joint capsule. The synovial membrane is composed of the

synovial lining (facing the cartilage and bone) which consists of a thin (1–3 cells) layer of synoviocytes and the sublining connective tissue layer that is highly vascularised. The synovial membrane covers almost all intra-articular structures except for cartilage. B. Like many other forms of arthritis, rheumatoid arthritis (RA) is initially characterized by an inflammatory response of the synovial membrane ('synovitis') that is characterised by an important influx of various types of mononuclear cells as well as by the activation of the local or infiltrated mononuclear cells. The lining layer becomes hyperplastic (it can have a thickness of >20 cells) and the synovial membrane expands. However, in addition, the hallmark of RA is joint destruction: the joint spaces narrow or disappear as a sign of cartilage degradation and destructions of the adjacent bone, also termed 'erosions', have occurred. The destructive portion of the synovial membrane is termed 'pannus'. Enzymes secreted by synoviocytes lead to cartilage degradation.

This analysis shows that the main effector responsible for RA-associated joint degradation is the pannus, where the synovial fibroblast, by producing diverse proteolytic enzymes, is the prime driver of cartilage and bone erosion. In the advanced RA patient, the pannus mediates the degradation of the adjacent cartilage, leading to the narrowing of the joint space, and has the potential to invade adjacent bone and cartilage. As bone and cartilage tissues are composed mainly of collagen type I or II, respectively, the pannus destructive and invasive properties are mediated by the secretion of collagenolytic proteases, principally the matrix metallo proteinases (MMPs). The erosion of the bone under and adjacent to the cartilage is also part of the RA process, and results principally from the presence of osteoclasts at the interface of bone and pannus. Osteoclasts adhere to the bone tissue and form a closed compartment, within which the osteoclasts secrete proteases (Cathepsin K, MMP9) that degrade the bone tissue. The osteoclast population in the joint is abnormally increased by osteoblast formation from precursor cells induced by the secretion of the receptor activator of NFkB ligand (RANKL) by activated SFs and T-cells.

Various collagen types have a key role in defining the stability of the extra-cellular matrix (ECM). Collagens type I and collagen type II, for example, are the

main components of bone and cartilage, respectively. Collagen proteins typically organise into multimeric structures referred to as collagen fibrils. Native collagen fibrils are very resistant to proteolytic cleavage. Only a few types of ECM-degrading proteins have been reported to have the capacity to degrade native collagen: matrix-metallo proteases (MMPs) and Cathepsins. Among the Cathepsins, cathepsin K, which is active mainly in osteoclasts, is the best characterised. Among the MMPs, MMP1, MMP2, MMP8 MMP13 and MMP14 are known to have collagenolytic properties. The correlation between an increased expression of MMP1 by synovial fibroblasts (SFs) and the progression of the arthritic disease is well-established and is predictive for joint erosive processes (Cunnane et al., 2001). In the context of RA, therefore, MMP1 represents a highly relevant collagen degrading protein. In vitro, the treatment of cultured SFs with cytokines relevant in the RA pathology (e.g. TNF-α and IL1ß) will increase the expression of MMP1 by these cells (Andreakos et al., 2003). Monitoring the levels of MMP1 expressed by SFs therefore is a relevant readout in the field of RA as it is indicative for the activation of SFs towards an erosive phenotype that, in vivo, is responsible for cartilage degradation. Inhibition of the MMP1 expression by SFs represents a valuable therapeutic approach towards the treatment of RA.

The activity of the ECM-degrading proteins can also be causative or correlate with the progression of various diseases different from RA, as e.g. other diseases that involve the degradation of the joints. These diseases include, but are not limited to, psoriatic arthritis, juvenile arthritis, early arthritis, reactive arthritis, osteo-arthritis, and ankylosing spondylitis. Other diseases that may be treatable with compounds identified according to the present invention and using the targets involved in the expression of MMPs as described herein are osteoporosis, muskulo skeletal diseases like tendinitis and periodontal disease (Gapski et al., 2004), cancer metastasis (Coussens et al., 2002), airway diseases (COPD, asthma) (Suzuki et al., 2004), lung, renal fibrosis (Schanstra et al., 2002), liver fibrosis associated with chronic hepatitis C (Reiff et al., 2005), cardio-vascular diseases like atherosclerosis and heart failure

(Creemers et al., 2001), and neurological diseases like neuroinflammation and multiple sclerosis (Rosenberg, 2002). Patients suffering from such diseases may benefit from stabilizing the ECM (by protecting it from degradation).

Reported Developments

NSAIDS (Non-steroidal anti-inflammatory drugs) are used to reduce the pain associated with RA and improve life quality of the patients. These drugs will not, however, put a brake on the RA-associated joint destruction.

Corticosteroids are found to decrease the progression of RA as detected radiographically and are used at low doses to treat part of the RA patients (30 to 60%). Serious side effects, however, are associated with long corticosteroid use (Skin thinning, osteoporosis, cataracts, hypertension, hyperlipidemia).

Synthetic DMARDs (Disease-Modifying Anti-Rheumatic Drugs) (e.g. methotrexate, leflunomide, sulfasalazine) mainly tackle the immuno-inflammatory component of RA. As a main disadvantage, these drugs only have a limited efficacy (joint destruction is only slowed down but not blocked by DMARDs such that disease progression in the long term continues). The lack of efficacy is indicated by the fact that, on average, only 30% of the patients achieve a ACR50 score after 24 months treatment with methotrexate. This means that, according to the American College of Rheumatology, only 30% of the patients do achieve a 50% improvement of their symptoms (O'Dell et al., 1996). In addition, the precise mechanism of action of DMARDs is often unclear.

Biological DMARDs (Infliximab, Etanercept, Adalimumab, Rituximab, CTLA4-Ig) are therapeutic proteins that do inactivate cytokines (e.g. TNF-α) or cells (e.g. T-cells or B-cells) that have an important role in the RA pathophysiology (Kremer et al., 2003; Edwards et al., 2004). Although the TNF-α-blockers (Infliximab, Etanercept, Adalimumab) and methotrexate combination therapy is the most effective RA treatment currently available, it is striking that even this therapy only achieves a 50% improvement (ACR50) in disease symptoms in 50-60% of patients after 12 months therapy (St Clair et al., 2004). Some adverse events warnings

for anti-TNF-α drugs exist, shedding a light on the side effects associated to this type of drugs. Increased risk for infections (tuberculosis) hematologic events and demyelinating disorders have been described for the TNF-α blockers. (see also Gomez-Reino et al., 2003). Besides the serious side effects, the TNF-α blockers do also share the general disadvantages of the biologicals class of therapeutics, which are the unpleasant way of administration (frequent injections accompanied by infusion site reactions) and the high production cost. Newer agents in late development phase target T-cell co-stimulatory molecules and B-cells. The efficacy of these agents is expected to be similar to that of the TNF-α blockers. The fact that a variety of targeted therapies have similar but limited efficacies, suggests that there is a multiplicity of pathogenic factors for RA. This is also indicative for the deficiencies in our understanding of pathogenic events relevant to RA.

The current therapies for RA are not satisfactory due to a limited efficacy (no adequate therapy exists for 30% of the patients). This calls for additional strategies to achieve remission. Remission is required since residual disease bears the risk of progressive joint damage and thus progressive disability. Inhibiting the immuno-inflammatory component of the RA disease, which represents the main target of drugs currently used for RA treatment, does not result in a blockade of joint degradation, the major hallmark of the disease.

The histological analysis of RA patient joints clearly identifies the pannus, as an aggressive, invasive tissue that represents the main culprit in joint degradation. Within the pannus, the synovial fibroblasts represent a link between the initiation of the abnormally triggered immune system that lies at the basis of RA pathogenesis, and the ultimate joint erosion. As no current RA therapy efficiently abolishes the erosive activity of the pannus in the long term, the discovery of novel drugs and/or drug targets that inhibit the generation, and/ or the activity, of the pannus would represent an important milestone for the development of novel RA treatments.

The present invention is based on the discovery of that certain proteins function in the pathway that results in the expression of extra-cellular matrix (ECM) degradation proteases, such as MMP1, and that inhibitors of the activity of these

proteins, are useful for the treatment of diseases involving the abnormally high expression of such proteases.

Summary of the Invention

The present invention relates to a method for identifying compounds that inhibit extra-cellular matrix (ECM) degradation, comprising contacting a compound with a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 (hereinafter "TARGETS") and fragments thereof under conditions that allow said polypeptide to bind to the compound, and measuring a compound-polypeptide property related to extra-cellular matrix (ECM) degradation.

Aspects of the present method include the *in vitro* assay of compounds using polypeptide of a TARGET and fragments thereof including selected from the group consisting of SEQ ID NO. 501-564, and cellular assays wherein TARGET inhibition is followed by observing indicators of efficacy including, for example, TARGET expression levels and/or Matrix Metallo Proteinase -1 levels.

The present invention also relates to expression inhibitory agents comprising a polynucleotide selected from the group of an antisense polynucleotide, a ribozyme, and a small interfering RNA (siRNA), wherein said polynucleotide comprises a nucleic acid sequence complementary to, or engineered from, a naturally occurring polynucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 and 501-564, pharmaceutical compositions comprising said agent, useful in the treatment, or prevention, of chronic joint degenerative diseases such as rheumatoid arthritis.

Another aspect of the invention is a method of treatment, or prevention, of a condition involving extra-cellular matrix (ECM) degradation, in a subject suffering or susceptible thereto, by administering a pharmaceutical composition comprising an effective TARGET-expression inhibiting amount of a expression-inhibitory agent.

A further aspect of the present invention is a method for diagnosis relating to disease conditions characterized by extra-cellular matrix (ECM) degradation comprising measurement of indicators of levels of TARGET expression in a subject.

Another aspect of this invention relates to the use of the present compound in a therapeutic method, a pharmaceutical composition, and the manufacture of such composition, useful for the treatment of a disease involving inflammation, and in particular, a disease characteristic of abnormal matrix metallo proteases activity.

Brief Description Of The Drawings

Figure 1. Schematic view of a normal joint and its changes in rheumatoid arthritis (From Smolen and Steiner, 2003).

Figure 2. Characterization of the expression of MMP1 by synovial fibroblasts. In panel A, the MMP1 mRNA levels present in the SF lysate are determined by real-time PCR. These MMP1 levels are normalized to the 18S levels that are also determined by real-time PCR for the same samples. Panel B shows the MMP1 signal detected from the supernatant that is subjected to Western blotting for detection of MMP1 protein levels using an MMP1-specific polyclonal antibody. Panel C shows the results of subjecting the supernatant to a commercially available MMP1 "activity ELISA" (Amersham Biosciences). The signal represented is proportional to the MMP1 activity present in the samples tested.

Figure 3. Increased expression of MMP1 by SFs triggered with various model adenoviruses. The SF supernatant uninfected SFs and SFs infected with the indicated model recombinant adenoviruses is subjected to the MMP1 ELISA and the MMP1 level measured by using a luminescence generating substrate is shown.

Figure 4. Layout and performance of the control plate produced for the MMP1 ELISA assay.

Figure 5. Representative example of the performance of the MMP1 ELISA run on a subset of 384 Ad-cDNAs of the FlexSelect collection that are tested in duplicate in a primary screen (A) and a rescreen (B).

Figure 6. Downscaling of the collagen degradation assay.

Figure 7. Matching of the collagen degradation assay readout to the visual assessment of collagen degradation.

Figure 8. Comparison of the degradation of FITC-labeled collagen type II and FITC-labeled Collagen type I in the collagen degradation assay.

Figure 9. Performance of the collagen degradation assay.

Figure 10. Activation of SFs by various complex cytokine mixtures. Shown are the raw luminescence signals from MMP1 ELISA measurements of the supernatant of SFs collected 72 hours after being triggered with the indicated recombinant cytokines or with the supernatant of THP1 cells activated with the indicated cytokines. These measurements are proportional to MMP1 levels.

Figure 11. Inhibition of the response of SFs to a complex cytokine mixture by two inhibitors.

Figure 12. Inhibition of the expression of MMP1 by SFs as a response to a complex cytokine mixture by infection with various "knock down" viruses.

Figure 13. Induction of the expression of MMP1 by SFs by adenovirus mediated expression of target genes

Figure 14. Reduction, at the protein level, of the expression of MAPKAPK5, PRKCE and CAMK4 by infection of the cells with various Ad-siRNA viruses targeting these genes

Figure 15. Inhibition of the collagen degradation by SFs as a response to a complex cytokine mixture by infection of the cells with various "knock down" viruses.

Figure 16. Structure of short-hairpin RNA (shRNA) targeted against Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2) mRNA.

Detailed Description

The following terms are intended to have the meanings presented therewith below and are useful in understanding the description and intended scope of the present invention.

The term "agent" means any molecule, including polypeptides, polynucleotides and small molecules.

The term "agonist" refers to a ligand that stimulates the receptor the ligand binds to in the broadest sense.

The term "assay" means any process used to measure a specific property of a compound. A "screening assay" means a process used to characterize or select compounds based upon their activity from a collection of compounds.

The term "binding affinity" is a property that describes how strongly two or more compounds associate with each other in a non-covalent relationship. Binding affinities can be characterized qualitatively, (such as "strong", "weak", "high", or "low") or quantitatively (such as measuring the K_D).

The term "carrier" means a non-toxic material used in the formulation of pharmaceutical compositions to provide a medium, bulk and/or useable form to a pharmaceutical composition. A carrier may comprise one or more of such materials such as an excipient, stabilizer, or an aqueous pH buffered solution. Examples of physiologically acceptable carriers include aqueous or solid buffer ingredients including phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

The term "complex" means the entity created when two or more compounds bind to each other.

The term "compound" is used herein in the context of a "test compound" or a "drug candidate compound" described in connection with the assays of the present invention. As such, these compounds comprise organic or inorganic compounds, derived synthetically or from natural sources. The compounds include inorganic or organic compounds such as polynucleotides, lipids or hormone analogs that are characterized by relatively low molecular weights. Other biopolymeric organic test compounds include peptides comprising from about 2 to about 40 amino acids and larger polypeptides comprising from about 40 to about 500 amino acids, such as antibodies or antibody conjugates.

The term "condition" or "disease" means the overt presentation of symptoms (i.e., illness) or the manifestation of abnormal clinical indicators (e.g., biochemical indicators). Alternatively, the term "disease" refers to a genetic or environmental risk of or propensity for developing such symptoms or abnormal clinical indicators.

The term "contact" or "contacting" means bringing at least two moieties together, whether in an in vitro system or an in vivo system.

The term "derivatives of a polypeptide" relates to those peptides, oligopeptides, polypeptides, proteins and enzymes that comprise a stretch of contiguous amino acid residues of the polypeptide and that retain the biological activity of the protein, e.g. polypeptides that have amino acid mutations compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may further comprise additional naturally occurring, altered, glycosylated, acylated or non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally occurring form of the polypeptide. It may also contain one or more non-amino acid substituents compared to the amino acid sequence of a naturally occurring form of the polypeptide, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence.

The term "derivatives of a polynucleotide" relates to DNA-molecules, RNA-molecules, and oligonucleotides that comprise a stretch or nucleic acid residues of the polynucleotide, e.g. polynucleotides that may have nucleic acid mutations as compared to the nucleic acid sequence of a naturally occurring form of the polynucleotide. A

derivative may further comprise nucleic acids with modified backbones such as PNA, polysiloxane, and 2'-O-(2-methoxy)ethyl-phosphorothioate, non-naturally occurring nucleic acid residues, or one or more nuclei acid substituents, such as methyl-, thio-, sulphate, benzoyl-, phenyl-, amino-, propyl-, chloro-, and methanocarbanucleosides, or a reporter molecule to facilitate its detection.

The terms "ECM-degrading protein" and "ECM-degrading activity" refer to a protein and activity, respectively, that is capable of degrading extra-cellular matrixes found in bone and cartilage.

The term "effective amount" or "therapeutically effective amount" means that amount of a compound or agent that will elicit the biological or medical response of a subject that is being sought by a medical doctor or other clinician.

The term "endogenous" shall mean a material that a mammal naturally produces. Endogenous in reference to the term "protease", "kinase", or G-Protein Coupled Receptor ("GPCR") shall mean that which is naturally produced by a mammal (for example, and not limitation, a human). In contrast, the term non-endogenous in this context shall mean that which is not naturally produced by a mammal (for example, and not limitation, a human). Both terms can be utilized to describe both "in vivo" and "in vitro" systems. For example, and not a limitation, in a screening approach, the endogenous or non-endogenous TARGET may be in reference to an in vitro screening system. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-endogenous TARGET, screening of a candidate compound by means of an in vivo system is viable.

The term "expressible nucleic acid" means a nucleic acid coding for a proteinaceous molecule, an RNA molecule, or a DNA molecule.

The term "expression" comprises both endogenous expression and overexpression by transduction.

The term "expression inhibitory agent" means a polynucleotide designed to interfere selectively with the transcription, translation and/or expression of a specific polypeptide or protein normally expressed within a cell. More particularly, "expression inhibitory agent" comprises a DNA or RNA molecule that contains a

nucleotide sequence identical to or complementary to at least about 17 sequential nucleotides within the polyribonucleotide sequence coding for a specific polypeptide or protein. Exemplary expression inhibitory molecules include ribozymes, double stranded siRNA molecules, self-complementary single-stranded siRNA molecules, genetic antisense constructs, and synthetic RNA antisense molecules with modified stabilized backbones.

The term "expressible nucleic acid" means a nucleic acid coding for a proteinaceous molecule, an RNA molecule, or a DNA molecule.

The term "fragment of a polynucleotide" relates to oligonucleotides that comprise a stretch of contiguous nucleic acid residues that exhibit substantially a similar, but not necessarily identical, activity as the complete sequence.

The term "fragment of a polypeptide" relates to peptides, oligopeptides, polypeptides, proteins and enzymes that comprise a stretch of contiguous amino acid residues, and exhibit substantially a similar, but not necessarily identical, functional activity as the complete sequence.

The term "hybridization" means any process by which a strand of nucleic acid binds with a complementary strand through base pairing. The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_{0t} or R_{0t} analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed). The term "stringent conditions" refers to conditions that permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature can increase stringency.

The term "inhibit" or "inhibiting", in relationship to the term "response" means that a response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

The term "inhibition" refers to the reduction, down regulation of a process or the elimination of a stimulus for a process that results in the absence or minimization of the expression of a protein or polypeptide.

The term "induction" refers to the inducing, up-regulation, or stimulation of a process that results in the expression of a protein or polypeptide.

The term "ligand" means an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

The term "pharmaceutically acceptable salts" refers to the non-toxic, inorganic and organic acid addition salts, and base addition salts, of compounds of the present invention. These salts can be prepared *in situ* during the final isolation and purification of compounds useful in the present invention.

The term "polypeptide" relates to proteins, proteinaceous molecules, fractions of proteins, peptides, oligopeptides, enzymes (such as kinases, proteases, GCPR's etc.).

The term "polynucleotide" means a polynucleic acid, in single or double stranded form, and in the sense or antisense orientation, complementary polynucleic acids that hybridize to a particular polynucleic acid under stringent conditions, and polynucleotides that are homologous in at least about 60 percent of its base pairs, and more preferably 70 percent of its base pairs are in common, most preferably 90 per cent, and in a special embodiment 100 percent of its base pairs. The polynucleotides include polyribonucleic acids, polydeoxyribonucleic acids, and synthetic analogues thereof. It also includes nucleic acids with modified backbones such as peptide nucleic acid (PNA), polysiloxane, and 2'-O-(2-methoxy)ethylphosphorothioate. The polynucleotides are described by sequences that vary in length, that range from about 10 to about 5000 bases, preferably about 100 to about 4000 bases, more preferably about 250 to about 2500 bases. One polynucleotide embodiment comprises from about 10 to about 30 bases in length. A special embodiment of polynucleotide is the

polyribonucleotide of from about 10 to about 22 nucleotides, more commonly described as small interfering RNAs (siRNAs). Another special embodiment are nucleic acids with modified backbones such as peptide nucleic acid (PNA), polysiloxane, and 2'-O-(2-methoxy)ethylphosphorothioate, or including non-naturally occurring nucleic acid residues, or one or more nucleic acid substituents, such as methyl-, thio-, sulphate, benzoyl-, phenyl-, amino-, propyl-, chloro-, and methanocarbanucleosides, or a reporter molecule to facilitate its detection.

The term "polypeptide" relates to proteins (such as TARGETS), proteinaceous molecules, fractions of proteins peptides and oligopeptides.

The term "solvate" means a physical association of a compound useful in this invention with one or more solvent molecules. This physical association includes hydrogen bonding. In certain instances the solvate will be capable of isolation, for example when one or more solvent molecules are incorporated in the crystal lattice of the crystalline solid. "Solvate" encompasses both solution-phase and isolable solvates. Representative solvates include hydrates, ethanolates and methanolates.

The term "subject" includes humans and other mammals.

The term "TARGET" or "TARGETS" means the protein(s) identified in accordance with the present assay to be involved in the induction of MMP1 levels. The preferred TARGETS are identified as SEQ ID NOS. 101-125 in Table 1. The more preferred TARGETS are the kinases, proteases and G-Protein Coupled Receptors (GPCRs) identified in Table 1.

"Therapeutically effective amount" means that amount of a drug or pharmaceutical agent that will elicit the biological or medical response of a subject that is being sought by a medical doctor or other clinician. In particular, with regard to treating an disease condition characterized by the degradation of extracellular matrix, the term "effective matrix metallo-protease inhibiting amount" is intended to mean that effective amount of an compound of the present invention that will bring about a biologically meaningful decrease in the production of MMP-1 in the subject's disease affected tissues such that extracellular matrix degradation is meaningfully reduced. A compound having matrix metallo-protease inhibiting properties or a

"matrix metallo-protease inhibiting compound" means a compound that provided to a cell in effective amounts is able to cause a biologically meaningful decrease in the production of MMP-I in such cells.

The term "treating" means an intervention performed with the intention of preventing the development or altering the pathology of, and thereby alleviating a disorder, disease or condition, including one or more symptoms of such disorder or condition. Accordingly, "treating" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treating include those already with the disorder as well as those in which the disorder is to be prevented. The related term "treatment," as used herein, refers to the act of treating a disorder, symptom, disease or condition, as the term "treating" is defined above.

Applicants' Invention Based on TARGET Relationship to Extra-cellular Matrix Degradation

As noted above, the present invention is based on the present inventors' discovery that the TARGET polypeptides are factors in the up-regulation and/or induction of extra-cellular matrix degradation. The activity of the ECM-degrading protein is believed to be causative and to correlate with the progression of various diseases associated with an increased degradation of the extra-cellular matrix, including diseases that involve the degradation of the joint.

The present invention relates to a method for assaying for drug candidate compounds that inhibit extra-cellular matrix degradation, comprising contacting the compound with a polypeptide comprising an amino acid sequence of SEQ ID NO: 101-125 and 501-564 under conditions that allow said polypeptide to bind to the compound, and detecting the formation of a complex between the polypeptide and the compound. One preferred means of measuring the complex formation is to determine the binding affinity of said compound to said polypeptide.

More particularly, the invention relates to a method for identifying an agent that inhibits extra-cellular matrix degradation, the method comprising further:

(a) contacting a population of mammalian cells with one or more compound that exhibits binding affinity for a TARGET polypeptide, and

(b) measuring a compound-polypeptide property related to extra-cellular matrix degradation.

The compound-polypeptide property referred to above is related to the expression of the TARGET, and is a measurable phenomenon chosen by the person of ordinary skill in the art. The measurable property may be, e.g., the binding affinity for a peptide domain of the polypeptide TARGET such as for SEQ ID NO: 501-564, or the level of any one of a number of biochemical marker levels of extra-cellular matrix degradation. Extra-cellular matrix degradation can e.g. be measured by measuring the level of enzymes that are induced during the process, such as expression of a MMP and/or a Cathepsin polypeptide.

In a preferred embodiment of the invention, the TARGET polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID No: 101-125 as listed in Table 1.

Table 1

Hit No.	Gene Name	Description	Ref/SEQ accession (DNA)	SEQ ID NO DNA	Ref/SEQ accession (Protein)	SEQ ID NO Protein	Protein Class	SEQ ID KD Target
H31-290	RIPK2	Homo sapiens receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA.	NM_003821	1	NP_003812	101	Kinase	201-205 317-319
H31-035	PRKCE	Homo sapiens protein kinase C, epsilon (PRKCE), mRNA.	NM_005400	2	NP_005391	102	Kinase	206-210 316
H31-319	MST3	Homo sapiens kinase SK246 from Manning et al., Science.	SK246	3		103	Kinase	211-215 313
			NM_003576	4		104	Kinase	211-215 313
H34-088	MAPKAPK5	Homo sapiens mitogen-activated protein kinase-activated protein kinase 5 (MAPKAPK5), transcript variant 1, mRNA.	NM_003668	5	NP_003659	105	Kinase	216-220 305-310
			NM_139078	6		106	Kinase	221-225 305-310
H34-087	MKNK1	Homo sapiens MAP kinase-interacting serine/threonine kinase 1 (MKNK1), mRNA.	NM_003684	7	NP_003675	107	Kinase	226-230 311-312
H31-	CAMK4	Homo sapiens calcium/calmodulin-	NM_001744	8	NP_001735	108	Kinase	231-235

031		dependent protein kinase IV (CAMK4), mRNA.						297
	CAMK4		SK061	9		109	Kinase	236-240 320
H31-347	SEPT1	Homo sapiens septin 1 (SEPT1), mRNA.	NM_052838	10	NP_443070	110	Secreted	241-245
H31-450	PGPEP1	Homo sapiens pyroglutamyl-peptidase I	NM_017712	11		111	Protease	241-245 314-315
H31-351	CD72	Homo sapiens CD72 antigen (CD72), mRNA.	NM_001782	12	NP_001773	112	Secreted	246-250
H31-301	TPST1	Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), mRNA.	NM_003596	13	NP_003587	113	Enzyme	251-255 299,322
H31-242	GPR21	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA.	NM_005294	14	NP_005285	114	GPCR	256-260 304
H31-047	USP21	Homo sapiens ubiquitin specific protease 21 (USP21), transcript variant 1, mRNA.	NM_012475	15	NP_036607	115	Protease	261-265 323-324
	USP21	Homo sapiens ubiquitin specific protease 21 (USP21), transcript variant 2, mRNA.	NM_016572	16	NP_057656	116	Protease	263-267 323-324
H34-092	FZD4	Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA.	NM_012193	17	NP_036325;	117	GPCR	268-272 301-303
			GAL_GPCR 0379	18	GAL_GPCR _0379	118	GPCR	268-272
H31-180	TM7SF1	Homo sapiens transmembrane 7 superfamily member 1 (upregulated in kidney) (TM7SF1), mRNA.	NM_003272	19	NP_003263	119	GPCR	273-277 321
H31-384	FXYD5	Homo sapiens FXYD domain containing ion transport regulator 5 (FXYD5), mRNA.	NM_014164	20	NP_054883	120	Secreted	278-282 300
H31-360	RIT1	Homo sapiens Ras-like without CAAX 1 (RIT1), mRNA	NM_006912	21	NP_008843	121	Enzyme	283-287
H31-049	CASP10	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), transcript variant A, mRNA.	NM_001230	22	NP_001221	122	Protease	288-292 295
	CASP10	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), transcript variant B, mRNA.	NM_032974	23	NP_116756	123	Protease	289-290 292-295 298
	CASP10	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), transcript variant C, mRNA.	NM_032976	24	NP_116758	124	Enzyme	288-292 295
	CASP10	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10), transcript variant D, mRNA.	NM_032977	25	NP_116759	125	Protease	289-292 295,298
		loop						26

Depending on the choice of the skilled artisan, the present assay method may be designed to function as a series of measurements, each of which is designed to determine whether the drug candidate compound is indeed acting on the polypeptide to thereby inhibit extra-cellular matrix degradation. For example, an assay designed to

determine the binding affinity of a compound to the polypeptide, or fragment thereof, may be necessary, but not sufficient, to ascertain whether the test compound would be useful for inhibiting extra-cellular matrix degradation when administered to a subject.

Such binding information would be useful in identifying a set of test compounds for use in an assay that would measure a different property, further down the biochemical pathway, such as for example MMP-1 expression. Such second assay may be designed to confirm that the test compound, having binding affinity for the polypeptide, actually inhibits extra-cellular matrix degradation. Suitable controls should always be in place to insure against false positive readings.

The order of taking these measurements is not believed to be critical to the practice of the present invention, which may be practiced in any order. For example, one may first perform a screening assay of a set of compounds for which no information is known respecting the compounds' binding affinity for the polypeptide. Alternatively, one may screen a set of compounds identified as having binding affinity for a polypeptide domain, or a class of compounds identified as being an inhibitor of the polypeptide. However, for the present assay to be meaningful to the ultimate use of the drug candidate compounds, a measurement of extra-cellular matrix degradation activity is necessary. Validation studies including controls, and measurements of binding affinity to the polypeptides of the invention are nonetheless useful in identifying a compound useful in any therapeutic or diagnostic application.

The present assay method may be practiced *in vitro*, using one or more of the TARGET proteins, or fragments thereof. The amino acid sequences of exemplary protein domain fragments of selected TARGETS are SEQ ID NO: 501-564, listed in Table 1A below.

Table 1A

Accession	Name	Protein Segment	SEQ ID NO Protein segment
NM_005294	GPR21	Extracellular domain	501
NM_005294	GPR21	Transmembrane domain	502
NM_005294	GPR21	Intracellular domain	503

NM_005294	GPR21	Transmembrane domain	504
NM_005294	GPR21	Extracellular domain	505
NM_005294	GPR21	Transmembrane domain	506
NM_005294	GPR21	Intracellular domain	507
NM_005294	GPR21	Transmembrane domain	508
NM_005294	GPR21	Extracellular domain	509
NM_005294	GPR21	Transmembrane domain	510
NM_005294	GPR21	Intracellular domain	511
NM_005294	GPR21	Transmembrane domain	512
NM_005294	GPR21	Extracellular domain	513
NM_005294	GPR21	Transmembrane domain	514
NM_005294	GPR21	Intracellular domain	515
NM_012193	FZD4	Extracellular domain	516
NM_012193	FZD4	Transmembrane domain	517
NM_012193	FZD4	Intracellular domain	518
NM_012193	FZD4	Transmembrane domain	519
NM_012193	FZD4	Extracellular domain	520
NM_012193	FZD4	Transmembrane domain	521
NM_012193	FZD4	Intracellular domain	522
NM_012193	FZD4	Transmembrane domain	523
NM_012193	FZD4	Extracellular domain	524
NM_012193	FZD4	Transmembrane domain	525
NM_012193	FZD4	Intracellular domain	526
NM_012193	FZD4	Transmembrane domain	527
NM_012193	FZD4	Extracellular domain	528
NM_012193	FZD4	Transmembrane domain	529
NM_012193	FZD4	Intracellular domain	530
NM_003272	TM7SF1	Extracellular domain	531
NM_003272	TM7SF1	Transmembrane domain	532
NM_003272	TM7SF1	Intracellular domain	533
NM_003272	TM7SF1	Transmembrane domain	534
NM_003272	TM7SF1	Extracellular domain	535
NM_003272	TM7SF1	Transmembrane domain	536
NM_003272	TM7SF1	Intracellular domain	537
NM_003272	TM7SF1	Transmembrane domain	538
NM_003272	TM7SF1	Extracellular domain	539
NM_003272	TM7SF1	Transmembrane domain	540
NM_003272	TM7SF1	Intracellular domain	541
NM_003272	TM7SF1	Transmembrane domain	542
NM_003272	TM7SF1	Extracellular domain	543
NM_003272	TM7SF1	Transmembrane domain	544
NM_003272	TM7SF1	Intracellular domain	545
NM_001782	CD72	Intracellular domain	546

NM_001782	CD72	Transmembrane domain	547
NM_001782	CD72	Extracellular domain	548
NM_014164	FXYD5	Extracellular domain	549
NM_014164	FXYD5	Transmembrane domain	550
NM_014164	FXYD5	Intracellular domain	551
GAL_GPCR0379	FZD4	Intracellular domain	552
GAL_GPCR0379	FZD4	Transmembrane domain	553
GAL_GPCR0379	FZD4	Extracellular domain	554
GAL_GPCR0379	FZD4	Transmembrane domain	555
GAL_GPCR0379	FZD4	Intracellular domain	556
GAL_GPCR0379	FZD4	Transmembrane domain	557
GAL_GPCR0379	FZD4	Extracellular domain	558
GAL_GPCR0379	FZD4	Transmembrane domain	559
GAL_GPCR0379	FZD4	Intracellular domain	560
GAL_GPCR0379	FZD4	Transmembrane domain	561
GAL_GPCR0379	FZD4	Extracellular domain	562
GAL_GPCR0379	FZD4	Transmembrane domain	563
GAL_GPCR0379	FZD4	Intracellular domain	564

The binding affinity of a compound with the polypeptide TARGET can be measured by methods known in the art, such as using surface plasmon resonance biosensors (Biacore), by saturation binding analysis with a labeled compound (e.g. Scatchard and Lindmo analysis), by differential UV spectrophotometer, fluorescence polarization assay, Fluorometric Imaging Plate Reader (FLIPR®) system, Fluorescence resonance energy transfer, and Bioluminescence resonance energy transfer. The binding affinity of compounds can also be expressed in dissociation constant (Kd) or as IC50 or EC50. The IC50 represents the concentration of a compound that is required for 50% inhibition of binding of another ligand to the polypeptide. The EC50 represents the concentration required for obtaining 50% of the maximum effect in any assay that measures TARGET function. The dissociation constant, Kd, is a measure of how well a ligand binds to the polypeptide, it is equivalent to the ligand concentration required to saturate exactly half of the binding-sites on the polypeptide. Compounds with a high affinity binding have low Kd, IC50 and EC50 values, i.e. in the range of 100 nM to 1 pM; a moderate to low affinity binding relates to a high Kd, IC50 and EC50 values, i.e. in the micromolar range.

The present assay method may also be practiced in a cellular assay, A host cell expressing the TARGET can be a cell with endogenous expression or a cell over-expressing the TARGET e.g. by transduction. When the endogenous expression of the polypeptide is not sufficient to determine a baseline that can easily be measured, one may use using host cells that over-express TARGET. Over-expression has the advantage that the level of the TARGET substrate end products is higher than the activity level by endogenous expression. Accordingly, measuring such levels using presently available techniques is easier.

One embodiment of the present method for identifying a compound that decreases extra-cellular matrix (ECM) degradation comprises culturing a population of mammalian cells expressing a TARGET polypeptide, or a functional fragment or derivative thereof; determining a first level of ECM degradation in said population of cells; exposing said population of cells to a compound, or a mixture of compounds; determining a second level of ECM degradation in said population of cells during or after exposure of said population of cells to said compound, or the mixture of said compounds; and identifying the compound(s) that decreases ECM degradation. As noted above, ECM degradation may be determined by measuring the expression and/or activity of the TARGET polypeptide and/or a known ECM-degrading protein. In a preferred embodiment, said ECM-degrading protein is able to degrade collagen, and more preferably, is able to degrade collagen type I and/or collagen type II. In another preferred embodiment of the present invention, said ECM-degrading protein is a Matrix Metallo Proteinase (MMP), and more preferably is selected from the group consisting of: MMP1, MMP2, MMP3, MMP8, MMP9, MMP13 and MMP14. In this context, the most preferred ECM-degrading protein is Matrix Metalloprotease 1 (MMP1). In yet another preferred embodiment, said ECM-degrading protein is Cathepsin K.

The expression of an ECM-degrading protein can be determined by methods known in the art such as Western blotting using specific antibodies, or an ELISA using antibodies specifically recognizing a particular ECM-degrading protein.

The activity of an ECM-degrading protein can be determined by using fluorogenic small peptide substrates. The specificity of these substrates, however, is often limited. In general, the use of these substrates is limited to the testing of purified proteases in biochemical assays, to avoid interference of other proteases.

The present inventors have developed a protocol allowing the detection, in a high throughput mode, of the activity of collagen degrading enzymes in complex media such as the supernatant of cultured cells. This protocol makes use of native collagen, being labelled with a fluorescent label, as a substrate.

The present inventors identified target genes involved in ECM-degradation by using a 'knock-in' library. This type of library is a screen in which cDNA molecules are transduced into cells by recombinant adenoviruses that induce the expression and activity of a specific gene and corresponding gene product in a cell. Each cDNA in a viral vector corresponds to a specific natural gene. By identifying a cDNA that stimulates ECM-degradation, a direct correlation between can be drawn between the specific gene expression and ECM degradation. The TARGET genes identified using the knock-in library (the protein expression products thereof herein referred to as "TARGET" polypeptides) are then used in the present inventive method for identifying compounds that can be used to prevent ECM-degradation. Indeed, shRNA compounds comprising the sequences listed in Table 3 (SEQ ID NO: 201-324) and the antisense sequences corresponding thereto inhibit the expression and/or activity of these TARGET genes and decrease the ECM-degrading activity of cells, confirming the role of these TARGET genes in ECM-degradation.

Table 3.

List of target sequences selected within the coding sequences of the genes identified as modulators of the collagenolytic activity of SFs for use in RNAi-based down-regulation of the expression of these genes.

DISPLAY_ID	ACCESSION	NAME	SIRNA_NAME	SEQ ID NO
CAMK4	NM_001744	A150100-CAMK4_v1	NM_001744_idx445	232
CAMK4	NM_001744	A150100-CAMK4_v10	NM_001744_idx1045	297
CAMK4	NM_001744	A150100-CAMK4_v11	NM_001744_idx1186	234
CAMK4	NM_001744	A150100-CAMK4_v2	NM_001744_idx258	235
CAMK4	NM_001744	A150100-CAMK4_v3	NM_001744_idx668	233

CAMK4	NM_001744	A150100-CAMK4_v9	NM_001744_idx427	231
CASP10	NM_001230	A150100-CASP10_v1	NM_001230_idx934	295
CASP10	NM_001230	A150100-CASP10_v10	NM_001230_idx1532	291
CASP10	NM_001230	A150100-CASP10_v13	NM_001230_idx1111	292
CASP10	NM_001230	A150100-CASP10_v2	NM_001230_idx382	290
CASP10	NM_001230	A150100-CASP10_v8	NM_032974_idx317	289
CASP10	NM_032974	A150100-CASP10_v1	NM_001230_idx934	295
CASP10	NM_032974	A150100-CASP10_v11	NM_032974_idx1674	293
CASP10	NM_032974	A150100-CASP10_v12	NM_032974_idx1829	294
CASP10	NM_032974	A150100-CASP10_v13	NM_001230_idx1111	292
CASP10	NM_032974	A150100-CASP10_v2	NM_001230_idx382	290
CASP10	NM_032974	A150100-CASP10_v7	NM_032974_idx981	298
CASP10	NM_032974	A150100-CASP10_v8	NM_032974_idx317	289
CASP10	NM_032976	A150100-CASP10_v1	NM_001230_idx934	295
CASP10	NM_032976	A150100-CASP10_v10	NM_001230_idx1532	291
CASP10	NM_032976	A150100-CASP10_v13	NM_001230_idx1111	292
CASP10	NM_032976	A150100-CASP10_v2	NM_001230_idx382	290
CASP10	NM_032976	A150100-CASP10_v8	NM_032974_idx317	289
CASP10	NM_032977	A150100-CASP10_v1	NM_001230_idx934	295
CASP10	NM_032977	A150100-CASP10_v10	NM_001230_idx1532	291
CASP10	NM_032977	A150100-CASP10_v13	NM_001230_idx1111	292
CASP10	NM_032977	A150100-CASP10_v2	NM_001230_idx382	290
CASP10	NM_032977	A150100-CASP10_v7	NM_032974_idx981	298
CASP10	NM_032977	A150100-CASP10_v8	NM_032974_idx317	289
CD72	NM_001782	A150100-CD72_v2	NM_001782_idx376	249
CD72	NM_001782	A150100-CD72_v3	NM_001782_idx742	246
CD72	NM_001782	A150100-CD72_v4	NM_001782_idx975	299
CD72	NM_001782	A150100-CD72_v5	NM_001782_idx1049	247
CD72	NM_001782	A150100-CD72_v6	NM_001782_idx1054	250
CD72	NM_001782	A150100-CD72_v7	NM_001782_idx901	248
FXYD5	NM_014164	A150100-FXYD5_v2	NM_014164_idx224	281
FXYD5	NM_014164	A150100-FXYD5_v3	NM_014164_idx417	280
FXYD5	NM_014164	A150100-FXYD5_v4	NM_014164_idx436	278
FXYD5	NM_014164	A150100-FXYD5_v5	NM_014164_idx542	282
FXYD5	NM_014164	A150100-FXYD5_v6	NM_014164_idx603	279
FXYD5	NM_014164	A150100-FXYD5_v7	NM_014164_idx672	300
FZD4	NM_012193	A150100-C(27)-3BETA-HSD_v3	NM_025193_idx1374	301
FZD4	NM_012193	A150100-FZD4_v10	NM_012193_idx849	271
FZD4	NM_012193	A150100-FZD4_v5	NM_012193_idx481	269
FZD4	NM_012193	A150100-FZD4_v6	NM_012193_idx1570	302
FZD4	NM_012193	A150100-FZD4_v7	NM_012193_idx745	272
FZD4	NM_012193	A150100-FZD4_v8	NM_012193_idx1160	303
FZD4	NM_012193	A150100-FZD4_v9	NM_012193_idx534	270
GPR21	NM_005294	A150100-GPR21_v10	NM_005294_idx638	257

GPR21	NM_005294	A150100-GPR21_v11	NM_005294_idx936	258
GPR21	NM_005294	A150100-GPR21_v12	NM_005294_idx168	304
GPR21	NM_005294	A150100-GPR21_v13	NM_005294_idx868	256
GPR21	NM_005294	A150100-GPR21_v14	NM_005294_idx988	260
GPR21	NM_005294	A150100-GPR21_v9	NM_005294_idx161	259
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v1	oKD102	219
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v10	NM_003668_idx856	305
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v11	NM_003668_idx1542	225
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v12	NM_003668_idx456	306
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v13	NM_003668_idx609	307
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v2	oKD103	308
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v8	oKD104	309
MAPKAPK5	NM_003668	A150100-MAPKAPK5_v9	NM_003668_idx686	310
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v1	oKD102	219
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v10	NM_003668_idx856	305
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v11	NM_003668_idx1542	225
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v12	NM_003668_idx456	306
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v13	NM_003668_idx609	307
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v2	oKD103	308
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v8	oKD104	309
MAPKAPK5	NM_139078	A150100-MAPKAPK5_v9	NM_003668_idx686	310
MKNK1	NM_003684	A150100-MKNK1_v1	oKD110	311
MKNK1	NM_003684	A150100-MKNK1_v14	oKD109	230
MKNK1	NM_003684	A150100-MKNK1_v15	oKD108	226
MKNK1	NM_003684	A150100-MKNK1_v16	NM_003684_idx384	228
MKNK1	NM_003684	A150100-MKNK1_v17	NM_003684_idx549	229
MKNK1	NM_003684	A150100-MKNK1_v18	NM_003684_idx1216	312
MST3	SK246	A150100-MST3_v2	SK246_idx413	215
MST3	SK246	A150100-MST3_v3	SK246_idx508	214
MST3	SK246	A150100-MST3_v4	SK246_idx918	212
MST3	SK246	A150100-STK24_v1	NM_003576_idx300	211
MST3	SK246	A150100-STK24_v2	NM_003576_idx950	313
MST3	SK246	A150100-STK24_v3	NM_003576_idx1020	213
PGPEP1	NM_017712	A150100-FLJ20208_v10	NM_017712_idx176	243
PGPEP1	NM_017712	A150100-FLJ20208_v11	NM_017712_idx404	241

PGPEP1	NM_017712	A150100-FLJ20208_v5	NM_017712_idx289	245
PGPEP1	NM_017712	A150100-FLJ20208_v6	NM_017712_idx164	242
PGPEP1	NM_017712	A150100-FLJ20208_v7	NM_017712_idx496	314
PGPEP1	NM_017712	A150100-FLJ20208_v8	NM_017712_idx198	244
PGPEP1	NM_017712	A150100-FLJ20208_v9	NM_017712_idx298	315
PRKCE	NM_005400	A150100-PRKCE_v10	NM_005400_idx760	208
PRKCE	NM_005400	A150100-PRKCE_v11	NM_005400_idx1276	209
PRKCE	NM_005400	A150100-PRKCE_v2	NM_005400_idx1240	206
PRKCE	NM_005400	A150100-PRKCE_v7	NM_005400_idx1109	207
PRKCE	NM_005400	A150100-PRKCE_v8	NM_005400_idx2050	210
PRKCE	NM_005400	A150100-PRKCE_v9	NM_005400_idx148	316
RIPK2	NM_003821	A150100-RIPK2_v1	oKD111	201
RIPK2	NM_003821	A150100-RIPK2_v10	NM_003821_idx993	317
RIPK2	NM_003821	A150100-RIPK2_v11	NM_003821_idx1416	318
RIPK2	NM_003821	A150100-RIPK2_v2	oKD112	203
RIPK2	NM_003821	A150100-RIPK2_v3	oKD113	204
RIPK2	NM_003821	A150100-RIPK2_v9	NM_003821_idx612	319
RIT1	NM_006912	A150100-RIT_v2	NM_006912_idx247	286
RIT1	NM_006912	A150100-RIT_v3	NM_006912_idx536	283
RIT1	NM_006912	A150100-RIT_v4	NM_006912_idx622	285
RIT1	NM_006912	A150100-RIT_v5	NM_006912_idx824	287
RIT1	NM_006912	A150100-RIT_v6	NM_006912_idx263	284
SEPT1	NM_052838	A150100-SEPT1_v2	NM_052838_idx305	320
SEPT1	NM_052838	A150100-SEPT1_v3	NM_052838_idx329	238
SEPT1	NM_052838	A150100-SEPT1_v4	NM_052838_idx480	239
SEPT1	NM_052838	A150100-SEPT1_v5	NM_052838_idx677	237
SEPT1	NM_052838	A150100-SEPT1_v6	NM_052838_idx954	236
SEPT1	NM_052838	A150100-SEPT1_v7	NM_052838_idx1218	240
MST3	NM_003576	A150100-MST3_v2	SK246_idx413	215
MST3	NM_003576	A150100-MST3_v3	SK246_idx508	214
MST3	NM_003576	A150100-MST3_v4	SK246_idx918	212
MST3	NM_003576	A150100-STK24_v1	NM_003576_idx300	211
MST3	NM_003576	A150100-STK24_v2	NM_003576_idx950	313
MST3	NM_003576	A150100-STK24_v3	NM_003576_idx1020	213
TM7SF1	NM_003272	A150100-TM7SF1_v11	NM_003272_idx637	277
TM7SF1	NM_003272	A150100-TM7SF1_v12	NM_003272_idx673	274
TM7SF1	NM_003272	A150100-TM7SF1_v13	NM_003272_idx764	321
TM7SF1	NM_003272	A150100-TM7SF1_v14	NM_003272_idx775	276
TM7SF1	NM_003272	A150100-TM7SF1_v9	NM_003272_idx275	273
TPST1	NM_003596	A150100-TPST1_v1	NM_003596_idx722	255
TPST1	NM_003596	A150100-TPST1_v2	NM_003596_idx1262	253
TPST1	NM_003596	A150100-TPST1_v3	NM_003596_idx425	251
TPST1	NM_003596	A150100-TPST1_v5	NM_003596_idx1229	252
TPST1	NM_003596	A150100-TPST1_v6	NM_003596_idx1260	254
TPST1	NM_003596	A150100-TPST1_v7	NM_003596_idx1444	322

USP21	NM_012475	A150100-USP21_v1	NM_012475_idx1574	261
USP21	NM_012475	A150100-USP21_v13	NM_012475_idx741	266
USP21	NM_012475	A150100-USP21_v14	NM_012475_idx928	323
USP21	NM_012475	A150100-USP21_v15	NM_012475_idx682	263
USP21	NM_012475	A150100-USP21_v16	NM_012475_idx733	267
USP21	NM_012475	A150100-USP21_v17	NM_012475_idx1573	262
USP21	NM_012475	A150100-USP21_v2	NM_012475_idx1224	265
USP21	NM_012475	A150100-USP21_v3	NM_012475_idx269	264
USP21	NM_012475	A150100-mmUsp21_v5	NM_013919_idx1120	324
USP21	NM_016572	A150100-USP21_v13	NM_012475_idx741	266
USP21	NM_016572	A150100-USP21_v14	NM_012475_idx928	323
USP21	NM_016572	A150100-USP21_v15	NM_012475_idx682	263
USP21	NM_016572	A150100-USP21_v16	NM_012475_idx733	267
USP21	NM_016572	A150100-USP21_v2	NM_012475_idx1224	265
USP21	NM_016572	A150100-USP21_v3	NM_012475_idx269	264
USP21	NM_016572	A150100-mmUsp21_v5	NM_013919_idx1120	324

It should be understood that the TARGET genes represented in Table 1 encode different kinds of polypeptides. For example, the TARGETS represented by SEQ ID NO: 114, 117-119 as disclosed herein (Table 1) are GPCRs. Each of these GPCRs is capable of activating an effector protein, resulting in changes in second messenger levels in the cell. The activity of a GPCR can be measured by measuring the activity level of such second messengers. Two important and useful second messengers in the cell are cyclic AMP (cAMP) and Ca^{2+}. The activity levels can be measured by methods known to persons skilled in the art, either directly by ELISA or radioactive technologies or by using substrates that generate a fluorescent or luminescent signal when contacted with Ca^{2+} or indirectly by reporter gene analysis.

The activity level of the one or more secondary messengers may typically be determined with a reporter gene controlled by a promoter, wherein the promoter is responsive to the second messenger. Promotors known and used in the art for such purposes are the cyclic-AMP responsive promoter that is responsive for the cyclic-AMP levels in the cell, and the NF-AT responsive promoter that is sensitive to cytoplasmic Ca^{2+}-levels in the cell. The reporter gene typically has a gene product that is easily detectable. The reporter gene can either be stably infected or transiently

transfected in the host cell. Useful reporter genes are alkaline phosphatase, enhanced green fluorescent protein, destabilized green fluorescent protein, luciferase and β-galactosidase.

Many of the TARGETS as disclosed herein are kinases and phospatases, such as the targets represented by SEQ ID NO: 101-108. Specific methods to determine the activity of a kinase or phosphatase by measuring the phosphorylation of a substrate by the kinase or phosphastase, which measurements are performed in the presence or absence of a compound, are well known in the art, whereas some are described in the examples.

The TARGETS represented by SEQ ID NO: 111, 115, 116, 122, 123, and 125 are proteases. Specific methods to determine the inhibition by the compound by measuring the cleavage of the substrate by the polypeptide, which is a protease, are well known in the art.

It should be understood that the cells expressing the polypeptides, may be cells naturally expressing the polypeptides, or the cells may be may be transfected to express the polypeptides, as described above.

In one embodiment it is preferred that the methods of the present invention further comprise the step of contacting the population of cells with an agonist of the polypeptide. This is useful in methods wherein the expression of the polypeptide in a certain chosen population of cells is too low for a proper detection of its activity. By using an agonist the polypeptide may be triggered, enabling a proper read-out if the compound inhibits the polypeptide. Similar considerations apply to the measurement of ECM degradation. In a preferred embodiment, the cells used in the present method are mammalian synovial fibroblasts and the triggers that may be used to induce the ECM-degrading activity are cytokines relevant in the field of arthritis: for instance TNFalpha, IL1beta, IL6, OSM, IL17, and MIF1alpha. In another preferred embodiment, the trigger is a mixture of factors generated by contacting cytokine-producing cells relevant in the field of arthritis, such as monocytes, macrophages, T-cells, and B-cells. The cytokine-producing cells will respond to the contact by producing a complex and unbiased mixture of factors. If the cytokine-producing cell

used is also found in a pannus, and the cytokine applied to this trigger is found in the synovial fluid of rheumatoid arthritis patients, the mixture of factors ultimately produced will contain part of the factors that are present in the joints of arthritis patients.

The present invention further relates to a method for identifying a compound that inhibits extra-cellular matrix degradation, comprising:

(a) contacting a compound with a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 and 501-564;

(b) determining the binding affinity of the compound to the polypeptide;

(c) contacting a population of mammalian cells expressing said polypeptide with the compound that exhibits a binding affinity of at least 10 micromolar; and

(d) identifying the compound that inhibits extra-cellular matrix degradation.

The population of cells may be exposed to the compound or the mixture of compounds through different means, for instance by direct incubation in the medium, or by nucleic acid transfer into the cells. Such transfer may be achieved by a wide variety of means, for instance by direct transfection of naked isolated DNA, or RNA, or by means of delivery systems, such as recombinant vectors. Other delivery means such as liposomes, or other lipid-based vectors may also be used. Preferably, the nucleic acid compound is delivered by means of a (recombinant) vector such as a recombinant virus.

For high-throughput purposes, libraries of compounds may be used such as antibody fragment libraries, peptide phage display libraries, peptide libraries (e.g. LOPAP^{TM}, Sigma Aldrich), lipid libraries (BioMol), synthetic compound libraries (e.g. LOPAC^{TM}, Sigma Aldrich) or natural compound libraries (Specs, TimTec).

Preferred drug candidate compounds are low molecular weight compounds. Low molecular weight compounds, i.e. with a molecular weight of 500 Dalton or less, are likely to have good absorption and permeation in biological systems and are consequently more likely to be successful drug candidates than compounds with a

molecular weight above 500 Dalton (Lipinski et al. (1997)). Peptides comprise another preferred class of drug candidate compounds. Many GPCRs have a peptide as an agonist or antagonist. Peptides may be excellent drug candidates and there are multiple examples of commercially valuable peptides such as fertility hormones and platelet aggregation inhibitors. Natural compounds are another preferred class of drug candidate compound. Such compounds are found in and extracted from natural sources, and which may thereafter be synthesized. The lipids are another preferred class of drug candidate compound. Many GPCRs have lipids as a ligand.

Another preferred class of drug candidate compounds is an antibody. The present invention also provides antibodies directed against a TARGET. These antibodies may be endogenously produced to bind to the TARGET within the cell, or added to the tissue to bind to TARGET polypeptide present outside the cell. These antibodies may be monoclonal antibodies or polyclonal antibodies. The present invention includes chimeric, single chain, and humanized antibodies, as well as FAb fragments and the products of a FAb expression library, and Fv fragments and the products of an Fv expression library. In another embodiment, the compound may be a nanobody, the smallest functional fragment of naturally occurring single-domain antibodies (Cortez-Retamozo et al. 2004).

In certain embodiments, polyclonal antibodies may be used in the practice of the invention. The skilled artisan knows methods of preparing polyclonal antibodies. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. Antibodies may also be generated against the intact TARGET protein or polypeptide, or against a fragment, derivatives including conjugates, or other epitope of the TARGET protein or polypeptide, such as the TARGET embedded in a cellular membrane, or a library of antibody variable regions, such as a phage display library.

It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic

proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants that may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). One skilled in the art without undue experimentation may select the immunization protocol.

In some embodiments, the antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using methods known in the art. The monoclonal antibodies of the present invention may be "humanized" to prevent the host from mounting an immune response to the antibodies. A "humanized antibody" is one in which the complementarity determining regions (CDRs) and/or other portions of the light and/or heavy variable domain framework are derived from a non-human immunoglobulin, but the remaining portions of the molecule are derived from one or more human immunoglobulins. Humanized antibodies also include antibodies characterized by a humanized heavy chain associated with a donor or acceptor unmodified light chain or a chimeric light chain, or vice versa. The humanization of antibodies may be accomplished by methods known in the art (see, e.g. Mark and Padlan, (1994) "Chapter 4. Humanization of Monoclonal Antibodies", The Handbook of Experimental Pharmacology Vol. 113, Springer-Verlag, New York). Transgenic animals may be used to express humanized antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter, (1991) J. Mol. Biol. 227:381-8; Marks et al. (1991). J. Mol. Biol. 222:581-97). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77; Boerner, et al (1991). J. Immunol., 147(1):86-95).

Techniques known in the art for the production of single chain antibodies can be adapted to produce single chain antibodies to the TARGET polypeptides and proteins of the present invention. The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and

modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain cross-linking. Alternatively; the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent cross-linking.

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens and preferably for a cell-surface protein or receptor or receptor subunit. In the present case, one of the binding specificities is for one domain of the TARGET; the other one is for another domain of the same or different TARGET.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, (1983) Nature 305:537-9). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. Affinity chromatography steps usually accomplish the purification of the correct molecule. Similar procedures are disclosed in Trauneeker, et al. (1991) EMBO J. 10:3655-9.

According to another preferred embodiment, the assay method uses a drug candidate compound identified as having a binding affinity for a TARGET, and/or has already been identified as having down-regulating activity such as antagonist activity vis-à-vis one or more TARGET.

The present invention further relates to a method for inhibiting extra-cellular matrix degradation comprising contacting mammalian cells with an expression inhibitory agent comprising a polyribonucleotide sequence that complements at least about 17 to about 30 contiguous nucleotides of the nucleotide sequence selected from the group consisting of SEQ ID NO: 1-25.

Another aspect of the present invention relates to a method for inhibiting extra-cellular matrix degradation, comprising by contacting mammalian cells with an expression-inhibiting agent that inhibits the translation in the cell of a

polyribonucleotide encoding a TARGET polypeptide. A particular embodiment relates to a composition comprising a polynucleotide including at least one antisense strand that functions to pair the agent with the TARGET mRNA, and thereby down-regulate or block the expression of TARGET polypeptide. The inhibitory agent preferably comprises antisense polynucleotide, a ribozyme, and a small interfering RNA (siRNA), wherein said agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence selected from the group consisting of SEQ ID NO: 1-25.

A special embodiment of the present invention relates to a method wherein the expression-inhibiting agent is selected from the group consisting of antisense RNA, antisense oligodeoxynucleotide (ODN), a ribozyme that cleaves the polyribonucleotide coding for SEQ ID NO: 1-25, a small interfering RNA (siRNA, preferably shRNA,) that is sufficiently homologous to a portion of the polyribonucleotide corresponding to SEQ ID NO: 1-25, such that the siRNA, preferably shRNA, interferes with the translation of the TARGET polyribonucleotide to the TARGET polypeptide.

Another embodiment of the present invention relates to a method wherein the expression-inhibiting agent is a nucleic acid expressing the antisense RNA, antisense oligodeoxynucleotide (ODN), a ribozyme that cleaves the polyribonucleotide encoded by SEQ ID NO: 1-25, a small interfering RNA (siRNA, preferably shRNA,) that is sufficiently complementary to a portion of the polyribonucleotide corresponding to SEQ ID NO: 1-25, such that the siRNA, preferably shRNA, interferes with the translation of the TARGET polyribonucleotide to the TARGET polypeptide. Preferably the expression-inhibiting agent is an antisense RNA, ribozyme, antisense oligodeoxynucleotide, or siRNA, preferably shRNA, comprising a polyribonucleotide sequence that complements at least about 17 to about 30 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-25. More preferably, the expression-inhibiting agent is an antisense RNA, ribozyme, antisense oligodeoxynucleotide, or siRNA, preferably shRNA, comprising a polyribonucleotide sequence that complements at least about 17 to about 25 contiguous nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-25. A

special embodiment comprises a polyribonucleotide sequence that complements a polynucleotide sequence selected from the group consisting of SEQ ID NO: 201-324.

The down regulation of gene expression using antisense nucleic acids can be achieved at the translational or transcriptional level. Antisense nucleic acids of the invention are preferably nucleic acid fragments capable of specifically hybridizing with all or part of a nucleic acid encoding a TARGET polypeptide or the corresponding messenger RNA. In addition, antisense nucleic acids may be designed which decrease expression of the nucleic acid sequence capable of encoding a TARGET polypeptide by inhibiting splicing of its primary transcript. Any length of antisense sequence is suitable for practice of the invention so long as it is capable of down-regulating or blocking expression of a nucleic acid coding for a TARGET. Preferably, the antisense sequence is at least about 17 nucleotides in length. The preparation and use of antisense nucleic acids, DNA encoding antisense RNAs and the use of oligo and genetic antisense is known in the art.

One embodiment of expression-inhibitory agent is a nucleic acid that is antisense to a nucleic acid comprising SEQ ID NO: 1-25. For example, an antisense nucleic acid (e.g. DNA) may be introduced into cells *in vitro*, or administered to a subject *in vivo*, as gene therapy to inhibit cellular expression of nucleic acids comprising SEQ ID NO: 1-25. Antisense oligonucleotides preferably comprise a sequence containing from about 17 to about 100 nucleotides and more preferably the antisense oligonucleotides comprise from about 18 to about 30 nucleotides. Antisense nucleic acids may be prepared from about 17 to about 30 contiguous nucleotides selected from the sequences of SEQ ID NO: 1-25, expressed in the opposite orientation.

The antisense nucleic acids are preferably oligonucleotides and may consist entirely of deoxyribo-nucleotides, modified deoxyribonucleotides, or some combination of both. The antisense nucleic acids can be synthetic oligonucleotides. The oligonucleotides may be chemically modified, if desired, to improve stability and/or selectivity. Since oligonucleotides are susceptible to degradation by intracellular nucleases, the modifications can include, for example, the use of a sulfur

group to replace the free oxygen of the phosphodiester bond. This modification is called a phosphorothioate linkage. Phosphorothioate antisense oligonucleotides are water soluble, polyanionic, and resistant to endogenous nucleases. In addition, when a phosphorothioate antisense oligonucleotide hybridizes to its TARGET site, the RNA-DNA duplex activates the endogenous enzyme ribonuclease (RNase) H, which cleaves the mRNA component of the hybrid molecule.

In addition, antisense oligonucleotides with phosphoramidite and polyamide (peptide) linkages can be synthesized. These molecules should be very resistant to nuclease degradation. Furthermore, chemical groups can be added to the 2' carbon of the sugar moiety and the 5 carbon (C-5) of pyrimidines to enhance stability and facilitate the binding of the antisense oligonucleotide to its TARGET site. Modifications may include 2'-deoxy, O-pentoxy, O-propoxy, O-methoxy, fluoro, methoxyethoxy phosphorothioates, modified bases, as well as other modifications known to those of skill in the art.

Another type of expression-inhibitory agent that reduces the levels of TARGETS is the ribozyme. Ribozymes are catalytic RNA molecules (RNA enzymes) that have separate catalytic and substrate binding domains. The substrate binding sequence combines by nucleotide complementarity and, possibly, non-hydrogen bond interactions with its TARGET sequence. The catalytic portion cleaves the TARGET RNA at a specific site. The substrate domain of a ribozyme can be engineered to direct it to a specified mRNA sequence. The ribozyme recognizes and then binds a TARGET mRNA through complementary base pairing. Once it is bound to the correct TARGET site, the ribozyme acts enzymatically to cut the TARGET mRNA. Cleavage of the mRNA by a ribozyme destroys its ability to direct synthesis of the corresponding polypeptide. Once the ribozyme has cleaved its TARGET sequence, it is released and can repeatedly bind and cleave at other mRNAs.

Ribozyme forms include a hammerhead motif, a hairpin motif, a hepatitis delta virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) motif or Neurospora VS RNA motif. Ribozymes possessing a hammerhead or hairpin structure are readily prepared since these catalytic RNA molecules can be expressed

within cells from eukaryotic promoters (Chen, et al. (1992) Nucleic Acids Res. 20:4581-9). A ribozyme of the present invention can be expressed in eukaryotic cells from the appropriate DNA vector. If desired, the activity of the ribozyme may be augmented by its release from the primary transcript by a second ribozyme (Ventura, et al. (1993) Nucleic Acids Res. 21:3249-55).

Ribozymes may be chemically synthesized by combining an oligodeoxyribonucleotide with a ribozyme catalytic domain (20 nucleotides) flanked by sequences that hybridize to the TARGET mRNA after transcription. The oligodeoxyribonucleotide is amplified by using the substrate binding sequences as primers. The amplification product is cloned into a eukaryotic expression vector.

Ribozymes are expressed from transcription units inserted into DNA, RNA, or viral vectors. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol (I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on nearby gene regulatory sequences. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Gao and Huang, (1993) Nucleic Acids Res. 21:2867-72). It has been demonstrated that ribozymes expressed from these promoters can function in mammalian cells (Kashani-Sabet, et al. (1992) Antisense Res. Dev. 2:3-15).

A particularly preferred inhibitory agent is a small interfering RNA (siRNA, preferably small hairpin RNA, "shRNA"). siRNA, preferably shRNA, mediate the post-transcriptional process of gene silencing by double stranded RNA (dsRNA) that is homologous in sequence to the silenced RNA. siRNA according to the present invention comprises a sense strand of 17-25 nucleotides complementary or homologous to a contiguous 17-25 nucleotide sequence selected from the group of sequences described in SEQ ID NO: 1-25, preferably from the group of sequences described in SEQ ID No: 201-324, and an antisense strand of 17-25 nucleotides complementary to the sense strand. The most preferred siRNA comprises sense and anti-sense strands that are 100 per cent complementary to each other and the TARGET

polynucleotide sequence. Preferably the siRNA further comprises a loop region linking the sense and the antisense strand.

A self-complementing single stranded shRNA molecule polynucleotide according to the present invention comprises a sense portion and an antisense portion connected by a loop region linker. Preferably, the loop region sequence is 4-30 nucleotides long, more preferably 5-15 nucleotides long and most preferably 8 nucleotides long. In a most preferred embodiment the linker sequence is UUGCUAUA (SEQ ID NO: 26; see Figure 16). Self-complementary single stranded siRNAs form hairpin loops and are more stable than ordinary dsRNA. In addition, they are more easily produced from vectors.

Analogous to antisense RNA, the siRNA can be modified to confirm resistance to nucleolytic degradation, or to enhance activity, or to enhance cellular distribution, or to enhance cellular uptake, such modifications may consist of modified internucleoside linkages, modified nucleic acid bases, modified sugars and/or chemical linkage the siRNA to one or more moieties or conjugates. The nucleotide sequences are selected according to siRNA designing rules that give an improved reduction of the TARGET sequences compared to nucleotide sequences that do not comply with these siRNA designing rules (For a discussion of these rules and examples of the preparation of siRNA, WO2004094636, published November 4, 2004, and UA20030198627, are hereby incorporated by reference).

The present invention also relates to compositions, and methods using said compositions, comprising a DNA expression vector capable of expressing a polynucleotide capable of inhibiting extra-cellular matrix degradation and described hereinabove as an expression inhibition agent.

A special aspect of these compositions and methods relates to the down-regulation or blocking of the expression of a TARGET polypeptide by the induced expression of a polynucleotide encoding an intracellular binding protein that is capable of selectively interacting with the TARGET polypeptide. An intracellular binding protein includes any protein capable of selectively interacting, or binding, with the polypeptide in the cell in which it is expressed and neutralizing the function of the

polypeptide. Preferably, the intracellular binding protein is a neutralizing antibody or a fragment of a neutralizing antibody having binding affinity to an epitope of the TARGET polypeptide of SEQ ID NO: 101-125, preferably to a domain of SEQ ID NO: 501-564. More preferably, the intracellular binding protein is a single chain antibody.

A special embodiment of this composition comprises the expression-inhibiting agent selected from the group consisting of antisense RNA, antisense oligodeoxynucleotide (ODN), a ribozyme that cleaves the polyribonucleotide coding for SEQ ID NO: 101-125, and a small interfering RNA (siRNA) that is sufficiently homologous to a portion of the polyribonucleotide corresponding to SEQ ID NO: 1-25, such that the siRNA interferes with the translation of the TARGET polyribonucleotide to the TARGET polypeptide,

The polynucleotide expressing the expression-inhibiting agent is preferably included within a vector. The polynucleic acid is operably linked to signals enabling expression of the nucleic acid sequence and is introduced into a cell utilizing, preferably, recombinant vector constructs, which will express the antisense nucleic acid once the vector is introduced into the cell. A variety of viral-based systems are available, including adenoviral, retroviral, adeno-associated viral, lentiviral, herpes simplex viral or a sendaviral vector systems, and all may be used to introduce and express polynucleotide sequence for the expression-inhibiting agents in TARGET cells.

Preferably, the viral vectors used in the methods of the present invention are replication defective. Such replication defective vectors will usually pack at least one region that is necessary for the replication of the virus in the infected cell. These regions can either be eliminated (in whole or in part), or be rendered non-functional by any technique known to a person skilled in the art. These techniques include the total removal, substitution, partial deletion or addition of one or more bases to an essential (for replication) region. Such techniques may be performed in vitro (on the isolated DNA) or in situ, using the techniques of genetic manipulation or by treatment with

mutagenic agents. Preferably, the replication defective virus retains the sequences of its genome, which are necessary for encapsidating, the viral particles.

In a preferred embodiment, the viral element is derived from an adenovirus. Preferably, the vehicle includes an adenoviral vector packaged into an adenoviral capsid, or a functional part, derivative, and/or analogue thereof. Adenovirus biology is also comparatively well known on the molecular level. Many tools for adenoviral vectors have been and continue to be developed, thus making an adenoviral capsid a preferred vehicle for incorporating in a library of the invention. An adenovirus is capable of infecting a wide variety of cells. However, different adenoviral serotypes have different preferences for cells. To combine and widen the TARGET cell population that an adenoviral capsid of the invention can enter in a preferred embodiment, the vehicle includes adenoviral fiber proteins from at least two adenoviruses. Preferred adenoviral fiber protein sequences are serotype 17, 45 and 51. Techniques or construction and expression of these chimeric vectors are disclosed in US Published Patent Applications 20030180258 and 20040071660, hereby incorporated by reference.

In a preferred embodiment, the nucleic acid derived from an adenovirus includes the nucleic acid encoding an adenoviral late protein or a functional part, derivative, and/or analogue thereof. An adenoviral late protein, for instance an adenoviral fiber protein, may be favorably used to TARGET the vehicle to a certain cell or to induce enhanced delivery of the vehicle to the cell. Preferably, the nucleic acid derived from an adenovirus encodes for essentially all adenoviral late proteins, enabling the formation of entire adenoviral capsids or functional parts, analogues, and/or derivatives thereof. Preferably, the nucleic acid derived from an adenovirus includes the nucleic acid encoding adenovirus E2A or a functional part, derivative, and/or analogue thereof. Preferably, the nucleic acid derived from an adenovirus includes the nucleic acid encoding at least one E4-region protein or a functional part, derivative, and/or analogue thereof, which facilitates, at least in part, replication of an adenoviral derived nucleic acid in a cell. The adenoviral vectors used in the examples

of this application are exemplary of the vectors useful in the present method of treatment invention.

Certain embodiments of the present invention use retroviral vector systems. Retroviruses are integrating viruses that infect dividing cells, and their construction is known in the art. Retroviral vectors can be constructed from different types of retrovirus, such as, MoMuLV ("murine Moloney leukemia virus" MSV ("murine Moloney sarcoma virus"), HaSV ("Harvey sarcoma virus"); SNV ("spleen necrosis virus"); RSV ("Rous sarcoma virus") and Friend virus. Lentiviral vector systems may also be used in the practice of the present invention. Retroviral systems and herpes virus system may be preferred vehicles for transfection of neuronal cells.

In other embodiments of the present invention, adeno-associated viruses ("AAV") are utilized. The AAV viruses are DNA viruses of relatively small size that integrate, in a stable and site-specific manner, into the genome of the infected cells. They are able to infect a wide spectrum of cells without inducing any effects on cellular growth, morphology or differentiation, and they do not appear to be involved in human pathologies.

In the vector construction, the polynucleotide agents of the present invention may be linked to one or more regulatory regions. Selection of the appropriate regulatory region or regions is a routine matter, within the level of ordinary skill in the art. Regulatory regions include promoters, and may include enhancers, suppressors, etc.

Promoters that may be used in the expression vectors of the present invention include both constitutive promoters and regulated (inducible) promoters. The promoters may be prokaryotic or eukaryotic depending on the host. Among the prokaryotic (including bacteriophage) promoters useful for practice of this invention are lac, lacZ, T3, T7, lambda P.sub.r, P.sub.l, and trp promoters. Among the eukaryotic (including viral) promoters useful for practice of this invention are ubiquitous promoters (e.g. HPRT, vimentin, actin, tubulin), intermediate filament promoters (e.g. desmin, neurofilaments, keratin, GFAP), therapeutic gene promoters (e.g. MDR type, CFTR, factor VIII), tissue-specific promoters (e.g. actin promoter in

smooth muscle cells, or Flt and Flk promoters active in endothelial cells), including animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift, et al. (1984) Cell 38:639-46; Ornitz, et al. (1986) Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, (1987) Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanahan, (1985) Nature 315:115-22), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl, et al. (1984) Cell 38:647-58; Adames, et al. (1985) Nature 318:533-8; Alexander, et al. (1987) Mol. Cell. Biol. 7:1436-44), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder, et al. (1986) Cell 45:485-95), albumin gene control region which is active in liver (Pinkert, et al. (1987) Genes and Devel. 1:268-76), alpha-fetoprotein gene control region which is active in liver (Krumlauf, et al. (1985) Mol. Cell. Biol., 5:1639-48; Hammer, et al. (1987) Science 235:53-8), alpha 1-antitrypsin gene control region which is active in the liver (Kelsey, et al. (1987) Genes and Devel., 1: 161-71), beta-globin gene control region which is active in myeloid cells (Mogram, et al. (1985) Nature 315:338-40; Kollias, et al. (1986) Cell 46:89-94), myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead, et al. (1987) Cell 48:703-12), myosin light chain-2 gene control region which is active in skeletal muscle (Sani, (1985) Nature 314.283-6), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason, et al. (1986) Science 234:1372-8).

Other promoters which may be used in the practice of the invention include promoters which are preferentially activated in dividing cells, promoters which respond to a stimulus (e.g. steroid hormone receptor, retinoic acid receptor), tetracycline-regulated transcriptional modulators, cytomegalovirus immediate-early, retroviral LTR, metallothionein, SV-40, E1a, and MLP promoters.

Additional vector systems include the non-viral systems that facilitate introduction of polynucleotide agents into a patient. For example, a DNA vector encoding a desired sequence can be introduced in vivo by lipofection. Synthetic

cationic lipids designed to limit the difficulties encountered with liposome-mediated transfection can be used to prepare liposomes for in vivo transfection of a gene encoding a marker (Felgner, et. al. (1987) Proc. Natl. Acad Sci. USA 84:7413-7); see Mackey, et al. (1988) Proc. Natl. Acad. Sci. USA 85:8027-31; Ulmer, et al. (1993) Science 259:1745-8). The use of cationic lipids may promote encapsulation of negatively charged nucleic acids, and also promote fusion with negatively charged cell membranes (Felgner and Ringold, (1989) Nature 337:387-8). Particularly useful lipid compounds and compositions for transfer of nucleic acids are described in International Patent Publications WO 95/18863 and WO 96/17823, and in U.S. Pat. No. 5,459,127. The use of lipofection to introduce exogenous genes into the specific organs in vivo has certain practical advantages and directing transfection to particular cell types would be particularly advantageous in a tissue with cellular heterogeneity, for example, pancreas, liver, kidney, and the brain. Lipids may be chemically coupled to other molecules for the purpose of TARGETing. Targeted peptides, e.g., hormones or neurotransmitters, and proteins for example, antibodies, or non-peptide molecules could be coupled to liposomes chemically. Other molecules are also useful for facilitating transfection of a nucleic acid in vivo, for example, a cationic oligopeptide (e.g., International Patent Publication WO 95/21931), peptides derived from DNA binding proteins (e.g., International Patent Publication WO 96/25508), or a cationic polymer (e.g., International Patent Publication WO 95/21931).

It is also possible to introduce a DNA vector in vivo as a naked DNA plasmid (see U.S. Pat. Nos. 5,693,622, 5,589,466 and 5,580,859). Naked DNA vectors for therapeutic purposes can be introduced into the desired host cells by methods known in the art, e.g., transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter (see, e.g., Wilson, et al. (1992) J. Biol. Chem. 267:963-7; Wu and Wu, (1988) J. Biol. Chem. 263:14621-4; Hartmut, et al. Canadian Patent Application No. 2,012,311, filed Mar. 15, 1990; Williams, et al (1991). Proc. Natl. Acad. Sci. USA 88:2726-30). Receptor-mediated DNA delivery approaches can also

be used (Curiel, et al. (1992) Hum. Gene Ther. 3:147-54; Wu and Wu, (1987) J. Biol. Chem. 262:4429-32).

The present invention also provides biologically compatible, extra-cellular matrix degradation inhibiting compositions comprising an effective amount of one or more compounds identified as TARGET inhibitors, and/or the expression-inhibiting agents as described hereinabove.

A biologically compatible composition is a composition, that may be solid, liquid, gel, or other form, in which the compound, polynucleotide, vector, and antibody of the invention is maintained in an active form, e.g., in a form able to effect a biological activity. For example, a compound of the invention would have inverse agonist or antagonist activity on the TARGET; a nucleic acid would be able to replicate, translate a message, or hybridize to a complementary mRNA of a TARGET; a vector would be able to transfect a TARGET cell and expression the antisense, antibody, ribozyme or siRNA as described hereinabove; an antibody would bind a TARGET polypeptide domain.

A preferred biologically compatible composition is an aqueous solution that is buffered using, e.g., Tris, phosphate, or HEPES buffer, containing salt ions. Usually the concentration of salt ions will be similar to physiological levels. Biologically compatible solutions may include stabilizing agents and preservatives. In a more preferred embodiment, the biocompatible composition is a pharmaceutically acceptable composition. Such compositions can be formulated for administration by topical, oral, parenteral, intranasal, subcutaneous, and intraocular, routes. Parenteral administration is meant to include intravenous injection, intramuscular injection, intraarterial injection or infusion techniques. The composition may be administered parenterally in dosage unit formulations containing standard, well-known non-toxic physiologically acceptable carriers, adjuvants and vehicles as desired.

A particularly preferred embodiment of the present composition invention is a extra-cellular matrix degradation inhibiting pharmaceutical composition comprising a therapeutically effective amount of an expression-inhibiting agent as described hereinabove, in admixture with a pharmaceutically acceptable carrier. Another

preferred embodiment is a pharmaceutical composition for the treatment or prevention of a condition involving ECM degradation, or a susceptibility to the condition, comprising an effective extra-cellular matrix degradation inhibiting amount of a TARGET antagonist or inverse agonist, its pharmaceutically acceptable salts, hydrates, solvates, or prodrugs thereof in admixture with a pharmaceutically acceptable carrier.

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient. Pharmaceutical compositions for oral use can be prepared by combining active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethyl-cellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate. Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinyl-pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate,

and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Preferred sterile injectable preparations can be a solution or suspension in a non-toxic parenterally acceptable solvent or diluent. Examples of pharmaceutically acceptable carriers are saline, buffered saline, isotonic saline (e.g. monosodium or disodium phosphate, sodium, potassium; calcium or magnesium chloride, or mixtures of such salts), Ringer's solution, dextrose, water, sterile water, glycerol, ethanol, and combinations thereof 1,3-butanediol and sterile fixed oils are conveniently employed as solvents or suspending media. Any bland fixed oil can be employed including synthetic mono- or di-glycerides. Fatty acids such as oleic acid also find use in the preparation of injectables.

The composition medium can also be a hydrogel, which is prepared from any biocompatible or non-cytotoxic homo- or hetero-polymer, such as a hydrophilic polyacrylic acid polymer that can act as a drug absorbing sponge. Certain of them, such as, in particular, those obtained from ethylene and/or propylene oxide are commercially available. A hydrogel can be deposited directly onto the surface of the tissue to be treated, for example during surgical intervention.

Embodiments of pharmaceutical compositions of the present invention comprise a replication defective recombinant viral vector encoding the polynucleotide inhibitory agent of the present invention and a transfection enhancer, such as poloxamer. An example of a poloxamer is Poloxamer 407, which is commercially available (BASF, Parsippany, N.J.) and is a non-toxic, biocompatible polyol. A poloxamer impregnated with recombinant viruses may be deposited directly on the surface of the tissue to be treated, for example during a surgical intervention. Poloxamer possesses essentially the same advantages as hydrogel while having a lower viscosity.

The active expression-inhibiting agents may also be entrapped in microcapsules prepared, for example, by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate)

microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences (1980) 16th edition, Osol, A. Ed.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g. films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™. (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

As defined above, therapeutically effective dose means that amount of protein, polynucleotide, peptide, or its antibodies, agonists or antagonists, which ameliorate the symptoms or condition. Therapeutic efficacy and toxicity of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio of toxic to therapeutic

effects is the therapeutic index, and it can be expressed as the ratio, LD50/ED50. Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually mice, rabbits, dogs, or pigs. The animal model is also used to achieve a desirable concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans. The exact dosage is chosen by the individual physician in view of the patient to be treated. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Additional factors which may be taken into account include the severity of the disease state, age, weight and gender of the patient; diet, desired duration of treatment, method of administration, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long acting pharmaceutical compositions might be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation.

The pharmaceutical compositions according to this invention may be administered to a subject by a variety of methods. They may be added directly to targeted tissues, complexed with cationic lipids, packaged within liposomes, or delivered to targeted cells by other methods known in the art. Localized administration to the desired tissues may be done by direct injection, transdermal absorption, catheter, infusion pump or stent. The DNA, DNA/vehicle complexes, or the recombinant virus particles are locally administered to the site of treatment. Alternative routes of delivery include, but are not limited to, intravenous injection, intramuscular injection, subcutaneous injection, aerosol inhalation, oral (tablet or pill

form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. Examples of ribozyme delivery and administration are provided in Sullivan et al. WO 94/02595.

Antibodies according to the invention may be delivered as a bolus only, infused over time or both administered as a bolus and infused over time. Those skilled in the art may employ different formulations for polynucleotides than for proteins. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

As discussed hereinabove, recombinant viruses may be used to introduce DNA encoding polynucleotide agents useful in the present invention. Recombinant viruses according to the invention are generally formulated and administered in the form of doses of between about 10^4 and about 10^{14} pfu. In the case of AAVs and adenoviruses, doses of from about 10^6 to about 10^{11} pfu are preferably used. The term pfu ("plaque-forming unit") corresponds to the infective power of a suspension of virions and is determined by infecting an appropriate cell culture and measuring the number of plaques formed. The techniques for determining the pfu titre of a viral solution are well documented in the prior art.

The present invention also provides methods of inhibiting extra-cellular matrix degradation, comprising administering, to a subject suffering from a disease condition involving extra-cellular matrix degradation, an extra-cellular matrix degradation inhibiting pharmaceutical composition as described herein, preferably a therapeutically effective amount of an expression-inhibiting agent of the present invention. The diseases involving extra-cellular marix degradation, include psoriatic arthritis, juvenile arthritis, early arthritis, reactive arthritis, osteoarthritis, ankylosing spondylitis. osteoporosis, muskulo skeletal diseases such as tendinitis and periodontal disease, cancer metastasis, airway diseases (COPD, asthma), renal and liver fibrosis, cardio-vascular diseases such as atherosclerosis and heart failure, and neurological diseases such as neuroinflammation and multiple sclerosis. More preferred diseases for treatment in accordance with the present invention are the degenerative joint diseases such as psoriatic arthritis, juvenile arthritis, early arthritis, reactive arthritis,

osteoarthritis, ankylosing spondylitis. The most preferred degenerative joint disease for treatment in accordance with the present method is rheumatoid arthritis,

Administering of the expression-inhibiting agent of the present invention to the subject patient includes both self-administration and administration by another person. The patient may be in need of treatment for an existing disease or medical condition, or may desire prophylactic treatment to prevent or reduce the risk for diseases and medical conditions affected by a disturbance in bone metabolism. The expression-inhibiting agent of the present invention may be delivered to the subject patient orally, transdermally, via inhalation, injection, nasally, rectally or via a sustained release formulation.

A preferred regimen of the present method comprises the administration to a subject in suffering from a disease condition characterized by inflammatory, with an effective inhibiting amount of an expression-inhibiting agent of the present invention for a period of time sufficient to reduce the abnormal levels of extracellular matrix degradation in the patient, and preferably terminate, the self-perpetuating processes responsible for said degradation. A special embodiment of the method comprises administering of an effective matrix metallo-protease inhibiting amount of a expression-inhibiting agent of the present invention to a subject patient suffering from or susceptible to the development of rheumatoid arthritis, for a period of time sufficient to reduce or prevent, respectively, collagen and bone degradation in the joints of said patient, and preferably terminate, the self-perpetuating processes responsible for said degradation.

The invention also relates to the use of an agent as described above for the preparation of a medicament for treating or preventing a disease involving extra-cellular matrix degradation.

Preferably the pathological condition is arthritis. More preferably, the pathological condition is rheumatoid arthritis.

The polypeptides and polynucleotides useful in the practice of the present invention described herein may be free in solution, affixed to a solid support, borne on

a cell surface, or located intracellularly. To perform the methods it is feasible to immobilize either the TARGET polypeptide or the compound to facilitate separation of complexes from uncomplexed forms of the polypeptide, as well as to accommodate automation of the assay. Interaction (e.g., binding of) of the TARGET polypeptide with a compound can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and microcentrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows the polypeptide to be bound to a matrix. For example, the TARGET polypeptide can be "His" tagged, and subsequently adsorbed onto Ni-NTA microtitre plates, or ProtA fusions with the TARGET polypeptides can be adsorbed to IgG, which are then combined with the cell lysates (*e.g.*, $(35)^{S}$-labelled) and the candidate compound, and the mixture incubated under conditions favorable for complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the plates are washed to remove any unbound label, and the matrix is immobilized. The amount of radioactivity can be determined directly, or in the supernatant after dissociation of the complexes. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of the protein binding to the TARGET protein quantified from the gel using standard electrophoretic techniques.

Other techniques for immobilizing protein on matrices can also be used in the method of identifying compounds. For example, either the TARGET or the compound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated TARGET protein molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with the TARGETS but which do not interfere with binding of the TARGET to the compound can be derivatized to the wells of the plate, and the TARGET can be trapped in the wells by antibody conjugation. As described above, preparations of a labeled candidate

compound are incubated in the wells of the plate presenting the TARGETS, and the amount of complex trapped in the well can be quantitated.

The polynucleotides encoding the TARGET polypeptides are identified as SEQ ID NO: 1-25. Applicants have shown that transfection of mammalian cells with these polynucleotides in an expressible form increase the release of factors that promote extra-cellular matrix degradation.

The present invention also relates to a method for diagnosis of a pathological condition involving ECM degradation, comprising determining the nucleic acid sequence of at least one of the genes of SEQ ID NO: 1-25 within the genomic DNA of a subject; comparing the sequence with the nucleic acid sequence obtained from a database and/or a healthy subject; and identifying any difference(s) related to the onset of the pathological condition.

Still another aspect of the invention relates to a method for diagnosing a pathological condition involving extra-cellular matrix degradation or a susceptibility to the condition in a subject, comprising determining the amount of polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 in a biological sample, and comparing the amount with the amount of the polypeptide in a healthy subject, wherein an increase of the amount of polypeptide compared to the healthy subject is indicative of the presence of the pathological condition.

The invention is further illustrated in the following figures and examples.

Examples

The following assays, when used in combination with arrayed adenoviral libraries (the production and use of which are described in WO99/64582), are useful for the discovery of factors that modulate the capacity of synovial fibroblasts (SFs) to degrade collagen, the main component of cartilage. Candidate factors are filtered first through a primary followed by a secondary assay. Example 1 describes the development and setup of the primary assay screen of an adenoviral cDNA library using an ELISA for detection of protein levels of Matrix Metalloprotease 1 (MMP1),

and is referred to herein as the "MMP1 assay". Example 2 describes the screening and its results. Examples 3 and 4 describe the secondary assay, which is more functionally oriented, detects collagen degradation in the supernatant of SFs, and is referred to herein as the "collagen degradation assay". Example 5 describes the testing for the endogenous expression of factors in SFs. This method in referred to as "expression profiling" of hits in various RA-derived SFs (RASFs). Example 6 describes the effect of the reduction in activity of various genes on the cytokine-induced SF MMP1 expression thereby determining the collagenolytic activity of RASF's.

Control viruses used:

The control viruses used in these studies are listed below. dE1/dE2A adenoviruses are generated from these adapter plasmids by co-transfection of the helper plasmid pWEAd5AflII-rITR.dE2A in PER.E2A packaging cells, as described in WO99/64582.

(A) Negative control viruses:

Ad5-LacZ: Described as pIPspAdApt6-lacZ in WO02/070744.

Ad5-ALPP: The 1.9 kb insert is isolated from pGT65-PLAP (Invitrogen) by digestion with NsiI; blunted; followed by digestion with EcoR1 and cloned into EcoRI and HpaI-digested pIPspAdApt6.

Ad5-eGFP: Described as pIPspAdApt6-EGFP in WO02/070744.

Ad5-eGFP_KD: Target sequence: GCTGACCCTGAAGTTCATC (SEQ ID NO: 401). Cloned using Sap1-sites into vector and virus generated as described in WO03/020931.

Ad5-Luciferase_KD_v13: Target sequence: GCTGACCCTGAAGTTCATC (SEQ ID NO: 402). Cloned using Sap1-sites into vector and virus generated as described in WO03/020931.

Ad5-M6PR_KD_v1: Target sequence: GCTGACCCTGAAGTTCATC. Cloned using Sap1-sites into vector and virus generated as described in WO03/020931.

(B) Positive control viruses:

Ad5-RELA: The cDNA encoding RELA is obtained by PCR on a human placenta cDNA library with the following primers:

upstream: GCGAAGCTTGCGGCATGGACGAACTGT (SEQ ID NO: 403) and

downstream: GCGGGATCCCAGGCGTCACCCCCTTAG (SEQ ID NO: 404).

A 1681bp DNA insert is generated of which the 5' sequence corresponds to NM_021975. Primers are designed such that the PCR products can be inserted into the pIPspAdapt6 vector by *Hind*III-*Bam*HI cloning.

Ad5-MMP1: The cDNA encoding MMP1, cloned into the pIPspAdapt6 plasmid, is isolated from a human placenta cDNA library (see WO02/070744) by classical filter colony hybridisation strategy. A human placental cDNA library is transformed into bacteria and plated out on agar plates. Thousands of individual colonies are picked (using a Q-pix device (Genetix)) and re-arrayed on agar plates. After growing bacteria up, these plates are overlayed on hybridisation filters. These filters are subjected to a classical hybridisation procedure with a MMP1 specific probe. This probe is obtained by PCR on a placenta cDNA library using the following primers:

upstream: GTTCTGGGGTGTGGTGTCTCACAGC (SEQ ID NO: 405); and

downstream: CAAACTGAGCCACATCAGGCACTCC (SEQ ID NO: 406).

A bacterial colony, at a position corresponding to that of a positive signal spot on the filter after hybridisation, is picked and used for plasmid preparation. 5' sequence verification confirms that the 5' sequence of the insert corresponds to NM_002421.

Ad5-TRAF6: The cDNA encoding TRAF6 is isolated according to the same colony hybridisation technique as the one described for MMP1. The TRAF6

specific probe is obtained by PCR on a placenta cDNA library using the following primers:

upstream: CCAGTCTGAAAGTGACTGCTGTGTGG (SEQ ID NO: 407); and

downstream: CAACTGGACATTTGTGACCTGCATCC (SEQ ID NO: 408).

A bacterial colony, at a position corresponding to that of a positive signal spot on the filter after hybridisation, is picked and used for plasmid preparation. 5' sequence verification confirms that the 5' sequence of the insert corresponds to NM_004620.2.

Ad5-MMP13: The cDNA of MMP13 is isolated from a cDNA preparation from human synovial fibroblasts by PCR. The 1498 bp PCR product is cloned into pIPspAdapt6 using a *Hind*III/*Eco*RI cloning strategy. Sequence verification confirms that the insert corresponds to bp 18 to 1497 of NM_002427.

Ad5-MYD88: This cDNA is isolated from a human placenta cDNA library constructed in pIPspAdapt6. The virus mediating the expression of MYD88 is identified as a hit in one of the genomic screen run at Galapagos Genomics. Sequence verification of the insert confirms that the insert corresponds to bp 40 to 930 of NM_002468.

Ad5TNFRIA: This virus is isolated from a human placenta cDNA library constructed in pIPspAdapt6. The virus mediating the expression of MYD88 is identified as a hit in one of the genomic screen run at Galapagos Genomics. 5' sequence verification of the 1.4 Kb insert reveals that the insert starts at bp 958 of NM_001065. Virus is generated as described in WO03/020931.

Ad5-MMP1_KD_v10: Target sequence: GCTGACCCTGAAGTTCATC (SEQ ID NO: 409). Cloned using SapI-sites into vector and virus generated as described in WO03/020931.

Example 1: Development of the MMP assay

Matrix Metallo Proteases (MMPs) possess various physiological roles, for example, they are involved in the maturation of other proteases, growth factors, and the degradation of extra-cellular matrix components. MMP1 is a member of the MMP family and is able to degrade native collagen, the main component of bone and cartilage. Increased expression of MMP1 by synovial fibroblasts (SFs) is diagnostic for the progression of the arthritic disease and is predictive for erosive processes in the joint (Cunnane et al., 2001). SF expression of MMP1 can be increased by the activation of SFs with triggers relevant for rheumatoid arthritis, such as the cytokines TNF-α and IL1ß (Andreakos et al., 2003). The measurement of the MMP1 levels produced by activated SFs is highly relevant in the context of RA as this event reflects the level of activation of SFs towards an erosive phenotype as it is seen in the pannus. If reduced expression of a candidate target protein in activated SFs leads to the reduction of MMP1 expression in these cells, then the target is shown to be involved in the regulation of MMP1 expression and thus considered relevant for the development of therapeutic strategies for the treatment of RA. The identification of such target proteins involves the screening of a collection of recombinant adenoviruses mediating the expression of a library of cDNAs, further referred to as "Ad-cDNAs". The collection used herein is further referred to as "adenoviral cDNA library" or the "FlexSelect collection" (see WO99/64582).

The MMP1 assay is developed by first testing the capacity of Synovial fibroblasts (SFs) to produce MMP1.

A. To evaluate the capacity of SFs to produce MMP1, a set of adenoviruses mediating the expression of TRAF6 and MYD88, adaptor molecules in the IL1β pathway, and p65/RelA, a subunit of the NFκB transcription factor that is known to increase expression of factors involved in the immune and inflammatory responses, both of which are expected to increase MMP1 expression (see Vincenti and Brinckerhoff, 2002) are used to infect SFs.

40,000 SFs are seeded per well of a 6-well plate in DMEM + 10% FBS and infected with a multiplicity of infection (MOI) of 7500 viral particles per cell (vp/cell). The expression of MMP1 by SFs is first determined at the mRNA level, by means of real-time, quantitative PCR. RNA of the cells infected with the control viruses is prepared 48 h post infection using the SV RNA isolation kit (Promega), according to the instructions of the manufacturer. cDNA is prepared from this RNA using Multiscribe reverse transcriptase (50 U/µl, Applied Biosystems) and random hexamers. cDNA synthesis is performed in 25 µl total volume consisting of 1x TaqMan buffer A (PE Applied Biosystems), 5 mM MgCl2, 500 mM total dNTPs, 2,5 mM random hexamers, 0.4 U/µl RNase Inhibitor, and 1.25 U/µl MultiScribe Reverse Transcriptase. The mixture is incubated for 10 min at 25°C, 30 min at 48°C, and 5 min at 95°C. Specific DNA products are amplified from the resulting cDNA with AmpliTaq Gold DNA polymerase (Applied BioSystems) during 40 PCR cycles using suited primer pairs. Amplification of the specific DNA products is monitored on an ABI PRISM® 7000 Sequence Detection System. The subsequent real time PCR reaction contained 5 µl of the RT reaction product in a total volume of 25 µl consisting of 1x SYBR Green mix (Applied Biosystems), 300 nM forward primer, and 300 nM reverse primer. Each sample is analyzed in duplicate. The PCR reaction is performed using the following program: 10 min at 95°C followed by 40 cycles of (15 sec 95°C, 1 min 60°C). After each PCR reaction the products are analysed by measuring the dissociation curve by incubating for 15 sec 95°C, and 15 sec at 60°C, followed by increasing the temperature to 95°C over a 20 min time period, ending with 15 sec at 95°C. The sequences of the primer pairs used for the detection of MMP1, 18S and β-actin expression are listed in Table 2.

Table 2. List of primers and their sequences used herein.

Hit number	Primer name	Primer sequence	SEQ ID NO
NA	pAdapt_FW	GGTGGGAGGTCTATATAAGC	410
	pAdapt_REV	GGACAAACCACAACTAGAATGC	411
NA	MMP2_For	CCCCAGGCACTGGTGTTG	412
	MMP2_Rev	ACGGACCACTTGGCCTTCT	413

NA	MMP1_For	CCGGTTTTTCAAAGGGAATAAGTAC	414
	MMP1_Rev	TTCACAGTTCTAGGGAAGCCAAAG	415
H31-031	CAMK4_For	CAGCATCCGTGGGTCACA	416
	CAMK4_Rev	TTCACCGCTGCCTTAAGCTT	417
H31-035	PRKCE_For	TGAGGACGACCTATTTGAGTCCAT	418
	PRKCE_Rev	GGGATTCTTCGTCATGAAAGCT	419
H31-047	USP21_For	CTGCGAAGCTGTGAATCCTACTC	420
	USP21_Rev	GGCATCCTGCTGGCTGTATC	421
H31-049	CASP10_For	TCCTGGCAGAACTCCTCTATATCATAC	422
	CASP10_Rev	TGACAGTTCGTAGAGCAGGTTTCTA	423
H31-180	TM7SF1_For	GAACTTGTACTTCACGCAGGTG	424
	TM7SF1_Rev	CAACAGGAAAACAAGGCTGATG	425
H31-242	GPR21_For	TGCGTGGTCCCTTCTTTATCAC	426
	GPR21_Rev	GCCATGGAGACGCTCTTCAG	427
H31-290	RIPK2_For	CATTAAATGAACTCCTACATAGGAAAAC	428
	RIPK2_Rev	AGGGCAATTTCATGCAGGAT	429
H31-301	TPST1_For	GGAGTGTCTCTGTCAAAAGTGGA	430
	TPST1_Rev	ACCCATTTTGATAGAGCTCCTACATT	431
H31-319	MST3_For	GACATTAAAGCGGCCAACGT	432
	MST3_Rev	CTCGGGTGCCATCCAGAA	433
H31-347	SEPT1_For	GCGAGAAAGACGAAGAGCTGC	434
	SEPT1_Rev	GCCTGGCTCTGCTGCATT	435
H31-351	CD72_For	CAGTGAAATTTATCCACAATCACAC	436
	CD72_Rev	AGAGCTGAGGCCAGTCCAATAT	437
H31-360	RIT_For	GGTGTAGGGAAGAGTGCCATGA	438
	RIT_Rev	GCATCTTCAATGGTGGGATCA	439
H31-384	FXYD5_For	TGGTCGCCTGTGTCTTCTCA	440
	FXYD5_Rev	GTGGTATCTTTCAACGTCTGTCCTC	441
H31-450	Q9ESW8_For	GAGGAAGGCGGTGGTAGTGA	442
	Q9ESW8_Rev	CTCAACCGGAATCTCGTACACA	443
H34-067	FZD6_For	TGGGAGATAACTTGGGTCTCTGAT	444
	FZD6_Rev	AAGCCAATTCTGGTCGAGCTT	445
H34-087	MKNK1_For	AGGGAGCCTATGCCAAAGTTC	446
	MKNK1_Rev	CTCGATGATTTTGACGGCATAC	447
H34-088	MAPKAPK5_For	GAGGAAGCTCCTGAAGGTCAAAC	448
	MAPKAPK5_Rev	CAACCACTGCCTTGTCCATC	449
H34-092	FZD4_For	AGCCAGCTGCAGTTCTTCCTT	450
	FZD4_Rev	TCACAGCGTCTCTTGACTGAAAG	451

MMP1 is detected using the SYBR Green method, whereas the levels of 18S rRNA, used as internal calibrator for the PCR reaction, is measured using a Taqman probe (TaqMan® Ribosomal RNA Control Reagents, Applied Biosystems). The

amplification plot and the resulting threshold Ct value are indicators for the amount of specific mRNAs present in the samples. Delta-delta Ct values are presented, meaning the normalized (relative to the 18S calibrator) levels of MMP1 mRNA in the samples infected with the positive control viruses relative to the expression levels in a Ad5-eGFP infected control sample. Results indicate a strong up-regulation of the MMP1 mRNA levels upon expression of p65/RelA, TRAF6 or MYD88 in SFs as compared to the non-infected or Ad5-eGFP-infected SFs.

The level of MMP1 expressed by SFs is also determined at the protein level by Western Blotting. Two days after infection, supernatant of cells, infected with various recombinant adenoviruses as indicated for the Real-time PCR experiment, is collected and concentrated 15 times by classical TCA precipitation. 15 µl of the supernatant are resolved by SDS-PAGE using a 10% polyacrylamide gel. For these experiments, the medium used is M199 medium + 1% FBS. For the MMP1 control sample, non-concentrated supernatant of cells infected with Ad5-MMP1 is loaded onto the gel. The resolved proteins are transferred onto a nitrocellulose membrane. The quality of the transfer and equal loading of the samples are verified by Ponceau-S staining of the membrane. Immunodetection is performed using a goat anti-MMP1 polyclonal antibody as primary antibody (R&D Systems, 1/500 dilution) and an HRP-linked rabbit anti-goat antibody (DAKO, 1/10000 dilution) as secondary antibody and ECL plus HRP substrate (Amersham Biosciences). The Western Blotting revealed a strongly increased level of MMP1 protein in the supernatant of the SFs infected with the adenoviruses mediating expression of Ad5-p65/RelA, Ad5-TRAF6 or Ad5-MYD88 as compared to the Ad5-eGFP infected cells. A very strong signal is detected for the supernatant of cells infected with Ad5-MMP1 (Figure 2, panels B and C).

The high levels of MMP1 protein present in the supernatant of the Ad5-p65/RelA, Ad5-TRAF6 or Ad5-MYD88 infected SFs are confirmed using a commercially available MMP1 activity ELISA (RPN2629, Amersham Biosciences). In this ELISA, MMP1 is captured by an antibody immobilized in a well and the amount is subsequently quantified based on the conversion of a MMP1 substrate. 50µl

of non-concentrated supernatant of SFs (prepared as indicated for the western blotting experiment) are processed in this ELISA as recommended by the manufacturer.

These experiments confirm the capacity of SFs, in general, and of the cell batch used for screening and validation experiments, to produce MMP1 protein upon triggering of inflammatory pathways.

A 384-well format ELISA for measurement of MMP1 is developed. Various primary antibodies are tested, as well as various ELISA protocols. The following protocol is developed and validated to measure MMP1 levels in SF supernatant in 384 well plates: white Lumitrac 600 384 well plates (Greiner) are coated with 2 µg/ml anti-MMP1 antibody MAB1346 (Chemicon). The antibody is diluted in buffer 40 (1.21 g Tris base (Sigma), 0.58 g NaCl (Calbiochem) and 5 ml 10% NaN3 (Sigma) in 1 L milliQ water and adjusted to pH 8.5). After overnight incubation at 4°C, plates are washed with PBS (80 g NaCl, 2g KCl (Sigma), 11.5 g Na2HPO4.7H2O and 2 g KH2PO4 in 10 L milliQ; pH 7.4) and blocked with 100 µl/well Casein buffer (2% Casein (VWR International) in PBS). Next day, casein buffer is removed from ELISA plates and replaced by 50 µl/well EC buffer (4 g casein, 2.13 g Na2HPO4 (Sigma), 2 g bovine albumin (Sigma), 0.69 g NaH2PO4.H2O (Sigma), 0.5 g CHAPS (Roche), 23.3 g NaCl, 4 ml 0,5 M EDTA pH 8 (Invitrogen), 5 ml 10% NaN3 in 1 L milliQ and adjusted to pH 7.0). 0,25 mM DTT (Sigma) is added to the thawed samples plates. After removal of the EC buffer, 20 µl of sample is transferred to the ELISA plates. After overnight incubation at 4°C plates are washed twice with PBS and once with PBST (PBS with 0,05% Tween-20 (Sigma)) and incubated with 35 µl/well biotinylated anti-MMP1 antibody solution (R&D). This secondary antibody is diluted in buffer C (0.82 g NaH2PO4.H2O, 4.82 g Na2HPO4, 46.6 g NaCl, 20 g bovine albumin and 4 ml 0,5M EDTA pH 8 in 2 L milliQ and adjusted to pH 7.0) at a concentration of 5 µg/ml. After 2 h of incubation at RT, plates are washed as described above and incubated with 50 µl/well streptavidin-HRP conjugate (Biosource). Streptavidin-HRP conjugate is diluted in buffer C at a concentration of 0.25 µg/ml. After 45 min, plates are washed as decribed above and incubated for 5 min with 50

µl/well BM Chem ELISA Substrate (Roche). Readout is performed on the Luminoscan Ascent Luminometer (Labsystems) with an integration time of 200 msec or with an Envision reader (Perkin Elmer).

Typical results obtained with the MMP1 ELISA developed are shown in Figure 3. For this experiment, 3000 SFs are seeded in a 96 well plate in DMEM + 10% FBS. 24 h later, SFs are either infected at an MOI of 10000 with adenoviruses mediating the expression of ALPP, MYD88, MMP1; or left uninfected. One day after the infection, the medium of the cells is replaced by M199 medium (Invitrogen) supplemented with 1% FBS. After an incubation time of 48hrs, the supernatant is harvested, transferred to a 384 well plate and subjected to the MMP1 ELISA procedure described above. A robust, more than 3.5-fold up-regulation of the signal is observed. This experiment demonstrated the robustness and specificity of the MMP1 ELISA.

The increase of MMP1 expression by SFs upon treatment with cytokines relevant in the field of RA (TNFα, IL1β and OSM) or a combination thereof is monitored. Results are shown in Figure 10 as white bars. For this experiment, SFs are seeded in 96 well plates at 3000 cells/well. 24 h later, the medium is changed to M199 medium supplemented with 1%FBS. One day after the medium change, cytokines or combinations thereof are added to the cultures, each cytokine being added to a final concentration of 25 ng/ml. 72 h after cytokine addition, the supernatant is collected and processed in the ELISA, as described for Figure 3. As shown in Figure 10, white bars, TNFα alone induces an almost 3-fold increase in MMP1 expression. Triggering of SFs with a combination of TNFα and OSM and/or IL1β leads to even higher MMP1 expression levels. This experiment demonstrates that the sensitivity of the MMP1 ELISA developed is sufficient to measure increases in MMP1 expression by SFs driven by cytokines involved in RA pathogenesis.

Example 2. Screening of 4224 recombinant adenoviruses in an MMP1 assay.

A 384 well control plate is generated to assess the quality of the assay during the different screening runs. The composition of this plate is shown in Figure 4A. Wells are filled with control viruses that are produced under the same conditions as the

FlexSelect adenoviral cDNA library. This control plate contains three sets of 48 positive control viruses (P_1 (Ad5-MMP1), P_2 (Ad5-TRAF6), P_3 (Ad5-MYD88)), arranged in diagonal, interspaced with three sets of 48 negative control viruses (N_1 (Ad5-eGFP), N_2 (Ad5-LacZ), N_3 (Ad5-ALPP), Bl: blanco, uninfected). Every well contains 50 µl of virus crude lysate. The viruses contained in the control plate are generated according to the protocol applied for the construction of the FlexSelect collection. Multiple aliquots of this control plate are produced and stored at -80°C.

Optimal screening protocol: RASFs are cultured in DMEM medium (Invitrogen) supplemented with 10% fetal calf serum (ICN), 100 units/ml penicillin (Invitrogen) and 100 µg/ml streptomycin (Invitrogen) and incubated at 37°C and 10% CO_2. The cells are passed once a week by a 1/3 split. The maximal passage number for RASFs used in the screening is 11. For screening, SFs are seeded in transparent 384 well plates (Greiner) coated with 0.1% gelatin (Merck) at a density of 1500 cells/well in 25 µl Synovial Cell growth medium (Cell Applications, Inc.). After overnight incubation, cells are infected with 3 µl Ad-cDNA from the Galapagos FlexSelect adenoviral cDNA library. As the average titer of the adenoviral library is $3x10^9$ virus particles/ml, this represents an MOI of 6000. 24 h after infection, the medium is changed to 50 µl of M199 medium supplemented with 1% FCS. 40 µl supernatant is collected 72 h later into new transparent 384 well plates (Greiner) and stored at –80°C until further processing in the MMP1 ELISA. The infection, medium change and medium collection steps are performed with a TECAN Freedom pipettor. The ELISA step is performed as indicated in Example 1.

A representative example of the performance of the control plate tested with the protocol described above is shown in Figure 4B. Synovial fibroblasts are infected with 3 µl of the viruses contained in the control plate in an arrayed fashion using a TECAN 384 channel pipettor. The medium is refreshed the day after infection and the supernatant is harvested after 72 h production time and subjected to the 384 well format MMP1 ELISA described in previous example. The raw luminescence signal obtained is shown.

A stringent cutoff is applied, that is the average of all 144 negative control viruses plus 4.5 times the standard deviation over these samples. As expected, the Ad5-MMP1 control virus scored very well in the assay, with all 48 Ad5-MMP1 viruses being picked up as a hit above this cutoff. The Ad5-MYD88 control virus also scored robustly, with 84% of the Ad5-MYD88 control viruses being picked up above the applied cutoff. The weaker Ad5-TRAF6 control, which gave rise to weaker increases in MMP1 mRNA levels (see Example 1) did not perform strongly, indicating that this cutoff will likely identify strong MMP1 inducers.

The MMP1 assay on RASFs described above is screened against the adenoviral cDNA libraries (FlexSelect™ collection) developed at Galapagos Genomics. The main part of this adenoviral collection contains cDNAs of genes from "drugable" classes like GPCRs, kinases, proteases, phosphodiesterases and nuclear hormone receptors. The majority of these cDNAs are obtained by a PCR-based approach briefly described below. Based on the sequences of the selected genes, which are obtained from the RefSeq database, PCR primers are designed for amplification of the complete open reading frame from ATG start codon to the stop codon. Primers are received in an arrayed format with forward and reverse primers mixed at a PCR ready concentration in 96 well plates. From this point on, the arrayed format is maintained throughout all the handlings (from PCR till virus production) resulting in an arrayed adenoviral cDNA library. As a template for the PCR reactions, placental, fetal liver, fetal brain and spinal cord cDNA libraries are used (from Invitrogen or Edge Biosystems). For the genes encoded by a single exon, PCR reactions are performed on human genomic DNA. After the amplification reactions, the size of the PCR products is estimated and compared to the predicted size based on sequence information. The PCR products obtained are purified with a 96-well PCR clean-up system (Wizard magnesil, Promega, Madison, WI, USA), digested with the appropriate restriction enzymes (*Asc*I, *Not*I or *Sal*I restriction sites are included in the primers) and directly cloned into the adenoviral adapter plasmid pIspAdAdapt-10-Zeo (described in US 6,340,595) using DNA ligation kit version 2 (TaKaRa, Berkeley, CA, USA). After a transformation and selection step, multiple clones per gene, one of which is sequence

verified, are used for the preparation of plasmid DNA and subsequent generation of adenovirus according to the procedure described in WO99/64582.

The total FlexSelect adenoviral cDNA library consisted of 11 x 384 well plates at the time it is screened. 4224 samples represents 1705 genes.

The MMP1 assay is screened against the FlexSelect adenoviral cDNA library using the optimized protocol described above. Every cDNA library plate is screened in duplicate in a primary screen and in a rescreen. As such, four data points are obtained for each cDNA clone. A representative example of screening results and of the analysis performed to identify hits is shown in Figure 5.

SFs are seeded in 384 well plates and infected with 3 µl of 384 different recombinant adenoviruses of the FlexSelect collection contained in an arrayed fashion (using a TECAN pipetor), in a 384 well plate. The medium is refreshed the day after infection; the supernatant is harvested after 72 h production time and subjected to the MMP1 ELISA using a luminescent substrate. The raw luminescence signal obtained is shown. For every individual virus, the viruses mediating he expression of PRKCE, CASP10 and USP21 in particular, the 2 datapoints (Figure 5A and B) obtained in the primary screen (Figure 5A) and in the rescreen (Figure 5B) are shown.

To determine the cutoff value for hit calling, the average as well as standard deviation are calculated on all data points obtained per screening batch after removal of the 10% highest and 10% lowest values. The cutoff value is then defined as 3 times the standard deviation added to the average. This cutoff is indicated as a horizontal line in the graph in Figure 5. Screening and rescreening results are presented in Figure 6 for 4 cDNA encoding PRKCE, 5 cDNAs encoding USP21 and 4 cDNAs encoding CASP10. All 4 PRKCE cDNA clones scored above cutoff in duplicate in both the primary screen and rescreen, 4 out of 5 USP21 clones scored above cutoff in primary screening and rescreening, and 3 out of 4 CASP10 cDNA clones scored in duplicate in primary screening and rescreening. These data are indicative of the quality of the screening and of the FlexSelect cDNA collection.

As mentioned, every screening plate is screened and rescreened in duplicate. Only samples that scored above the cutoff value (the average plus 3 times standard

deviation) for 3 out of the 4 datapoints are selected as hits. In addition, if multiple clones scored positive, maximally 2 clones per gene are further processed through the collagen degradation assay. As such, 253 hit Ad-cDNAs, representing 229 genes, are finally picked, propagated and tested in the collagen degradation assay.

'Knock-in viruses' mediating the expression of various target genes listed in Table 1 are tested as follows. On day 1, SFs are seeded, in Synovial growth medium, in gelatin coated 96 well plates at a density of 3000 cells per well or in 384 well plates at a density of 1500 cells per well. 1 day after seeding, the cells are infected at the volumes or MOIs indicated on the figures. On day 3, the medium is refreshed to M199 medium supplemented with 1% FBS. On day 6, the supernatant is collected and subjected to the MMP1 ELISA according to the protocol described above. The Ad5-Luciferase, Ad5-eGFP or Ad5-Empty viruses are used as negative control viruses. Infection of SFs with recombinant adenoviruses driving the expression of SEPT1, TPST1, USP21, MKNK1, RIPK2 (Figure 13 A), PGPEP1, RIT1 (Figure 13 B), CAMK4, MST3, PRKCE (Figure 13 C) and CD72, TM7SF1, GPR21 (Figure 13 D) clearly mediated an increased expression of MMP1 by the infected SFs. The results shown in Figure 13 are the averages of duplicate datapoints.

Example 3. Development of a screening method for the measurement of the collagenolytic activity of primary synovial fibroblasts (SFs): collagen degradation assay.

The MMP1 assay is used as a first filter to select hits that mediated an increase in the MMP1 expression in SFs. The amount of MMP1 present in the supernatant of SFs might not, however, be sufficient to mediate the degradation of native collagen. In addition, besides MMP1, additional proteases might be expressed by SFs that, alone or in synergy with MMP1, mediate collagen breakdown. In order to rank our hits according to their potential to increase the collagenolytic activity of SFs, the present inventors developed a functional assay that determines the extent of degradation of native collagen in the supernatant of SFs. The various reagents and buffers used to perform the assay described below are from Chondrex (Redmond, USA), unless mentioned otherwise.

In first instance, the assay is developed to be compatible with a cDNA library screening on primary human cells. As a second development step, the assay is miniaturized to be compatible with an arrayed, medium throughput assay. Experiments confirmed that the sensitivity of the collagen assay performed on primary cells in miniaturized configuration is conserved as compared to the assay in non-miniaturized configuration. The results of a typical experiment illustrating this finding are shown in Figure 6. For this experiment, SFs (seeded at a density of 3000 cells/well in a 96 well plate in M199 medium supplemented with 1% FBS) are infected (MOI 10,000) with Ad5-ALPP, AD5-TRAF6 or Ad5-MYD88. After an incubation time of 48hrs (post infection), the supernatant is harvested and tested in both the miniaturized and non-miniaturized collagen degradation assays. Fluorescence signal, which is proportional to the level of collagen degradation, is indicated.

"Non-miniaturized" collagen degradation assay protocol: 100 µl of the SF supernatant or 100 µl of M199 medium + 1% FBS supplemented with the indicated amount of rMMP1 (R&D systems) or chymotrypsin (Sigma) are mixed with 90 µl of buffer B. These mixes are added to either 10 µl of trypsin activating solution, or 10 µl of APMA (4-aminophenyl mercuric acetate, 2mM final, Sigma) activating solution. These activating solutions mediate the removal of the pro-domain of MMPs that keep these proteases in an inactive state. In the case of trypsin activation, the mixture is incubated for 60 min at 35°C, followed by the addition of SBTI (soybean trypsin inhibitor) to inactivate all non-collagenolytic proteases, whereas in the case of APMA activation, the mixture is incubated for 10 min at 35°C. 100 µl of Buffer A and 100 µl of native FITC-labeled bovine collagen type I (1 mg/ml, in 0.01N acetic acid) are mixed and added to the activated samples followed by an incubation step of 2 h at 35°C during which collagenases cleave the FITC-labeled collagen in the typical ¼ and ¾ fragments. The reaction is stopped by addition of 10 µl of the stop solution (1,10 phenantroline, 10mM final, Sigma). The large collagenase pieces are further digested by the addition of 10 µl of elastase (the "enhancer" solution) and incubation for 30 min at 35°C. After cooling down the samples, 400 µl of extraction buffer is added to precipitate the non-cleaved collagen fragments. These fragments are separated from

the digested collagen pieces by a centrifugation step (10,000 rpm, 10 min). 200 µl sample is transferred to a black 96 well plate for a fluorescence measurement (520nm, 480nm as emission and excitation wavelengths, respectively) performed on a Fluostar reader (BMG).

"Miniaturized collagen degradation assay" protocol: A 96 well plate (V-bottom, Greiner) is filled with 9 µl of solution B and 1 µl of trypsin solution per well. 10 µl of sample is added per well, followed by incubation for 15 min at 34°C. After incubation, 1 µl SBTI is added. 20 µl of FITC-Collagen mix (10 µl FITC-labeled collagen type I + 10 µl solution A) are added to the activated sample followed by incubation for 24 h at 34°C. One µl of 1.10 Phenantroline (Sigma) is added to the reaction mixture. One µl of enhancer solution (elastase) is added, followed by incubation for 30 min at 34°C. When the reaction mixture is at room temperature, 40 µl extraction buffer are added and the plate is sealed (Nunc seals) and vortexed. After centrifugation for 25 min at 4000 rpm (Beckman centrifuge), 50 µl of the supernatant are transferred into a black F-bottom plate (Greiner) and fluorescence is measured on a Fluostar reader (BMG), 480nm excitation wavelength, 520nm emission wavelength). The results of the experiment are shown in Figure 8, and shows increased collagen type I degradation in the supernatant of Ad5-TRAF6 as well as Ad5-MYD88 infected cells. As such, the 2 positive controls identified for the "MMP1 assay" on SFs also mediate increased collagenolytic capacity of SFs. This suggests that the potency of a cDNA in the "MMP1 assay" is predictive for its capacity to increase the global collagenolytic activity of SFs. Although the levels of the fluorescent signal in the miniaturized assay are lower as compared to the non-miniaturized assay, the relative increase in fluorescence in the positive samples as compared to the Ad5-ALPP control is maintained. Thus, a miniaturized collagen degradation assay on SFs has been developed that has a sensitivity level comparable to the non-miniaturized assay. This result establishes that the method used for the collagen degradation assay described above is compatible with the screening of cDNA libraries (in adenoviral format in this example) on primary cells (human SFs in this example). Various experiments established that following aspects of the protocol are important:

- the use of trypsin for the activation of the latent MMPs in the supernatant of the cells is useful for the detection of collagenase activity using the assay.
- the supernatant of non-infected cells does not contain any detectable background collagenase activity. It is held that the use of medium without phenol red (M199 medium, no phenol red, Invitrogen) with low serum content (1% FBS) is preferred to obtain this low background signal.
- the collagen used for this assay is mostly in native, triple helix conformation, as no collagen degradation is mediated by chymotrypsin, an enzyme that has the capacity to degrade denatured collagen (gelatin). The native character of the collagen used is also preferred for this assay.

The above miniaturized assay is compared to another low-throughput detection method for collagen degradation, in which the following samples are tested: supernatant of SFs (cultured in 96 well plates in M199 medium supplemented with 1% FBS) uninfected or infected with Ad5-ALPP, Ad5-TRAF6, Ad5-PRKCD, Ad5-MMP13 (MMP13 is a potent collagenase), or Ad5-TNFR1A, all at an MOI of 10,000. The results of the miniaturized collagen degradation assay run on these samples (following the protocol described in former example) is shown in Figure 7: Supernatant obtained after infection of SFs with the indicated recombinant adenoviruses and a 48hrs production time, is subjected to both the miniaturized (fluorescence-based) collagen degradation assay and the lower throughput visual assessment of collagen degradation. For the latter test, the various supernatants are incubated with native collagen. The reaction mixtures are resolved on a polyacrylamide gel and degradation of the heterotrimeric collagen type I fibrils from the native (bands A and B) to the ¾ N-terminal TC^A fragments (bands C and D) is assessed after Coomassie staining.

A cutoff value for hits versus non-hits in this experiment is defined as the average over the data points for the uninfected control samples plus 3 times the standard deviation over these data points and is indicated as a dotted line on the bar graph in Figure 7. These data indicate that, in addition to the Ad5-TRAF6 and Ad5-

MMP13 positive controls, the collagenolytic potential of SFs increased upon overexpression of PRKCD and TNFR1A. As TNFalpha is a well-known trigger involved in RA pathogenesis, it can be expected that the overexpression of TNFR1A, the TNFa receptor, will lead to an increase in collagen degradation. This result further validates our approach to identify relevant cDNAs involved in RA pathogenesis. In this experiment, PRKCD is identified as another relevant mediator of collagen degradation by SFs.

The same samples are then tested in the following setup: a 10 µl sample is mixed with 10 µl EDANS buffer (50 mM Tris-HCl, pH 7.5; 150 mM NaCl; 10 mM $CaCL_2$; 0.05% Brij-35, 50 µM $ZnCl_2$), 10 µl of a solution of collagen type I (IBFB, Germany, 1 mg/ml dissolved in 0.01N acetic acid). APMA is added to this reaction mixture to a final concentration of 2 mM. The reaction mixture is incubated for 48 h at 35°C. 25 µl of the reaction mixture is then boiled and resolved on a 8% SDS poly acryl amide gel (Novex) which is then subjected to a coomassie blue staining. Native collagen type I is a triple helix composed of 2 α1 and 1 α2 chains. These chains are visible on the gel in the control samples and are indicated by arrows A and B in the lower part of Figure 7. In the positive control samples, Ad5-MMP13, Ad5-TRAF6 and Ad5-PRKCD, these 2 bands are cleaved into the $^{3/4}$N-terminal "TC^{A}" fragments, indicated by arrows C and D. This typical restriction pattern is indicative for the action of MMP-type collagenases, which cleaves the collagen triple helix at a single position, thereby generating characteristic ¼ C-terminal "TC^{B}" and ¾ N-terminal "TC^{A}" fragments. These results confirm in a visual way the direct relationship that exists between the signal obtained in the collagen degradation assay and the collagen degrading activity present in the tested samples. These data also confirm that the signal obtained in the collagen degradation assay is the result of the activity of MMP-type collagenases.

As the main component of cartilage is collagen type II, we compared the collagen degradation assay readout performed with FITC-labeled collagen type I and with FITC-labeled collagen type II. Results of a representative experiment are shown in Figure 8. For this experiment, supernatant is used of SFs (cultured in 96 wells

plates, 3000 cells/well in M199 + 1% FBS) that are infected with Ad5-TRAF6, Ad5-ALPP or Ad5-MYD88 at an MOI of 10,000. Supernatant of these cells is harvested 48h post-infection and subjected to the non-miniaturized collagen degradation assay procedure described for Figure 8 with either FITC-labeled native collagen type I or FITC-labeled collagen type II (same amounts as FITC-labeled collagen type I). Results shown in Figure 8 indicate that the degradation of collagen type II gave rise to lower fluorescent signals, suggesting a higher resistance of collagen type II to proteolytic degradation as compared to collagen type I. Notwithstanding the lower signal levels obtained when using collagen type II, cDNAs mediating increased collagen type II degradation are identified, as exemplified here with Ad5-TRAF6. The order of potency of the hits towards induction of collagen degradation is maintained in the collagen degradation assay run with collagen type II as compared to the assay run with collagen type I. These results indicate that the capacity of a hit to induce the degradation of collagen type I in this assay is predictive for its capacity to induce the degradation of collagen type II.

Example 4. Testing of 253 hits of the "MMP1 assay" and screening of 1679 recombinant adenoviruses in the collagen degradation assay

The adenoviruses identified as hits in the MMP1 assay on primary synovial fibroblasts (SFs) are picked from the FlexSelect adenoviral cDNA library and are re-propagated in 96 well plate format by infection of PER.E2A producer cells (see WO99/64582). These plates are further referred to as the "MMP1 hit propagation plates". On these plates, 4 Ad5-ALPP and 4 Ad5-Luciferase control viruses are also included. The border wells of these plates are not used to avoid eventual "border effects" in the experiments. The MMP1 hit propagation plates contain 50 hit viruses and 10 negative control viruses. This virus material is then tested at 3 MOI's in duplicate in the collagen type I degradation assay on SFs as follows. SFs are trypsinized and seeded in 96 well plates (Nunc, transparant plates, tissue culture treated). Trypsinized SFs are resuspended in Synoviocyte Growth medium (Cell Applications) at a density of 30,000 cells/ml and 100 µl of this suspension is dispensed

in each well using a multidrop dispenser (Labsystems). Approximately 24 h after seeding of the cells, a duplicate infection of the cells is performed with 6, 12 or 18 µl of the virus material present in 96 well MMP1 hit propagation plates using a Tecan Freedom 200 pipettor (Tecan). As such, the content of the MMP1 hit propagation plates is transferred to 6 96 well plates containing the seeded SFs. 6 data points in the collagen degradation assay are generated per hit virus. Approximately 24 h after infection, virus and medium are removed from the cells using an 8 channel Vacusafe device (Integra) and 60 µl M199 medium supplemented with + 0.5% FBS is added to every well.

72 h after medium refreshment, supernatant is transferred to a 96 well plate (V-bottom, Greiner) with the Tecan Freedom 200 pipettor. The supernatant is stored at –80°C until use. To perform the assay, the supernatant is thawed and the assay is performed according to the protocol of the miniaturized collagen type I degradation assay described above in Example 3.

Hit selection is performed as follows: For each plate, the average and standard deviation are calculated for the fluorescence measurements obtained for the 8 wells infected with control viruses. The cutoff for hits versus no-hit is defined as the average plus 2 times the standard deviation for these control samples. A virus is considered a hit if it induced a signal above the cutoff value for at least 3 out of 6 data points. 253 hits identified in the MMP1 assay have been retested according to this procedure. Out of these, 61 Ad-cDNAs significantly increased the collagenolytic activity of SFs, representing 55 individual genes when redundancy is taken into account. Besides these 55 hits, two Ad-cDNAs picked up in the screening delivered a proof of principle for the screening. One of these hits encoded MMP1. Another hit encodes IKKβ (IKBKB). This kinase has a central role in the response of cells to inflammatory triggers as e.g. TNFα. Small drug inhibitors, with RA as therapeutic indication, are currently being designed against IKKβ (Andreakos et al., 2003). The fact that hits, relevant in the field of RA, are picked up confirms the quality of our screening concept and the quality if the materials (assays and libraries) used.

As final quality control on these hit Ad-cDNAs, their identity is checked by sequence analysis. The procedure for sequence analysis is as follows. The hit viruses are propagated using PER.E2A producer cells in a 96 well plate. PER.E2A cells are seeded in 96 well plates at a density of 40,000 cells/well in 180 µl medium. Cells are incubated overnight at 39°C in a 10% $C0_2$ humidified incubator. One day later, cells are infected with 1 µl of crude cell lysate from FlexSelect stocks containing the hit Ad-cDNA. Cells are incubated further at 34°C, 10% CO_2 until appearance of cytopathic effect (as revealed by the swelling and rounding up of the cells, typically 7 days post infection). The supernatant is collected and the virus crude lysate is treated with proteinase K: 12 µl crude lysate is added to 4 µl Lysis buffer (1x Expand High Fidelity buffer with $MgCl_2$ (Roche Molecular Biochemicals, Cat. No 1332465) supplemented with 1 mg/ml proteinase K (Roche Molecular Biochemicals, Cat No 745 723) and 0.45% Tween-20 (Roche Molecular Biochemicals, Cat No 1335465) in sterile PCR tubes. These are incubated at 55°C for 2 h followed by a 15 min inactivation step at 95°C. For the PCR reaction, 1 µl lysate is added to a PCR master mix composed of 5 µl 10x Expand High Fidelity buffer with $MgCl_2$, 0.5 µl of dNTP mix (10 mM for each dNTP), 1 µl of 'Forward primer' (10 mM stock, sequence: 5' GGT GGG AGG TCT ATA TAA GC; SEQ ID NO: 452), 1 µl of 'Reverse Primer' (10 mM stock, sequence: 5' GGA CAA ACC ACA ACT AGA ATG C; SEQ ID NO: 453), 0.2 µl of Expand High Fidelity DNA polymerase (3.5 U/µl, Roche Molecular Biochemicals) and 41.3 µl of H_2O.

PCR is performed in a PE Biosystems GeneAmp PCR system 9700 as follows: the PCR mixture (50 µl in total) is incubated at 95°C for 5 min; each cycle runs at 95°C for 15 sec, 55°C for 30 sec, 68°C for 4 min, and is repeated for 35 cycles. A final incubation at 68°C is performed for 7 min. 5 µl of the PCR mixture is mixed with 2 µl of 6 x gel loading buffer, loaded on a 0.8% agarose gel containing 0.5 µg/µl ethidium bromide to resolve the amplification products. The size of the amplified fragments is estimated from a standard DNA ladder loaded on the same gel. For sequencing analysis, the cDNAs expressed by the target adenoviruses are amplified by PCR using primers complementary to vector sequences flanking the SapI site of the pIPspAdapt6

plasmid. The sequence of the PCR fragments is determined and compared with the expected sequence.

Screening of the FlexSelect collection subset in the collagen degradation assay

The possibility exists that certain factors mediate an increased collagenolytic activity of SFs through collagenases other than MMP1. In order to identify such factors, a subset of the FlexSelect collection is screened in the collagen degradation assay on SFs. 384 well plates from the FlexSelect collection containing mainly Ad-cDNAs mediating the expression of kinases and GPCRs are screened. The following screening protocol is applied. SFs are trypsinized and resuspended in Synoviocyte Growth medium (Cell Applications) at a density of 30,000 cells/ml. 100 µl of this cell suspension is dispensed in each well of 96 well plates (Nunc, tissue culture treated) using a `multidrop` dispenser (Labsystems). Approximately 24 h after seeding of the cells, they are infected with the library Ad-cDNAs as follows. The FlexSelect library aliquot plates (384 well format, stored at –80°C) to be processed are thawed at RT in a laminar air flow cabinet for 1 h. Plates are then stored at 4°C until further processing.

For every well of a quadrant of a 384-well adenoviral cDNA library aliquot plate, 10 µl of virus crude lysate is transferred to a well of a 96 well plate containing the SFs. This action is performed with the 96 needle head of a TECAN Freedom 200 pipettor. Each virus is assayed in duplicate. As such, for every 384-well virus library aliquot plates, 8 96-well plates containing SF are infected. In between every pipeting step, needles of the pipettor are emptied in a bleach wash station and rinsed two times with 175 µl of bleach (5%) and two times with 200 µl of water and finally with 200 µl of ethanol (20%). Approximately 24 h after infection, the medium of the cells is refreshed. Virus and medium are removed with the Vacusafe (Integra) and 60 µl of fresh M199 medium + 0.5% FBS is added. 72 h after refreshment of the medium, the cell supernatant is transferred from the 96 well plates containing the infected SFs to a 96 well plate (V-bottom, Greiner) with the TECAN Freedom 200 pipettor. The samples are then subjected to the miniaturized collagen type I degradation assay. In total, 1679 samples are screened in duplicate in this assay, representing 449 genes.

The following analysis is performed for hit selection: Per screening batch, the average and standard deviation is calculated on all samples after removal of the 10% highest and 10% lowest values. As mentioned above, 2 data points are obtained for every Ad-cDNA sample screened. The Ad-cDNA samples for which one of the 2 data points scored above the average plus 4 times the standard deviation as well as the samples for which both data points scored above the average plus 2 times standard deviation are selected as hits. A representative example of the results obtained during screening for 96 viruses (1 assay plate) screened in duplicate is shown in Figure 9. For every individual virus, the 2 datapoints (A and B) obtained in the primary screen are shown. Viruses mediating the expression of CASP10 and MMP3 are indicated. The signal obtained for the samples is expressed relative to the standard deviation and average using following formula: [Times standard deviation difference from average=(Value Sample-Value Average)/Standard deviation]. The cutoff for hit calling (average plus 2 or 4 times standard deviation) is indicated as a full or dotted line, respectively. Among the 96 Ad-cDNAs for which screening results are shown, 4, out of which 3 scored according to the selection criterion, mediated the expression of MMP3 and 4, out of which 3 scored according to the selection criterion, mediated the expression of CASP10. 108 Ad-cDNAs, representing 79 genes when taking redundancy into account, are selected as hits according to this procedure.

These hits are re-propagated and rescreened using the procedure described for the screening of the hits of the MMP1 assay in the collagen degradation assay. 31 hits, representing 20 individual genes, out of the 108 primary hits mediated a significant level of collagen type I degradation in the rescreen procedure. As 4 genes out of the 55 identified as hits through the "MMP1 assay" and validated in the collagen degradation assay are also present among the 20 genes identified as hits in the screening of a subset of the FlexSelect collection in the collagen degradation assay, a total of 71 genes are identified that increased the collagenolytic potential when expressed or activated in primary human SFs. The preferred hit genes identified in this assay are listed in Table 1. The performance of these in the collagen degradation assay in summarized in Table 4.

Table 4 - Summary of the Features of the TARGET Genes

Gene Symbol	Experiment Description				
	Knock-in	Knock-in		Knock down	Knock down
	MMP1 induction	Induction of collagen degradation	Expression in primary RASFs	Inhibition of cytokine induced MMP1	Inhibition of cytokine induced collagen degradation
RIPK2	SP	SP	SP	SP	NT
PRKCE	SP	SP	P	SP	SP
MST3	SP	SP	P	P	NT
MAPKAPK5	N	N	P	SP	SP
MKNK1	SP	SP	P	N	NT
CAMK4	P	P	P	SP	SP
SEPT1	P	P	P	SP	NT
PGPEP1	P	P	P	SP	NT
CD72	P	P	P	SP	NT
TPST1	P	P	SP	SP	P
GPR21	P	P	P	SP	NT
USP21	SP	SP	P	P	NT
FZD4	N	N	P	SP	NT
TM7SF1	P	P	P	SP	NT
FXYD5	N	N	SP	SP	NT
RIT1	P	P	P	SP	SP
CASP10	SP	SP	P	N	NT

P: positive response in the assay
SP: Strong positive response in the assay
NT: not tested
N: negative response in the assay

Example 5. Expression analysis of the TARGETS identified in human primary synovial fibroblasts derived from synovium of RA patients

Expression levels for all the TARGETS identified are determined in at least three different isolates of primary human synovial fibroblasts.

One isolate of RASF's is obtained as cryopreserved passage 2 cells from Cell Applications Inc. (Cat.No.404-05). These cells are cultured and propagated in DMEM (Invitrogen) supplemented with 10% (v/v) heat-inactivated FBS (ICN) and 1x Pen/Strep (Invitrogen).

Two other isolates are established starting from synovial membrane biopsy specimens obtained during knee arthroscopy of patients who are diagnosed as suffering from RA. Upon removal, the tissue samples are frozen in DMEM (Invitrogen) containing 15 % (v/v) heat-inactivated FBS, 1X sodium pyruvate (Invitrogen), 1X antibiotics (Invitrogen) and 10% (v/v) DMSO (Sigma) and stored in liquid nitrogen. Cell culture is initiated from these synovial tissue specimens as follows: the tissues are washed thoroughly with Hanks balanced salt solution (Invitrogen) supplemented with 2X antibiotics and are digested overnight at 37°C with 0.2% (w/v) Type IV Collagenase (Invitrogen) in DMEM containing 10% (v/v) heat-inactivated FBS, 1X sodium pyruvate, 2X antibiotics. Cells are collected, washed, resuspended in growth medium (DMEM supplemented with 10% heat-inactivated FBS, 1X sodium pyruvate, 1X antibiotics) and finally plated in 3 different wells of a 6-wells tissue culture plate. Non-adherent cells are removed after 3 days by changing growth medium. When cells reached 90-95% confluency, they are harvested by trypsinization (0.25% trypsin/1 mM EDTA) and passaged to a 25-cm2 tissue culture flask. Further passaging is done by 1/3 splitting and growth medium is changed twice a week. For expression analysis, cells are used at passages 6 to 10.

For RNA preparation, the primary human synovial fibroblasts are seeded in 10-cm Petri dishes (500,000 cells/dish). After overnight incubation, medium is refreshed to 6 ml of M199 medium supplemented with 1% (v/v) heat-inactivated FBS containing 1X Pen/Strep. 24 h later, total RNA is extracted using the 'SV Total RNA Isolation kit' (Promega). Certain samples are stimulated before harvesting. In this case, the

following medium is added to the dishes for 24 h before harvesting: supernatant of THP1 cells (a human monocytic cell line) triggered with recombinant human TNFα (25 ng/ml) for 72 h in M199 medium + 1% FBS diluted 2 fold in fresh M199 + 1% FBS.

The concentration of RNA in each sample is fluorimetrically quantified using the 'Ribogreen RNA quantitation kit' (Molecular Probes). A similar amount of RNA from each preparation is reverse transcribed into first strand cDNA with the 'Taqman reverse transcription kit' from Applied Biosystems. Briefly, 40 ng RNA is included per 20 µl reaction mix containing 50 pmol of random hexamers, 10 U Rnase inhibitor, 25 U Multiscribe reverse transcriptase, 5 mM $MgCl_2$ and 0.5 mM of each dNTP. The reaction mixture is incubated at 25°C for 10 min, followed by 30 min incubation at 48°C and heat inactivation (5 min 95°C) of the reverse transcriptase in a thermocycler (Dyad, MJ Research). Reactions are immediately chilled to 4°C at the end of the program. To avoid multiple freeze/thaw cycles of the obtained cDNA, the different samples are pooled in 96-well plates, aliquoted and stored at -20°C.

Real-time PCR reactions are performed and monitored using the 'ABI PRISM 7000 Sequence Detection System Instrument' (Applied Biosystems). Primers are designed with 'Primer Express software version 2.0' (Applied Biosystems) and purchased from Sigma-Genosys. The specificity of the primers is confirmed by BLASTN searches. The PCR mixture consisted of 1X Sybr Green PCR Master mix (Aplied Biosystems), 7.5 pmol of forward and reverse primers and 2 µl of the retrotranscription reaction product in a total volume of 25 µl. After an initial denaturation step at 95°C for 10 min, the cDNA products are amplified with 40 cycles consisting of 95°C for 15 s and 60°C for 1 min, followed by a dissociation protocol, which is defined as a slow ramp from 60 to 95°C. Using the dissociation protocol single peaks are confirmed in each of the PCR reactions for the various genes to exclude non-specific amplification. In order to normalize for variability in the initial quantities of cDNA between different samples, amplification reactions with the same cDNA are performed for the housekeeping genes ß-actin/ 18S rRNA using either home made ß -actin primers and SYBR Green PCR Master Mix or the 'predeveloped

primer and Taqman probe mix' for human 18S rRNA and 'Taqman Universal PCR Mastermix no AmpErase UNG' (all Applied Biosystems) according to the manufacturer's instruction. To identify any contamination resulting from residual genomic DNA, real-time PCR reactions with product from a control (-RT) reverse transcription reaction that is performed under the same conditions but without the addition of the reverse transcriptase are included for each sample. Threshold cycle values (Ct), i.e. the cycle number at which the amount of amplified gene of interest reached a fixed threshold are determined for each sample. For each sample, the ΔCt value is determined by substracting the Ct value of the endogenous control (ß -actin) from the Ct value obtained for the target gene. A gene is considered as expressed in primary human SFs if the ΔCt value obtained for this hit is lower as 13.3 in at least one of the 3 synovial isolates, activated or not, that are available. The results of the expression profiling experiments are summarized in Table 5. The DCt value relative to ß -actin obtained for all target genes (listed in Table 1) in untriggered SFs or SFs triggered with 25% 'complex cytokine mixture' are given in this Table 5. The primers used in this study are listed in Table 2.

Table 5 - Expression of target genes in primary synovial fibroblasts

Gene symbol	Untriggered RASFs	Triggered RASFs
RIPK2	6.7	3.7
PRKCE	8.8	7.8
MST3	6.4	5.2
MAPKAPK5	7.5	6.0
MKNK1	5.9	5.6
CAMK4	14.2	11.6
SEPT1	7.0	7.1
PGPEP1	8.7	8.1
CD72	9.0	9.1
TPST1	5.1	3.1
GPR21	11.5	9.8
USP21	8.1	6.9
FZD4	7.4	7.3
TM7SF1	7.6	7.1
FXYD5	2.8	2.1
RIT1	6.5	4.4
CASP10	14.5	11.9

Example 6A. Testing of the TARGETS identified using siRNA technology

When the adenoviral expression or the activation of a factor in SFs increases the collagen degrading potency of these cells, activation of this factor is sufficient to increase collagen degradation by these cells. This indicates that the factor controls or is acting on signaling pathways that are important for the regulation of MMP1 and/or other proteases involved in collagen degradation. However, to confirm that a factor is indispensable for the expression of MMP1 or degradation of collagen, the following "reverse MMP1 assay" experiments are performed. These experiments are key in determining whether the inhibition of a TARGET protein will reduce the cytokine-

induced MMP1 expression, collagen degradation and thus has therapeutic potential for diseases involving ECM degradation.

This assay used multiple "knock down" viruses corresponding to the TARGET genes that, when overexpressed or activated in SFs, increase the potency of these cells to express MMP1 or to degrade collagen. Certain "knock down" viruses are also designed against 3 other target genes (MAPKAPK5, FXYD5 and FZD4) that are not identified through the screening of the FlexSelect collection in the "MMP assay". A "knock down" virus is defined as an adenovirus that drives the expression of a self-complementing single-stranded siRNA molecule polynucleotide, resulting in the reduction of the corresponding mRNAs levels that encode the target polypeptides. The siRNA polynucleotides are designed based on the sequence of the gene encoding the TARGET polypeptide and selected according to siRNA designing rules that give an improved reduction of the target sequence expression compared to nucleotide sequences that do not comply with these siRNA designing rules (See PCT/EP03/04362). Multiple viruses are generated and tested for each TARGET gene as not every siRNA is as efficient in reducing the mRNA levels for a given TARGET gene.

SFs are seeded in 384 or 96 well plates and infected at various MOI's with the knockdown viruses generated against the targets identified as players modulating SF MMP1 expression in, or SF collagen degradation. Five days after infection, at the time the levels of the target mRNA in the SFs are efficiently reduced by the knock down virus, the SFs are "activated" with a trigger or a mixture of triggers relevant in the field of arthritis. I n uninfected SFs, or SFs infected with control knock down viruses, this trigger or mix of triggers lead to an increase in the expression of MMP1 and the potency of the cells to degrade collagen.

Two days after application of the trigger, the levels of MMP1 in the supernatant of the SFs are measured in an MMP1 ELISA, or the degradation of collagen by the supernatant of the SFs is measured in the collagen degradation assay. If the reduction in the expression level for a certain target gene leads to a reduced response of the cells to the RA-relevant trigger applied, this indicates that this target

gene is indispensable for the SFs to respond to this trigger. The inhibition of the activity of the polypeptide product of this gene, or the reduction in expression of this gene, might thus represent a suitable approach for treatment of RA.

In order to work in an unbiased way, a complex mixture of factors relevant in the field of RA is generated as follows: THP-1 cells, a representative human monocyte cell line, is cultured in the presence of human recombinant TNFalpha (Sigma, 25 ng/ml) for 48 h. Supernatant of this cell line is then collected and stored at –80°C until further use. The monocytes respond to the TNF-alpha trigger by the production of a variety of other cytokines and factors, most of which will be pro-inflammatory. As monocytes (macrophages) as well as high levels of TNF-alpha are present in the affected joints of RA patients, the trigger mixture produced in this way is relevant in the field of RA and will be representative for the mixture of factors present in the joints of RA patients. The unbiased character of this method represents an important advantage, as the mixture produced is very complex and might contain factors unknown to be involved in RA or even factors unknown to date.

The white bars in Figure 10 show the increase of SF MMP1 expression upon treatment with cytokines relevant in the field of RA (TNFα, IL1β and OSM) or a combination thereof. For this experiment, SFs are seeded in 96 well plates, 3,000 cells/well. 24 h later, the medium is changed to M199 medium supplemented with 1% FBS. One day after the medium change, cytokines or combinations thereof are added to the cultures, each cytokine being added to a final concentration of 25 ng/ml. 72 h after cytokine addition, the supernatant is collected and processed in the MMP1 ELISA. In parallel with this experiment, SFs are triggered, using the same protocol, with the supernatant of THP1 cells (2-fold diluted in M199 + 1% FBS) that are left untreated or are treated with the same cytokines or combinations of cytokines for 48 h in M199 medium + 1% FBS. MMP1 levels for these samples are shown in Figure 10 as grey bars. The induction of the MMP1 expression levels by the supernatants of TNFα-treated THP1 cells is stronger (>4.5 fold induction) as compared to the induction by recombinant TNFα alone (3-fold induction) and almost equals the 5-fold induction obtained by a mixture of 3 purified cytokines (TNFalpha, IL1b, OSM). This

result indicates that the supernatant of TNFα-induced THP1 cells contains additional pro-inflammatory factors that trigger the SFs towards MMP1 production.

In another experiment, inhibition of the response of SFs to the SN (supernatant) of TNFα-triggered THP1 cells is investigated. SFs are seeded in 384 well plates at 1500 cells/well and left uninfected or infected with the control knock-down virus Ad5-eGFP_KD or the control knock-in virus Ad5-MMP1. One day after infection, dexamethasone, a classical anti-inflammatory agent and SB203580 (an inhibitor of p38alpha and p38beta (kinases involved in the response of cells to TNFα and other cytokines), purchased at Calbiochem, dissolved in 100% DMSO), are added to the SF cultures at a final concentration of 100 nM and 5 μM respectively, 1 h before triggering of the cells with 2-fold diluted SN of TNFα-activated THP1 cells. 72 h after treatment, the SN is collected and subjected to the MMP1 ELISA. Results are depicted in Figure 11: SFs are left uninfected or are infected with a control knock-in virus (Ad5-MMP1_KI) or a control knock–down virus (Ad5-eGFP_KD). Raw luminescence signals, which are proportional to the MMP1 levels, are shown.

Triggering of the cells led to a 6-fold increase of MMP1 expression. Even higher MMP1 levels are measured in the samples infected with Ad5-MMP1, indicating that the THP1 SN-induced MMP1 levels are not saturating for the MMP1 ELISA. The MMP1 levels obtained in the dexamethasone and SB203580 treated samples are 4 and 3 fold lower as the control levels, respectively, indicating that the assay as set up is suitable for the identification of inhibitors of the inflammatory response of SFs. Efficient reduction of gene expression in SFs can be obtained by RNAi (RNA interference) using knockdown viruses or transfection of siRNA duplexes.

Example 6B. Analysis of the Reduction
in mRNA Expression of TARGET Genes by Ad-siRNA

Primary human synovial fibroblasts are seeded in gelatin coated 6-well plates (75,000 cells/well) in 2 ml synovial growth medium (Cell Applications Inc.) supplemented with 1x Pen/Strep (Invitrogen). After overnight incubation, cells are

infected with the Ad5-siRNA targeting the gene of interest at an MOI of 3000. As a negative control, other wells are infected at the same MOI with Ad5-siRNA targeting the firefly luciferase gene. Five days post infection, medium is refreshed with 2 ml M199 medium supplemented with 1% (v/v) heat-inactivated FBS. At the same time, parallel samples are stimulated by refreshing the medium with 2 ml of a 2-fold dilution of the 'complex cytokine mixture' in M199 + 1% FBS. 48 h later, total RNA is extracted using the 'SV Total RNA Isolation kit' (Promega). RNA is quantitated and cDNA is prepared as described in Example 5. For each sample, real-time PCR reactions are performed for the TARGET and the 18S rRNA genes and ΔCt values are calculated as previously described in Example 5. To calculate the % knock-down of the endogenous TARGET mRNA after infection with the Ad5-siRNA, values are first expressed relative to the control samples that are infected with Ad5-luciferase-v13_KD virus using the equation: relative expression = $2^{-\Delta\Delta Ct}$ with $\Delta\Delta Ct = \Delta Ct_{(\text{sample infected with Ad5-luciferase-v13\_KD})} - \Delta Ct_{(\text{sample infected with TARGETspecific Ad5-siRNA})}$. The DCt values indicate the expression relative to ß-actin as indicated in Example 5. Table 6 shows that after infection with most of the selected Ad5-siRNAs, more than 60% reduction of the TARGET mRNA, irrespective of whether the cells are stimulated with the 'complex cytokine mixture'. The abbreviation "Rel Expr" means relative expression.

Table 6

		no trigger				triggered			
TARGET	Ad5-siRNA	DCt	DDCt	Rel. Expr.	% KD	DCt	DDCt	Rel. Expr.	% KD
CAMKIV	Ad5-CamK4-v1_KD	16.7	-2.9	0.13	86.6	18.3	-3.8	0.07	92.8
	Ad5-Luciferase-v13_KD	13.8	0	1.00	0.0	14.5	0	1.00	0.0
PRKCE	Ad5-PRKCE-v11_KD	10	-1.1	0.47	53.3	8.7	-0.9	0.54	46.4
	Ad5-Luciferase-v13_KD	8.9	0	1.00	0.0	7.8	0	1.00	0.0
MMP1	Ad5-MMP1-v10_KD	13.4	-4.9	0.03	96.7	5	-3.2	0.11	89.1
	Ad5-Luciferase-v13_KD	8.5	0	1.00	0.0	1.8	0	1.00	0.0
MAPKAPK5	Ad5-MAPKAPK5-v2_KD	9.3	-2.3	0.20	79.7	7.4	-3	0.13	87.5
	Ad5-MAPKAPK5-v8_KD	9.2	-2.2	0.22	78.2	7.3	-2.9	0.13	86.6
	Ad5-Luciferase-v13_KD	7	0	1.00	0.0	4.4	0	1.00	0.0
RIT	Ad5-RIT-v5_KD	7.1	-1.2	0.44	56.5	6.5	-1.9	0.27	73.2

	Ad5-Luciferase-v13_KD	5.9	0	1.00	0.0	4.6	0	1.00	0.0
TPST1	Ad5-TPST1-v1_KD	7.3	-0.9	0.54	46.4	8.2	-2.3	0.20	79.7
	Ad5-Luciferase-v13_KD	6.4	0	1.00	0.0	5.9	0	1.00	0.0
USP21	Ad5-USP21-v3_KD	9.5	-1.2	0.44	56.5	8.9	-1.3	0.41	59.4
	Ad5-Luciferase-v13_KD	8.3	0	1.00	0.0	7.6	0	1.00	0.0
MST3	Ad5-MST3-v4_KD	6.9	-2	0.25	75.0	7.1	-2.1	0.23	76.7
	Ad5-STK24-v1_KD	7.8	-2.9	0.13	86.6	6.4	-1.4	0.38	62.1
	Ad5-Luciferase-v13_KD	4.9	0	1.00	0.0	5	0	1.00	0.0

Example 6C: Ad-siRNA Viruses Function to Knock Down Expression of MAPKAPK5, PRKCE and CAMK4 at the protein level.

Figure 14 illustrates the functionality of Ad-siRNAs for reducting expression of TARGET genes (PRKCE, MAPKAPK5 and CAMK4) at the protein level in human cells.

Recombinant adenoviruses mediating the expression of siRNA's targeting MAPKAPK5, PRKCE and CAMK4 are generated according to the procedure described in WO03/020931. The target sequences in these genes based on which the siRNAs were designed and that were used to generate the recombinant adenoviruses are listed in Table 3.

The functionality of MAPKAPK5 targeting adenoviruses is tested as follows: On day 1, 500.000 primary human SFs are seeded per petri dish. One day later, the cells are infected with Ad5-MAPKAPK5-v2_KD, Ad5-MAPKAPK5-v8_KD or Ad5-eGFP-v5_KD at an MOI of 4000 (based on the titers (number of virus particles per ml) defined for the viruses by Q-rt-PCR). On day 7, cells are detached from the petri dish according to standard procedure using a trypsin EDTA solution. The trypsin is then neutralized by addition of DMEM growth medium supplemented with 10%FBS. The cells are then collected by a centrifugation step (1000 rpm, 5 min). The pellet is lysed in 100µl of fresh RIPA buffer (50mM Tris pH7.5, 150mM NaCl, 1% deoxycholate, 1% Triton X100, 0.1% SDS). The samples are then sonicated for 10sec. The protein concentration of the samples is then determined using the BCA kit (Pierce, Cat N°

23227) as described by the provider, using BSA as a standard. To 30µg of cell lysate diluted to 19.5µl in RIPA buffer, 3.5µl of reducing agent (NuPage reducing agent N°10, Invitrogen NP0004) and 7.5µl of sample buffer (NuPage LDS sample buffer, Invitrogen NP0007) are added. The 30µl sample is then boiled for 5min and loaded on a 10% polyacrylamide gel (Invitrogen NP0301). The gel is then run for 2 hours at 100V in 1x MOPS/SDS NuPage running buffer (Invitrogen NP001). 10µl of Seablue Plus Prestained standard (Invitrogen LC5925) is used to estimate protein size on the gel. The proteins on the gel are then transferred onto a PVDF membrane (Invitrogen LC2002) by a wet blotting procedure using a transfer buffer prepared by mixing 100ml Nupage Transfer buffer 20* (NP0006-1), 400ml methanol and 1500ml Milli Q water. Before the transfer, the membrane is first soaked in methanol and in transfer buffer. The transfer is performed at 100V for 90 minutes. The membrane is then blocked by 30 min soaking in blocking buffer (2% blocking blocking powder (Amersham, RPN 2109) prepared in PBST (PBS supplemented with 0,1% Tween 20 (Sigma, P1379)). After blocking, the immunodetection is performed using a mouse monoclonal antibody against MAPKAPK5 (BD Biosciences, Cat N°612080) diluted 250 fold in blocking buffer. After overnight incubation with this primary antibody, the membrane is washed 3 times with PBST and incubated 1 hr with the secondary antibody ((Polyclonal goat anti-mouse Ig, HRP conjugated (DAKO P0447) diluted 50000 fold in blocking buffer. The blot is then washed 3 times in PBST and the detection is performed with ECL advance (RPN2109, Amersham) on a Kodakimager according to the manufacturers instructions. The Western Blotting revealed a lower expression level of MAPKAPK5 in the Ad5-MAPKAPK5-v2_KD and Ad5-MAPKAPK5-v8_KD infected cells compared to the cells infected with the Ad5-eGFP-v5_KD negative control virus. Equal loading of the 30µg samples is demonstrated by immunodetection of ß-actin after removal of the MAPKAPK5 antibody by a 'stripping procedure' (5 minutes boiling of the membrane in PBST). Immunodetection of ß-actin is performed according to the method described for MAPKAPK5 detection, but using a goat polyclonal antibody against ß-actin (Santa Cruz, Cat N° SC-1615) at a 1000 fold

dilution as primary antibody and a rabbit anti goat antibody at a 50000 fold dilution as a secondary antibody. Results of this experiment are shown in Figure 14 C.

The functionality of the PRKCE targeting adenovirus (Ad5-PRKCE-v11_KD) is tested according to the same protocol as the one described above for MAPKAPK5, with the difference that an MOI of 2000 is used for infection of the cells. The western blotting procedure is the same as the one described for MAPKAPK5 detection, with the difference that a PRKCE specific antibody is used (BD Biosciences, Cat N° 610085) at a dilution of 250-fold. The same secondary antibody is used as for the detection of MAPKAPK5. Results are shown in Figure 14 B.

The functionality of the CAMK4 targeting adenovirus is tested as follows: These adenoviruses are used to infect Hek293T cells cultured in 6-well plates as follows. On day 1, 400000 Hek293T cells are seeded per 6-well plate in DMEM + 10% FBS. One day later, the cells are infected with Ad5-CAMK4-v1_KD, CAMK4-CAMK4-v9_KD or Ad5-eGFP-v5_KD at an MOI (multiplicity of infection) of 500 (based on the titers (number of virus particles per ml) defined for the viruses by Q-rt-PCR). One day after the infection, the medium is refreshed. On day 7, cells are detached from the petri dish according to standard procedure using a trypsin EDTA solution. The handling of the cell pellet, the running/blotting of the gel and the immunodetection procedure is identical to what is described for MAPKAPK5, with the difference that 40µg protein is loaded on the gel and that a mouse monoclonal antibody against CAMK4 (Santa Cruz, Sc-17762, diluted 100-fold in blocking buffer) is used. The Western Blotting reveals a lower expression level of CAMK4 in the Ad5-CAMK4-v1_KD and the Ad5-CAMK4-v9_KD infected cells compared to the cells infected with the Ad5-eGFP-v5_KD negative control virus. Equal loading of the 30µg samples is demonstrated by immunodetection of ß-actin after removal of the CAMK4 antibody by a 'stripping procedure'. Results of this experiment are given in Figure 14 A.

These experiments demonstrate that the Ad-siRNA virus function to reduce the expression levels of the corresponding MAPKAPK5, CAMK4 and PRKCE polpeptides in human cells.

Example 6D: Reduction of the Expression in Primary SFs of various TARGET Genes by Ad-siRNAs Inhibit SF-induced MMP1 Expression

Figure 12 illustrates the reduction of cytokine-induced SF MMP1 expression by Ad-siRNAs reducing the expression of TARGET genes. These Ad-siRNAs are generated according to the procedure described in WO03/020931. The target sequences (KD SEQ) in these genes, based on which the siRNAs were designed and that were used to generate the recombinant adenoviruses, are listed in Table 3.

The efficacy of Ad5-siRNAs in the 'MMP assay' is tested as follows. Day 1, SFs (passage 9 to 10) are seeded in 96 well plates at a density of 3000 cells per well in complete synovial growth medium (Cell Applications). One day later, the cells are infected with increasing amounts (3, 7.5, 12 or 15 µl in experiment shown in Figure 12 A; 3, 6, 9, 12 and 15 µl in experiment shown in Figure 12 B; and 3, 6, 9, and 12µl in the experiments represented on Figures 12 C and 12 D) of the Ad-siRNA's. The following viruses are used as negative control: Ad5-eGFP-v5_KD, Ad5-Luciferase-v13_KD and Ad-M6PR-v1_KD. Ad5-MMP1-v10_KD is used as a positive control virus. The virus load is corrected by addition of the neutral virus Ad5-Luciferase-v13_KD to bring the final virus volume on the cells to 15µl in every well. This correction guarantees that the effects observed do not result from differences in the virus load applied to the cells. The cells are then incubated for 5 days before the activation step. This step involves the replacement, in every well, of the growth medium by 75µl of M199 medium supplemented with 25µl of 'complex trigger'. 48 hrs after the activation step, the supernatant is collected and subjected to the MMP1 ELISA as described above.

The results of the experiment are shown in Figure 12A, B, C and D. The average of duplicate data points is shown in these Figures. The quality of the experiment is demonstrated by the efficacy of the Ad-siRNA virus targeting MMP1

itself. This positive control virus strongly reduces the MMP1 expression by SFs, whereas the negative control viruses, designed to target the expression of luciferase, M6PR and eGFP do not influence the levels of MMP1 expression, as expected. The Ad-siRNAs designed against TARGET genes (GPR21, FZD4, TM7SF1, PGPEP1, SEPT1, CD72, FXYD5 (Figure 12 A.); PRKCE, CAMK4, MAPKAPK5 (Figure 12 B.), RIPK2, RIT1 (Figure 12 C.) and PPST1, USP21 and STK24 (Figure 12 D.), also lead to a clear reduction of the complex trigger induced MMP1 expression by primary human SFs. For certain TARGET genes (e.g. CAMK4, MAPKAPK5), 2 independent Ad-siRNAs showed efficacy in reducing cytokine induced MMP1 expression by SFs. In Figure 12 A and B, the MMP1 expression levels are shown in terms of raw data (RLU) whereas in Figures 12 C and 12 D, the MMP1 expression levels are expressed relative to the samples infected with Ad5-luciferase-v13_KD only set to 100%.

For most TARGET genes, at least 1 of the 5 Ad-siRNAs designed per TARGET gene mediated a reduction of the cytokine-induced MMP1 expression by SFs. This was not the case for MKNK1 and CASP10. The effects observed were weaker for USP21 and MST3.

It can be concluded, from this experiment, that these genes represent valuable drug targets that are shown to modulate MMP1 expression in SFs. Similarly, the inhibition of the activity of the protein product of these genes by a small molecule compound is expected to reduce the 'complex cytokine' induced MMP1 expression in the 'MMP assay'. The inhibition of the activity of the protein products of these genes by small molecule compounds is also predicted to reduce the degradation of the joint associated with RA.

Example 6E: Reduction of the Expression in Primary SFs of MAPKAPK5 and CAMK4 by Ad-siRNAs Inhibit cytokine-induced Collagen Degradation

This experiment measures the ability of Ad-siRNAs to reduce cytokine-induced degradation of collagen type I, which is even more stringent than the MMP1 ELISA, as the degradation of native collagen might be due to the action of proteases

different from MMP1. The Ad-siRNAs used in this experiment are generated according to the procedure described in WO03/020931. The recombinant Ad-siRNAs used in this experiment were generated based on target sequences in the target genes that are listed in Table 3.

The efficacy of Ad5-siRNAs in the 'miniaturized native collagen type I degradation assay' described above is tested as follows: Day 1, SFs (passage 9 to 10) are seeded in 96 well plates at a density of 3000 cells per well in complete synovial growth medium (Cell Applications). One day later, the cells are infected with increasing amounts (3, 6, 9, 12 and 15 µl)of the Ad-siRNA's indicated on the figure. The following viruses are used as negative control: Ad5-eGFP-v5_KD, and Ad5-Luciferase-v13_KD. The virus load is corrected by addition of the neutral virus Ad5-Luciferase-v13_KD to bring the final virus volume added to each well to 15µl. This correction guarantees that the effects observed do not result from differences in the virus load applied to the cells. The cells are then incubated for 5 days before the activation step. This step involves the replacement, in every well, of the growth medium by 45µl of M199 medium supplemented with 15µl of 'complex trigger'. 4 days later, the supernatant is collected and subjected to the miniaturized collagen type I degradation assay according to the protocol as described above. The results of the experiment are shown in Figure 15.

The negative control viruses, designed to target the expression of luciferase and eGFP, do not influence the levels of collagen degradation, as expected. The Ad-siRNAs targeting MAPKAPK5 and CAMK4 do mediate a clear reduction of the complex trigger-induced collagen degradation by primary human SFs. It can be concluded, from this experiment, that these genes represent valuable drug targets that are shown to modulate collagen degradation by SFs. Similarly, the inhibition of the activity of the protein product of these genes by a small molecule compound is expected to reduce the 'complex cytokine' induced collagen degradation by SFs. The inhibition of the activity of the protein products of these genes by small molecule compounds is also predicted to reduce the degradation of the joint associated with RA. In similar experiments, the Ad5-MMP1-v10_KD virus is shown to strongly reduce the

cytokine induced collagen degradation by SFs, which implies the fact that MMP1 itself is the main collagenase responsible for the cytokine induced collagen degradation by SFs. As such, this means that modulation of MMP1 expression by SFs is sufficient to reduce cartilage degradation associated with RA.

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It will be appreciated by those skilled in the art that the foregoing description is exemplary and explanatory in nature, and is intended to illustrate the invention and its preferred embodiments. Through routine experimentation, an artisan will recognise apparent modifications and variations that may be made without departing from the spirit of the invention. Thus, the invention is intended to be defined not by the above description, but by the following claims and their equivalents.

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<SEQ ID NO: 14; DNA; Homo sapiens>

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EDEIEDIQQEITVLSQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLEPGPLDETQ
IATILREILKGLDYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFV
GTPFWMAPEVIKQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE
GNYSKPLKEFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYKRWKAEQSH
DDSSSEDSDAETDGQASGGSDSGDWIFTIREKDPKNLENGALQPSDLDRNKMKDIPKRPF
SQCLSTIISPLFAELKEKSQACGGNLGSIEELRGAIYLAEEVCPGISDTMVAQLVQRLQR
YSLSGGGTSSH
<SEQ ID NO: 104; PRT; Homo sapiens>
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VVAIKIIDLEEAEDEIEDIQQEITVLSQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSAL
DLLEPGPLDETQIATILREILKGLDYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQ
LTDTQIKRNTFVGTPFWMAPEVIKQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVL
FLIPKNNPPTLEGNYSKPLKEFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELI
DRYKRWKAEQSHDDSSSEDSDAETDGQASGGSDSGDWIFTIREKDPKNLENGALQPSDLD
RNKMKDIPKRPFSQCLSTIISPLFAELKEKSQACGGNLGSIEELRGAIYLAEEACPGISD

TMVAQLVQRLQRYSLSGGGTSSH
<SEQ ID NO: 105; PRT; Homo sapiens>
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NEVRLHMMCATHPNIVQIIEVFANSVQFPHESSPRARLLIVMEMMEGGELFHRISQHRHF
TEKQASQVTKQIALALRHCHLLNIAHRDLKPENLLFKDNSLDAPVKLCDFGFAKIDQGDL
MTPQFTPYYVAPQVLEAQRRHQKEKSGIIPTSPTPYTYNKSCDLWSLGVIIYVMLCGYPP
FYSKHHSRTIPKDMRRKIMTGSFEFPEEEWSQISEMAKDVVRKLLKVKPEERLTIEGVLD
HPWLNSTEALDNVLPSAQLMMDKAVVAGIQQAHAEQLANMRIQDLKVSLKPLHSVNNPIL
RKRKLLGTKPKDSVYIHDHENGAEDSNVALEKLRDVIAQCILPQAGENEDEKLNEVMQEA
WKYNRECKLLRDTLQSFSWNGRGFTDKVDRLKLAEIVKQVIEEQTTSHESQ
<SEQ ID NO: 106; PRT; Homo sapiens>
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TEKQASQVTKQIALALRHCHLLNIAHRDLKPENLLFKDNSLDAPVKLCDFGFAKIDQGDL
MTPQFTPYYVAPQVLEAQRRHQKEKSGIIPTSPTPYTYNKSCDLWSLGVIIYVMLCGYPP
FYSKHHSRTIPKDMRRKIMTGSFEFPEEEWSQISEMAKDVVRKLLKVKPEERLTIEGVLD
HPWLNSTEALDNVLPSAQLMMDKAVVAGIQQAHAEQLANMRIQDLKVSLKPLHSVNNPIL
RKRKLLGTKPKDSVYIHDHENGAEDSNVALEKLRDVIAQCILPQAGKGENEDEKLNEVMQ
EAWKYNRECKLLRDTLQSFSWNGRGFTDKVDRLKLAEIVKQVIEEQTTSHESQ
<SEQ ID NO: 107; PRT; Homo sapiens>
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AKVQGAVSLQNGKEYAVKIIEKQAGHSRSRVFREVETLYQCQGNKNILELIEFFEDDTRF
YLVFEKLQGGSILAHIQKQKHFNEREASRVVRDVAAALDFLHTKDKVSLCHLGWSAMAPS
GLTAAPTSLGSSDPPTSASQVAGTTGIAHRDLKPENILCESPEKVSPVKICDFDLGSGMK
LNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDLWSLGVVLYIMLSGYPP
FVGHCGADCGWDRGEVCRVCQNKLFESIQEGKYEFPDKDWAHISSEAKDLISKLLVRDAK
QRLSAAQVLQHPWVQGQAPEKGLPTPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENEL
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<SEQ ID NO: 108; PRT; Homo sapiens>
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VTGGELFDRIVEKGYYSERDAADAVKQILEAVAYLHENGIVHRDLKPENLLYATPAPDAP
LKIADFGLSKIVEHQVLMKTVCGTPGYCAPEILRGCAYGPEVDMWSVGIITYILLCGFEP
FYDERGDQFMFRRILNCEYYFISPWWDEVSLNAKDLVRKLIVLDPKKRLTTFQALQHPWV
TGKAANFVHMDTAQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHGSIQESHKASRDPS
PIQDGNEDMKAIPEGEKIQGDGAQAAVKGAQAELMKVQALEKVKGADINAEEAPKMVPKA
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<SEQ ID NO: 109; PRT; Homo sapiens>
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ESGLNRKNIQDSRVHCCLYFISPFGRGLRPLDVAFLRAVHEKVNIIPVIGKADALMPQET
QALKQKIRDQLKEEEIHIYQFPECDSDEDEDFKRQDAEMKESIPFAVVGSCEVVRDGGNR
PVRGRRYSWGTVEVENPHHCDFLNLRRMLVQTHLQDLKEVTHDLLYEGYRARCLQSLARP
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LWEKHSPQLVVHVGVSGMATTVTLEKCGHNKGYKGLDNCRFCPGSQCCVEDGPESIDSII
DMDAVCKRVTTLGLDVSVTISQDAGRKKPFPAKGDCVFCRRRRARSLQAQCGFSLTPALE
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<SEQ ID NO: 111; PRT; Homo sapiens>
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LWEKHSPQLVVHVGVSGMATTVTLEKCGHNKGYKGLDNCRFCPGSQCCVEDGPESIDSII
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LGRALRAIIEEMLDLLEQSEGKINYCHKH
<SEQ ID NO: 112; PRT; Homo sapiens>
MAEAITYADLRFVKAPLKKSISSRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLG
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VSQQLQQTNRVLEVTNSSLRQQLRLKITQLGQSAEDLQGSRRELAQSQEALQVEQRAHQA
AEGQLQACQADRQKTKETLQSEEQQRRALEQKLSNMENRLKPFFTCGSADTCCPSGWIMH
QKSCFYISLTSKNWQESQKQCETLSSKLATFSEIYPQSHSYYFLNSLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRTYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD
<SEQ ID NO: 113; PRT; Homo sapiens>
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KTFAYHKDMPLIFIGGVPRSGTTLMRAMLDAHPDIRCGEETRVIPRILALKQMWSRSSKE
KIRLDEAGVTDEVLDSAMQAFLLEIIVKHGEPAPYLCNKDPFALKSLTYLSRLFPNAKFL
LMVRDGRASVHSMISRKVTIAGFDLNSYRDCLTKWNRAIETMYNQCMEVGYKKCMLVHYE
QLVLHPERWMRTLLKFLQIPWNHSVLHHEEMIGKAGGVSLSKVERSTDQVIKPVNVGALS
KWVGKIPPDVLQDMAVIAPMLAKLGYDPYANPPNYGKPDPKIIENTRRVYKGEFQLPDFL
KEKPQTEQVE
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HHTTSYFIQTMAYADLFVGVSCVVPSLSLLHHPLPVEESLTCQIFGFVVSVLKSVSMASL
ACISIDRYIAITKPLTYNTLVTPWRLRLCIFLIWLYSTLVFLPSFFHWGKPGYHGDVFQW
CAESWHTDSYFTLFIVMMLYAPAALIVCFTYFNIFRICQQHTKDISERQARFSSQSGETG
EVQACPDKRYAMVLFRITSVFYILWLPYIIYFLLESSTGHSNRFASFLTTWLAISNSFCN
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<SEQ ID NO: 115; PRT; Homo sapiens>
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ERLKKLELGRGRTSGPRPRGPLRADHGVPLPGSPPPTVALPLPSRTNLARSKSVSSGDLR
PMGIALGGHRGTGELGAALSRLALRPEPPTLRRSTSLRRLGGFPGPPTLFSIRTEPPASH
GSFHMISARSSEPFYSDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDFC
LRRDFRQEVPGGGRAQELTEAFADVIGALWHPDSCEAVNPTRFRAVFQKYVPSFSGYSQQ
DAQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLEEPELSDDDRANLMWK
RYLEREDSKIVDLFVGQLKSCLKCQACGYRSTTFEVFCDLSLPIPKKGFAGGKVSLRDCF
NLFTKEEELESENAPVCDRCRQKTRSTKKLTVQRFPRILGLDLNRFSASRGSIKKSSVGV
DFPLQRLSLGDFASDKAGSPVYQLYALCNHSGSVHYGHYTALCRCQTGWHVYNDSRVSPV
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<SEQ ID NO: 116; PRT; Homo sapiens>
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GSFHMISARSSEPFYSDDKMAHHTLLLGSGHVGLRNLGNTCFLNAVLQCLSSTRPLRDFC
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DAQEFLKLLMERLHLEINRRGRRAPPILANGPVPSPPRRGGALLEEPELSDDDRANLMWK
RYLEREDSKIVDLFVGQLKSCLKCQACGYRSTTFEVFCDLSLPIPKKGFAGGKVSLRDCF
NLFTKEEELESENAPVCDRCRQKTRSTKKLTVQRFPRILGLDLNRFSASRGSIKKSSVGV
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<SEQ ID NO: 117; PRT; Homo sapiens>

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CLSVKRRCEPVLKEFGFAWPESLNCSKFPPQNDHNHMCMEGPGDEEVPLPHKTPIQPGEE
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FLIDSSRFSYPERPIIFLSMCYNIYSIAYIVRLTVGRERISCDFEEAAEPVLIQEGLKNT
GCAIIFLLMYFFGMASSIWWVILTLTWFLAAGLKWGHEAIEMHSSYFHIAAWAIPAVKTI
VILIMRLVDADELTGLCYVGNQNLDALTGFVVAPLFTYLVIGTLFIAAGLVALFKIRSNL
QKDGTKTDKLERLMVKIGVFSVLYTVPATCVIACYFYEISNWALFRYSADDSNMAVEMLK
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<SEQ ID NO: 118; PRT; Homo sapiens>
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EEVPLPHKTPIQPGEECHSVGTNSDQYIWVKRSLNCVLKCGYDAGLYSRSAKEFTDIWMA
VWASLCFISTAFTVLTFLIDSSRFSYPERPIIFLSMCYNIYSIAYIVRLTVGRERISCDF
EEAAEPVLIQEGLKNTGCAIIFLLMYFFGMASSIWWVILTLTWFLAAGLKWGHEAIEMHS
SYFHIAAWAIPAVKTIVILIMRLVDADELTGLCYVGNQNLDALTGFVVAPLFTYLVIGTL
FIAAGLVALFKIRSNLQKDGTKTDKLERLMVKIGVFSVLYTVPATCVIACYFYEISNWAL
FRYSADDSNMAVEMLKIFMSLLVGITSGMWIWSAKTLHTWQKCSNRLVNSGKVKREKRGN
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PVCLQFFTLTLMNLYFTQVIFKAKSKYSPELLKYRLPLYLASLFISLVFLLVNLTCAVLV
KTGNWERKVIVSVRVAINDTLFVLCAVSLSICLYKISKMSLANIYLESKGSSVCQVTAIG
VTVILLYTSRACYNLFILSFSQNKSVHSFDYDWYNVSDQADLKNQLGDAGYVLFGVVLFV
WELLPTTLVVYFFRVRNPTKDLTNPGMVPSHGFSPRSYFFDNPRRYDSDDDLAWNIAPQG
LQGGFAPDYYDWGQQTNSFLAQAGTLQDSTLDPDKPSLG
<SEQ ID NO: 120; PRT; Homo sapiens>
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PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNRCR
<SEQ ID NO: 121; PRT; Homo sapiens>
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VRRTDDTPVVLVGNKSDLKQLRQVTKEEGLALAREFSCPFFETSAAYRYYIDDVFHALVR
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ELSEGIDSENLKDMIFLLKDSLPKTEMTSLSFLAFLEKQGKIDEDNLTCLEDLCKTVVPK
LLRNIEKYKREKAIQIVTPPVDKEAESYQGEEELVSQTDVKTFLEALPRAAVYRMNRNHR
GLCVIVNNHSFTSLKDRQGTHKDAEILSHVFQWLGFTVHIHNNVTKVEMEMVLQKQKCNP
AHADGDCFVFCILTHGRFGAVYSSDEALIPIREIMSHFTALQCPRLAEKPKLFFIQACQG
EEIQPSVSIEADALNPEQAPTSLQDSIPAEADFLLGLATVPGYVSFRHVEEGSWYIQSLC
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QGTHKDAEILSHVFQWLGFTVHIHNNVTKVEMEMVLQKQKCNPAHADGDCFVFCILTHGR
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QAPTSLQDSIPAEADFLLGLATVPGYVSFRHVEEGSWYIQSLCNHLKKLVPRMLKFLEKT
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<SEQ ID NO: 124; PRT; Homo sapiens>
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We claim:

1. A method for identifying a compound that inhibits extra-cellular matrix (ECM) degradation, comprising
   contacting a compound with a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 and 501-564; and measuring a compound-polypeptide property related to related to extra-cellular matrix (ECM) degradation.
2. The method according to claim 1, wherein said polypeptide is in an *in vitro* cell-free preparation.
3. The method according to claim 1, wherein said polypeptide is present in a mammalian cell.
4. The method of claim 1, wherein said property is a binding affinity of said compound to said polypeptide.
5. The method of claim 3, wherein said property is activation of a biological pathway producing a biochemical marker indicative of extra-cellular matrix (ECM) degradation.
6. The method of claim 5 wherein said indicator is MMP1.
7. The method of claim 6 wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125.
8. The method according to claim 1, wherein said compound is selected from the group consisting of compounds of a commercially available screening library and compounds having binding affinity for a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 and 501-564.
9. The method according to claim 2, wherein said compound is a peptide in a phage display library or an antibody fragment library.
10. An agent for inhibiting extra-cellular matrix (ECM) degradation, selected from the group consisting of an antisense polynucleotide, a ribozyme, and a small interfering RNA (siRNA), wherein said agent comprises a nucleic acid sequence complementary to, or engineered from, a naturally-occurring polynucleotide sequence of about 17 to about 30 contiguous nucleotides of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-25.

11. The agent according to claim 10, wherein a vector in a mammalian cell expresses said agent.
12. The agent according to claim 11, wherein said vector is an adenoviral, retroviral, adeno-associated viral, lentiviral, a herpes simplex viral or a sendaiviral vector.
13. The agent according to claim 10, wherein said antisense polynucleotide and said siRNA comprise an antisense strand of 17-25 nucleotides complementary to a sense strand, wherein said sense strand is selected from 17-25 continuous nucleotides of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1-25.
14. The agent according to claims 13, wherein said siRNA further comprises said sense strand.
15. The agent according to claim 14, wherein said sense strand is selected from the group consisting of SEQ ID NO: 201-324.
16. The agent according to claim 15, wherein said siRNA further comprises a loop region connecting said sense and said antisense strand.
17. The agent according to claim 16, wherein said loop region comprises a nucleic acid sequence defined of SEQ ID NO: 26.
18. The agent according to claim 17, wherein said agent is an antisense polynucleotide, ribozyme, or siRNA comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 201-324.
19. The agent according to claim 18, wherein said agent is an antisense polynucleotide, ribozyme, or siRNA comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 201-324.
20. An ECM degradation inhibiting pharmaceutical composition comprising a therapeutically effective amount of an agent of claim 10 in admixture with a pharmaceutically acceptable carrier.
21. A method of treating and/or preventing a disease involving extra-cellular matrix (ECM) degradation in a subject suffering from or susceptible to the disease, comprising administering to said subject a pharmaceutical composition according to claim 20.
22. The method according to claim 22 wherein the disease is a joint degenerative disease.
23. The method according to claim 23, wherein the disease is rheumatoid arthritis.

24. Use of an agent according to claims 10-19 in the manufacture of a medicament for the treatment and/or prevention of a disease involving extra-cellular matrix (ECM) degradation.
25. Use according to claim 24, wherein the disease is selected from the group consisting of joint degenerative and inflammation diseases.
26. Use according to claim 24 or 25, wherein the disease is rheumatoid arthritis.
27. A method of treatment of a condition characterised by abnormal matrix metallo proteinase activity, which comprises administering a therapeutically effective amount of a matrix metallo proteinase inhibiting agent according to claim 10.
28. A method of treatment of a condition selected from diseases involving abnormal cellular expression of MMP1, which comprises administering a therapeutically effective matrix metallo proteinase inhibiting amount of a agent according to claim 10.

A method for diagnosing a pathological condition involving extra-cellular matrix (ECM) degradation or a susceptibility to the condition in a subject, comprising determining a first amount of polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 101-125 present in a biological sample obtained from said subject, and comparing said first amount with the ranges of amounts of the polypeptide determined in a population of healthy subjects, wherein an increase of the amount of polypeptide in said biological sample compared to the range of amounts determined for healthy subjects is indicative of the presence of the pathological condition.

Figure 1

Schematic view of a normal joint and its changes in rheumatoid arthritis
(From Smolen and Steiner, 2003).

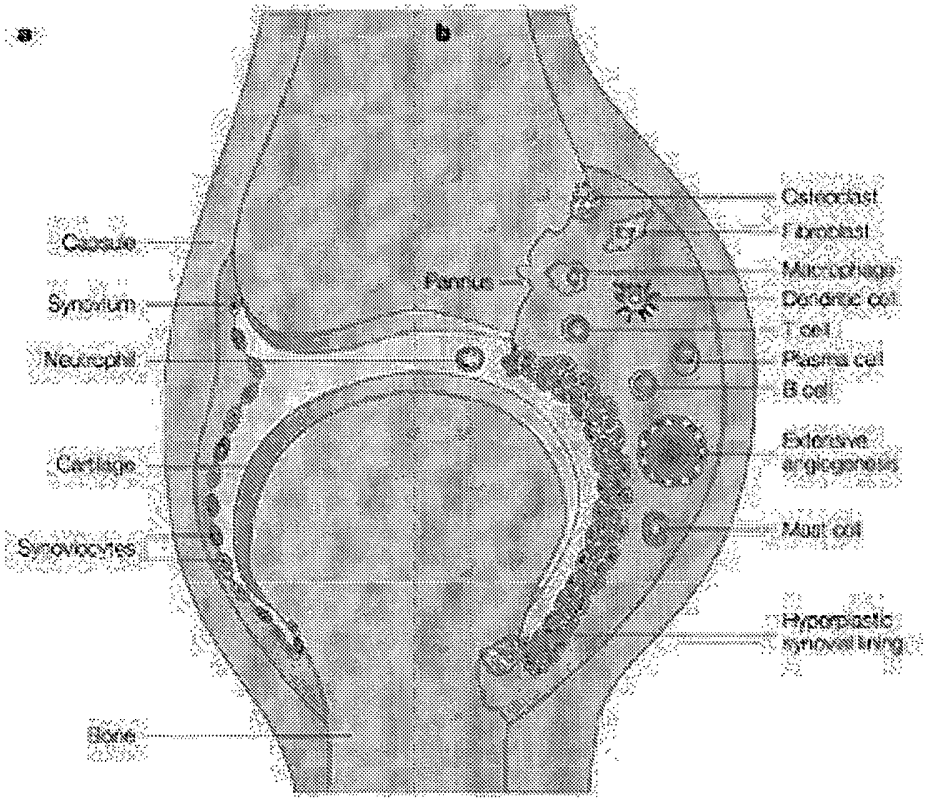
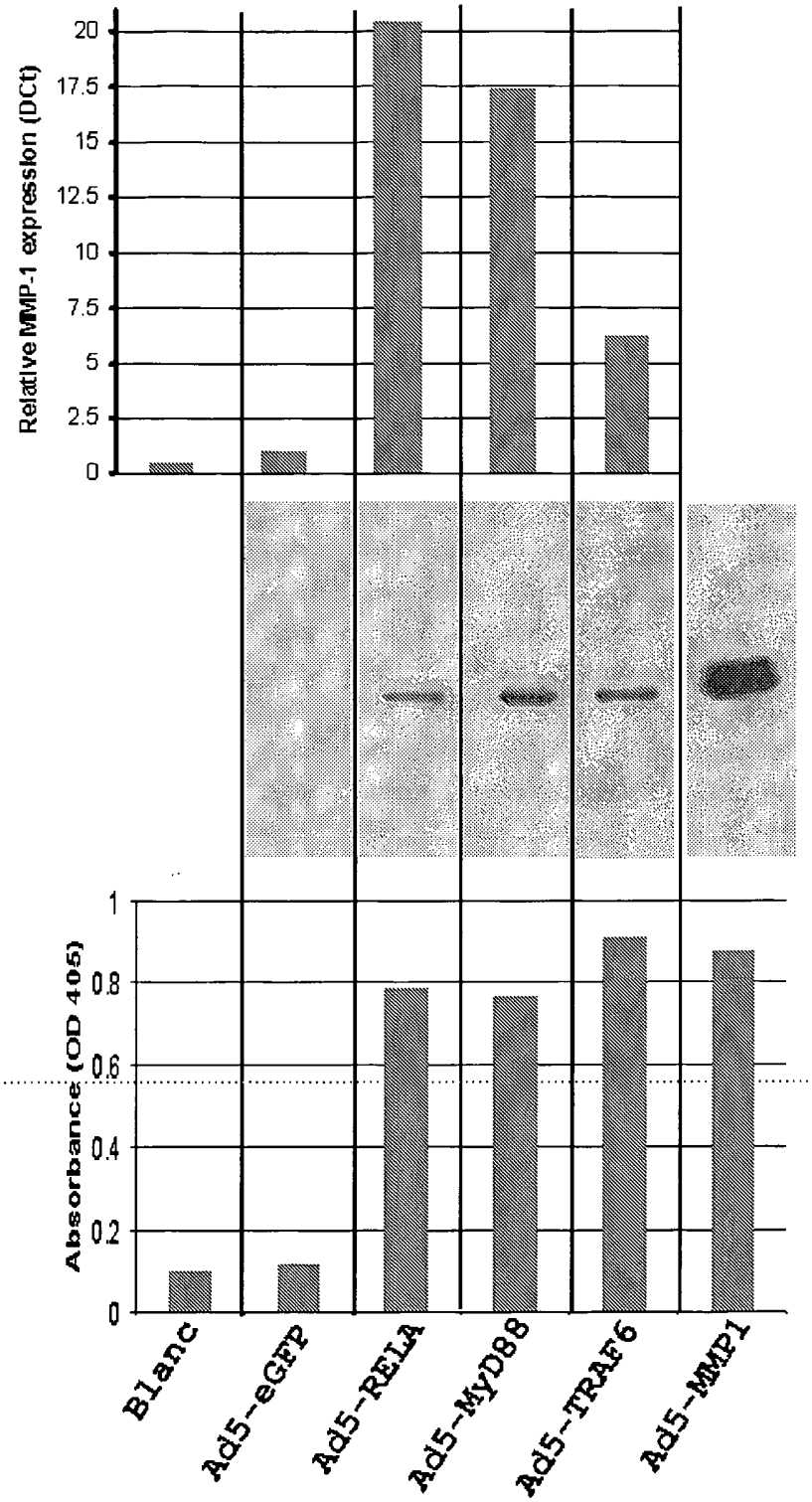


Figure 2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15
12.5
10
7.5
5
2.5
0
Absorbance (OD 405)
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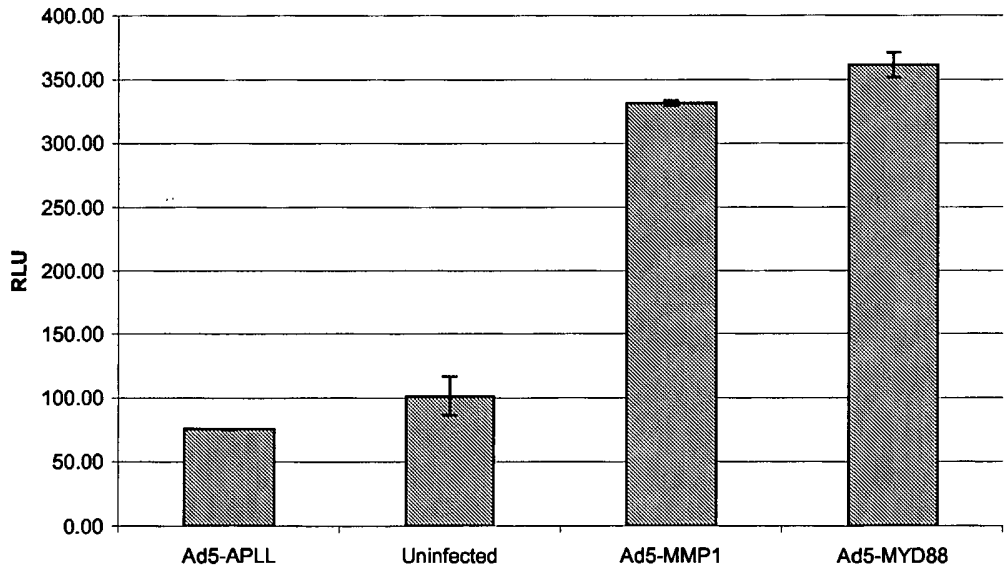
0.8
0.6
0.4
0.2
0
Blanc
Ad5-eGFP
Ad5-RELA
Ad5-MyD88
Ad5-TRAF6
Ad5-MMP1

Figure 3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Ad5-MMP1
Ad5-MYD88

Figure 4A

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D	N1	BI	P2	BI	N2	BI	P3	BI	N3	BI	P1	BI	N1	BI	P2	BI	N2	BI	P3	BI	N3	BI	P1	BI
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K	N3	N3	P1	P1	N1	N1	P2	P2	N2	N2	P3	P3	N3	N3	P1	P1	N1	N1	P2	P2	N2	N2	P3	P3
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B	992.8	170.8	88.18	92.83	233	75.43	96.47	125.2	348.3	140.2	195.1	152.9	957.7	97.15	56.59	62.11	154.3	60.83	58.3	84.43	330.1	106.8	101.7	222
C	143.3	96.54	184.6	181.9	60.6	81.66	253.3	187.8	149.3	129.4	678.9	805.5	56.91	49.2	136.3	157	51.8	57.02	243.5	279.8	102.6	79.42	873.8	876.2
D	122.5	84.52	190	78.55	71.05	72.69	370.9	68.15	101.4	192.1	729.9	138.4	54.43	49.88	178.3	65.32	56.24	72.54	296.3	127.9	120.9	169.1	911.6	159.1
E	290	191.1	66.24	66.15	300.6	225.8	77	119.3	789.4	784.5	69.82	100.3	191.1	167.2	49.07	56.66	299.2	316.3	87.45	139.6	878.9	837	91.33	123.6
F	225.8	112.8	86.46	81.71	404.4	129.2	82.93	102.4	1016	78.39	35.99	64.43	195.4	42.95	56.57	103.9	409.9	160.9	103	94.56	880.5	102.9	54.46	94.26
G	75.32	79.75	397.4	311.8	109.2	77.27	885.8	786	84.34	45.91	201.6	197.5	45.24	56.54	402.6	411.9	121.8	108	807.3	769.6	57.79	51.29	147.7	169.2
H	89.63	84.49	384.6	91.71	77.39	91.73	1041	127.2	79.02	39.25	222.2	43.08	104.9	70.67	449.1	92.62	93.1	162	686	85.4	39.69	48.42	209.3	83.59
I	427.2	377.4	88.99	100.6	986.7	864.5	95	58.82	232.7	132.9	40.48	57.62	447.6	344	53.04	90.58	821.9	787.5	61.57	39.16	154.7	191.2	58.64	77.35
J	375	112.8	86.11	123.5	1059	109.9	60.77	54.79	214.3	37.14	42.64	52.62	350.5	71.41	115.8	105.3	861.1	124.2	55.32	41.83	152.4	51.95	64.58	56.2
K	110.3	114.8	793.7	853.7	88.13	66.26	194	188.1	65.01	46.06	361.7	217.7	50.76	85.24	844.8	844.8	69.67	36.25	161.3	156.4	36.62	41.18	233.5	196.9
L	119.3	115.7	1086	183.8	62.63	75.35	181.2	59.04	67.11	61.1	549.2	53.32	41.78	106.6	915.1	110	37.98	38.69	120.7	34.53	37.55	42.84	252.9	81.5
M	769.4	898.9	133	73.79	316.9	157.7	38.5	60.48	233	278.8	48.15	77.91	847.2	852.1	48.46	44.7	161.4	132.3	27.47	31.59	195.5	240.6	53.8	50.51
N	931.1	114.9	110.7	72.61	203	59.08	45.58	69.04	459.3	84.81	45.86	74.3	943.1	130.3	35.8	34.82	159.7	31.86	27.37	35.96	168.7	65.82	72.94	67.72
O	171.5	101	237.9	239	68.45	70.38	414.5	446.4	96.57	107.4	879.4	826.3	64.7	43.68	123.1	206.2	33.01	35.37	153.9	161.5	30.86	59.61	778.1	829.8
P	142.9	126	213.5	99.46	71.39	85.74	517.6	79.77	89.75	98.73	905.7	99.69	54.82	46.37	174.4	55.53	44.08	49.29	219.3	45.78	51.97	70.09	712.4	140.6

Figure 4B

		Average	Standard deviation	Cutoff	% positive	
Ad5-MMP-1	P1	856.0	91.8		100.0	of 48
Ad5-TRAF6	P2	187.2	38.9		16.7	of 48
Ad5-MYD88	P3	325.7	96.8		83.3	of 48
Ad5-eGFP	N1	75.0	32.9		0.0	of 48
Ad5-LacZ	N2	60.6	19.7		0.0	of 48
Ad5-PLAP	N3	93.8	32.1		0.0	of 48
	Blanco	89.6	39.5		1.0	of 96
	All positives	456.3	300.0			
	All negatives	76.4	31.8	219.4		

Figure 5

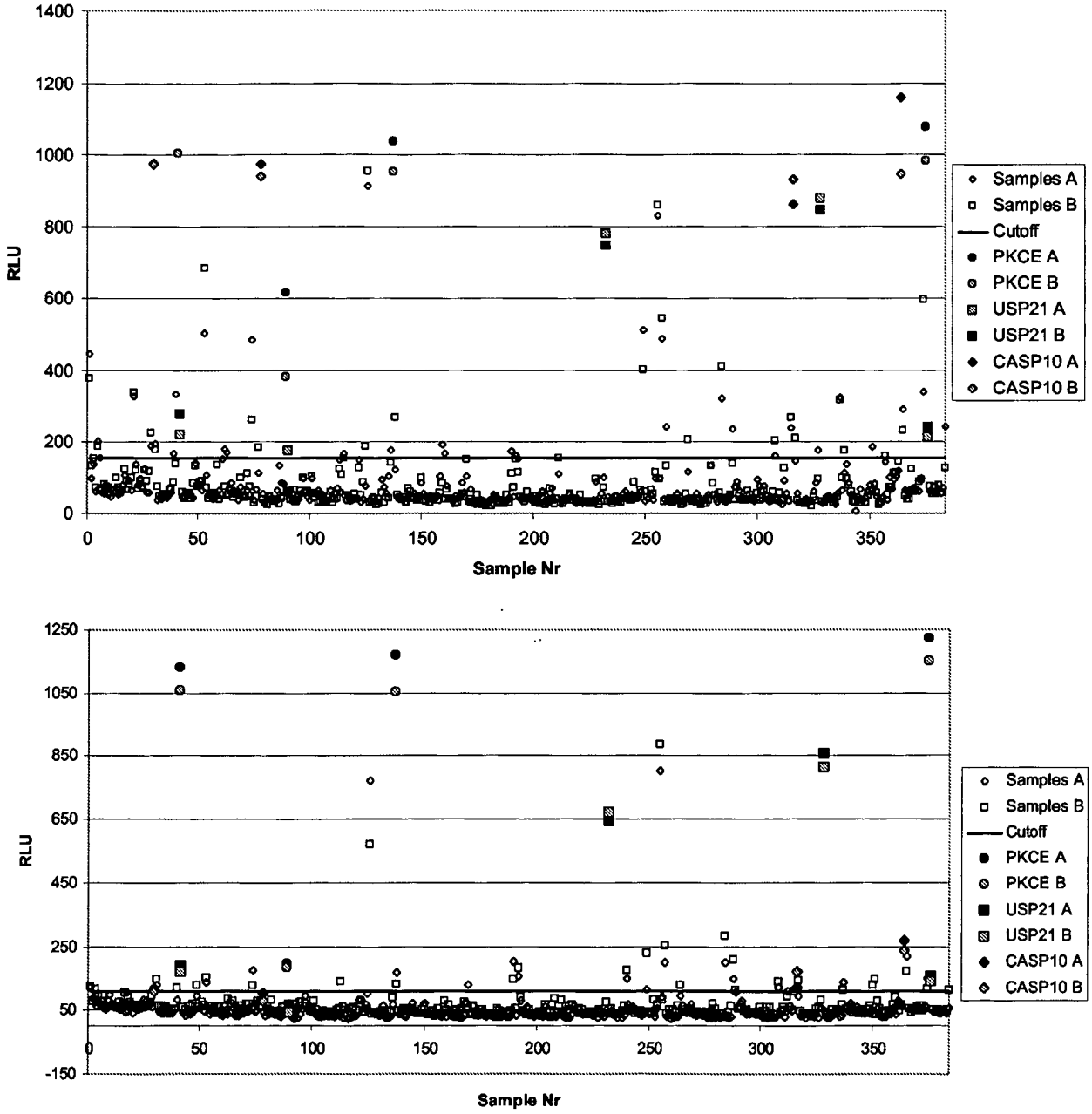

1400
1200
1000
800
600
400
200
0
RLU
0
50
100
150
200
250
300
350
Sample Nr
Samples A
Samples B
Cutoff
PKCE A
PKCE B
USP21 A
USP21 B
CASP10 A
CASP10 B
1250
1050
850
650
450
250
50
-150
RLU
0
50
100
150
200
250
300
350
Sample Nr
Samples A
Samples B
Cutoff
PKCE A
PKCE B
USP21 A
USP21 B
CASP10 A
CASP10 B

Figure 6

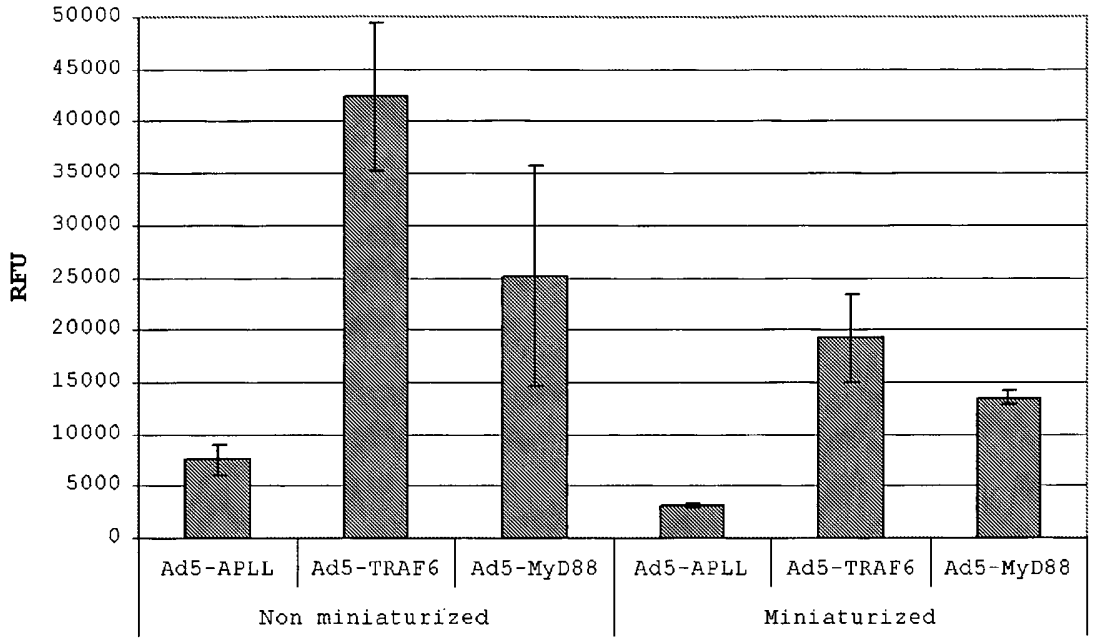

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
RFU
Ad5-APLL
Ad5-TRAF6
Ad5-MyD88
Ad5-APLL
Ad5-TRAF6
Ad5-MyD88
Non miniaturized
Miniaturized

Figure 7

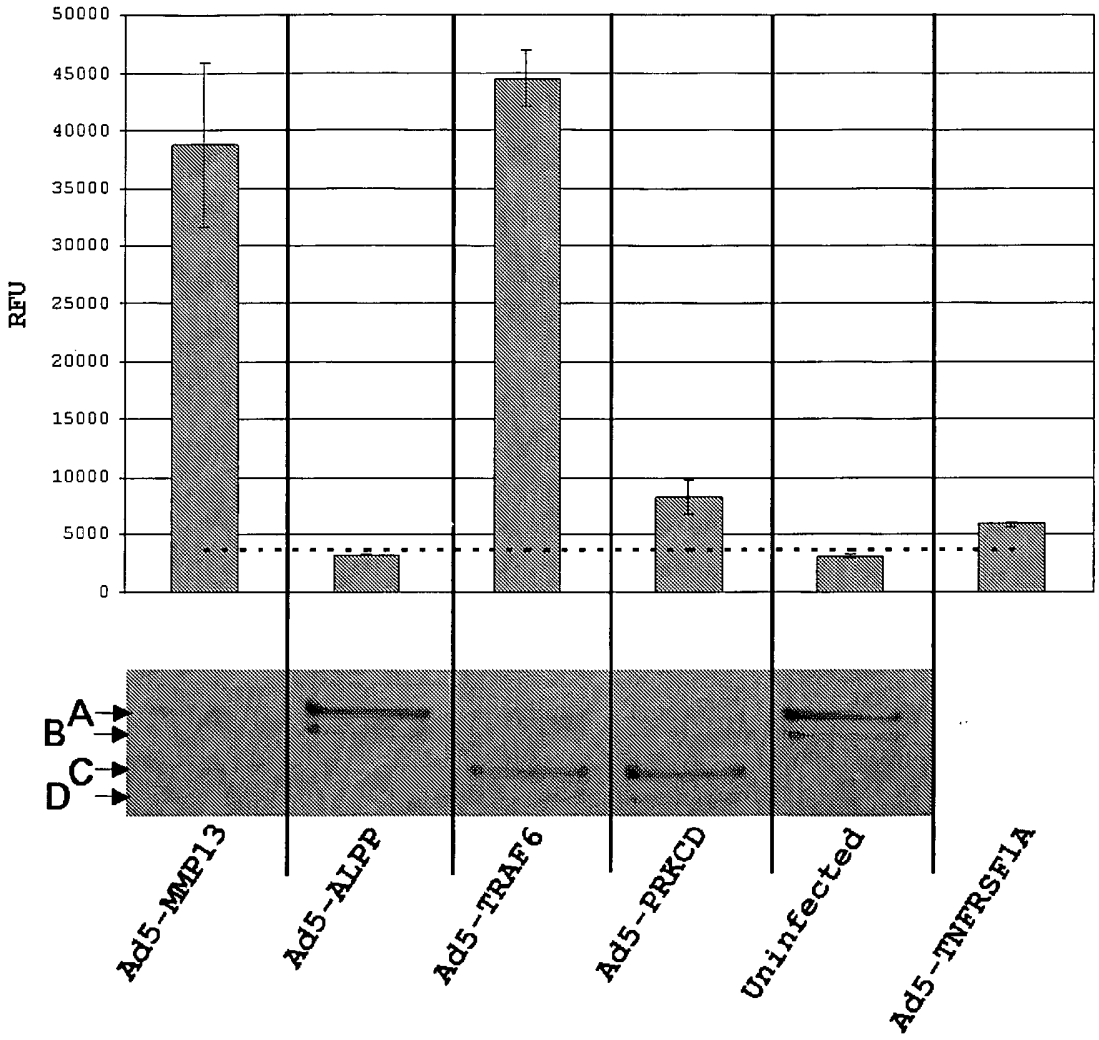

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
RFU
A
B
C
D
Ad5-MMP13
Ad5-ALPP
Ad5-TRAF6
Ad5-PRKCD
Uninfected
Ad5-TNFRSF1A

Figure 8

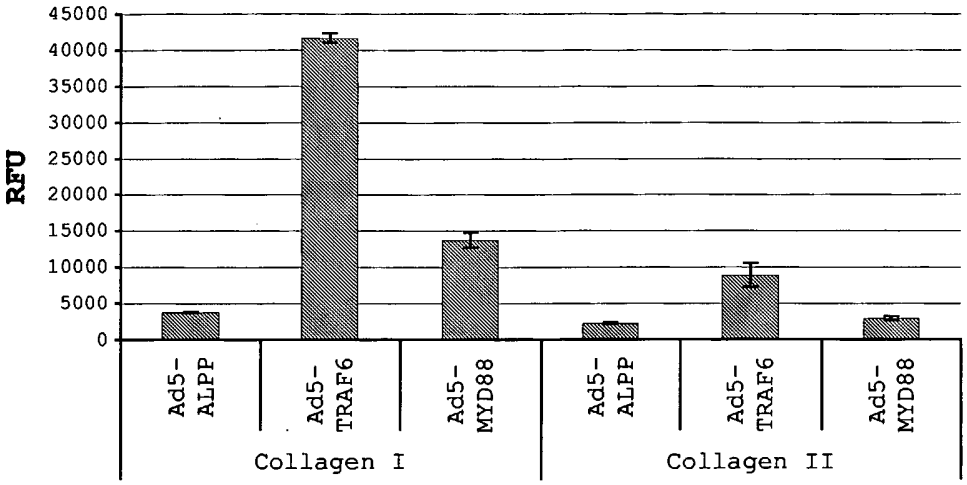

45000
40000
35000
30000
25000
20000
15000
10000
5000
0
RFU
Ad5-ALPP
Ad5-TRAF6
Ad5-MYD88
Ad5-ALPP
Ad5-TRAF6
Ad5-MYD88
Collagen I
Collagen II

Figure 9

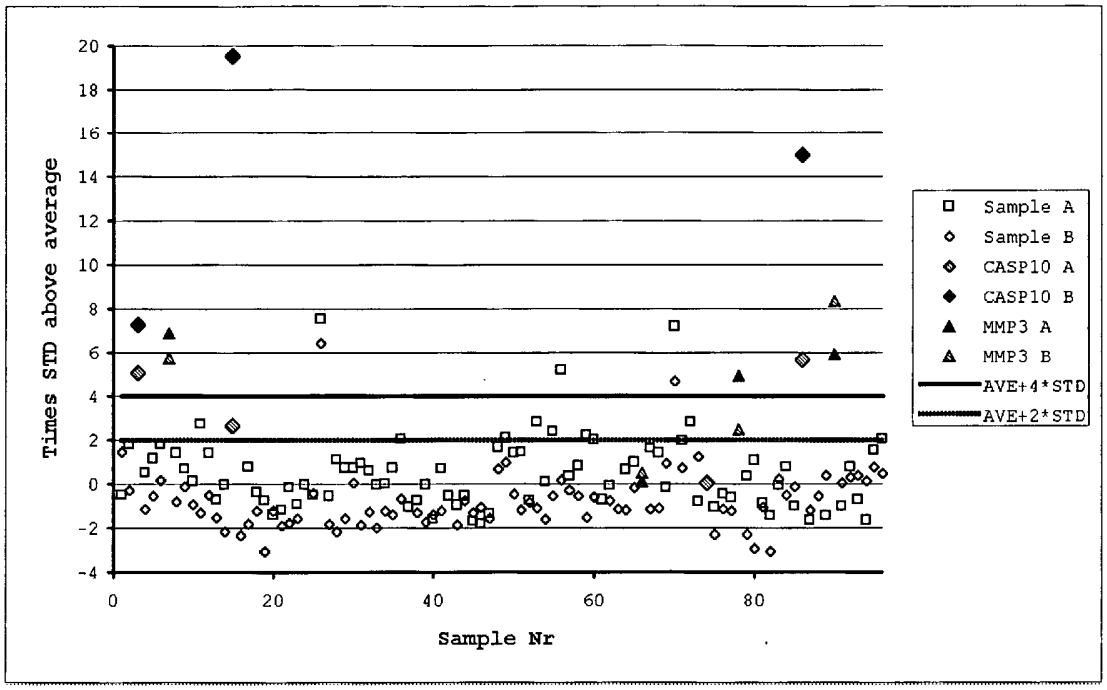

Times STD above average
20
18
16
14
12
10
8
6
4
2
0
-2
-4
0
20
40
60
80
Sample Nr
Sample A
Sample B
CASP10 A
CASP10 B
MMP3 A
MMP3 B
AVE+4*STD
AVE+2*STD

Figure 10

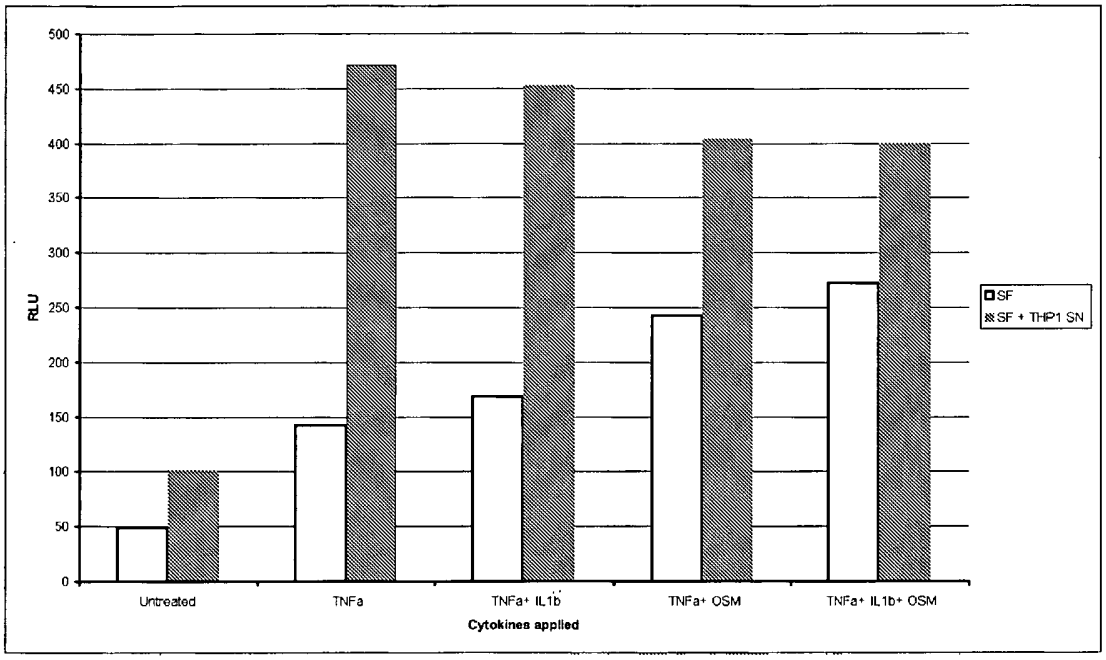

500
450
400
350
300
250
200
150
100
50
0
RLU
Untreated
TNFa
TNFa+ IL1b
TNFa+ OSM
TNFa+ IL1b+ OSM
Cytokines applied
SF
SF + THP1 SN

Figure 11

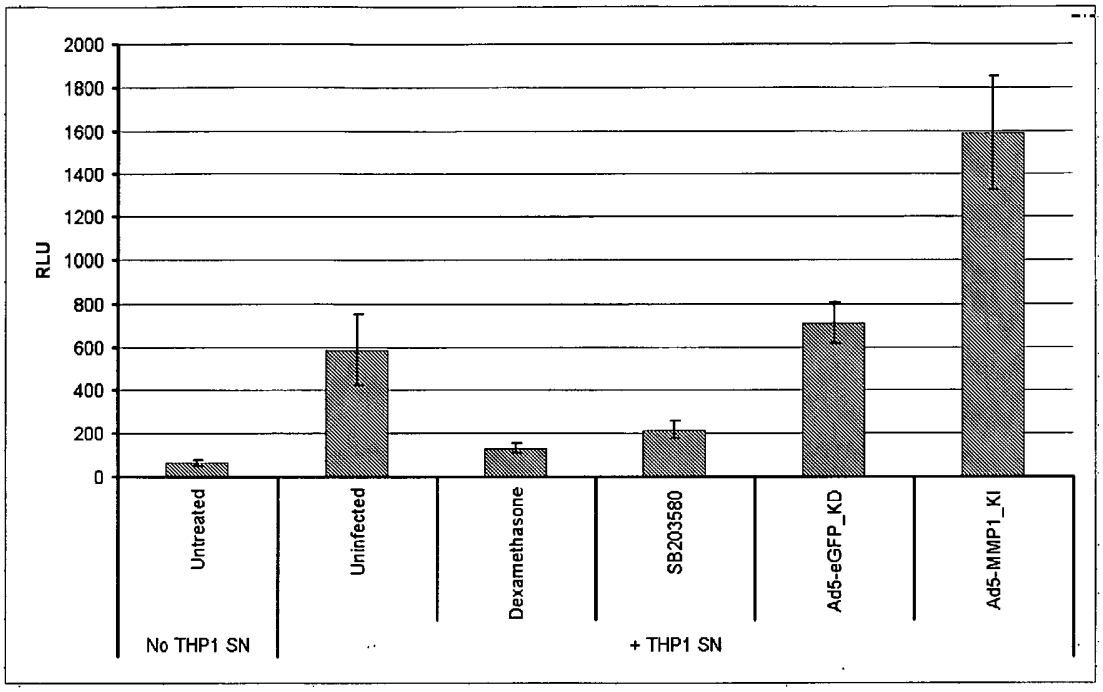

2000
1800
1600
1400
1200
1000
800
600
400
200
0
RLU
Untreated
Uninfected
Dexamethasone
SB203580
Ad5-eGFP_KD
Ad5-MMP1_KI
No THP1 SN
+ THP1 SN

Figure 12

Ad-siRNA mediated reduction in the expression of various target genes in SF's reduces the capacity of these cells to express MMP1 as a response to cytokines.

Figure 12 A

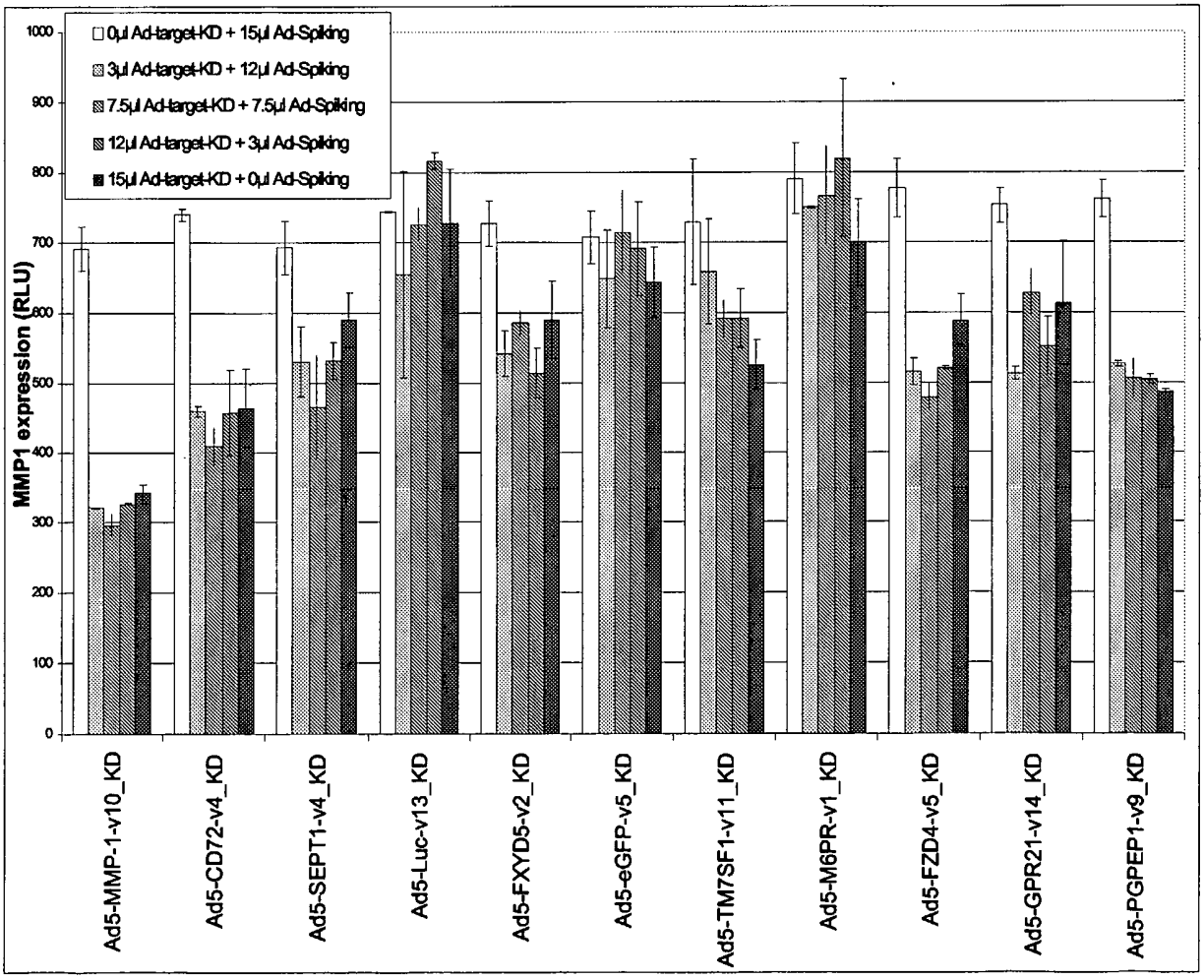


Figure 12 B

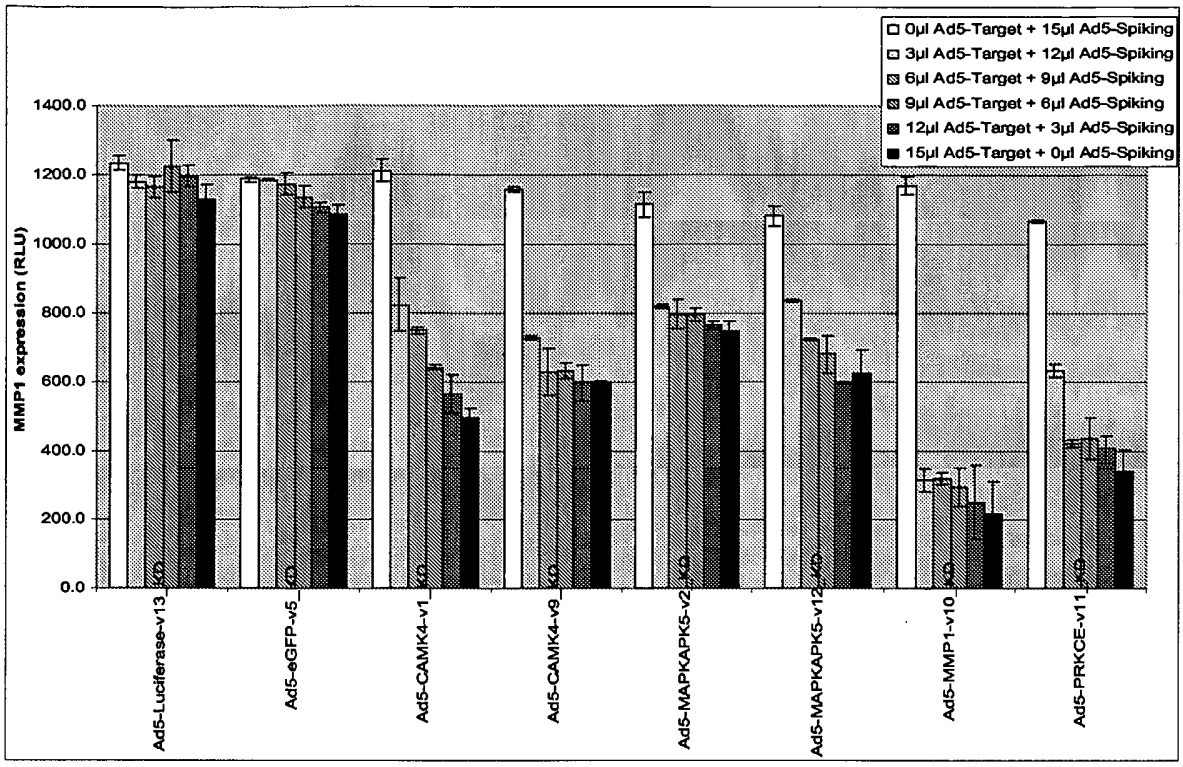


Figure 12 C

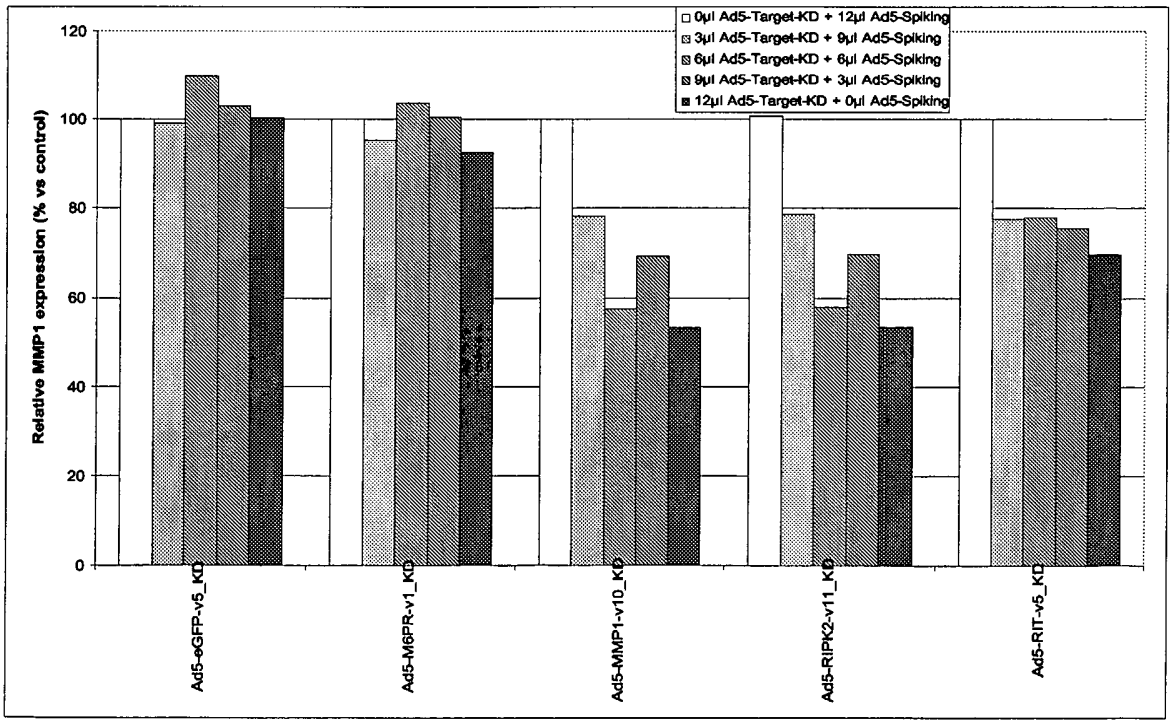


Figure 12 D

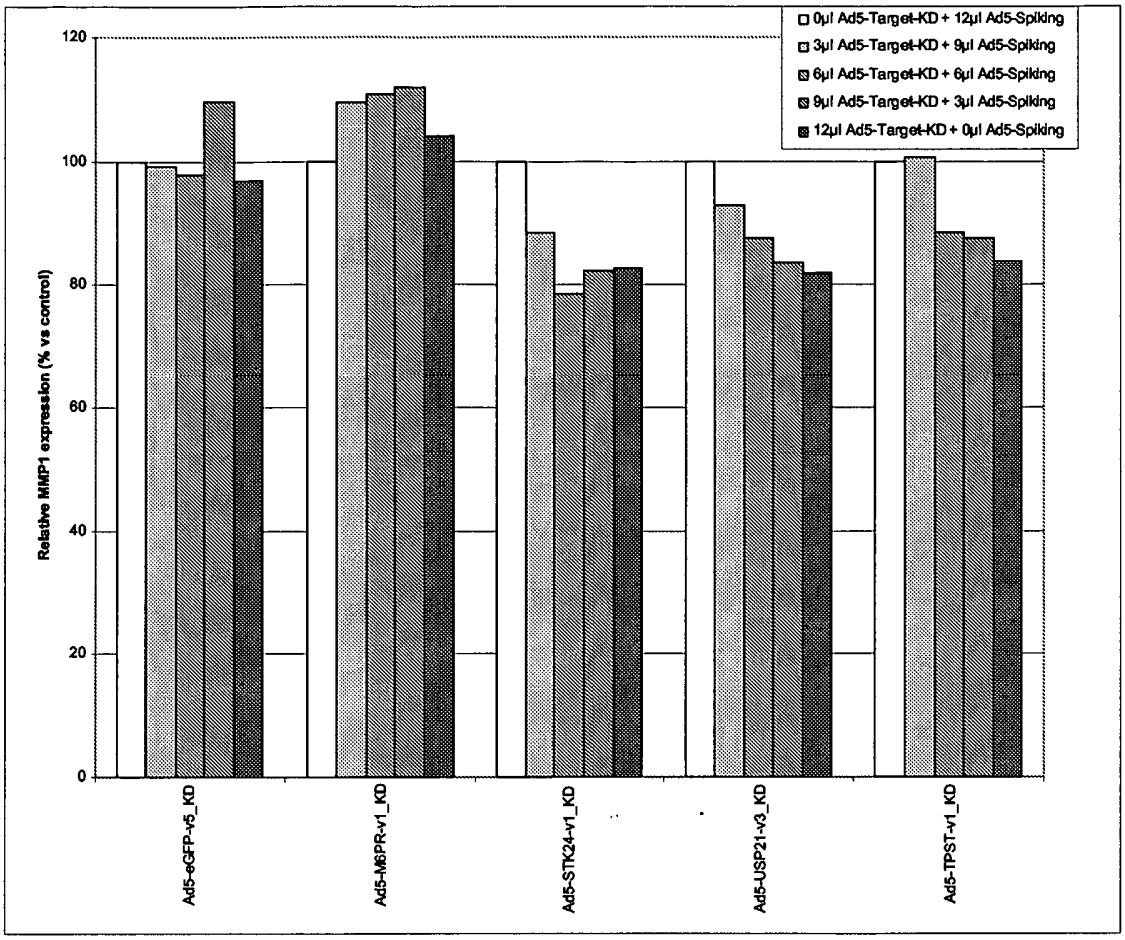

0µl Ad5-Target-KD + 12µl Ad5-Spiking
3µl Ad5-Target-KD + 9µl Ad5-Spiking
6µl Ad5-Target-KD + 6µl Ad5-Spiking
9µl Ad5-Target-KD + 3µl Ad5-Spiking
12µl Ad5-Target-KD + 0µl Ad5-Spiking
Relative MMP1 expression (% vs control)
120
100
80
60
40
20
0
Ad5-eGFP-v5_KD
Ad5-M6PR-v1_KD
Ad5-STK24-v1_KD
Ad5-USP21-v3_KD
Ad5-TPST-v1_KD

Figure 13

Recombinant adenovirus-driven expression of various target genes in primary human SFs induces MMP1 expression

Figure 13 A

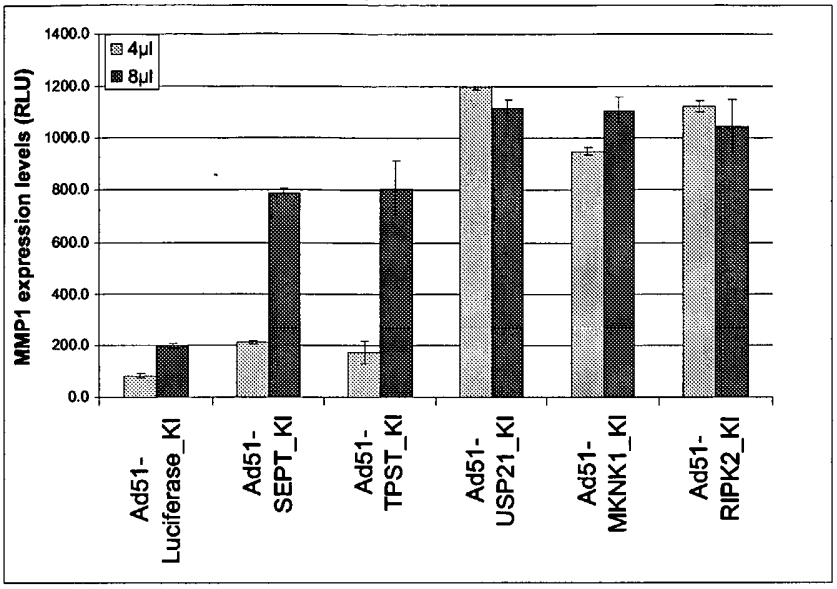


Figure 13 B

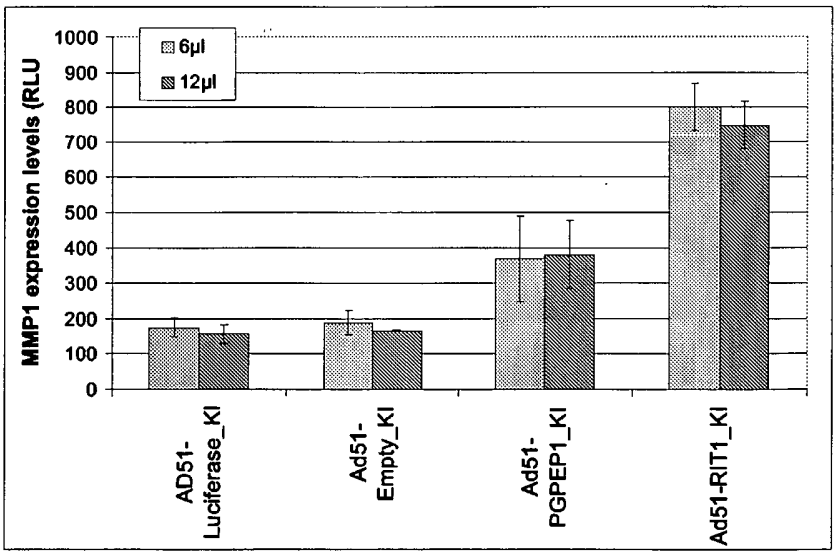


Figure 13 C

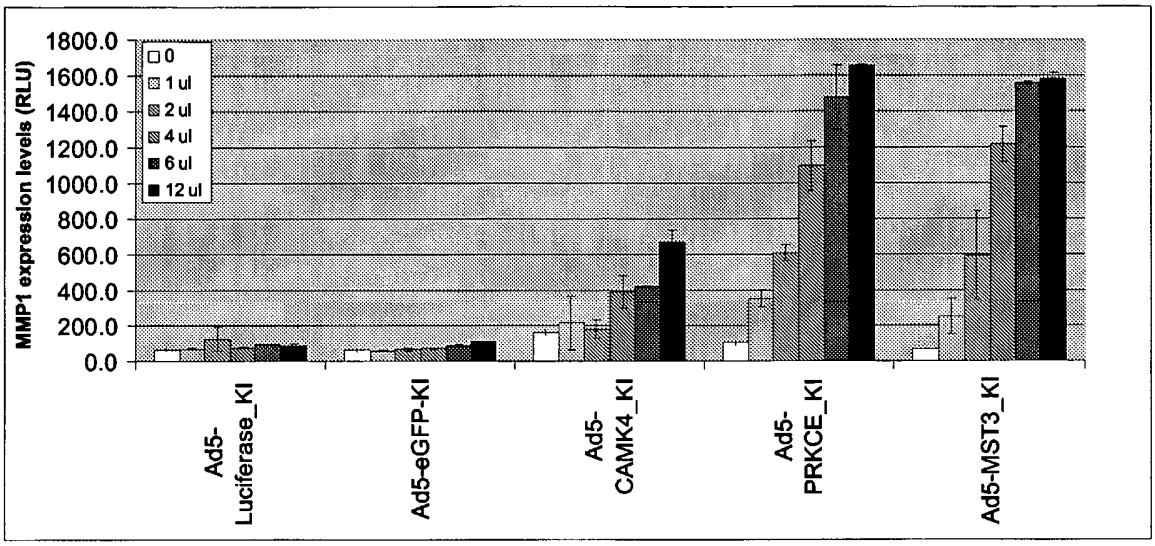


Figure 13 D

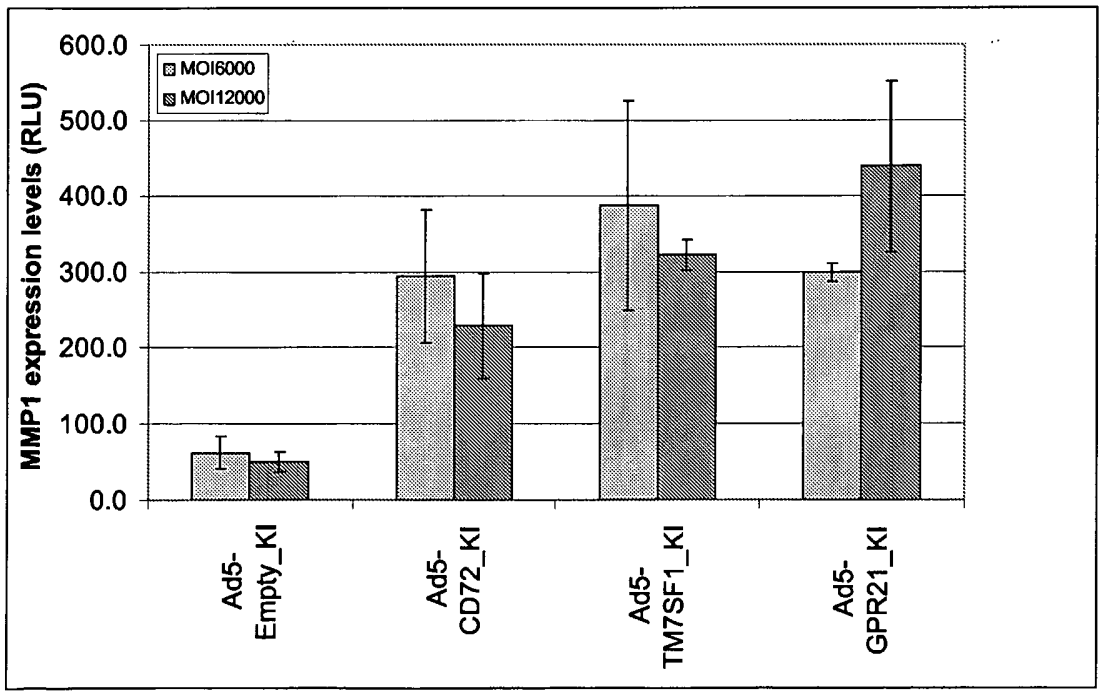


Figure 14

Reduction, at the protein level, of the expression of MAPKAPK5, PRKCE and CAMK4 by infection of the cells with various Ad-siRNA viruses targeting these genes.

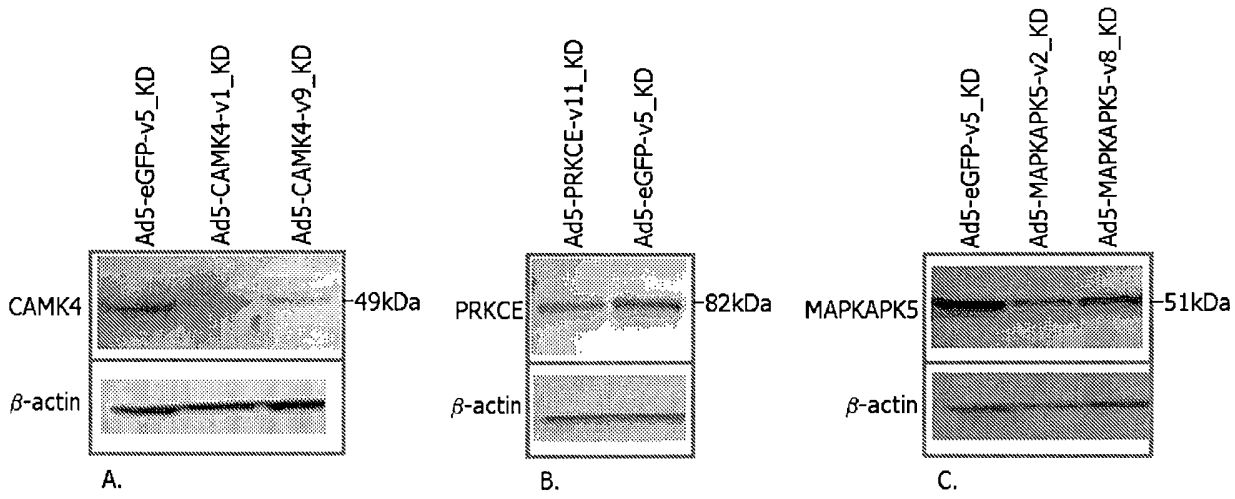


Figure 15

Ad-siRNA Mediated Reduction in the Expression of MAPKAPK5 or CAMK4 in SFs Reduces the Capacity of these Cells to Degrade Native Collagen as a Response to Cytokines.

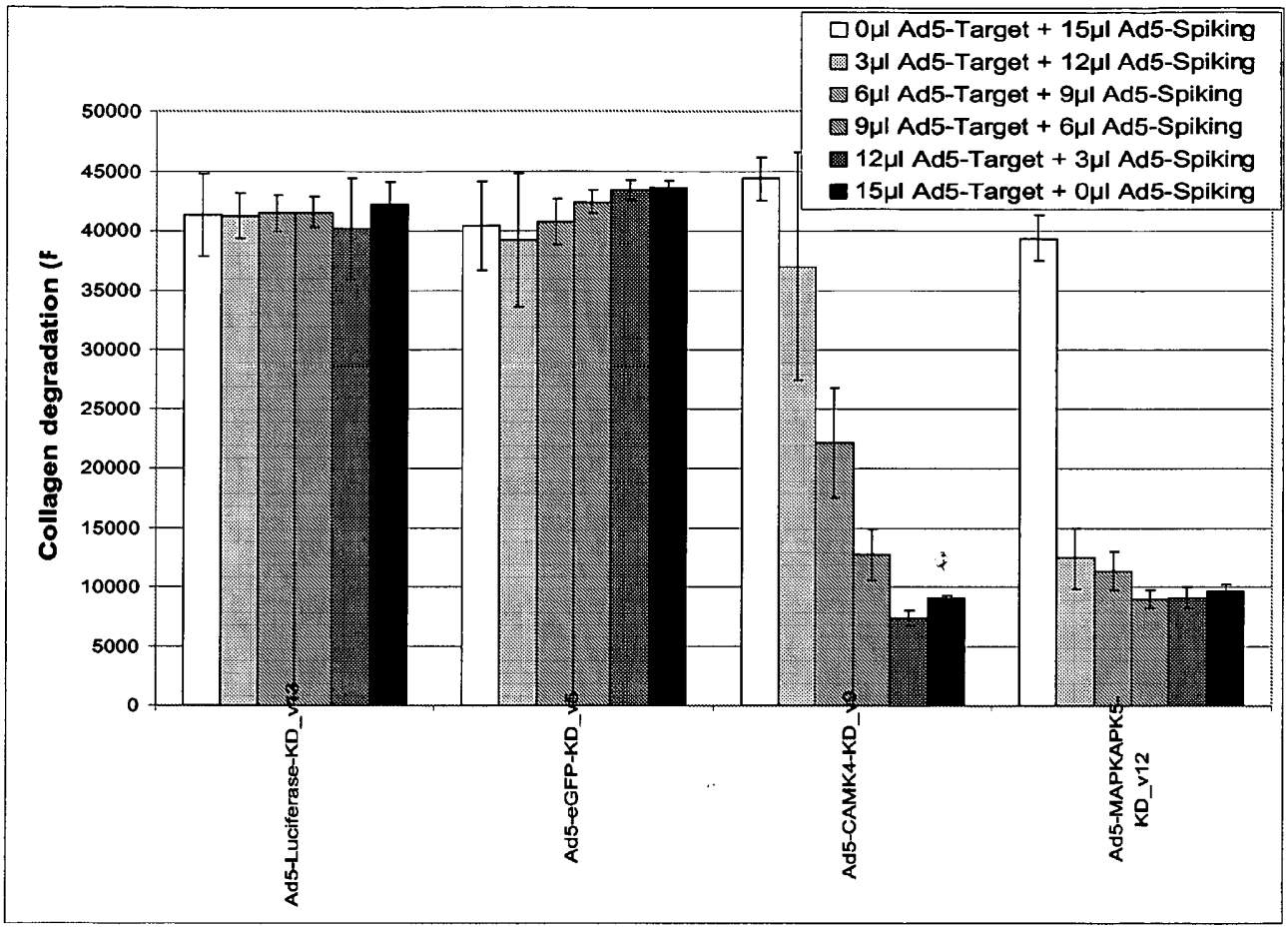
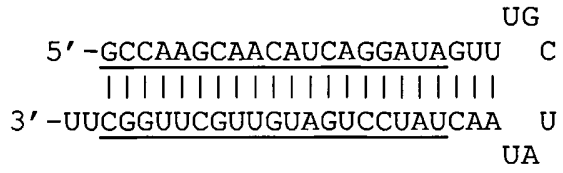


Figure 16

shRNA Constructed from KD Target sequence for RIPK2:



Written linearly:
5′-GCCAAGCAACAUCAGGAUAGUUUGCUAUAACUAUCCUGAUGUUGCUUGGCUU-3′ (SEQ ID NO: 325)

Homologous to target sequence /Loop/ Antisense to target sequence

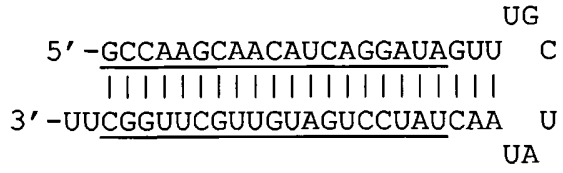
Homologous to target sequence: GCCAAGCAACAUCAGGAUA (SEQ ID NO: 326)

Loop region: UUGCUAUA (SEQ ID NO: 26)

Antisense to target sequence: UAUCCUGAUGUUGCUUGGC (SEQ ID NO: 327)

Figure 16

shRNA Constructed from KD Target sequence for RIPK2:



Written linearly:
5′-GCCAAGCAACAUCAGGAUAGUUUGCUAUAACUAUCCUGAUGUUGCUUGGCUU-3′ (SEQ ID NO: 325)

Homologous to target sequence /Loop/ Antisense to target sequence

Homologous to target sequence: GCCAAGCAACAUCAGGAUA (SEQ ID NO: 326)

Loop region: UUGCUAUA (SEQ ID NO: 26)

Antisense to target sequence: UAUCCUGAUGUUGCUUGGC (SEQ ID NO: 327)