



(86) **Date de dépôt PCT/PCT Filing Date:** 2014/07/04
(87) **Date publication PCT/PCT Publication Date:** 2015/01/08
(85) **Entrée phase nationale/National Entry:** 2016/01/04
(86) **N° demande PCT/PCT Application No.:** KR 2014/006033
(87) **N° publication PCT/PCT Publication No.:** 2015/002513
(30) **Priorité/Priority:** 2013/07/05 (KR10-2013-0079311)

(51) **Cl.Int./Int.Cl. C12N 15/113** (2010.01),
A61K 48/00 (2006.01), **A61P 11/00** (2006.01),
C07H 21/02 (2006.01)

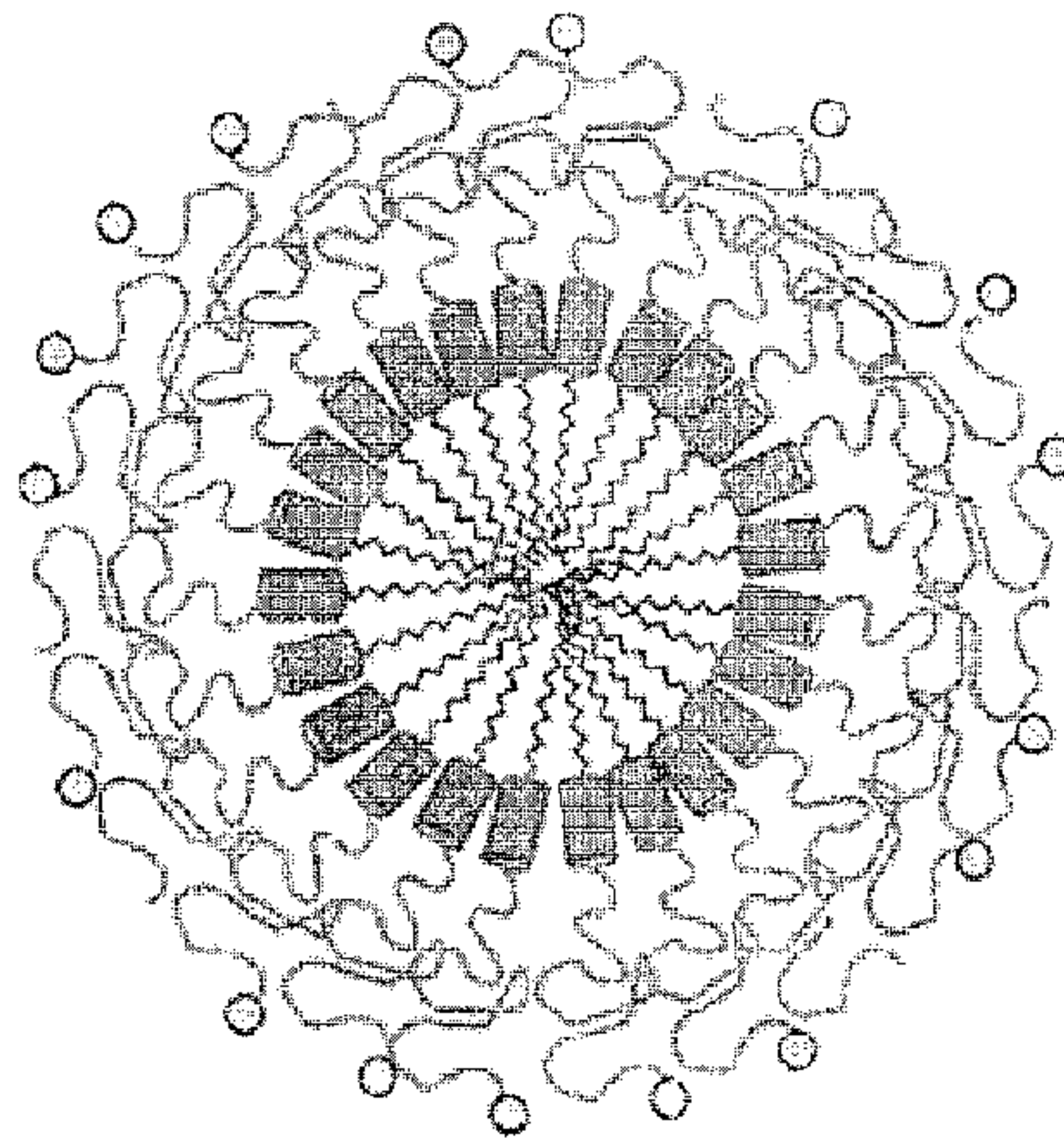
(71) **Demandeurs/Applicants:**
BIONEER CORPORATION, KR;
YUHAN CORPORATION, KR

(72) **Inventeurs/Inventors:**
CHAE, JEIWOOK, KR;
PARK, HAN OH, KR;
YOON, PYOUNG OH, KR;
HAN, BORAM, KR;
KIM, MI NA, KR

(74) **Agent:** NEXUS LAW GROUP LLP

(54) **Titre : ARNSI SPECIFIQUE DU GENE ASSOCIE A UNE MALADIE RESPIRATOIRE, STRUCTURE OLIGO-ARN DOUBLE HELICE
CONTENANT L'ARNSI, COMPOSITION CONTENANT CETTE STRUCTURE POUR PREVENIR OU TRAITER UNE MALADIE
RESPIRATOIRE**

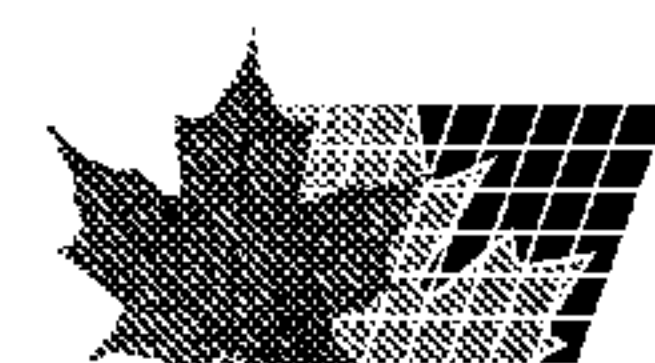
(54) **Title: RESPIRATORY DISEASE-RELATED GENE SPECIFIC SIRNA, DOUBLE-HELICAL OLIGO RNA STRUCTURE
CONTAINING SIRNA, COMPOSITON CONTAINING SAME FOR PREVENTING OR TREATING RESPIRATORY DISEASE**



: Oligonucleotide structure
: Hydrophobic Material
: Oligonucleotide
: Hydrophilic Material
○ : Target-Oriented Ligand

(57) **Abrégé/Abstract:**

The present invention relates to respiratory diseases, especially to gene specific siRNA related to idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease (COPD), and a highly efficient double-helical oligo RNA structure containing the same, wherein the double-helical oligo RNA structure has a structure in which hydrophilic and hydrophobic materials are bonded at the both ends of the double-helical RNA (siRNA) using a simple covalent bond or a linker-mediated covalent bond to be effectively transferred into a cell, and is converted into nanoparticles by the hydrophobic interaction of the double-helical oligo RNA structure in a solution. It is desirable that the siRNA contained in the double-helical oligo RNA structure is a siRNA specific to a CTGF, Cyr61, or Plekho1, which are genes related to respiratory diseases, particularly idiopathic pulmonary fibrosis and COPD. In addition, the present invention relates to a method for producing the double-helical oligo RNA structure and a pharmaceutical composition containing the double-helical oligo RNA structure for preventing or treating respiratory diseases, particularly idiopathic pulmonary fibrosis and COPD.



(12) 특허협력조약에 의하여 공개된 국제출원

(19) 세계지식재산권기구
국제사무국(43) 국제공개일
2015년 1월 8일 (08.01.2015)(10) 국제공개번호
WO 2015/002513 A3

- (51) 국제특허분류:
C12N 15/113 (2010.01) A61K 48/00 (2006.01)
C07H 21/02 (2006.01) A61P 11/00 (2006.01)
- (21) 국제출원번호: PCT/KR2014/006033
- (22) 국제출원일: 2014년 7월 4일 (04.07.2014)
- (25) 출원언어: 한국어
- (26) 공개언어: 한국어
- (30) 우선권정보:
10-2013-0079311 2013년 7월 5일 (05.07.2013) KR
- (71) 출원인: (주)바이오니아 (BIONEER CORPORATION)
[KR/KR]; 306-220 대전시 대덕구 문평서로 8-11, Daejeon (KR).
- (72) 발명자: 채제욱 (CHAE, Jeiwook); 305-761 대전시 유성구 엑스포로 448 엑스포아파트 104-201, Daejeon (KR). 박한오 (PARK, Han Oh); 305-761 대전시 유성구 엑스포로 448 엑스포아파트 208-601, Daejeon (KR). 윤평오 (YOON, Pyoung Oh); 305-751 대전시 유성구 구죽로 25 송강그린아파트 306-1205, Daejeon (KR). 한보람 (HAN, Boram); 422-753 경기도 부천시 소사구 범안로 95 번길 32 부천범박힐스테이트 3단지 아파트 310-1204, Gyeonggi-do (KR). 김미나 (KIM, Mi Na); 305-770 대전시 유성구 노은서로 210 번길 32 열매마을 4단지 아파트 401-402, Daejeon (KR).

- (74) 대리인: 이처영 (LEE, Cheo Young) 등; 135-748 서울시 강남구 테헤란로 123 (여삼빌딩 11층), Seoul (KR).
- (81) 지정국 (별도의 표시가 없는 한, 가능한 모든 종류의 국내 권리의 보호를 위하여): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.
- (84) 지정국 (별도의 표시가 없는 한, 가능한 모든 종류의 역내 권리의 보호를 위하여): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), 유라시아 (AM, AZ, BY, KG, KZ, RU, TJ, TM), 유럽 (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

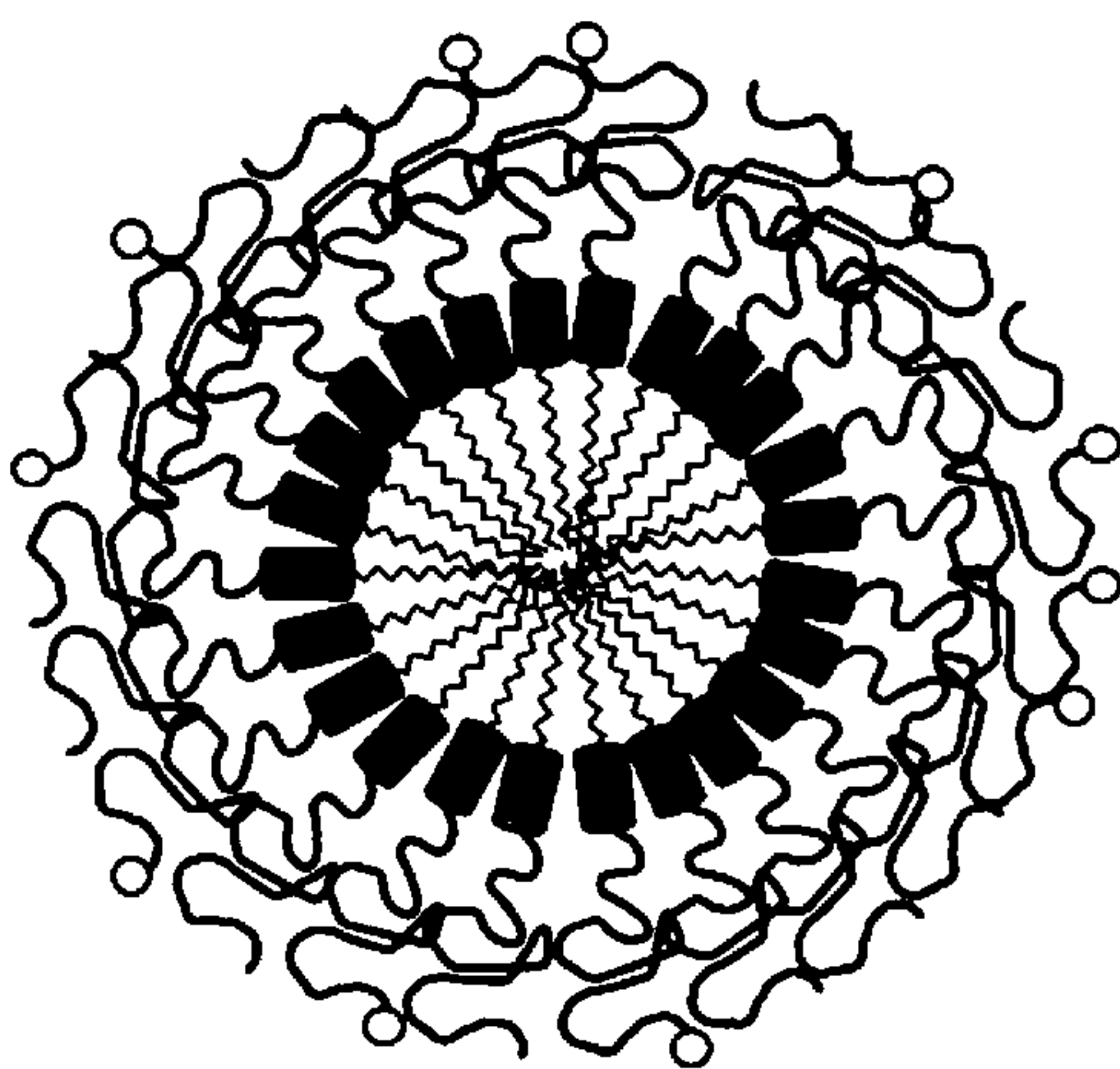
공개:

— 국제조사보고서와 함께 (조약 제 21 조(3))

[다음 쪽 계속]

(54) Title: RESPIRATORY DISEASE-RELATED GENE SPECIFIC SIRNA, DOUBLE-HELICAL OLIGO RNA STRUCTURE CONTAINING SIRNA, COMPOSITON CONTAINING SAME FOR PREVENTING OR TREATING RESPIRATORY DISEASE

(54) 발명의 명칭: 호흡기 질환 연관 유전자 특이적 siRNA, 그러한 siRNA를 포함하는 이중나선 올리고 RNA 구조체 및 이를 포함하는 호흡기 질환 예방 또는 치료용 조성물



AA ... 올리고뉴클레오타이드 구조체
BB ... 소수성 물질
CC ... 올리고뉴클레오타이드
DD ... 친수성 고분자 물질
EE ... 표적지향 리간드

AA ... Oligonucleotide structure
BB ... Hydrophobic material
CC ... Oligonucleotide
DD ... Hydrophilic polymer material
EE ... Target-oriented ligand

(57) Abstract: The present invention relates to respiratory diseases, especially to gene specific siRNA related to idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease (COPD), and a highly efficient double-helical oligo RNA structure containing the same, wherein the double-helical oligo RNA structure has a structure in which hydrophilic and hydrophobic materials are bonded at the both ends of the double-helical RNA (siRNA) using a simple covalent bond or a linker-mediated covalent bond to be effectively transferred into a cell, and is converted into nanoparticles by the hydrophobic interaction of the double-helical oligo RNA structure in a solution. It is desirable that the siRNA contained in the double-helical oligo RNA structure is a siRNA specific to a CTGF, Cyr61, or Plekho1, which are genes related to respiratory diseases, particularly idiopathic pulmonary fibrosis and COPD. In addition, the present invention relates to a method for producing the double-helical oligo RNA structure and a pharmaceutical composition containing the double-helical oligo RNA structure for preventing or treating respiratory diseases, particularly idiopathic pulmonary fibrosis and COPD.

(57) 요약서:

[다음 쪽 계속]

WO 2015/002513 A3

WO 2015/002513 A3



- 청구범위 보정 기한 만료 전의 공개이며, 보정서를 접수하는 경우 그에 관하여 별도 공개함 (규칙 48.2(h))

— 명세서의 서열목록 부분과 함께 (규칙 5.2(a))
- (88) 국제조사보고서 공개일:

2015년 3월 5일

본 발명은 호흡기 질환, 특히 특발성폐섬유화증 및 만성폐쇄성폐질환(COPD) 연관 유전자 특이적 siRNA 및 이를 포함하는 고효율 이중나선 올리고 RNA 구조체에 관한 것으로, 상기 이중나선 올리고 RNA 구조체는 세포 내로 효율적으로 전달되도록 하기 위하여 이중나선 RNA(siRNA)의 양 말단에 친수성 물질 및 소수성 물질을 단순 공유결합 또는 링커-매개(linker-mediated) 공유결합을 이용하여 접합된 형태의 구조를 가지며, 수용액에서 상기 이중나선 올리고 RNA 구조체들의 소수성 상호작용에 의해 나노입자 형태로 전환될 수 있다. 상기 이중나선 올리고 RNA 구조체에 포함된 siRNA는 호흡기 질환, 특히 특발성폐섬유화증 및 COPD 연관 유전자인 CTGF, Cyr61 또는 Plekho1 특이적 siRNA인 것이 바람직하다. 또한 본 발명은 상기 이중나선 올리고 RNA 구조체의 제조방법 및 상기 이중나선 올리고 RNA 구조체를 포함하는 호흡기 질환, 특히 특발성폐섬유화증 및 COPD를 예방 또는 치료하기 위한 약제학적 조성물에 관한 것이다.

RESPIRATORY DISEASE-RELATED GENE SPECIFIC siRNA,
DOUBLE-HELICAL OLIGO RNA STRUCTURE CONTAINING siRNA,
COMPOSITON CONTAINING SAME FOR PREVENTING OR TREATING
RESPIRATORY DISEASE

5

Technical Field

The present invention relates to a respiratory disease-related gene-specific siRNA and a high efficient structure comprising double helical-oligo RNA ('double
10 helical-oligo RNA structure') containing the siRNA. The double helical-oligo RNA structure has a structure in which a hydrophilic material and a hydrophobic material are conjugated to both ends of double helical RNA (siRNA) by using a simple covalent bond or a linker-mediated covalent
15 bond so as to be effectively delivered into cells, wherein the structure may be converted into a nanoparticle form by hydrophobic interactions of the double helical-oligo RNA structures in an aqueous solution. The siRNA included in the double helical-oligo RNA structure is preferably a
20 siRNA specific to CTGF, Cyr61, or Plekhol (hereinafter, referred to as a CTGF, Cyr61 or Plekhol-specific siRNA), which is a gene related with respiratory diseases, particularly, idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease (COPD).

25 Further, the present invention relates to a method for producing the double-helical oligo RNA structure and a pharmaceutical composition containing the double-helical

oligo RNA structure for preventing or treating respiratory diseases, particularly, idiopathic pulmonary fibrosis and COPD.

5

Background Art

Technologies for inhibiting gene expression are important tools in the development of a therapeutic agent and target validation for treating diseases. Among the technologies, since a role of an RNA interference
10 (hereinafter, referred to as 'RNAi') had been found, it was found that the RNA interference acts on a sequence-specific mRNA in various kinds of mammalian cells (Silence of the transcripts: RNA interference in medicine. J. Mol. Med. (2005) 83: 764-773). When a long-chain double-stranded RNA
15 is delivered into a cell, the delivered double-stranded RNA is converted into a small interfering RNA (hereinafter, referred to as 'siRNA') which is processed to 21 to 23 base pairs (bp) by Dicer endonuclease. siRNA is bonded to an RNA-induced silencing complex (RISC), whereby a guide
20 (antisense) strand recognizes and decomposes a target mRNA to sequence-specifically inhibit expression of a target gene (NUCLEIC-ACID THERAPEUTICS: BASIC PRINCIPLES AND RECENT APPLICATIONS. Nature Reviews Drug Discovery. 2002. 1, 503-514).

25

Bertrand et al., found that as compared to an antisense oligonucleotide (ASO) on the same target gene, siRNA has an effect of significantly inhibiting mRNA

expression in vitro and in vivo, and the corresponding effect is maintained for a long time (Comparison of antisense oligonucleotides and siRNAs in cell culture and in vivo. Biochem. Biophys. Res. Commun. 2002. 296: 1000-
5 1004). In addition, since siRNA is complementarily coupled to a target mRNA to sequence-specifically regulate an expression of the target gene, a mechanism of the siRNA has an advantage in that a target to be applicable may be remarkably increased as compared to the existing antibody-
10 based medical product or chemical pharmaceuticals (small molecular drug) (Progress Towards in Vivo Use of siRNAs. MOLECULAR THERAPY. 2006 13(4):664-670).

In order to develop the siRNA as a therapeutic agent even with excellent effect and variously usable range of
15 the siRNA, the siRNA needs to be effectively delivered to a target cell with improved stability and a more efficient cell delivery of the siRNA (Harnessing In Vivo siRNA Delivery for Drug Discovery and Therapeutic Development. Drug Discov. Today. 2006 Jan; 11(1-2):67-73.

20 In order to solve the problems, research into modification of some nucleotides or backbone of siRNA to have a nucleic acid lyase resistance, or use of carriers such as viral vectors, liposomes or nanoparticles, etc. for improving stability in vivo, has been actively attempted.

25 Delivery systems using viral vectors such as adenovirus, retrovirus, etc, have high transfection efficacy, and also have high immunogenicity and

oncogenicity. Meanwhile, a non-viral delivery system including nanoparticles has a low cell delivery efficiency as compared to the viral delivery system, but has high stability in vivo and is possible to be target-specifically delivered, has highly improved delivery effects such as uptake, internalization, etc., of RNAi oligonucleotide into cells or tissues, and rarely has cytotoxicity and immune stimulation, such that the non-viral delivery system is currently evaluated as a viable delivery method as compared to the viral delivery systems (Nonviral delivery of synthetic siRNA *s in vivo*. J Clin Invest. 2007 December 3; 117(12): 3623-3632).

In a method using a nanocarrier in the non-viral delivery systems, various polymers such as liposomes, cationic polymer composites, etc., are used to form nanoparticles, and a siRNA is supported on the nanoparticles, that is, nanocarrier, to be delivered into the cells. Among the methods using nanocarriers, a method using polymeric nanoparticle, polymer micelle, lipoplex, or the like, is mainly used, wherein the lipoplex consists of cationic lipid to interact with anionic lipid of endosome of a cell, thereby eliciting a destabilization effect of the endosome to deliver the siRNA into a cell (Proc. Natl. Acad. Sci. 15; 93(21):11493-8, 1996).

In addition, it is known that chemical materials, etc., are connected to end portions of a siRNA passenger (sense) strand to provide promoted pharmacokinetics

characteristics, such that high efficacy may be induced in vivo (Nature 11; 432(7014):173-8, 2004). Here, stability of the siRNA may vary depending on properties of the chemical materials bonded to ends of the siRNA sense (passenger) or antisense (guide) strand. For example, a siRNA to which a polymer compound such as polyethylene glycol (PEG) is conjugated, interacts with an anionic phosphate group of siRNA in the presence of cationic materials to form a complex, thereby being a carrier having an improved siRNA stability (J. Control Release 129(2):107-16, 2008). In particular, micelle consisting of polymer complexes has an extremely small size, significantly uniform distribution, and is spontaneously form, thereby being easy to manage quality of formulation and secure reproducibility, as compared to other systems used as a drug delivery vehicle, such as microsphere, nanoparticle, etc.

Further, in order to improve an intracellular delivery efficiency of siRNA, technology of using a siRNA conjugate in which hydrophilic material which is a biocompatible polymer (for example, polyethylene glycol (PEG)) is conjugated to the siRNA by a simple covalent bond or a linker-mediated covalent bond, to thereby secure stability of siRNA and have effective cell membrane permeability was developed (see Korean Patent Publication No. 883471). However, the chemical modification of the siRNA and the conjugation with the polyethylene glycol (PEG) (PEGylation) still have disadvantages that stability

in vivo is low and delivery into a target organ is not smooth. In order to solve the disadvantages, a double-helical oligo RNA structure in which a hydrophilic material and a hydrophobic material are bonded to oligonucleotides, in particular, double helical RNA such as siRNA, was developed, wherein the double-helical oligo RNA structure forms a self assembled nanoparticle named a self assembled micelle inhibitory RNA (SAMITMRNA) by a hydrophobic interaction of a hydrophobic material (see Korean Patent Publication No. 1224828), the SAMITMRNA technology has an advantage in that homogenous nanoparticles having a significantly small size are capable of being obtained as compared to the existing delivery technologies.

As a specific example of the SAMITMRNA technology, PEG (polyethylene glycol) is used as a hydrophilic material, wherein PEG is synthetic polymer, which is used for increasing solubility of pharmaceuticals, particularly, protein, and for controlling pharmacokinetics. PEG is a polydisperse material, a polymer in one batch consists of the sum of different number of monomers, a molecular weight is shown in the Gaussian curve, and polydispersity values (M_w/M_n) express the homogeneity degree of a material. That is, when PEG has a low molecular weight (3 to 5 kDa), the polydisperse value is about 1.01, and when PEG has a high molecular weight (20 kDa), the polydisperse value is about 1.2, which is high, such that as the molecular weight is higher, the homogeneity of the material is relatively low

(F. M. Veronese. Peptide and protein PEGylation: a review of problems and solutions. Biomaterials (2001) 22:405-417). Accordingly, when the PEG is combined to the pharmaceuticals, polydispersed characteristic of PEG is reflected on the conjugate, such that it is not easy to perform verification of single material, and accordingly, production of materials having a low polydisperse value through synthesis of PEG and improvement of purification processes is on a rising trend, but has still problems due to polydispersed characteristic of the material, particularly, when PEG is combined to a material having a small molecular weight, there is difficult in confirming whether or not the combination is easily performed, etc. (Francesco M. Veronese and Gianfranco Pasut. PEGylation, successful approach to drug delivery. DRUG DISCOVERY TODAY (2005) 10(21):1451-1458).

Accordingly, recently, as an improved technology of SAMiRNA™ which is the existing self-assembled nanoparticles, a technology of a new form of carrier having a significantly small size as compared to the existing SAMiRNA™ and remarkably improved polydispersity has been developed by blocking the hydrophilic material of the double helical RNA structure configuring SAMiRNA™ as a base unit including 1 to 15 uniform monomers having a predetermined molecular weight and a linker as needed, and using the appropriate number of blocked hydrophilic materials as needed.

Meanwhile, since biopharmaceuticals specifically act to a target gene sequence or a protein structure, in order to evaluate the efficacy and safety in a non-clinical surrogate model, a material acting with the same mechanism
5 as the corresponding biopharmaceuticals in human is additionally required even in species of the surrogate model. Therefore, in order to avoid difficulty in additionally finding the material including the same mechanism as human, a material acting with the same
10 mechanism both in human (treatment target) in the mouse (the non-clinical surrogate model), is required to be developed.

Idiopathic Pulmonary Fibrosis (hereinafter, abbreviated as 'IPF') is a disease in which chronic
15 inflammatory cells penetrate into a wall of an alveolar wall (lung alveolus) to make the lung become hard, causing severe structural change in lung tissue, such that lung function is gradually reduced to induce death. However, an effective treatment thereof does not exist yet, and
20 Idiopathic Pulmonary Fibrosis is generally diagnosed when symptoms appear at last, and has extremely bad prognosis since a median survival time is only about three to five years. It is reported that the incidence frequency of the foreign countries is about 3-5 people per 100,000, and it
25 is known that the incidence is generally high after the age of 50, and men have a two-times higher incidence than women.

The cause of IPF has not been clearly identified yet,

and it is merely reported that high frequency is shown in smokers, antidepressants, chronic pulmonary inhalation due to gastroesophageal reflux, metal dust, wood dust, solvent inhalation, etc., are regarded as risk factors related with
5 IPF occurrence. However, definitive causal factors cannot be found in the majority of patients.

It is known that IPF is continuously worsen with no treatment, and about 50% of patients die within 3-5 years, and once a lung is completely hardened by fibrosis as the
10 disease progresses, there is no improvement despite any treatment, and accordingly, it is predicted that an early treatment increases efficacy. As the currently used therapeutic agent, a combination therapy method using steroid and azathioprine or cyclophosphamide, has been
15 known, but it is difficult to say that there are special effects, and attempts of several fibrosis inhibitors in animal experiments and small group of patients failed in proving clear effects. In particular, there is no other effective treatment in patients with end-stage IPF, in
20 addition to lung transplantation. Therefore, development of more effective therapeutic agent against IPF is desperately required.

Meanwhile, COPD, one of representative lung diseases together with asthma, is different from asthma in that it
25 is accompanied by irreversible airway obstruction, and is a respiratory disease which is accompanied by abnormal inflammatory response of lung caused by repeated infection,

harmful particles, gas inlet or smoking, and is not fully reversible, but shows increasingly progressed airflow limitation (Pauwels et al, *Am J Respir Crit Care Med*, 163:1256-1276, 2001). COPD is a disease caused by
5 pathological changes of bronchioles and lung parenchyma by airway and lung parenchyma inflammation, and is characterized by obstructive bronchiolitis and emphysema (destruction of lung parenchyma). Types of COPD include chronic obstructive bronchitis, chronic bronchiolitis and
10 emphysema. In COPD, the number of neutrophils is increased, and secretion of cytokines such as GM-CSF, TNF- α , IL-8, and MIP-2 is increased. Further, airway inflammation, a thickened muscle wall, and bronchial closure due to increased mucus secretion are also shown. When bronchus is
15 closed, alveoli are expanded and damaged, such that an exchange ability of oxygen and carbon dioxide is damaged to increase respiratory failure.

The severity of COPD is emerging around the world since it is predicted that COPD ranked 6th in 1990 among
20 causes of death due to disease, but will rank in third place in 2020, and is the only disease of which the incidence is increased in 10 diseases. COPD has a high prevalence rate, causes a respiratory disorder, and requires a large amount of direct medical costs required
25 for diagnosis and treatment of COPD, and a significant amount of indirect expenses such as losses due to dyspnea and leave of absence or loss due to premature death, which

is a social and economic problem in the world (Chronic obstructive pulmonary disease (COPD) treatment guidelines 2005. Chronic obstructive airway disease Clinical Research Center. p.30-31).

5 Existing therapeutic drugs have not been confirmed as relieving reduction in long time lung function which is a characteristic of COPD. Accordingly, drug treatment in COPD has a main purpose of reducing symptoms or complications. Among the therapeutic drugs, a bronchodilator is a typical
10 COPD allopathic drug, and an anti-inflammatory drug or corticosteroid is usually prescribed, but the effect is not significant, the application range is narrow, and there is great concern for side effects. As other drugs, it is known that only the influenza vaccine reduces serious symptoms
15 and death by about 50% in patients with COPD (chronic obstructive pulmonary disease (COPD) treatment guidelines 2005. Chronic obstructive airway disease Clinical Research Center. p.52-58).

Meanwhile, many genetic factors are estimated as
20 increasing (or decreasing) the risk of individual COPD. A genetic risk factor which has been demonstrated so far is genetic deficiency of α 1-antitrypsin. Smoking significantly increases the risk of COPD, but occurrence of panlobular emphysema and reduction in lung function that rapidly
25 progress at a young age are shown by both of smokers and non-smokers having significant genetic deficiency. Although other genes confirmed to be related with the COPD

pathogenesis do not exist yet in addition to α 1-antitrypsin, attempt for identifying biomarkers of the disease to be utilized for diagnosis through research into cellular, molecular, and genetic abnormal states that are basically shown in patients with COPD or attempt for finding a new treatment method is being progressed (P.J. Barnes and R.A. Stockely. COPD: current therapeutic interventions and future approaches. Eur Respir J. (2005) 25:1084-1106). In particular, research into diagnosis of COPD and selection of target for treatment through methods such as gene microarray, proteomics, etc., has been actively conducted, and analyses of genetic factors for obtaining COPD sensitivity (susceptibility) and causes of the worsen COPD symptoms induced by smoking have been mainly conducted (Peter J. Castaldi et al. The COPD genetic association compendium. Human Molecular Genetics, 2010, Vol. 19, No. 3 526-534).

CTGF (connective tissue growth factor; CCN2), which is one of matricellular proteins included in CCN family, is known to be a secretion cytokine involved in various biological processes such as cell adhesion, migration, proliferation, angiogenesis, wound repair, etc. Over-expression of CTGF is regarded as being main cause of symptoms such as scleroderma, fibrotic disease, and scar formation (Brigstock DR. Connective tissue growth factor (CCN2, CTGF) and organ fibrosis: lessons from transgenic animals. J Cell Commun Signal (2010) 4 (1): 1-4). In

particular, regarding fibrosis, CTGF is known to cause sustained fibrosis together with TGF- β (Transforming growth factor- β) or to promote production of ECM (extracellular matrix) under a condition in which fiber formation is
5 caused, and recently, it is known to be capable of treating ocular disorders or muscular dystrophy caused by abnormal expression of CTGF by treating samples or materials that hinder expression of CTGF or inhibiting action thereof, but relevancy with a respiratory disease has not been suggested
10 (U.S. Patent No. 7,622,454, and U.S Patent Application Publication No. 20120164151).

CYR61 (Cysteine-rich angiogenic inducer 61) is an extracellular matrix (ECM)-related signaling protein included in CCN family, which is known to control various
15 cellular activities such as cell adhesion, migration, proliferation, differentiation, apoptosis, etc. The purified CYR61 promotes attachment and spreading of endothelial cells in a similar manner to fibronectin, and does not have mitogenic activity, but acts to reinforce a
20 mitogen effect of a fibroblast growth factor (MARIA L. KIREEVA et al. Cyr61, a Product of a Growth Factor-Inducible Immediate-Early Gene, Promotes Cell Proliferation, Migration, and Adhesion. MOLECULAR AND CELLULAR BIOLOGY, Apr. 1996, p. 1326-1334).

25 It is reported that Plekhol (Pleckstrin homology domain-containing family O member 1) is present in a plasma membrane or nucleus, acts as a non-enzymatic regulator of

protein kinase CK2 α 1(Casein kinase 2, alpha 1), and is involved in apoptosis by inhibition of AP-1 action through C-terminal piece produced when being decomposed by Caspase 3 (Denis G. Bosc et al. Identification and Characterization of CKIP-1, a Novel Pleckstrin Homology Domain-containing Protein That Interacts with Protein Kinase CK2. The Journal of Biological Chemistry(2000) 275, 14295-14306; Lingqiang Zhang et al. Role for the pleckstrin homology domain containing protein CKIP-1 in AP-1 regulation and apoptosis. The EMBO Journal (2005) 24, 766-778).

As described above, prevalence of the respiratory diseases, particularly, idiopathic pulmonary fibrosis and COPD has increased, but therapeutic agents being capable of basically preventing and treating the idiopathic pulmonary fibrosis and COPD do not exist yet. Therefore, the demand for the therapeutic agent for the idiopathic pulmonary fibrosis and COPD showing high level of prevention and treatment effects without side effects is significantly largely present in the market.

20

DISCLOSURE OF INVENTION

An object of the present invention is to provide a novel siRNA specific to CTGF, Cyr61 or Plekhol (hereinafter, referred to as a CTGF, Cyr61 or Plekhol-specific siRNA), capable of inhibiting expression thereof at a significantly high efficiency, a double helical-oligo RNA structure containing the siRNA, and a method for producing the

double-helical oligo RNA structure.

Another object of the present invention is to provide a pharmaceutical composition including the CTGF, Cyr61 or Plekhol-specific siRNA or the double-helical oligo RNA
5 structure containing the siRNA as an effective component, for preventing or treating respiratory diseases, particularly, idiopathic pulmonary fibrosis and COPD.

Another object of the present invention is to provide a method for preventing or treating respiratory diseases,
10 particularly, idiopathic pulmonary fibrosis and COPD, by using the CTGF, Cyr61 or Plekhol-specific siRNA or the double-helical oligo RNA structure containing the siRNA.

BRIEF Description of THE Drawings

15 FIG. 1 is a schematic diagram of a nanoparticle formed of a double-helical oligo polymer structure according to the present invention.

FIG. 2 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a
20 human fibroblast cell line with siRNA having sequence of SEQ ID NOs: 1 to 10, 101 to 110, and 201 to 210 as a sense strand according to the present invention.

A : Graph showing CTGF expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ ID
25 NOs: 1 to 10 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ

ID NOs: 101 to 110 as a sense strand.

C : Graph showing Plekhol expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ ID NOs: 201 to 210 as a sense strand.

5 FIG. 3 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a human fibroblast cell line with siRNA having sequence of SEQ ID NO: 1, 3, 4, 8, 9, 10, 102, 104, 105, 106, 107, 108, 109, 204, 206, 207, 208, 209 or 210 as a sense strand
10 according to the present invention.

A : Graph showing CTGF expression amount according to treatment of 0.2 or 1 nM of siRNA having sequence of SEQ ID NO: 1, 3, 4, 8, 9 or 10 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 0.2 or 1 nM of siRNA having sequence of SEQ ID NO: 102, 104, 105, 106, 107, 108 or 109 as a sense strand.
15

C : Graph showing Plekhol expression amount according to treatment of 0.2 or 1 nM of siRNA having sequence of SEQ ID NO: 204, 206, 207, 208, 209, or 210 as a sense strand.
20

FIG. 4 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a human lung cancer cell line with siRNA having sequence of SEQ ID NO: 35, 42, 59, 602, 603, 604, 124, 153, 166, 187, 197, 212, 218, 221 or 223 as a sense strand according to
25 the present invention.

A : Graph showing CTGF expression amount according to

treatment of 0.04, 0.2 or 1 nM of siRNA having sequence of SEQ ID NO: 35, 42, 59, 602, 603, or 604 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 0.5, 1 or 5 nM of siRNA having sequence of
5 SEQ ID NO: 124, 153, 166, 187, or 197 as a sense strand.

C : Graph showing Plekhol1 expression amount according to treatment of 0.5, 1 or 5 nM of siRNA having sequence of SEQ ID NO: 212, 218, 221 or 223 as a sense strand.

FIG. 5 is a graph showing an inhibition amount of
10 target gene expression, confirmed after transforming a human lung cancer cell line with SAMiRNA having sequence of SEQ ID NO: 42, 59, or 602 as a sense strand according to the present invention.

FIG. 6 is a graph showing an inhibition amount of
15 target gene expression, confirmed after transforming a mouse fibroblast cell line with siRNA having sequence of SEQ ID NOs: 301 to 330, 401 to 430, 501 to 530 as a sense strand according to the present invention.

A : Graph showing CTGF expression amount according to
20 treatment of 20 nM of siRNA having sequence of SEQ ID NOs: 301 to 330 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 20 nM of siRNA having sequence of SEQ ID NOs: 401 to 430 as a sense strand.

25 C : Graph showing Plekhol1 expression amount according to treatment of 20 nM of siRNA having sequence of SEQ ID NOs: 501 to 530 as a sense strand.

FIG. 7 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a mouse fibroblast cell line with siRNA having sequence of SEQ ID NO: 404 to 406, 408 to 410, 414 to 418, 420 to 422, 5 424, 427, 429, 430, 503 to 509, 514 to 517, 519, 521 to 526 or 528 as a sense strand according to the present invention.

A: Graph showing Cyr61 expression amount according to treatment of 5 nM of siRNA having sequence of SEQ ID NOs: 404 to 406, 408 to 410, 414 to 418, 420 to 422, 424, 427, 10 429, or 430 as a sense strand.

B : Graph showing Plekhol1 expression amount according to treatment of 5 nM of siRNA having sequence of SEQ ID NO: 503 to 509, 514 to 517, 519, 521 to 526 or 528 as a sense strand.

15 FIG. 8 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a mouse fibroblast cell line with siRNA having sequence of SEQ ID NO: 301, 303, 307, 323, 410, 422, 424, 507, 515 or 525 as a sense strand according to the present invention.

20 A : Graph showing CTGF expression amount according to treatment of 0.2, 1, or 5 nM of siRNA having sequence of SEQ ID NO: 301, 303, 307 or 323 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 0.2, 1, or 5 nM of siRNA having sequence of 25 SEQ ID NO: 410, 422 or 424 as a sense strand.

C : Graph showing Plekhol1 expression amount according to treatment of 0.2, 1 or 5 nM of siRNA having sequence of

SEQ ID NO: 507, 515 or 525 as a sense strand.

FIG. 9 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a mouse fibroblast cell line with siRNA having a SEQ ID NO: 4,
5 5, 6, 8, 9, 102, 104, 105, 107, 108, 109, 202, 204, 206 to 209, 307, 424 or 525 as a sense strand according to the present invention.

A : Graph showing CTGF expression amount according to treatment of 5 nM of siRNA having sequence of SEQ ID NO: 4,
10 5, 6, 8, 9 or 307 as a sense strand.

B : Graph showing Cyr61 expression amount according to treatment of 5 nM of siRNA having sequence of SEQ ID NO: 102, 104, 105, 107, 108, 109 or 424 as a sense strand.

C : Graph showing Plekhol expression amount according to treatment of 5 nM of siRNA having sequence of SEQ ID NO:
15 202, 204, 206 to 209 or 525 as a sense strand.

FIG. 10 is a graph showing an inhibition amount of target gene expression, confirmed after transforming a mouse fibroblast cell line with siRNA having sequence of
20 SEQ ID NO: 6, 8, 102, 104, 105, 204, 207, 208, 307, 424 or 525 as a sense strand according to the present invention.

A : Graph showing CTGF expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ ID NO: 6, 8 or 307 as a sense strand.

25 B : Graph showing Cyr61 expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ ID NO: 102, 104, 105 or 424 as a sense strand.

C : Graph showing Plekhol expression amount according to treatment of 5 or 20 nM of siRNA having sequence of SEQ ID NO: 204, 207, 208 or 525 as a sense strand.

5

BEST MODE FOR CARRYING OUT THE INVENTION

In order to achieve the foregoing objects, the present invention provides a CTGF, Cyr61 or Plekhol (respiratory diseases-related gene)-specific siRNA consisting of first oligonucleotide which is a sense strand including any one sequence selected from the group consisting of SEQ ID NOs: 1 to 600 and 602 to 604 and a second oligonucleotide which is an antisense strand including a complementary sequence thereto.

The siRNA in the present invention includes all materials having a general RNAi (RNA interference) action, and accordingly, it is obvious to a person skilled in the art that CTGF, Cyr61 or Plekhol-specific siRNA includes CTGF, Cyr61 or Plekhol-specific shRNA, etc.

SEQ ID NOs: 1 to 100, or 602 to 604 are sense strand sequences of CTGF (Homo sapiens)-specific siRNA, SEQ ID NOs: 101 to 200 are sense strand sequences of Cyr61 (Homo sapiens)-specific siRNA, SEQ ID NOs: 201 to 300 are sense strand sequences of Plekhol (Homo sapiens)-specific siRNA, SEQ ID NOs: 301 to 400 are sense strand sequences of CTGF (Mus musculus)-specific siRNA, SEQ ID NOs: 401 to 500 are sense strand sequences of Cyr61 (Mus musculus)-specific siRNA, and SEQ ID NOs: 501 to 600 are sense strand

sequences of Plekhol1(*Mus musculus*)-specific siRNA.

The siRNA according to the present invention is preferably CTGF-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 1 to 10,
 5 35, 42, 59, 602, 603, 604, 301 to 303, 305 to 307, 309, 317, 323 and 329, as a sense strand,

Cyr61-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 101 to 110, 124, 153, 166, 187, 197, 409, 410, 415, 417, 418, 420,
 10 422, 424, 427 and 429, as a sense strand, or

Plekhol1-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 201 to 210, 212, 218, 221, 223, 504 to 507, 514, 515 and 522 to 525, as a sense strand.

15 More preferably, the siRNA according to the present invention is CTGF-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 4, 5, 8, 9, 35, 42, 59, 601, 602, 604, 301, 303, 307 and 323, as a sense strand,

20 Cyr61-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 102, 104, 107, 108, 124, 153, 166, 187, 197, 410, 422 and 424, as a sense strand, or

Plekhol1-specific siRNA including any one sequence
 25 selected from the group consisting of SEQ ID NOs: 206 to 209, 212, 218, 221, 223, 507, 515 and 525, as a sense strand.

Most preferably, the siRNA according to the present invention is CTGF-specific siRNA including any one sequence selected from the group consisting of SEQ ID NO: 42, 59, 602 and 323, as a sense strand,

5 Cyr61-specific siRNA including any one sequence selected from the group consisting of SEQ ID NO: 124, 153, 187, 197 and 424, as a sense strand, or Plekhol-specific siRNA including any one sequence selected from the group consisting of SEQ ID NO: 212, 218, 221, 223 and 525, as a
10 sense strand.

In particular, it was confirmed that some of human CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention is capable of simultaneously inhibiting expression of mouse CTGF, Cyr61 or Plekhol.

15 The siRNA capable of simultaneously inhibiting the expression of human and mouse CTGF, Cyr61 or Plekhol preferably includes a sense strand of CTGF-specific siRNA according to SEQ ID NO: 6 or 8, a sense strand of Cyr61-specific siRNA according to SEQ ID NO: 102, 104 or 105, or
20 a sense strand of Plekhol-specific siRNA according to SEQ ID NO: 204, 207 or 208.

Most preferably, the siRNA includes a sense strand of CTGF-specific siRNA according to SEQ ID NO: 6, a sense strand of Cyr61-specific siRNA according to SEQ ID NO: 102,
25 or a sense strand of Plekhol-specific siRNA according to SEQ ID NO: 207.

The sense strand or the antisense strand of the siRNA

according to the present invention preferably has 19 to 31 nucleotides, and the siRNA includes a sense strand including any one sequence selected from SEQ ID NOS: 1 to 604 and an antisense strand complementary thereto.

5 Since the CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention has a base sequence designed to be capable of being complementarily bonded to mRNA encoding the corresponding gene, expression of the corresponding gene is capable of being effectively
10 inhibited. Further, the CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention may include overhang which is a structure including one or two or more unpaired nucleotide(s) at 3' end of the siRNA, and

may include various modifications of the siRNA to
15 provide nucleic acid lyase resistance, and to decrease non-specific immune response for improving stability in vivo. The modification of the first oligonucleotide or the second oligonucleotide configuring the siRNA may be one or more combinations selected from modification in which -OH group
20 at 2' carbon in a sugar structure in one or more nucleotides is substituted with -CH₃(methyl), -OCH₃ (methoxy), -NH₂, -F(fluorine), -O-2-methoxyethyl, -O-propyl, -O-2-methylthioethyl, -O-3-aminopropyl, -O-3-dimethylaminopropyl, -O-N-methylacetamido or -O-
25 dimethylamidooxyethyl; modification in which oxygen in a sugar structure in nucleotides is substituted with sulfur; and modification to phosphorothioate or boranophosphate,

methy1 phosphonate bindings from nucleotides bindings, or
may be modification to peptide nucleic acid (PNA),
modification to locked nucleic acid (LNA), or modification
to unlocked nucleic acid (UNA) (Ann. Rev. Med. 55, 61-65
5 2004; US 5,660,985; US 5,958,691; US 6,531,584; US
5,808,023; US 6,326,358; US 6,175,001; Bioorg. Med. Chem.
Lett. 14:1139-1143, 2003; RNA, 9:1034-1048, 2003; Nucleic
Acid Res. 31:589-595, 2003; Nucleic Acids Research, 38(17)
5761-5773, 2010; Nucleic Acids Research, 39(5) 1823-1832,
10 2011).

The CTGF, Cyr61 and/or Plekhol-specific siRNA
according to the present invention may inhibit expression
of the corresponding gene, and may remarkably inhibit
expression of the corresponding protein.

15 The present invention also provides a conjugate in
which a hydrophilic material and a hydrophobic material are
conjugated to both ends of siRNA, for effective in vivo
delivery and for improving stability, of the respiratory
diseases-related gene-specific siRNA, particularly, the
20 CTGF, Cyr61 or Plekhol-specific siRNA.

In the siRNA conjugate in which a hydrophilic
material and a hydrophobic material are bonded to the siRNA,
a self-assembled nanoparticle is formed by a hydrophobic
interaction of the hydrophobic material (see Korean Patent
25 Publication No. 1224828), wherein the self-assembled
nanoparticle has advantages in that internal delivery
efficiency and stability in vivo are significantly

excellent, and uniformity of a particle size is excellent, such that quality control (QC) is easily performed, whereby a process for producing drugs is easy.

In one preferable exemplary embodiment, a double-
 5 helical oligo RNA structure containing the CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention preferably has a structure represented by the following Structural Formula (1):

10 Structural Formula 1

A-X-R-Y-B

In Structural Formula (1), A is a hydrophilic material, B is a hydrophobic material, X and Y are each
 15 independently a simple covalent bond or a linker-mediated covalent bond, and R is CTGF, Cyr61, or Plekhol-specific siRNA.

More preferably, the double-helical oligo RNA structure containing the CTGF, Cyr61 or Plekhol-specific
 20 siRNA according to the present invention has a structure represented by the following Structural Formula (2):

Structural Formula 2

A-X-S-Y-B

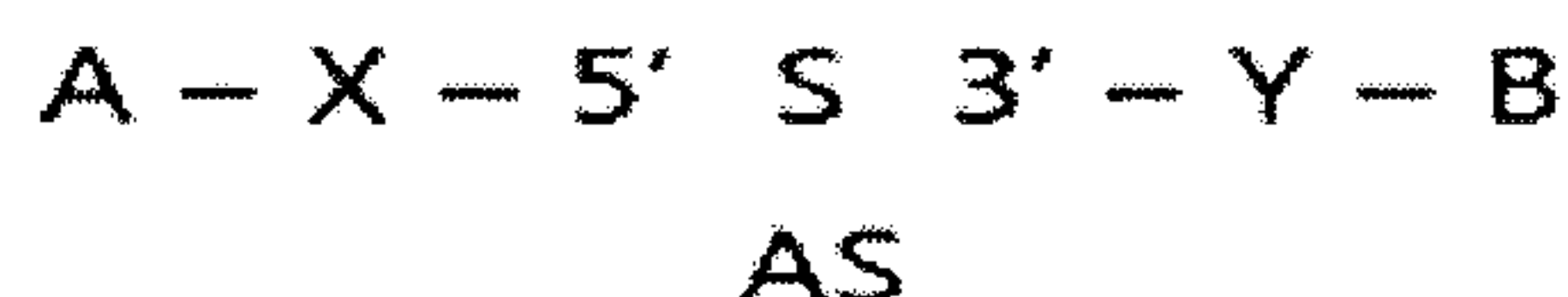
AS

25 In Structural Formula (2), A, B, X and Y are the same

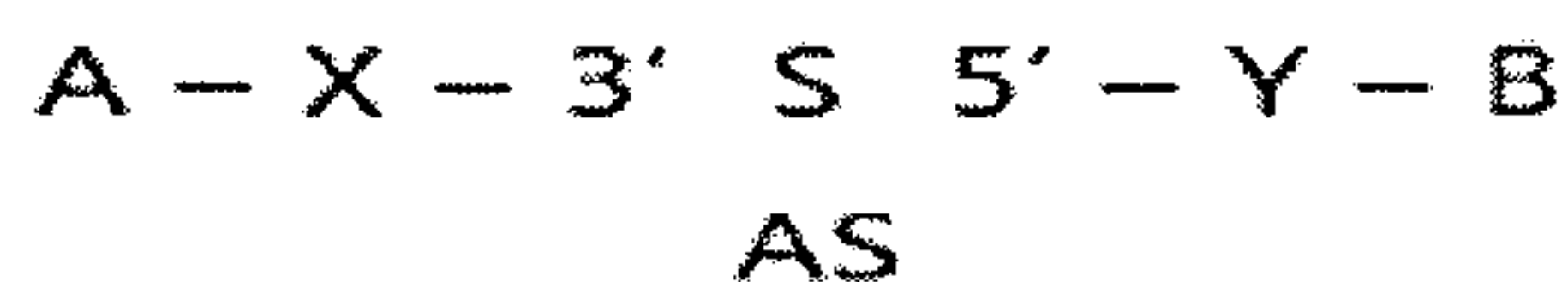
as being defined in Structural Formula (1), S is a sense strand of the CTGF, Cyr61 or Plekhol-specific siRNA, and AS is an antisense strand of the CTGF, Cyr61 or Plekhol-specific siRNA.

5 More preferably, the double-helical oligo RNA structure containing the CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention has a structure represented by the following Structural Formula (3) or (4):

10 Structural Formula 3



Structural Formula 4



15 In Structural Formulas (3) and (4), A, B, S, AS, X and Y are the same as being defined in Structural Formula (1), and 5' and 3' mean 5' end and 3' end of the sense strand of the CTGF, Cyr61 or Plekhol-specific siRNA.

It is obvious to a person skilled in the art that in
20 Structural Formulas (1) to (4), one to three phosphate group(s) may be bonded to 5' end of the antisense strand of the double-helical oligo RNA structure containing the CTGF, Cyr61 or Plekhol-specific siRNA, and shRNA is capable of being used instead of using siRNA.

25 The hydrophilic material in Structural Formulas (1)

to (4) is preferably a cationic or non-ionic polymer material having a molecular weight of 200 to 10,000, more preferably, a non-ionic polymer material having a molecular weight of 1,000 to 2,000. For example, non-ionic
 5 hydrophilic polymer compounds such as polyethylene glycol, polyvinyl pyrrolidone, polyoxazoline, etc., are preferably used as the hydrophilic polymer material, but the present invention is not necessarily limited thereto.

In particular, the hydrophilic material (A) in
 10 Structural Formulas (1) to (4) may be used in a hydrophilic material block form represented by the following Structural Formula (5) or (6), and by using an appropriate number (n in Structural Formula (5) or (6)) of hydrophilic material blocks as needed, problems caused by polydispersibility
 15 that may occur in a case of using a general synthetic polymer material, etc., may be largely improved.

Structural Formula 5



20 Structural Formula 6



In Structural Formula (5), A' is a hydrophilic material monomer, J is a linker for connecting hydrophilic
 25 material monomers (the sum is m) therebetween or a linker

for connecting hydrophilic material monomers (the sum is m)
 to siRNA, m is an integer of 1 to 15, n is an integer of 1
 to 10, and the repeating unit represented by (A'_m-J) or (J-
 A'_m) corresponds to a base unit of the hydrophilic material
 5 block.

When the hydrophilic material block is represented by
 Structural Formula (5) or (6), the double-helical oligo RNA
 structure containing the CTGF, Cyr61 or Plekhol-specific
 siRNA according to the present invention may have a
 10 structure represented by the following Structural Formula
 (7) or (8):

Structural Formula 7



15 Structural Formula 8



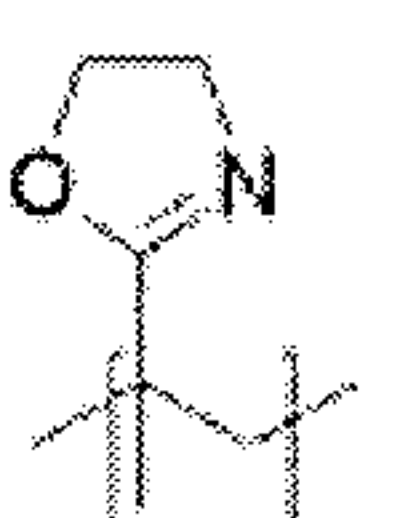
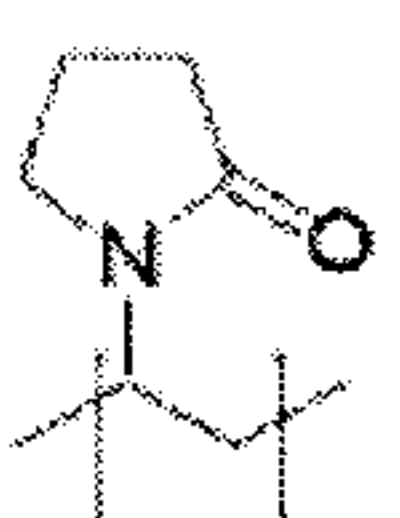
In Structural Formulas (7) and (8), X, R, Y and B are
 the same as being defined in Structural Formula (1), and A',
 20 J, m and n are the same as being defined in Structural
 Formulas (5) and (6).

In Structural Formulas (5) and (6), the hydrophilic
 material monomer A' is usable without limitation as long as
 25 it meets the objects of the present invention among the

monomers of the non-ionic hydrophilic polymer. The hydrophilic material monomer A' is preferably a monomer selected from the following compounds (1) to (3) shown in Table 1, more preferably, a monomer of the compound (1), and G in the compound (1) may be preferably selected from CH₂, O, S and NH.

In particular, among the hydrophilic material monomers, the monomer of Compound (1) may have various functional groups introduced thereinto and good affinity in vivo, and induce a little immune response, thereby having excellent bio-compatibility, and further, may increase stability in vivo of the oligonucleotide included in the structure of Structural Formula (7) or (8), and may increase delivery efficiency, which is significantly suitable for producing the structure according to the present invention.

[Table 1] Monomer structure of hydrophilic material in the present invention

Compound (1)	Compound (2)	Compound (3)
 G is CH₂, O, S or NH		

20

In particular, the hydrophilic material in Structural Formulas (5) to (8) preferably has total molecular weight of 1,000 to 2,000. Therefore, for example, when

hexaethylene glycol represented by Compound (1), that is, G is 0, and m is 6, is used in Structural Formulas (7) and (8), a molecular weight of hexaethylene glycol spacer is 344, such that the repeating number (n) is preferred to be 3 to 5. In particular, the repeating unit of the hydrophilic group, that is, hydrophilic material block, represented by (A'_m-J) or $(J-A'_m)_n$ in Structural Formulas (5) and (6), is capable of being used in an appropriate number represented by n, as needed. A which is the hydrophilic material monomer and J which is the linker included in each hydrophilic material block may be independently the same as each other or be different from each other. That is, when 3 hydrophilic material blocks are used ($n = 3$), the hydrophilic material monomer of the compound (1) is used in the first block, the hydrophilic material monomer of the compound (2) is used in the second block, the hydrophilic material monomer of the compound (3) is used in the third block, etc. That is, different hydrophilic material monomers for all hydrophilic material blocks may be used, and any one hydrophilic material monomer selected from the hydrophilic material monomers of compounds (1) to (3) may also be equally used in all hydrophilic material blocks. Similarly, linkers mediating the combination of the hydrophilic material monomer may also be same as each other or different from each other for all hydrophilic material blocks. Further, m which is the number of hydrophilic material monomers may be the same as

each other or different from each other among all hydrophilic material blocks. That is, 3 hydrophilic material monomers ($m=3$) are connected in the first hydrophilic material block, 5 hydrophilic material monomers (5) ($m=5$) are connected in the second hydrophilic material block, 4 hydrophilic material monomers ($m=4$) are connected in the third hydrophilic material block, etc. That is, hydrophilic material monomers each having different numbers or each having the same number may be used in all 10 hydrophilic material blocks.

Further, in the present invention, the linker (J) is preferably selected from the group consisting of PO_3^- , SO_3 and CO_2 , but the present invention is not limited thereto. It is obvious to a person skilled in the art that any 15 linker may be used depending on the used hydrophilic material monomer, etc., as long as it meets the objects of the present invention.

The hydrophobic material (B) in Structural Formulas (1) to (4), (7) and (8) serves to form a nanoparticle 20 formed of the oligonucleotide structures according to Structural Formulas (1) to (4), (7) and (8) through hydrophobic interaction. The hydrophobic material preferably has a molecular weight of 250 to 1,000, and may include a steroid derivative, a glyceride derivative, 25 glycerol ether, polypropylene glycol, C_{12} to C_{50} unsaturated or saturated hydrocarbon, diacylphosphatidylcholine, fatty acid, phospholipid, lipopolyamine, etc., but the present

invention is not limited thereto. It is obvious to a person skilled in the art that any hydrophobic material may be used as long as it meets the objects of the present invention.

5 The steroid derivative may be selected from the group consisting of cholesterol, cholestanol, cholic acid, cholesteryl formate, cholestanyl formate, and cholesteryl amine, and the glyceride derivative may be selected from mono-, di- and tri-glyceride, etc., wherein the fatty acid
10 of the glyceride is preferred to be C₁₂ to C₅₀ unsaturated or saturated fatty acid.

 In particular, among the hydrophobic materials, saturated or unsaturated hydrocarbon or cholesterol is preferred since it is capable of easily being bonded in a
15 synthetic step of the oligonucleotide structure according to the present invention, and C₂₄ hydrocarbon, particularly, tetradocosane including a disulfide bond is the most preferred.

 The hydrophobic material is bonded to the distal end
20 of the hydrophilic material, and it does not matter if the hydrophobic material is bonded to any position of the sense strand or the antisense strand of the siRNA.

 The hydrophilic material or the hydrophobic material in Structural Formulas (1) to (4), (7) and (8) according to
25 the present invention is bonded to the CTGF, Cyr61, or Plekhol-specific siRNA by a simple covalent bond or a linker-mediated covalent bond (X or Y). In addition, the

linker mediating the covalent bond is covalently bonded to the hydrophilic material or the hydrophobic material at the end of the CTGF, Cyr61 or Plekhol-specific siRNA, and is not particularly limited as long as the bond that is possible to be decomposed in a specific environment is provided as needed. Therefore, any compound for the binding to activate the CTGF, Cyr61 or Plekhol-specific siRNA and/or the hydrophilic material (or the hydrophobic material) in production of the double-helical oligo RNA structure according to the present invention, may be used as the linker. The covalent bond may be any one of a non-degradable bond or a degradable bond. Here, examples of the non-degradable bond may include an amide bond or a phosphorylation bond, and examples of the degradable bond may include a disulfide bond, an acid degradable bond, an ester bond, an anhydride bond, a biodegradable bond or an enzymatically degradable bond, and the like, but the present invention is not limited thereto.

In addition, any CTGF, Cyr61 or Plekhol-specific siRNA represented by R (or S and AS) in Structural Formulas (1) to (4), (7), and (8) is usable without limitation as long as it is siRNA capable of being specifically bonded to CTGF, Cyr61 or Plekhol. Preferably, the CTGF, Cyr61 or Plekhol-specific siRNA consists of a sense strand including any one sequence selected from SEQ ID NOs: 1 to 600 and 602 to 604 and an antisense strand including a complementary sequence thereto.

In particular, the siRNA included in Structural Formulas (1) to (4), (7) and (8) according to the present invention is preferably CTGF-specific siRNA including any one sequence selected from the group consisting of SEQ ID
5 NOs: 1 to 10, 35, 42, 59, 602 to 604 or 301 to 303, 305 to 307, 309, 317, 323 and 329, as a sense strand,

Cyr61-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 101 to 110, 124, 153, 166, 187, 197, 409, 410, 415, 417, 418, 420,
10 422, 424, 427 and 429, as a sense strand, or

Plekhol1-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 201 to 210, 212, 218, 221, 223, 504 to 507, 514, 515 and 522 to 525, as a sense strand.

15 More preferably, the siRNA according to the present invention is CTGF-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 4, 5, 8, 9, 35, 42, 59, 602, 603, 604, 301, 303, 307 and 323, as a sense strand,

20 Cyr61-specific siRNA including any one sequence selected from the group consisting of SEQ ID NOs: 102, 104, 107, 108, 124, 153, 166, 187, 197, 410, 422 and 424, as a sense strand, or

Plekhol1-specific siRNA including any one sequence
25 selected from the group consisting of SEQ ID NOs: 206 to 209, 212, 218, 221, 223, 507, 515 and 525, as a sense strand.

Most preferably, the siRNA according to the present invention is CTGF-specific siRNA including any one sequence of SEQ ID NO: 42, 59, 602 or 323, as a sense strand,

Cyr61-specific siRNA including any one sequence of
5 SEQ ID NO: 124, 153, 187, 197 or 424, as a sense strand, or

Plekhol-specific siRNA including any one sequence of
SEQ ID NO: 212, 218, 221, 223 or 525, as a sense strand.

In addition, siRNA including human and mouse CTGF-
10 specific siRNA sense strand according to SEQ ID NO: 6 or 8,
siRNA including human and mouse Cyr61-specific siRNA sense
strand according to SEQ ID NO: 102, 104 or 105, and siRNA
including human and mouse Plekhol-specific siRNA sense
strand according to SEQ ID NO: 204, 207 or 208, are
15 particularly preferred, which is because the siRNA having
the sequence as the sense strand has an effect of
simultaneously inhibiting expression of human and mouse
CTGF, Cyr61 or Plekhol, such that siRNA including human and
mouse CTGF-specific siRNA sense strand according to SEQ ID
20 NO: 6, siRNA including human and mouse Cyr61-specific siRNA
sense strand according to SEQ ID NO: 102, and siRNA
including human and mouse Plekhol-specific siRNA sense
strand according to SEQ ID NO: 207 are the most preferred.

In the double helical-oligo RNA structure containing
25 the CTGF, Cyr61 or Plekhol-specific siRNA according to the
present invention, an amine group or a polyhistidine group
may be additionally introduced into a portion of the distal

end bonded with the siRNA of the hydrophilic material in the structure.

This makes it easy to perform intercellular introduction and escape from the endosome of the double
5 helical-oligo RNA structure containing the CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention, and a possibility of introducing an amine group and using a polyhistidine group to easily perform the intercellular introduction and the escape from the endosome of the
10 carriers such as Quantum dot, Dendrimer, liposome, etc., and the effect thereof, have been reported.

Specifically, it is known that the primary amine group expressed at the end or the outside of the carrier is protonated in vivo pH to form a conjugate with a negatively
15 charged gene by an electrostatic interaction, and the escape from the endosome is easily performed due to internal tertiary amines having a buffer effect at a low pH of the endosome after being introduced into the cells, thereby being capable of protecting the carrier from
20 decomposition of lysosome (gene delivery and expression inhibition using a polymer-based hybrid material. *Polymer Sci. Technol.*, Vol. 23, No.3, pp254-259).

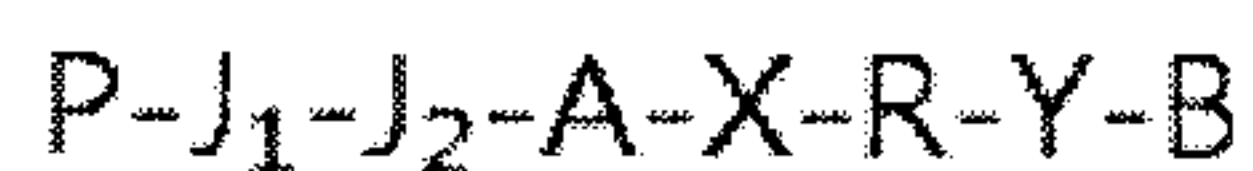
In addition, it is known that histidine which is one of non-essential amino acids, has an imidazole ring (pKa3
25 6.04) at a residue (-R) to increase a buffer capacity in the endosome and the lysosome, such that histidine expression may be used to increase an escape efficiency

from the endosome in non-viral gene carriers including liposome (Novel histidine-conjugated galactosylated cationic liposomes for efficient hepatocyte selective gene transfer in human hepatoma HepG2 cells. J. Controlled Release 118, pp262-270).

The amine group or the polyhistidine group may be linked to the hydrophilic material or the hydrophilic material block through at least one linker.

When the amine group or the polyhistidine group is introduced into the hydrophilic material of the double-helical oligo RNA structure represented by Structural Formula (1), the double helical-oligo RNA structure may have a structure represented by Structural Formula (9) below:

Structural Formula 9



In Structural Formula (9), A, B, R, X and Y are the same as being defined in Structural Formula (1),

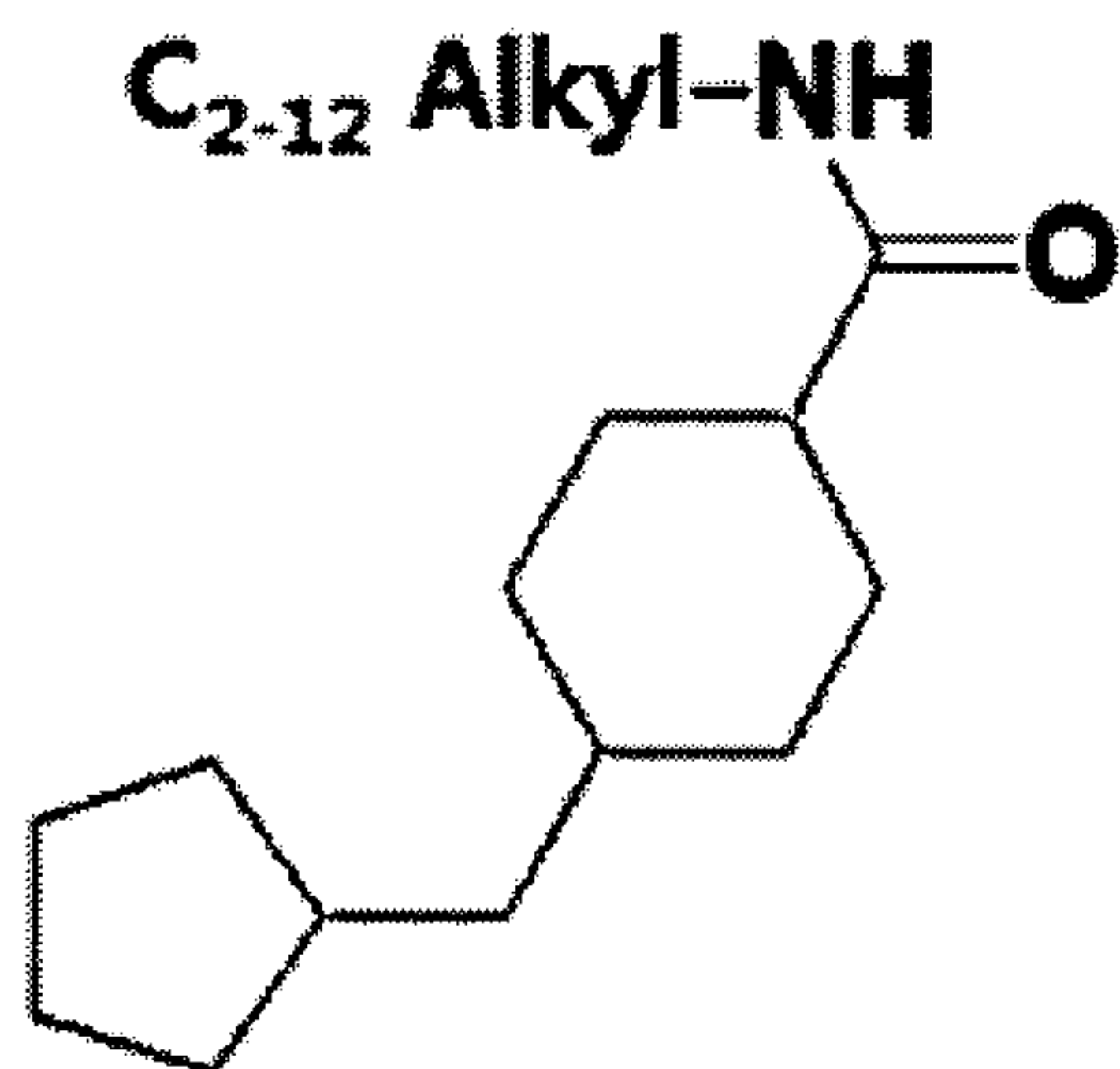
P is an amine group or a polyhistidine group. J_1 and J_2 are linkers and may be each independently selected from a simple covalent bond, PO_3^- , SO_3 , CO_2 , C_{2-12} alkyl, alkenyl, and alkynyl, but the present invention is not limited thereto. It is obvious to a person skilled in the art that any linker is usable as J_1 and J_2 as long as it meets the objects of the present invention depending on the used

hydrophilic material.

Preferably, when the amine group is introduced, J_2 is preferably a simple covalent bond or PO_3^- , and J_1 is preferably C_6 alkyl, but the present invention is not
5 limited thereto.

Further, when the polyhistidine group is introduced, in Structural Formula (9), J_2 is preferably a simple covalent bond or PO_3^- , and J_1 is preferably the following Compound (4), but the present invention is not limited
10 thereto.

Compound 4



Further, when the hydrophilic material of the double-helical oligo RNA structure represented by Structural Formula (9) is a hydrophilic material block represented by Structural Formula (5) or (6), and the amine group or the polyhistidine group is introduced, the double-helical oligo
15 RNA structure may be represented by Structural Formula (10) or (11):
20

Structural Formula 10Structural Formula 11

5

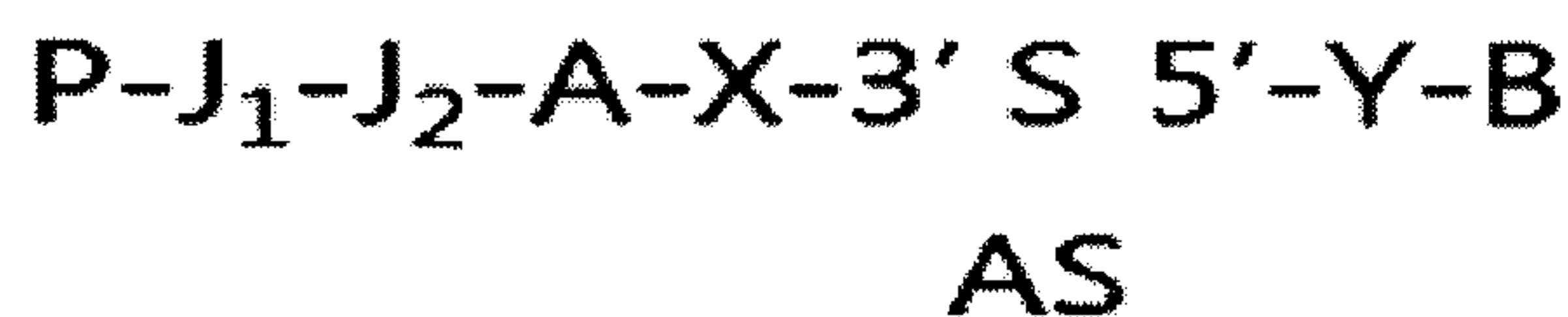
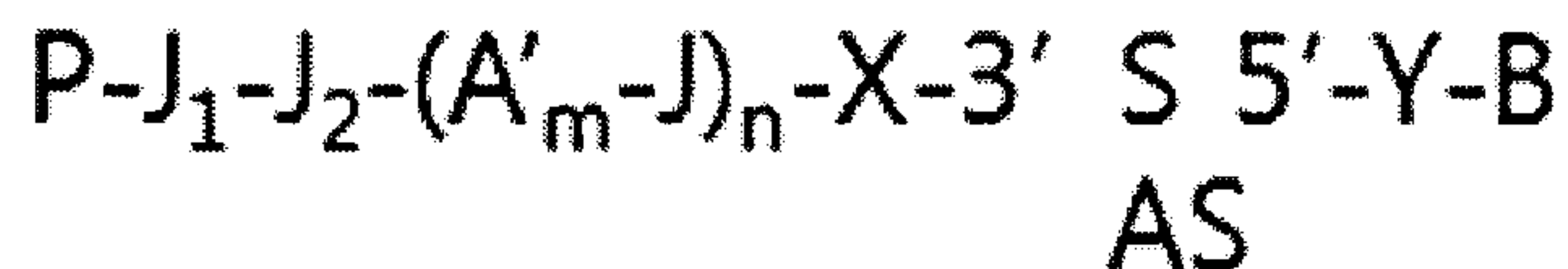
In Structural Formulas (10) and (11), X, R, Y, B, A', J, m and n are the same as being defined in Structural Formula (5) or (6), and P, J1 and J2 are the same as being defined in Structural Formula (9).

10

In particular, in Structural Formulas (10) and (11), the hydrophilic material is preferably bonded to 3' end of the sense strand of the CTGF, Cyr61 or Plekhol-specific siRNA, and in this case, Structural Formulas (9) to (11) may be represented by the following Structural Formulas

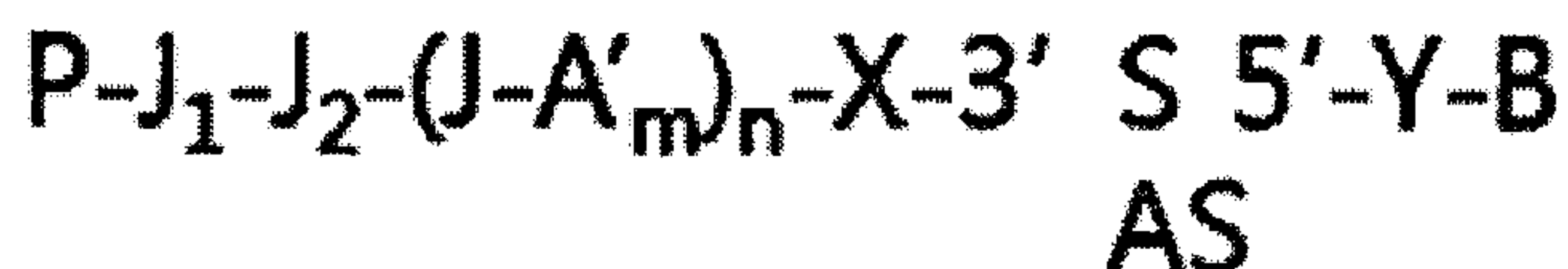
15

(12) to (14):

Structural Formula 12Structural Formula 13

20

Structural Formula 14



In Structural Formulas (12) to (14), X, R, Y, B, A, A' J, m, n, P, J₁ and J₂ are the same as being defined in Structural Formulas (9) to (11), and 5' and 3' mean 5' end
 5 and 3' end of the sense strand of the CTGF, Cyr61 or Plekhol-specific siRNA.

The amine group that may be introduced in the present invention may be primary to tertiary amine groups, and the primary amine group is particularly preferred. The
 10 introduced amine group may be present as an amine salt. For example, the salt of the primary amine group may be present in a form of NH₃⁺.

Further, the polyhistidine group that may be introduced in the present invention preferably includes 3
 15 to 10 histidines, more preferably, 5 to 8 histidines, and the most preferably, 6 histidines. In addition to histidine, at least one cystein may be additionally included.

Meanwhile, when a targeting moiety is provided in the double-helical oligo RNA structure containing the CTGF,
 20 Cyr61, or Plekhol-specific siRNA according to the present invention and the nanoparticle formed therefrom, delivery to the target cell is effectively promoted to achieve delivery to the target cell even in a relatively low concentration of dosage, thereby showing a high control
 25 function for target gene expression, and thereby preventing

non-specific delivery of the CTGF, Cyr61, or Plekhol-specific siRNA into other organs and cells.

Accordingly, the present invention provides a double-helical oligo RNA structure in which a ligand (L), particularly, a ligand specifically bonded to a receptor that promotes target cell internalization through receptor-mediated endocytosis (RME), is additionally bonded to the structure according to Structural Formulas (1) to (4), (7) and (8). For example, the form in which the ligand is bonded to the double-helical oligo RNA structure according to Structural Formula (1), has a structure represented by the following Structural Formula (15):

Structural Formula 15

(L_i-Z)-A-X-R-Y-B

In Structural Formula (15), A, B, X and Y are the same as being defined in Structural Formula (1), L is a ligand specifically bonded to a receptor that promotes target cell internalization through receptor-mediated endocytosis (RME), and i represents an integer from 1 to 5, preferably, an integer of 1 to 3.

The ligand in Structural Formula (15) may be preferably selected from the group consisting of a target receptor-specific antibody or aptamer, peptide that has properties of RME for promoting cell internalization in a target cell-specific manner; or folate (generally, folate

and folic acid are intersectionally used, and the folate in the present invention means folate in a natural state or in an activated state in a human body), chemicals such as sugar, carbohydrate, etc., including hexoamines such as N-
5 acetyl galactosamine (NAG), etc., glucose, mannose, but the present invention is not limited thereto.

Further, the hydrophilic material A in Structural Formula (15) may be used in the form of the hydrophilic material block represented by Structural Formulas (5) and
10 (6).

The present invention also provides a method for producing the double-helical oligo RNA structure containing the CTGF, Cyr61, or Plekhol-specific siRNA.

The method for producing the double-helical oligo RNA
15 structure containing the CTGF, Cyr61, or Plekhol-specific siRNA according to the present invention may include the following steps:

(1) binding a hydrophilic material based on a solid support;

20 (2) synthesizing an RNA single strand based on the solid support containing the hydrophilic material bonded thereto;

(3) covalently binding a hydrophobic material to 5' end of the RNA single strand;

25 (4) synthesizing an RNA single strand having a complementary sequence to a sequence of the RNA single strand;

(5) separating and purifying an RNA-polymer structure and the RNA single strand from the solid support when the synthesizing of the RNA single strand is completed; and

(6) producing the double-helical oligo RNA structure
5 by annealing the RNA-polymer structure and an RNA single strand having a complementary sequence thereto.

The solid support in the present invention is preferably a controlled pore glass (CPG), but the present invention is not limited thereto, but may be polystyrene,
10 silica gel, cellulose paper, etc. In the CPG, a diameter is preferably 40 to 180 μm , and a pore size is preferably 500 to 3000Å. After step (5) above, when the production is completed, it may be confirmed whether the purified RNA-polymer structure and the purified RNA single strand are
15 produced as the desired RNA-polymer structure and the desired RNA single strand by measuring molecular weights by MALDI-TOF mass spectrometer. In the production method, Step (4) which is a step of synthesizing the RNA single strand having a complementary sequence to a sequence of the RNA
20 single strand synthesized in Step (2) may be performed before Step (1) or may be performed during any one step of Steps (1) to (5).

In addition, the RNA single strand having a complementary sequence to the RNA single strand synthesized
25 in Step (2) may contain a phosphate group bonded to 5' end thereof.

Meanwhile, the present invention provides a method for producing a double-helical oligo RNA structure in which a ligand is additionally bonded to the double-helical oligo RNA structure containing the CTGF, Cyr61, or Plekhol-
5 specific siRNA.

The method for producing the double-helical oligo RNA structure containing the ligand-bonded CTGF, Cyr61, or Plekhol-specific siRNA according to the present invention may include the following steps:

10 (1) binding a hydrophilic material to a solid support containing a functional group bonded thereto;

(2) synthesizing an RNA single strand based on the solid support containing a functional group-hydrophilic material bonded thereto;

15 (3) covalently binding a hydrophilic material to 5' end of the RNA single strand;

(4) synthesizing an RNA single strand having a complementary sequence to a sequence of the RNA single strand;

20 (5) separating a functional group-RNA-polymer structure and the RNA single strand having the complementary sequence from the solid support when the synthesizing of the RNA single strand is completed;

(6) producing a ligand-RNA-polymer structure single
25 strand by binding a ligand to an end of the hydrophilic material using the functional group; and

(7) producing a ligand-double-helical oligo RNA

structure by annealing the ligand-RNA-polymer structure and an RNA single strand having a complementary sequence thereto.

After step (6) above, when the production is completed, whether the desired ligand-double-helical oligo RNA structure and the desired RNA single strand having a complementary sequence thereto are prepared may be confirmed by separating and purifying the ligand-RNA-polymer structure and the RNA single strand having a complementary sequence thereto, and measuring molecular weights by MALDI-TOF mass spectrometer. The ligand-double-helical oligo RNA structure may be produced by annealing the prepared ligand-RNA-polymer structure and the RNA single strand having a complementary sequence thereto. In the production method, Step (4) which is a step of synthesizing the RNA single strand having a complementary sequence to a sequence of the RNA single strand synthesized in Step (3), is an independent synthesis process, and may be performed before Step (1) or may be performed during any one step of Steps (1) to (6).

The present invention also provides a nanoparticle including the double-helical oligo RNA structure containing the CTGF, Cyr61, or Plekhol-specific siRNA.

As described above, the double-helical oligo RNA structure containing the CTGF, Cyr61, or Plekhol-specific siRNA is amphipathic structure containing both of hydrophobic materials and hydrophilic materials, wherein

the hydrophilic materials have affinity through an interaction such as a hydrogen bond, etc., with water molecules present in the body to face toward the outside, and the hydrophobic materials face toward the inside through a hydrophobic interaction therebetween, thereby forming a thermodynamically stable nanoparticle. That is, the hydrophobic materials are positioned in the center of the nanoparticle, and the hydrophilic materials are positioned in the outside direction of the CTGF, Cyr61, or Plekhol-specific siRNA to form nanoparticles protecting the CTGF, Cyr61, or Plekhol-specific siRNA. These formed nanoparticles improve intracellular delivery of the CTGF, Cyr61, and/or Plekhol-specific siRNA and improve siRNA effect.

The nanoparticles according to the present invention may be formed of only the double-helical oligo RNA structure containing siRNAs each having the same sequence as each other, or may be formed of the double-helical oligo RNA structure containing siRNAs each having different sequence, wherein it is construed in the present invention that the siRNAs each having different sequence includes siRNA having different target genes, for example, CTGF, Cyr61, or Plekhol-specific siRNA, or siRNA having the same target gene-specificity, but having different sequence.

Further, the double-helical oligo RNA structure containing other respiratory diseases-related gene-specific siRNA in addition to the CTGF, Cyr61, or Plekhol-specific

siRNA may also be included in the nanoparticle according to the present invention.

Further, the present invention provides a composition for preventing or treating respiratory diseases, particularly, idiopathic pulmonary fibrosis and COPD, including: the CTGF, Cyr61, or Plekhol-specific siRNA, the double-helical oligo RNA structure containing the siRNA, and/or the nanoparticle formed of the double-helical oligo RNA structure.

The composition including the CTGF, Cyr61, or Plekhol-specific siRNA according to the present invention, the double-helical oligo RNA structure containing the siRNA, and/or the nanoparticle formed of the double-helical oligo RNA structure as effective components, inhibits pulmonary artery remodeling and airway remodeling, such that the CTGF, Cyr61, or Plekhol-specific siRNA or the composition containing the siRNA has an effect of preventing or treating the respiratory diseases.

In particular, the composition for preventing or treating respiratory diseases, including the double-helical oligo RNA structure according to the present invention may include:

a double-helical oligo RNA structure including a CTGF-specific siRNA that includes a sense strand including any one sequence selected from the group consisting of SEQ ID NOs: 1 to 100 or 602 to 604 and 301 to 400, preferably, any one sequence selected from the group consisting of SEQ

ID NOs: 1 to 10, 35, 42, 59, 602 to 604, 301 to 303, 305 to 307, 309, 317, 323 and 329, more preferably, any one sequence selected from the group consisting of SEQ ID NOs: 4, 5, 8, 9, 35, 42, 59, 602 to 604, 301, 303, 307 and 323, the most preferably, any one sequence of SEQ ID NO: 42, 59, 602 or 323, and an antisense strand including a complementary sequence thereto;

a double-helical oligo RNA structure including a Cyr61-specific siRNA that includes a sense strand including any one sequence selected from the group consisting of SEQ ID NOs: 101 to 200 and 401 to 500, preferably, any one sequence selected from the group consisting of SEQ ID NOs: 101 to 110, 124, 153, 166, 187, 197, 409, 410, 415, 417, 418, 420, 422, 424, 427 and 429, more preferably, any one sequence selected from the group consisting of SEQ ID NOs: 102, 104, 107, 108, 124, 153, 166, 187, 197, 410, 422 and 424, the most preferably, any one sequence of SEQ ID NO: 124, 153, 187, 197 or 424, and an antisense strand including a complementary sequence thereto; or

a double-helical oligo RNA structure including a Plekhol-specific siRNA that includes a sense strand including any one sequence selected from the group consisting of SEQ ID NOs: 201 to 300 and 501 to 600, preferably, any one sequence selected from the group consisting of SEQ ID NOs: 201 to 210, 212, 218, 221, 223, 504 to 507, 514, 515 and 522 to 525, more preferably, any one sequence selected from the group consisting of SEQ ID

Nos: 206 to 209, 212, 218, 221, 223, 507, 515, and 525, the most preferably, any one sequence of SEQ ID NO: 212, 218, 221, 223 or 525, and an antisense strand including a complementary sequence thereto.

5 In addition, the composition for preventing or treating respiratory diseases, including the double-helical oligo RNA structure according to the present invention may include: a double-helical oligo RNA structure including a CTGF-specific siRNA that includes a sense strand of human
10 and mouse CTGF-specific siRNA according to sequence of SEQ ID NO: 6 or 8, preferably, SEQ ID NO: 6 and an antisense strand including a complementary sequence thereto;

 a double-helical oligo RNA structure including a Cyr61-specific siRNA that includes a sense strand of human
15 and mouse Cyr61-specific siRNA according to any one sequence of SEQ ID NO: 102, 104 and 105, preferably, SEQ ID NO: 102 and an antisense strand including a complementary sequence thereto; or

 a double-helical oligo RNA structure including a
20 Plekhol1-specific siRNA that includes a sense strand of human and mouse Plekhol1-specific siRNA according to any one sequence of SEQ ID NO: 204, 207 and 208, preferably, SEQ ID NO: 207 and an antisense strand including a complementary sequence thereto.

25 In addition, a double-helical oligo RNA structure containing the CTGF-specific siRNA, a double-helical oligo RNA structure containing the Cyr61-specific siRNA, and/or a

double-helical oligo RNA structure containing the Plekhol-
specific siRNA may be mixed and included in the composition,
and additionally, siRNA specific to the other respiratory
diseases-related gene in addition to CTGF, Cry61 or Plekhol
5 or a double-helical oligo RNA structure containing the
other respiratory diseases-related gene-specific siRNA may
also be included in the composition according to the
present invention.

At the time of using a composition for preventing or
10 treating respiratory diseases additionally including the
double-helical oligo RNA structure containing the other
respiratory diseases-related gene-specific siRNA together
with the CTGF, Cyr61, and/or Plekhol-specific siRNA, or the
double-helical oligo RNA structure containing the CTGF,
15 Cyr61, and/or Plekhol-specific siRNA, a synergistic effect
like that of a combination therapy may be obtained.

Examples of the respiratory diseases capable of being
prevented or treated by the composition of the present
invention include idiopathic pulmonary fibrosis, asthma,
20 chronic obstructive pulmonary disease (COPD), acute or
chronic bronchitis, allergic rhinitis, cough and phlegm,
acute lower respiratory tract infection, bronchitis, and
bronchiolitis, acute upper respiratory tract infection,
pharyngitis, tonsillitis, laryngitis, etc., but the present
25 invention is not limited thereto.

Further, the nanoparticle included in the composition
for preventing or treating the respiratory disease,

including the nanoparticle formed of the double-helical oligo RNA structure according to the present invention may purely consist of only any one structure selected from the double-helical oligo RNA structure containing the CTGF, 5 Cyr61, or Plekhol-specific siRNA, or may be configured in a form in which two or more kinds of the double-helical oligo RNA structures including the CTGF, Cyr61, or Plekhol-specific siRNA are mixed with each other.

The composition of the present invention may be 10 prepared by additionally including at least one pharmaceutically acceptable carrier in addition to the effective components. The pharmaceutically acceptable carrier is required to be compatible with the effective components of the present invention, and may be used by 15 mixing one or more components selected from saline, sterile water, Ringer's solution, buffered saline, dextrose solution, maltodextrin solution, glycerol and ethanol, and other conventional additives such as antioxidant, buffer, fungistat, and the like, may be added thereto as needed. In 20 addition, the composition may be prepared as a formulation for injection, such as an aqueous solution, suspension, emulsion, and the like, by additionally adding diluent, dispersant, surfactant, binder and lubricant thereto. In particular, it is preferred to provide the composition 25 prepared as a lyophilized formulation. To prepare the lyophilized formulation, any method which is generally known in the technical field of the present invention may

be used, wherein a stabilizer for lyophilization may be added thereto. In addition, appropriate methods in the art or a method disclosed in Remington's pharmaceutical Science, Mack Publishing Company, or Easton PA may be preferably
5 used for formulation depending on each disease or component.

The dosage and administration method of the effective components, etc, included in the pharmaceutical composition of the present invention may be determined based on symptoms of the general patient and severity of the disease
10 by general experts in the art. In addition, the composition may be formulated with various types such as powder, tablet, capsule, solution, injection, ointment, syrup, and the like, and may be provided as a unit-dose or a multi-dose container, for example, a sealed ampoule, bottle, and the
15 like.

The pharmaceutical composition of the present invention may be orally or parenterally administered. Examples of an administration route of the pharmaceutical composition according to the present invention may include
20 oral, intravenous, intramuscular, intra-arterial, intramedullary, intradural, intracardiac, transdermal, subcutaneous, intraperitoneal, intestinal, sublingual or topical administration, but the present invention is not limited thereto. Particularly, the administration route may
25 also include administration into lung via drip infusion in respiratory organs for treatment of respiratory diseases. The administration amount of the composition may have

various ranges depending on weight, age, gender, health condition, diet, administration time, method, excretion rate, the severity of disease, and the like, of a patient, and may be easily determined by a general expert in the art.

5 In addition, the composition of the present invention may be formulated into an appropriate dosage form by using known technologies for clinical administration.

Further, the present invention provides a method for preventing or treating respiratory diseases, particularly,
10 idiopathic pulmonary fibrosis and COPD, including: administering the double-helical oligo RNA structure according to the present invention and the nanoparticle including the double-helical oligo RNA structure to a patient requiring such treatment.

15

EXAMPLES

Hereinafter, the present invention will be described in detail with reference to the following Examples. These examples are only for exemplifying the present invention,
20 and it will be obvious to those skilled in the art that the scope of the present invention is not construed to be limited to these examples.

Example 1. Design of target sequence of CTGF, Cyr61
25 or Plekhol and production of siRNA

604 types of target sequences (sense strands) capable of being bonded to mRNA sequence of CTGF(*Homo sapiens*) gene

(NM_001901), mRNA sequence of Cyr61(*Homo sapiens*) gene
 (NM_001554), mRNA sequence of Plekhol(*Homo sapiens*) gene
 (NM_016274), mRNA sequence of CTGF(*Mus musculus*) gene
 (NM_010217), mRNA sequence of Cyr61(*Mus musculus*) gene
 5 (NM_010516), or mRNA sequence of Plekhol(*Mus musculus*) gene
 (NM_023320) were designed, and siRNAs of antisense strands
 having complementary sequences to the target sequences were
 produced.

First, a gene design program (Turbo si-Designer)
 10 developed by Bioneer Co., was used to design target
 sequence that the siRNA is capable of being bonded from
 mRNA sequences of the corresponding genes. The siRNA for
 respiratory disease-related genes according to the present
 invention has a double stranded structure including a sense
 15 strand consisting of 19 nucleotides and an antisense strand
 complementary thereto. Further, siCONT (having sequence of
 SEQ ID NO: 601 as a sense strand) which is siRNA having a
 sequence in which expression of any gene is not inhibited,
 was produced. The siRNA was produced by linking
 20 phosphodiester bonds forming an RNA backbone structure by
 using β -cyanoethyl phosphoramidite (Nucleic Acids Research,
 12:4539-4557, 1984). Specifically, a reaction product
 including RNA having a desired length was obtained by
 repeating a series of processes of deblocking, coupling,
 25 oxidation and capping, on a solid support to which
 nucleotide is attached, using RNA synthesizer (384
 Synthesizer, BIONEER, Korea). RNA of the reaction product

was separated and purified by HPLC LC918 (Japan Analytical Industry, Japan) equipped with Daisogel C₁₈ (Daiso, Japan) column, and it was confirmed whether or not the purified RNA meets the target sequence by MALDI-TOF mass spectrometer (Shimadzu, Japan). Then, the desired double-stranded siRNA (SEQ ID NOs: 1 to 604) was produced by binding the RNA sense strand to the RNA antisense strand.

Example 2. Production of double-helical oligo RNA structure (PEG-SAMiRNA).

The double-helical oligo RNA structure (PEG-SAMiRNA) produced in the present invention has a structure represented by the following Structural Formula (16):

Structural Formula 16

C₂₄-5'-S-3'-PEG

AS

In Structural Formula (16), S is a sense strand of siRNA; AS is an antisense strand of siRNA; PEG is a hydrophilic material, that is, polyethylene glycol; C₂₄ is a hydrophobic material and tetradocosane including a disulfide bond; and 5' and 3' mean directions of the double-helical oligo RNA end.

The sense strand of siRNA of Structural Formula (16) was produced by synthesizing a double-helical oligo RNA-

hydrophilic material structure of a sense strand in which polyethylene glycol is bonded to 3' end by the above-described method in which phosphodiester bonds forming an RNA backbone structure are linked by using β -cyanoethyl phosphoramidite, based on 3' polyethylene glycol (PEG, Mn=2,000)-CPG produced by Example 1 of Korean Patent Laid-Open Publication No. 10-2012-0119212, as a supporter, and binding tetradocosane including a disulfide bond to 5' end, thereby producing a sense strand of a desired RNA-polymer structure. For an antisense strand in which annealing is performed with the sense strand, the antisense strand having a complementary sequence to the sense strand was produced by the above-described reaction.

When the synthesis was completed, the RNA single strand and the RNA-polymer structure synthesized by treating 28%(v/v) ammonia in water bath at 60°C were separated from CPG and protecting moieties were removed therefrom by a deprotection reaction, respectively. The RNA single strand and the RNA-polymer structure from which the protecting moieties were removed were treated with N-methylpyrrolidone, triethylamine and triethylaminetrihydrofluoride at a volume ratio of 10:3:4 in an oven at 70°C, to remove 2' TBDMS(tert-butyldimethylsilyl).

RNA of the reaction product was separated and purified by HPLC LC918 (Japan Analytical Industry, Japan) equipped with Daisogel C18(Daiso, Japan) column, and it was

confirmed whether or not the purified RNA meets the target sequence by MALDI-TOF mass spectrometer (Shimadzu, Japan). Then, to produce each double-helical oligo RNA structure, the sense strand and the antisense strand each having the same amount were mixed with each other, put in 1X annealing buffer (30 mM HEPES, 100 mM potassium acetate, 2 mM magnesium acetate, pH 7.0 ~7.5), and reacted in a constant-temperature water bath at 90°C for 3 minutes, and reacted again at 37°C, thereby producing each double-helical oligo RNA structure including siRNA having sequence of SEQ ID NO: 42, 59, 602, 124, 153, 187, 197, 212, 218, 221, 223, 323, 424, 525 or 601 as the sense strand (hereinafter, referred to as SAMiRNALP-hCTGF, SAMiRNALP-hCyr, SAMiRNALP-hPlek, SAMiRNALP-mCTGF, SAMiRNALP-mCyr, and SAMiRNALP-mPlek, SAMiRNALP-CONT, respectively). It was confirmed that the produced double-helical oligo RNA structure was annealed by electrophoresis.

Example 3. Production of improved double-helical oligo RNA structure (Mono-HEG-SAMiRNA).

The improved double-helical oligo RNA structure produced in the present invention is obtained by using $[\text{PO}_3^- \text{-hexaethylene glycol}]_4$ (hereinafter, referred to as 'Mono-HEG-SAMiRNA', see Structural Formula (17)) which is the hydrophilic material block instead of using PEG which is the hydrophilic material, and has the following Structure Formula (17):

Structure Formula 17

5 In Structural Formula (17), S is a sense strand of siRNA; AS is an antisense strand of siRNA; [Hexa Ethylene Glycol]₄ is a hydrophilic material monomer; C₂₄ is a hydrophobic material and tetradocosane including a disulfide bond; and 5' and 3' mean directions of the

10 double-helical oligo RNA sense strand end.

The structure of Mono-HEG SAMiRNA according to Structural Formula (17) may be represented by the following Structural Formula (18):

15 Structural Formula 18



RNA of the reaction product was separated and purified by HPLC LC918 (Japan Analytical Industry, Japan) equipped with Daisogel C₁₈ (Daiso, Japan) column, and it was

20 confirmed whether or not the purified RNA meets the target sequence by MALDI-TOF mass spectrometer (Shimadzu, Japan). Then, to produce each double-helical oligo RNA structure, the sense strand and the antisense strand each having the

25 same amount were mixed with each other, put in 1X annealing

buffer (30 mM HEPES, 100 mM potassium acetate, 2 mM magnesium acetate, pH 7.0 ~7.5), and reacted in a constant-temperature water bath at 90°C for 3 minutes, and reacted again at 37°C, thereby producing each double-helical oligo RNA structure including siRNA having sequence of SEQ ID NO: 42, 59, 602, 124, 153, 187, 197, 212, 218, 221, 223, 323, 424, 525 or 601 as the sense strand (hereinafter, referred to as Mono-HEG-SAMiRNALP-hCTGF, Mono-HEG-SAMiRNALP-hCyr, Mono-HEG-SAMiRNALP-hPlek, Mono-HEG-SAMiRNALP-mCTGF, Mono-HEG-SAMiRNALP-mCyr, Mono-HEG-SAMiRNALP-mPlek, and Mono-HEG-SAMiRNALP-CONT, respectively). It was confirmed that the produced double-helical oligo RNA structure was annealed by electrophoresis.

Example 4. Production of nanoparticles formed of improved double-helical oligo RNA structure (Mono-HEG-SAMiRNA) and measurement of size thereof

The double-helical oligo RNA structure (Mono-HEG-SAMiRNA) produced by Example 3 forms a nanoparticle, that is, micelle by a hydrophobic interaction between the hydrophobic materials bonded to the end of the double-helical oligo RNA (FIG. 1).

It was confirmed that the nanoparticle (SAMiRNA) formed of the corresponding Mono-HEG-SAMiRNA was formed by analyzing PDI (polydispersity index) of the nanoparticles formed of Mono-HEG-SAMiRNA-hCTGF, Mono-HEG-SAMiRNA-hCyr, Mono-HEG-SAMiRNA-hPlek, Mono-HEG-SAMiRNA-mCTGF, Mono-HEG-

SAMiRNA-mCyr, Mono-HEG-SAMiRNA-mPlek and Mono-HEG-SAMiRNA-CONT.

Example 4-1. Production of nanoparticle

5 The Mono-HEG-SAMiRNA-hCTGF was dissolved in 1.5 ml DPBS (Dulbecco's Phosphate Buffered Saline) at a concentration of 50 $\mu\text{g/ml}$, the obtained mixture was freeze-dried at -75°C and 5mTorr condition for 48 hours to produce nanoparticle powder, and the nanoparticle powder was
10 dissolved in DPBS which is a solvent to produce homogenized nanoparticles. The nanoparticles formed of Mono-HEG-SAMiRNA-hCyr, Mono-HEG-SAMiRNA-hPlek, Mono-HEG-SAMiRNA-mCTGF, Mono-HEG-SAMiRNA-mCyr, Mono-HEG-SAMiRNA-mPlek, and Mono-HEG-SAMiRNA-CONT were produced by the same method.

15

Example 4-2. Measurement of size and polydispersity index (PDI) of nanoparticle

A size of the nanoparticle was measured by zeta-potential measurement. A size of the homogenized
20 nanoparticles produced by Example 4-1 was measured by zeta-potential measurement (Nano-ZS, MALVERN, England), under conditions in which a refractive index to the material is 1.459, an absorption index is 0.001, a temperature of a solvent: DPBS is 25°C and the corresponding viscosity and
25 refractive index are 1.0200 and 1.335, respectively. Once measurement was conducted by a size measurement including repeating 15 times and then repeating six times.

As the PDI value is decreased, the corresponding particles become uniformly distributed, and thus, it could be appreciated that the nanoparticles of the present invention have a significantly uniform size.

5

Example 5. Confirmation of inhibition of target gene expression using target gene-specific siRNA for human in human fibroblast cell line (MRC-5).

Human fibroblast (MRC-5) which is a fibroblast cell line was transformed by siRNAs having sequences of SEQ ID NOs: 1 to 10, 101 to 110, 201 to 210 and 601 produced by Example 1 as the sense strand, and the expression aspect of the target gene was analyzed in the transformed fibroblast cell line (MRC-5).

15

Example 5-1. Culture of human fibroblast cell line

A human fibroblast cell line (MRC-5) obtained from Korean Cell line bank (KCLB) was cultured in RPMI-1640 culture medium (GIBCO/Invitrogen, USA, 10% (v/v) fetal bovine serum, penicillin 100 units/ml and 100 $\mu\text{g}/\text{ml}$ of streptomycin) under condition of 37 °C and 5%(v/v) CO₂.

Example 5-2. Transfection of target siRNA into human fibroblast cell line

1.8 $\times 10^5$ fibroblast cell line (MRC-5) cultured by Example 5-1 was cultured in RPMI 1640 medium for 18 hours in 6-well plate under condition of 37°C and 5 %(v/v) CO₂,

and the medium was removed, and 500 μ l of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

Meanwhile, 3.5 μ l of Lipofectamine™ RNAi Max (Invitrogen, USA) was mixed with 246.5 μ l of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. siRNA solutions each having a final concentration of 5 or 20 nM were prepared by adding 5 or 20 μ l of siRNAs (1 pmole/ μ l) having sequences of SEQ ID NOs: 1 to 10, 101 to 110, 201 to 210 and 601 by Example 1, as the sense strand, to 230 μ l of Opti-MEM medium. The Lipofectamine™ RNAi Max mixture and the siRNA solution were mixed and reacted at room temperature for 15 minutes, thereby preparing a solution for transfection.

Then, 500 μ l of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under condition of 37 $^{\circ}$ C and 5%(v/v) CO₂ for 24 hours.

Example 5-3. Quantitative analysis of target gene mRNA

cDNA was produced by extracting total RNA from the transfected cell line by Example 5-2, and an mRNA expression amount of the target gene was subjected to relative-quantification by real-time PCR.

Example 5-3-1. RNA separation from transfected cell
and cDNA production

Total RNA was extracted from the transfected cell
5 line of Example 5-2 by RNA extraction kit (AccuPrep Cell
total RNA extraction kit, BIONEER, Korea), and the
extracted RNA was used to produce cDNA by RNA reverse
transcriptase (AccuPower CycleScript RT Premix/dT20,
Bioneer, Korea) according to the following method.
10 Specifically, 1 μ g of the extracted RNA per each tube was
added to AccuPower CycleScript RT Premix/dT20 (Bioneer,
Korea) contained in 0.25ml Eppendorf tube, and distilled
water treated with DEPC (diethyl pyrocarbonate) was added
thereto so as to have a total volume of 20 μ l. A process of
15 hybridizing RNA and primers at 30°C for 1 minute by a gene
amplifier (MyGenie™ 96 Gradient Thermal Block, BIONEER,
Korea) and a process of producing cDNA at 52°C for 4
minutes were repeated 6 times, and then, an amplification
reaction was completed by inactivating the enzyme at 90°C
20 for 5 minutes.

Example 5-3-2. Relative-quantitative analysis of
target gene mRNA

A relative amount of the respiratory disease-related
25 gene mRNA was quantified by the following method through
real-time PCR having the cDNA produced by Example 5-3-1 as
a template. cDNA produced by Example 5-3-1 was diluted 5

times with distilled water in each well of 96-well plate. Then, 3 μ l of the diluted cDNA, 25 μ l of 2 × GreenStar™ PCR master mix (BIONEER, Korea), 19 μ l of distilled water, and 3 μ l of qPCR primers (Table 2; F and R each having 10 pmole/ μ l; BIONEER, Korea) were added thereto to prepare each mixed solution. Meanwhile, RPL13A (ribosomal protein L13a) which is a housekeeping gene (hereinafter, referred to as HK gene) was determined as a standard gene to normalize the expression amount of the target gene mRNA.

The following reaction was performed on 96-well plate containing the mixture by Exicycler™ 96 Real-Time Quantitative Thermal Block (BIONEER, Korea). After the reaction at 95°C for 15 minutes to activate the enzyme and remove a secondary structure of cDNA, four processes including a process of denaturing at 94°C for 30 seconds, a process of annealing at 58°C for 30 seconds, a process of extension at 72°C for 30 seconds, and a process of SYBR green scan were repeated 42 times, and final extension was performed at 72°C for 3 minutes. Then, the temperature was maintained at 55°C for 1 minute, and a melting curve was analyzed from 55°C up to 95°C. After PCR was completed, for Ct (threshold cycle) value of each of the obtained target gene, Ct values of the target gene corrected through GAPDH gene were calculated, and then the difference (Δ Ct) was obtained by using a test group treated with siRNA (SEQ ID NO: 601, siCONT) having a control sequence preventing inhibition of gene expression, as a control group.

The expression amount of the target gene of the cell treated with the CTGF (Homo sapiens)-specific siRNA (having sequence of SEQ ID NOs: 1 to 10 as the sense strand) was relatively quantified by using the ΔC_t value and calculation formula $2^{(-\Delta C_t)} \times 100$ (FIG. 2A). Further, the expression amount of the target gene of the cell treated with the Cyr61 (Homo sapiens)-specific siRNA (having sequence of SEQ ID NOs: 101 to 110 as the sense strand) was relatively quantified (FIG. 2B), and the expression amount of the target gene of the cell treated with the Plekhol1 (Homo sapiens)-specific siRNA (having sequence of SEQ ID NOs: 201 to 210 as the sense strand) was relatively quantified (FIG. 2C).

As a result, it could be confirmed that several kinds of siRNA of the present invention showed high inhibition level of target gene expression. In addition, in order to select siRNA with high efficiency, siRNAs having sequences of SEQ ID NOs: 1, 3, 4, 8, 9, 10, 102, 104, 105, 106, 107, 108, 109, 204, 206, 207, 208, 209 and 210 in which the mRNA expression amount for each gene at 5 nM concentration is significantly decreased, as the sense strand, were selected.

Table 2 qPCR primer sequences

(m, *Mus musculus*; h, *Homo sapiens*; F, Forward primer; R- reverse primer)

Name	Sequences or product name
hCTGF-F	P199255(qPCR primer #, BIONEER)
hCTGF-R	
hAREG-F	ACACCTACTCTGGGAAGCGT
hAREG-R	GCCAGGTATTGTGGTTCGT
hCYR61-F	AAAGGAAGCCTTGCCTATTC
hCYR61-R	TCAACTOCACAAGCTCCAAA
hPlekho1-F	P299777(qPCR primer #, BIONEER)
hPlekho1-R	
mRPL13A-F	AGCTCATGAGGCTACGGAAA
mRPL13A-R	CGTACATTCAGGGCAACA
mCTGF-F	GGGCCCTCTCTCCGATTTC
mCTGF-R	ATCCAGGCAAGTGCATTTGTA
mAREG-F	GGTCTTAGGCTCAGGCCATTA
mAREG-R	CGCTTATGGTGGAAACCTCTC
mCYR61-F	CTGCGCTAAACAACCTCAACGA
mCYR61-R	GCAGATCCCTTTCAGAGCGG
mPlekho1-F	AATCTGCGGGAAAAGGGATT
mPlekho1-R	AACACCTCTGACTGTTTTCTC
mRPL13A-F	CGTGTGCTCTCAAGGTGTG
mRPL13A-R	CGATAGTGCATCTTGGCCCTT

Example 6. Selection of target gene-specific siRNA for human with high efficiency in human fibroblast cell line (MRC-5)

5 Human fibroblast cell line (MRC-5) was transformed by using siRNAs having sequences of SEQ ID NOs: 1, 3, 4, 8, 9, 10, 102, 104, 105, 106, 107, 108, 109, 204, 206, 207, 208, 209, 210 and 601 selected by Example 5-3-2, as the sense strand, and the expression aspect of the target gene was
10 analyzed in the transformed fibroblast cell line (MRC-5) to select siRNA with high efficiency.

Example 6-1. Culture of human fibroblast cell line

Human fibroblast cell line (MRC-5) obtained from
15 Korean Cell line bank (KCLB, Korea) was cultured under the same condition as Example 5-1.

Example 6-2. Transfection of target siRNA into human fibroblast cell line

1.8×10⁵ fibroblast cell line (MRC-5) cultured by Example 6-1 was cultured in RPMI 1640 medium for 18 hours in 6-well plate under condition of 37°C and 5 % (v/v) CO₂, and the medium was removed, and 500μℓ of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

Meanwhile, 3.5μℓ of Lipofectamine™ RNAi Max (Invitrogen, USA) was mixed with 246.5μℓ of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. siRNA solutions each having a final concentration of 0.2 or 1 nM were prepared by adding 0.2 or 1μℓ of siRNAs (1 pmole/μℓ) having sequences of SEQ ID NOs: 1, 3, 4, 8, 9, 10, 102, 104, 105, 106, 107, 108, 109, 204, 206, 207, 208, 209, 210 and 601 by Example 1, as the sense strand, to 230μℓ of Opti-MEM medium. The Lipofectamine™ RNAi Max mixture and the siRNA solution were mixed and reacted at room temperature for 15 minutes, thereby preparing a solution for transfection.

Then, 500μℓ of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under condition of 37°C and 5% (v/v) CO₂ for 24 hours.

Example 6-3. Quantitative analysis of target gene mRNA

cdNA was produced by extracting total RNA from the

transfected cell line by Example 6-2 through the same method as Example 4-3, and an mRNA expression amount of the target gene was subjected to relative-quantification by real-time PCR. The inhibition amount of the target gene expression according to low concentration siRNA treatment was observed to clearly confirm each siRNA efficacy, and it was confirmed that siRNAs having sequence of SEQ ID NOs: 8, 107 and 206 as the sense strand showed relatively high level of inhibition for target gene expression even at a significantly low concentration (FIG. 3).

Example 7. Confirmation of inhibition of target gene expression using target gene-specific siRNA for human in human lung cancer cell line (A549).

Human lung cancer cell line (A549) which is a lung tumor cell line was transformed by siRNAs having sequences of SEQ ID NOs: 35, 42, 59, 602, 603, 604, 124, 153, 166, 187, 197, 212, 218, 221, 223 and 601 produced by Example 1 as the sense strand, and the expression aspect of the target gene was analyzed in the transformed lung cancer cell line (A549).

Example 7-1. Culture of human lung cancer cell line

A human lung cancer cell line (A549) obtained from American Type Culture Collection (ATCC) was cultured in DMEM culture medium (GIBCO/Invitrogen, USA, 10% (v/v) fetal bovine serum, penicillin 100 units/ml and 100 μ g/ml of

streptomycin) under condition of 37 °C and 5%(v/v) CO₂.

Example 7-2. Transfection of target siRNA into human lung cancer cell line

5 1.2×10⁵ lung cancer cell line (A549) cultured by Example 7-1 was cultured in DMEM medium for 18 hours in 6-well plate under condition of 37°C and 5 %(v/v) CO₂, and the medium was removed, and 500μℓ of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

10 Meanwhile, 3.5μℓ of Lipofectamine™ RNAi Max (Invitrogen, USA) was mixed with 246.5μℓ of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. siRNA solutions each having a final concentration of 5nM, 1nM, 0.5nM, 0.2nM

15 or 0.04nM were prepared by adding 1μℓ of siRNAs (1 pmole/μℓ) having sequences of SEQ ID NOs: 35, 42, 59, 602, 603, 604, 124, 153, 166, 187, 197, 212, 218, 221 and 223 by Example 1, as the sense strand, to 230μℓ of Opti-MEM medium. The Lipofectamine™ RNAi Max mixture and the siRNA solution

20 were mixed and reacted at room temperature for 15 minutes, thereby preparing a solution for transfection.

Then, 500μℓ of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and

25 the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under condition of 37°C and 5%(v/v) CO₂ for 24 hours.

Example 7-3. Quantitative analysis of target gene mRNA

5 cDNA was produced by extracting total RNA from the transfected cell line by Example 7-2, and an mRNA expression amount of the target gene was subjected to relative-quantification by real-time PCR.

Example 7-3-1. RNA separation from transfected cell
10 and cDNA production

Total RNA was extracted from the transfected cell line of Example 5-2 by RNA extraction kit (AccuPrep Cell total RNA extraction kit, BIONEER, Korea), and the extracted RNA was used to produce cDNA by RNA reverse
15 transcriptase (AccuPower CycleScript RT Premix/dT20, Bioneer, Korea) according to the following method. Specifically, 1 μ g of the extracted RNA per each tube was added to AccuPower CycleScript RT Premix/dT20 (Bioneer, Korea) contained in 0.25ml Eppendorf tube, and distilled
20 water treated with DEPC (diethyl pyrocarbonate) was added thereto so as to have a total volume of 20 μ l. A process of hybridizing RNA and primers at 30 $^{\circ}$ for 1 minute by a gene amplifier (MyGenie™ 96 Gradient Thermal Block, BIONEER, Korea) and a process of producing cDNA at 52 $^{\circ}$ for 4 minutes
25 were repeated 6 times, and then, an amplification reaction was completed by inactivating the enzyme at 90 $^{\circ}$ for 5 minutes.

Example 7-3-2. Relative quantitative analysis of target gene mRNA

A relative amount of the respiratory disease-related gene mRNA was quantified by the following method through real-time PCR having the cDNA produced by Example 7-3-1 as a template. cDNA produced by Example 6-3-1 was diluted 5 times with distilled water in each well of 96-well plate. Then, 3 μ l of the diluted cDNA, 25 μ l of 2 $\times$ GreenStar™ PCR master mix (BIONEER, Korea), 19 μ l of distilled water, and 3 μ l of qPCR primers (Table 2; F and R each having 10 pmole/ μ l; BIONEER, Korea) were added thereto to prepare each mixed solution. Meanwhile, RPL13A (ribosomal protein L13a) which is a housekeeping gene (hereinafter, referred to as HK gene) was determined as a standard gene to normalize the expression amount of the target gene mRNA. The following reaction was performed on 96-well plate containing the mixture by Exicycler™ 96 Real-Time Quantitative Thermal Block (BIONEER, Korea). After the reaction at 95 $^{\circ}$ C for 15 minutes to activate the enzyme and remove a secondary structure of cDNA, four processes including a process of denaturing at 94 $^{\circ}$ C for 30 seconds, a process of annealing at 58 $^{\circ}$ C for 30 seconds, a process of extension at 72 $^{\circ}$ C for 30 seconds, and a process of SYBR green scan were repeated 42 times, and final extension was performed at 72 $^{\circ}$ C for 3 minutes. Then, the temperature was maintained at 55 $^{\circ}$ C for 1 minute, and a melting curve was

analyzed from 55° up to 95°. After PCR was completed, for Ct (threshold cycle) value of each of the obtained target gene, Ct values of the target gene corrected through GAPDH gene were calculated, and then the difference (ΔC_t) was
 5 obtained by using a test group treated with siRNA (SEQ ID NO: 601, siCONT) having a control sequence preventing inhibition of gene expression, as a control group.

The expression amount of the target gene of the cell treated with the CTGF (Homo sapiens)-specific siRNA (having
 10 sequence of SEQ ID NOs: 132, 42, 59, 602, 603, 604 as the sense strand) was relatively quantified by using the ΔC_t value and calculation formula $2^{(-\Delta C_t)} \times 100$ (FIG. 4A). Further, the expression amount of the target gene of the cell treated with the Cyr61(Homo sapiens)-specific siRNA
 15 (having sequence of SEQ ID NOs: 124, 153, 166, 187, and 197 as the sense strand) was relatively quantified (FIG. 4B), and the expression amount of the target gene of the cell treated with the Plekho1(Homo sapiens)-specific siRNA (having sequence of SEQ ID NOs: 212, 218, 221, and 223 as
 20 the sense strand) was relatively quantified (FIG. 4C).

As a result, it could be confirmed that several kinds of siRNA of the present invention showed high inhibition level of target gene expression. In addition, in order to select siRNA with high efficiency, siRNAs having sequences
 25 of SEQ ID NOs: 42, 59, 602, 124, 153, 187, 197, 212, 218, 221 and 223 in which the mRNA expression amount for each gene at 5 nM concentration is significantly decreased, as

the sense strand, were selected.

Example 8. Inhibition of target gene expression in human lung cancer cell line (A549) by nanoparticle (SAMIrNA) formed of double-helical oligo polymer structure

Human lung cancer cell line (A549) was transformed by using the nanoparticle formed of SAMiRNA LP including siRNA having sequences of SEQ ID NOs: 42, 59, 602, 124, 153, 187, 197, 212, 218, 221 and 223 selected by Example 7-3-2, as the sense strand, and the expression aspect of the target gene was analyzed in the transformed lung cancer cell line (A549).

Example 8-1. Culture of human lung cancer cell line Human lung cancer cell line (A549) obtained from American Type Culture Collection (ATCC) was cultured under the same condition as Example 7-1.

Example 8-2. Transfection of target SAMiRNA into human lung cancer cell line

1.2×10^5 lung cancer cell line (A549) cultured by Example 8-1 was cultured in RPMI 1640 medium for 18 hours in 12-well plate under condition of 37°C and 5 % (v/v) CO_2 , and the medium was removed, and the same amount of Opti-MEM medium (GIBCO, USA) for each well was dispensed. $100\mu\text{l}$ of Opti-MEM medium and SAMiRNALP and monoSAMIrNALP produced by Example 4-2 were added to DPBS at a concentration of 50

$\mu\text{g/ml}$, the obtained mixture was freeze-dried at -75°C and 5mTorr condition for 48 hours by the same method as Example 5-1 to produce homogenized nanoparticles. Then, each well of the tumor cell line in which the Opti-MEM is dispensed was treated with a transfection solution at a concentration of 200 nM, and cultured at 37°C and 5 % (v/v) CO_2 for the total of 48 hours.

Example 8-3. Relative-quantitative analysis of target gene mRNA

cDNA was produced by extracting total RNA from the transfected cell line by Example 8-2 through the same method as Example 6-3, and an mRNA expression amount of the target gene was subjected to relative quantification by real-time PCR. The inhibition amount of the target gene expression according to low concentration siRNA treatment was observed to clearly confirm each siRNA efficacy, and it was confirmed that siRNAs having sequence of SEQ ID NOs: 42, 59 and 602 as the sense strand showed relatively high level of inhibition for target gene expression even at a significantly low concentration (FIG. 5).

Example 9. Confirmation of inhibition of target gene expression using target gene-specific siRNA for mouse in mouse fibroblast cell line (NIH3T3).

Mouse fibroblast (NIH3T3) which is a fibroblast cell line was transformed by siRNAs having sequences of SEQ ID

NOs: 301 to 330, 401 to 430, 501 to 530 and 601 produced by Example 1 as the sense strand, and an expression aspect of the target gene was analyzed in the transformed fibroblast cell line (NIH3T3).

5

Example 9-1. Culture of mouse fibroblast cell line

A mouse fibroblast cell line (NIH3T3) obtained from American Type Culture Collection (ATCC) was cultured in RPMI-1640 culture medium (GIBCO/Invitrogen, USA, 10% (v/v) fetal bovine serum, penicillin 100 units/ml and 100 $\mu\text{g}/\text{ml}$ of streptomycin) under condition of 37 $^{\circ}\text{C}$ and 5% (v/v) CO_2 .

10

Example 9-2. Transfection of target siRNA into mouse fibroblast cell line

1×10^5 fibroblast cell line (NIH3T3) cultured by Example 9-1 was cultured in RPMI 1640 medium for 18 hours in 12-well plate under condition of 37 $^{\circ}\text{C}$ and 5 % (v/v) CO_2 , and the medium was removed, and 500 μl of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

15

Meanwhile, 1.5 μl of LipofectamineTM RNAi Max (Invitrogen, USA) was mixed with 248.5 μl of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. 5 or 20 μl of siRNAs (1 pmole/ μl) having sequences of SEQ ID NOs: 301 to 330, 401 to 430, 501 to 530 and 601 produced by Example 1, as the sense strand, were added to 230 μl of Opti-MEM medium, thereby preparing siRNA solutions each having a final

20

25

concentration of 5 or 20 nM. The Lipofectamine™ RNAi Max mixture and the siRNA solution were mixed and reacted at room temperature for 20 minutes, thereby preparing a solution for transfection.

5 Then, 500 μ l of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under
10 condition of 37°C and 5%(v/v) CO₂ for 24 hours.

Example 9-3. Quantitative analysis of target gene mRNA

cDNA was produced by extracting total RNA from the
15 transfected cell line by Example 9-2 through the same method as Example 5-3, and an mRNA expression amount of the target gene was subjected to relative quantification by real-time PCR.

The expression amount of the target gene of the cell
20 treated with the CTGF (Mus musculus)-specific siRNA (having sequence of SEQ ID NOs: 301 to 330 as the sense strand) was relatively quantified (FIG. 6A). Further, the expression amount of the target gene of the cell treated with the Cyr61(Mus musculus)-specific siRNA (having sequence of SEQ
25 ID NOs: 401 to 430 as the sense strand) was relatively quantified (FIG. 6B), and the expression amount of the target gene of the cell treated with the Plekhol(Mus

musculus)-specific siRNA (having sequence of SEQ ID NOs: 501 to 530 as the sense strand) was relatively quantified (FIG. 6C).

As a result, it could be confirmed that several kinds of siRNA of the present invention showed high inhibition level of target gene expression. In addition, in order to select siRNA with high efficiency, siRNA having sequence of SEQ ID NO: 301, 302, 303, 305, 306, 307, 309, 317, 323 or 329 in which the mRNA expression amount for CTGF(Mus musculus) at 20 nM concentration is significantly decreased, as the sense strand, was selected, siRNA having sequence of SEQ ID NO: 409, 410, 415, 417, 418, 420, 422, 424, 427 or 429 in which the mRNA expression amount for Cyr61(Mus musculus) at 20 nM concentration is significantly decreased, as the sense strand, was selected, and siRNA having sequence of SEQ ID NO: 504, 505, 506, 507, 514, 515, 522, 523, 524 or 525 in which the mRNA expression amount for Plekhol(Mus musculus) at 20 nM concentration is significantly decreased, as the sense strand, was selected.

Further, in order to select siRNA with more preferable efficiency, siRNA having sequence of SEQ ID NO: 301, 303, 307 or 323 in which the mRNA expression amount for CTGF(Mus musculus) at 5 nM concentration is significantly decreased, as the sense strand, was selected, siRNA having sequence of SEQ ID NO: 410, 422, or 424 in which the mRNA expression amount for Cyr61(Mus musculus) at 5 nM concentration is significantly decreased, as the sense

strand, was selected, and siRNA having sequence of SEQ ID NO: 507, 515, or 525 in which the mRNA expression amount for Plekhol(Mus musculus) at 5 nM concentration is significantly decreased, as the sense strand, was selected (FIG. 7).

Example 10. Selection of target gene-specific siRNA for mouse with high efficiency in mouse fibroblast cell line (NIH3T3)

The expression aspect of the target gene was analyzed in the mouse fibroblast cell line (NIH3T3) using siRNAs having sequences of SEQ ID NOs: 301, 303, 307, 323, 410, 422, 424, 507, 515, 525 and 601 selected by Example 9-3, as the sense strand, to select siRNA with high efficiency.

15

Example 10-1. Culture of mouse fibroblast cell line

Mouse fibroblast cell line (NIH3T3) obtained from American Type Culture Collection (ATCC) was cultured under the same condition as Example 9-1.

20

Example 10-2. Transfection of target siRNA into mouse fibroblast cell line

1×10^5 fibroblast cell line (NIH3T3) cultured by Example 10-1 was cultured in RPMI 1640 medium for 18 hours in 12-well plate under condition of 37°C and 5 % (v/v) CO₂, and the medium was removed, and 500 μ l of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

Meanwhile, 1.5 μ l of Lipofectamine™ RNAi Max (Invitrogen, USA) was mixed with 248.5 μ l of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. 0.2, 1 or 5 μ l of siRNAs (1 pmole/ μ l) having sequences of SEQ ID NOs: 301, 303, 307, 323, 410, 422, 424, 507, 515, 525 and 601 produced by Example 1, as the sense strand, were added to 230 μ l of Opti-MEM medium, thereby preparing siRNA solutions each having a final concentration of 0.2, 1 or 5 nM. The Lipofectamine™ RNAi Max mixture and the siRNA solution were mixed and reacted at room temperature for 20 minutes, thereby preparing a solution for transfection.

Then, 500 μ l of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under condition of 37°C and 5%(v/v) CO₂ for 24 hours.

Example 10-3. Quantitative analysis of target gene mRNA

cDNA was produced by extracting total RNA from the transfected cell line by Example 10-2 through the same method as Example 5-3, and an mRNA expression amount of the target gene was subjected to relative quantification by real-time PCR. The expression amount of the target gene of the cell treated with the CTGF (Mus musculus)-specific

siRNA (having sequence of SEQ ID NOs: 301, 303, 307, and 323 as the sense strand) was relatively quantified (FIG. 8A). Further, the expression amount of the target gene of the cell treated with the Cyr61 (Mus musculus)-specific siRNA (having sequence of SEQ ID NOs: 410, 422 and 424, as the sense strand) was relatively quantified (FIG. 8B), and the expression amount of the target gene of the cell treated with the Plekhol (Mus musculus)-specific siRNA (having sequence of SEQ ID NOs: 507, 515, and 525 as the sense strand) was relatively quantified (FIG. 8C).

As a result, it was confirmed that each target gene-specific siRNA inhibits the expression of the target gene in a concentration-dependent manner, and it was confirmed that siRNAs having sequences of SEQ ID NOs: 307, 424 and 525 as the sense strand showed relatively high level of inhibition for target gene expression even at a significantly low concentration, to select siRNA with high efficiency.

Example 11. Confirmation of inhibition of target gene expression using target gene-specific siRNA for human in mouse fibroblast cell line (NIH3T3).

Since biopharmaceuticals have species-specific action sites such as protein structure or gene sequence, identity of treatment drug is significantly important for securing efficiency in developing biopharmaceutical novel drug. Gene sequence homology between the target gene-specific siRNA

for human and the target gene-specific siRNA for mouse designed in Example 1 was analyzed to select siRNA sequences that may confirm the inhibition effect of the target gene expression in the mouse fibroblast cell.

5 The selected siRNA sequences are siRNAs having sequences of SEQ ID NOs: 4, 5, 6, 8, 9, 102, 104, 105, 107, 108, 109, 202, 204, 206, 207, 208 and 209, as the sense strand, which are the target gene-specific siRNAs for human produced by Example 1, siRNAs having sequences of SEQ ID
10 NOs: 307, 424 and 525, as the sense strand, which are the target gene-specific siRNAs for mouse, and siRNA having sequence of SEQ ID NO: 601, as the sense strand, which is a control group. The expression aspect of the target gene was analyzed in the mouse fibroblast cell line (NIH3T3)
15 using these selected siRNAs, and efficacy thereof was confirmed in the mouse cell of siRNA designed based on the human gene.

Example 11-1. Culture of mouse fibroblast cell line

20 Mouse fibroblast cell line (NIH3T3) obtained from American Type Culture Collection (ATCC) was cultured under the same condition as Example 9-1.

Example 11-2. Transfection of target siRNA into mouse
25 fibroblast cell line

1.8×10⁵ fibroblast cell line (NIH3T3) cultured by Example 11-1 was cultured in RPMI 1640 medium for 18 hours

in 6-well plate under condition of 37°C and 5 % (v/v) CO₂, and the medium was removed, and 500 µl of Opti-MEM medium (GIBCO, USA) for each well was dispensed.

Meanwhile, 3.5 µl of Lipofectamine™ RNAi Max (Invitrogen, USA) was mixed with 246.5 µl of Opti-MEM medium to prepare a mixed solution, and the mixed solution was reacted at room temperature for 5 minutes. siRNA solutions each having a final concentration of 5 or 20 nM were prepared by adding 5 or 20 µl of siRNAs (1 pmole/µl) having sequences of SEQ ID NOs: 4, 5, 6, 8, 9, 102, 104, 105, 107, 108, 109, 202, 204, 206, 207, 208, 209, 307, 424, 525 and 601 produced by Example 1, as the sense strand, to 230 µl of Opti-MEM medium. The Lipofectamine™ RNAi Max mixture and the siRNA solution were mixed and reacted at room temperature for 15 minutes, thereby preparing a solution for transfection.

Then, 500 µl of each transfection solution was dispensed in each well of the tumor cell line containing Opti-MEM dispensed therein, and cultured for 6 hours, and the Opti-MEM medium was removed. Here, 1 ml of RPMI 1640 culture medium was dispensed therein and cultured under condition of 37°C and 5% (v/v) CO₂ for 24 hours.

Example 11-3. Quantitative analysis of target gene mRNA¹

cDNA was produced by extracting total RNA from the transfected cell line by Example 11-2 through the same

method as Example 5-3, and an mRNA expression amount of the target gene was subjected to relative quantification by real-time PCR. The expression amount of the target gene of the cell treated with the CTGF (Mus musculus)-specific siRNA (SEQ ID NO: 307) or treated with the CTGF(Homo sapiens)-specific siRNA (SEQ ID NO: 4, 5, 6, 8 or 9) was relatively quantified (FIG. 9A). The expression amount of the target gene of the cell treated with Cyr61(Mus musculus)-specific siRNA (having a sequence of SEQ ID NO: 424 as the sense strand) or treated with Cyr61(Homo sapiens)-specific siRNA (having a sequence of SEQ ID NO: 102, 104, 105, 107, 108 or 109 as the sense strand) was relatively quantified (FIG. 9B), and the expression amount of the target gene of the cell treated with Plekhol1(Mus musculus)-specific siRNA (having a sequence of SEQ ID NO: 525 as the sense strand) or treated with Plekhol1(Homo sapiens)-specific siRNA (having a sequence of SEQ ID NO: 202, 204, 206, 207, 208 or 209 as the sense strand) was relatively quantified (FIG. 9C).

As a result, it was confirmed that each target gene-specific siRNA for human inhibits the expression of the target gene according to sequence homology, and it was confirmed that siRNAs having sequences of SEQ ID NOs: 6, 8, 102, 104, 105, 204, 207 and 208 as the sense strand showed relatively high level of inhibition for target gene expression at 20nM, and among them, IC50(inhibition concentration 50%) was less than 20nM in siRNAs having

sequences of SEQ ID NOs: 6, 102 and 207 even in mouse cell lines. Therefore, it was confirmed that relatively high level of inhibition for target gene expression was maintained even at a low concentration, that is, these
5 siRNAs had high efficiency (FIG. 10).

ADVANTAGEOUS EFFECTS

The CTGF, Cyr61 or Plekhol-specific siRNA according to the present invention, the double-helical oligo RNA
10 structure containing the siRNA, and the pharmaceutical composition containing the double-helical oligo RNA structure for treatment, are capable of inhibiting expression of CTGF, Cyr61 or Plekhol at a high efficiency without side effects to provide treatment effects for
15 respiratory diseases, particularly, idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease (COPD), which may be significantly usefully used for treating respiratory diseases in which there is no appropriate therapeutic agent at present, particularly, idiopathic
20 pulmonary fibrosis and chronic obstructive pulmonary disease (COPD).

From the foregoing, it will be understood by those skilled in the art to which the present invention pertains
25 that the present invention can be carried out in other concrete embodiments without changing the technical spirit or essential feature thereof. In this regard, it should be

understood that the aforementioned examples are of illustrative in all aspects but not is limited. The scope of the present invention should be construed to include the meaning and scope of the appended claims, and all the
5 alterations and modified forms which are derived from the equivalent concept thereof, rather than the detailed description.

【CLAIMS】**【Claim 1】**

A CTGF, Cyr61 or Plekhol specific siRNA comprising a sense strand and an anti-sense strand complementary to the sense strand, wherein the sense strand and the anti-sense strand comprise any one sequence selected from the group consisting of SEQ ID NOS: 1 to 600 and 602 to 604.

【Claim 2】

The CTGF, Cyr61 or Plekhol specific siRNA according to claim 1, wherein the sense strand or anti-sense strand has 19 to 31 nucleotides.

【Claim 3】

The CTGF, Cyr61 or Plekhol specific siRNA according to claim 1, wherein the sense strand and the anti-sense strand complementary to the sense strand comprise any one sequence selected from the group consisting of SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 35, 42, 59, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 124, 153, 166, 187, 197, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 212, 218, 221, 223, 301, 302, 303, 305, 306, 307, 309, 317, 323, 329, 409, 410, 415, 417, 418, 420, 422, 424, 427, 429, 504, 505, 506, 507, 514, 515, 522, 523, 524, 525, 602, 603 and 604.

【Claim 4】

The CTGF, Cyr61 or Plekhol specific siRNA according to any one of claims 1 to 3, wherein the sense strand or the anti-sense strand of the siRNA comprises more than one chemical modification.

【Claim 5】

The CTGF, Cyr61 or Plekhol specific siRNA according to claim 4,

wherein the chemical modification is more than any one selected from the group consisting of:

5 substitution of -OH group at 2' carbon in a sugar structure of nucleotides with -CH₃(methyl), -OCH₃ (methoxy), -NH₂, -F(fluorine), -O-2-methoxyethyl, -O-propyl, -O-2-methylthioethyl, -O-3-aminopropyl, -O-3-dimethylaminopropyl, -O-N-methylacetamido or -O-dimethylamidooxyethyl;

10 substitution of oxygen in a sugar structure of nucleotides with sulfur;

modification of bindings between nucleotides to phosphorothioate boranophosphate, or methyl phosphonate; and

15 modification of nucleotide to peptide nucleic acid (PNA), modification to locked nucleic acid (LNA), or modification to unlocked nucleic acid (UNA).

【Claim 6】

The CTGF, Cyr61 or Plekhol specific siRNA according to 20 any one of claims 1 to 5, more than one phosphate group(s) is bonded to 5' end of the antisense strand of siRNA.

【Claim 7】

A structure comprising double-helical oligo RNA, represented by the following Structural Formula (1):

25 Structural Formula 1

A-X-R-Y-B

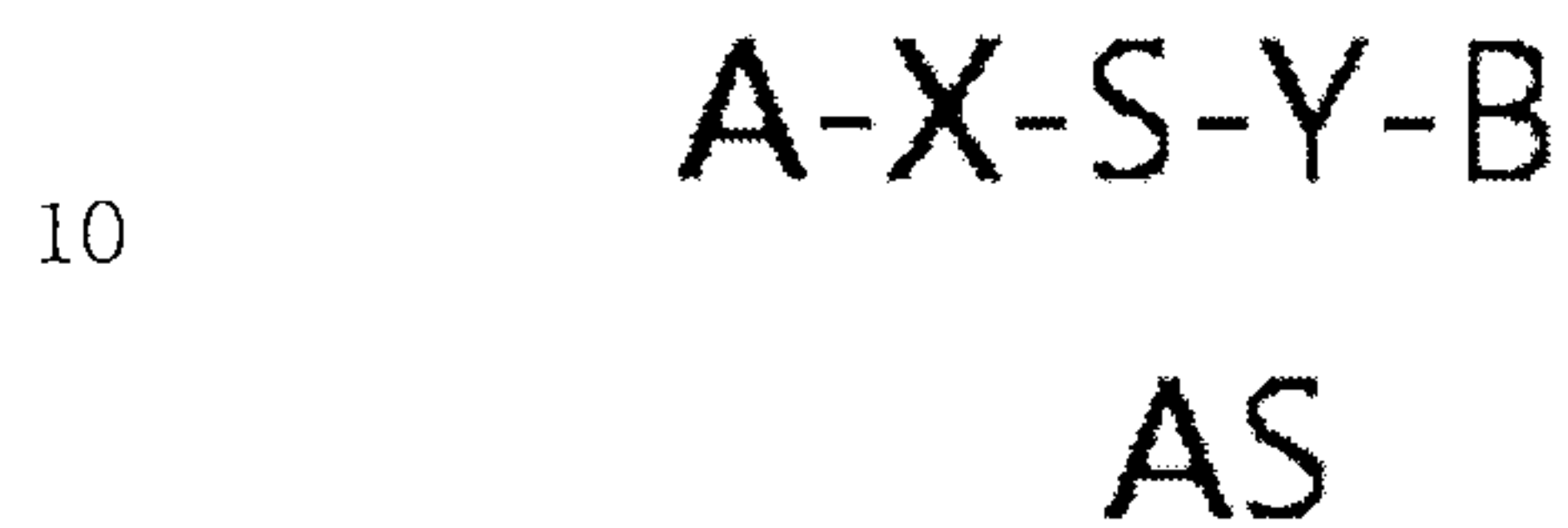
wherein A is a hydrophilic material, B is a

hydrophobic material, X and Y are each independently a simple covalent bond or a linker-mediated covalent bond, and R is CTGF, Cyr61, or Plekhol-specific siRNA.

[Claim 8]

5 The structure according to claim 7, wherein the structure comprising double-helical oligo RNA represented by the following Structural Formula (2):

Structural Formula 2



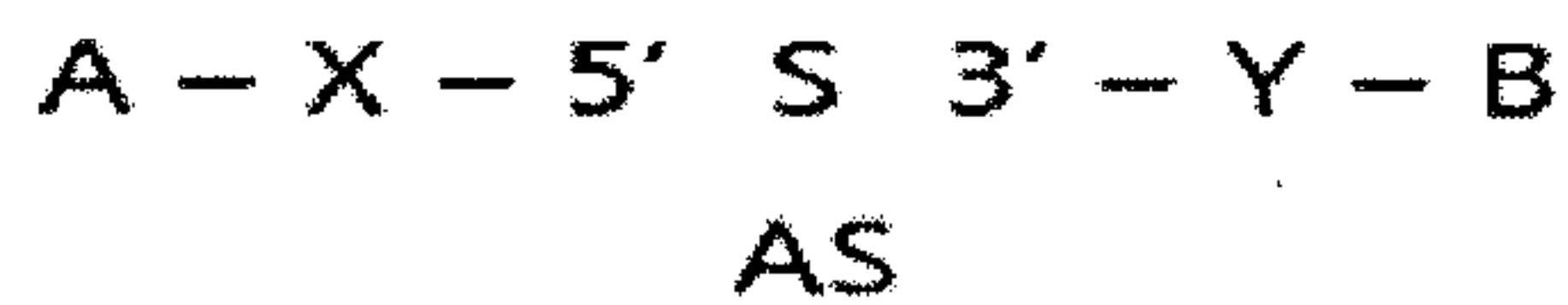
 wherein S is sense strand of the siRNA of claim 7, and AS is an antisense strand of claim 7, A, B, X and Y are the same as being defined in claim 7.

[Claim 9]

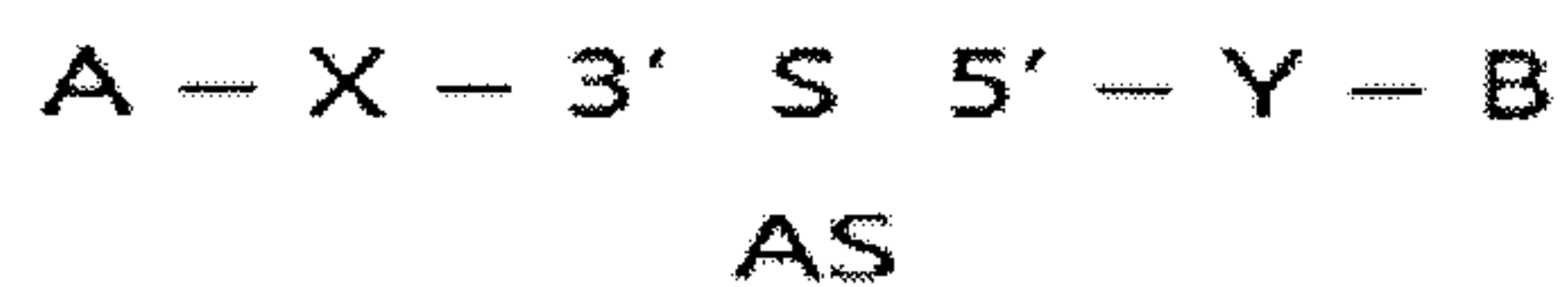
 The structure according to claim 8, wherein the structure comprising double-helical oligo RNA represented by the following Structural Formula (3) or Structural

20 Formula (4):

Structural Formula 3



Structural Formula 4



25 wherein A, B, X, Y S and AS are the same as being defined in claim 8, and 5' and 3' mean 5' end and 3' end of

the sense strand of siRNA.

【Claim 10】

The structure according to any one of claims 7 to 9,
wherein the CTGF, Cyr61 or Plekhol-specific siRNA is siRNA
5 according to any one of claims 1 to 6.

【Claim 11】

The structure according to any one of claims 7 to 10,
wherein the hydrophilic material has a molecular weight of
200 to 10,000.

10 **【Claim 12】**

The structure according to claim 11, wherein the
hydrophilic material is any one selected from the group
consisting of polyethylene glycol, polyvinyl pyrrolidone
and polyoxazoline.

15 **【Claim 13】**

The structure according to any one of claims 7 to 10,
wherein the hydrophilic material has the structure
represented by the following Structural Formula (5) or
Structural Formula (6):

20 Structural Formula 5



Structural Formula 6



25

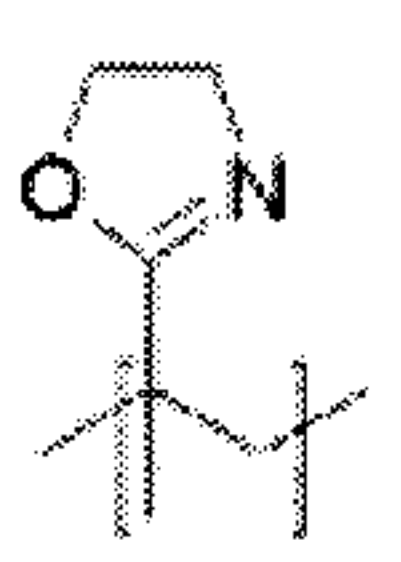
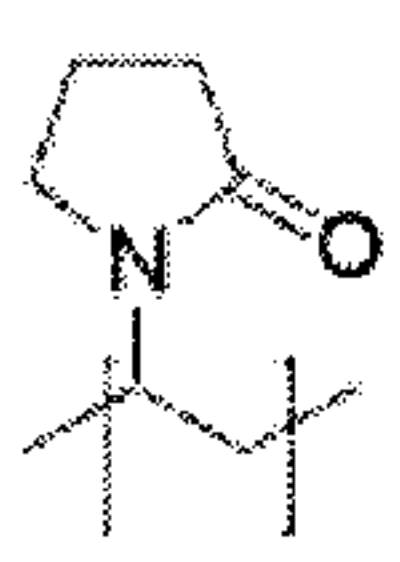
wherein A' is a hydrophilic material monomer,

J is a linker for connecting between m hydrophilic
material monomers, or a linker for connecting between m

hydrophilic material monomers with siRNA, m is an integer of 1 to 15, n is an integer of 1 to 10,

the hydrophilic material monomer A' is a compound selected from the group consisting of compounds (1) to (3),
5 and

the linker J is selected from the group consisting of PO_3^- , SO_3 and CO_2 .

Compound (1)	Compound (2)	Compound (3)
 G is CH_2 , O, S or NH		

【Claim 14】

The structure according to any one of claims 7 to 10,
10 wherein the hydrophobic material has a molecular weight of 250 to 1,000.

【Claim 15】

The structure according to claim 14, wherein the hydrophobic material is one selected from the group
15 consisting of a steroid derivative, a glyceride derivative, glycerol ether, polypropylene glycol, C_{12} to C_{50} unsaturated or saturated hydrocarbon, diacylphosphatidylcholine, fatty acid, phospholipid and lipopolyamine.

【Claim 16】

20 The structure according to claim 15, wherein the steroid derivative is selected from the group consisting of cholesterol, cholestanol, cholic acid, cholesteryl formate, cholestanyl formate, and cholesteryl amine.

【Claim 17】

The structure according to claim 15, wherein the glyceride derivative is selected from the group consisting of mono-, di- and tri-glyceride.

【Claim 18】

5 The structure according to any one of claims 7 to 17, wherein the covalent bond represented by X or Y is non-degradable bond or a degradable bond.

【Claim 19】

10 The structure according to claim 18, wherein the non-degradable bond is amide bond or a phosphorylation bond.

【Claim 20】

15 The structure according to claim 18, wherein the degradable bond is a disulfide bond, an acid degradable bond, an ester bond, an anhydride bond, a biodegradable bond or an enzymatically degradable bond.

【Claim 21】

20 The structure according to any one of claims 7 to 20, further comprising a ligand bonded to the hydrophilic material, which is specifically bonded to a receptor that promotes target cell internalization through receptor-mediated endocytosis (RME).

【Claim 22】

25 The structure according to claim 21, wherein the ligand is selected from the group consisting of a target receptor-specific antibody, aptamer, peptide, N-acetyl galactosamine (NAG), glucose and mannose.

【Claim 23】

The structure according to any one of claims 7 to 20, further comprising amine group or polyhistidine introduced into the distal end bonded with the siRNA in the hydrophilic material.

5 **【Claim 24】**

The structure according to claim 23, wherein the amine group or polyhistidine is bonded to hydrophilic material or hydrophilic block with more than a linker.

【Claim 25】

10 The structure according to claim 23, wherein the amine group is one selected from the group consisting of primary to tertiary amine groups.

【Claim 26】

15 The structure according to claim 23, wherein the polyhistidine comprises 3 to 10 histidines.

【Claim 27】

Nanoparticle(s) comprising the structure according to any one of claims 7 to 26.

【Claim 28】

20 The nanoparticle(s) according to claim 27, wherein the structure comprising the double-helical oligo RNA containing siRNAs with different sequences, is mixed in the nanoparticle(s).

【Claim 29】

25 A pharmaceutical composition comprising siRNA according to any one of claims 1 to 6, the structure according to any one of claims 7 to 26, or the nanoparticle(s) according to claim 27 or 28 as an active

ingredient.

【Claim 30】

The pharmaceutical composition according to claim 29,
wherein the composition is for prevention or treatment of
5 respiratory diseases.

【Claim 31】

The pharmaceutical composition according to claim 30,
wherein the respiratory diseases is selected from the group
consisting of asthma, idiopathic pulmonary fibrosis,
10 chronic obstructive pulmonary disease (COPD), acute or
chronic bronchitis, allergic rhinitis, cough and phlegm,
acute lower respiratory tract infection, bronchitis,
bronchiolitis, acute upper respiratory tract infection,
pharyngitis, tonsillitis, and laryngitis.

15 **【Claim 32】**

The pharmaceutical composition according to claim 30,
wherein the respiratory diseases is idiopathic pulmonary
fibrosis or chronic obstructive pulmonary disease (COPD).

【Claim 33】

20 A lyophilized formulation comprising the
pharmaceutical composition according to any one claims 29
to 32.

【Claim 34】

A method of preventing or treating respiratory
25 diseases comprising: administering siRNA, the structure
comprising double-helical oligo RNA, the nanoparticle(s),
the pharmaceutical composition or the formulation according
to any one of claims 1 to 33.

【Claim 35】

The method according to claim 34, wherein the respiratory diseases is selected from the group consisting of asthma, idiopathic pulmonary fibrosis, chronic
5 obstructive pulmonary disease (COPD), acute or chronic bronchitis, allergic rhinitis, cough and phlegm, acute lower respiratory tract infection, bronchitis, bronchiolitis, acute upper respiratory tract infection, pharyngitis, tonsillitis, and laryngitis.

10 **【Claim 36】**

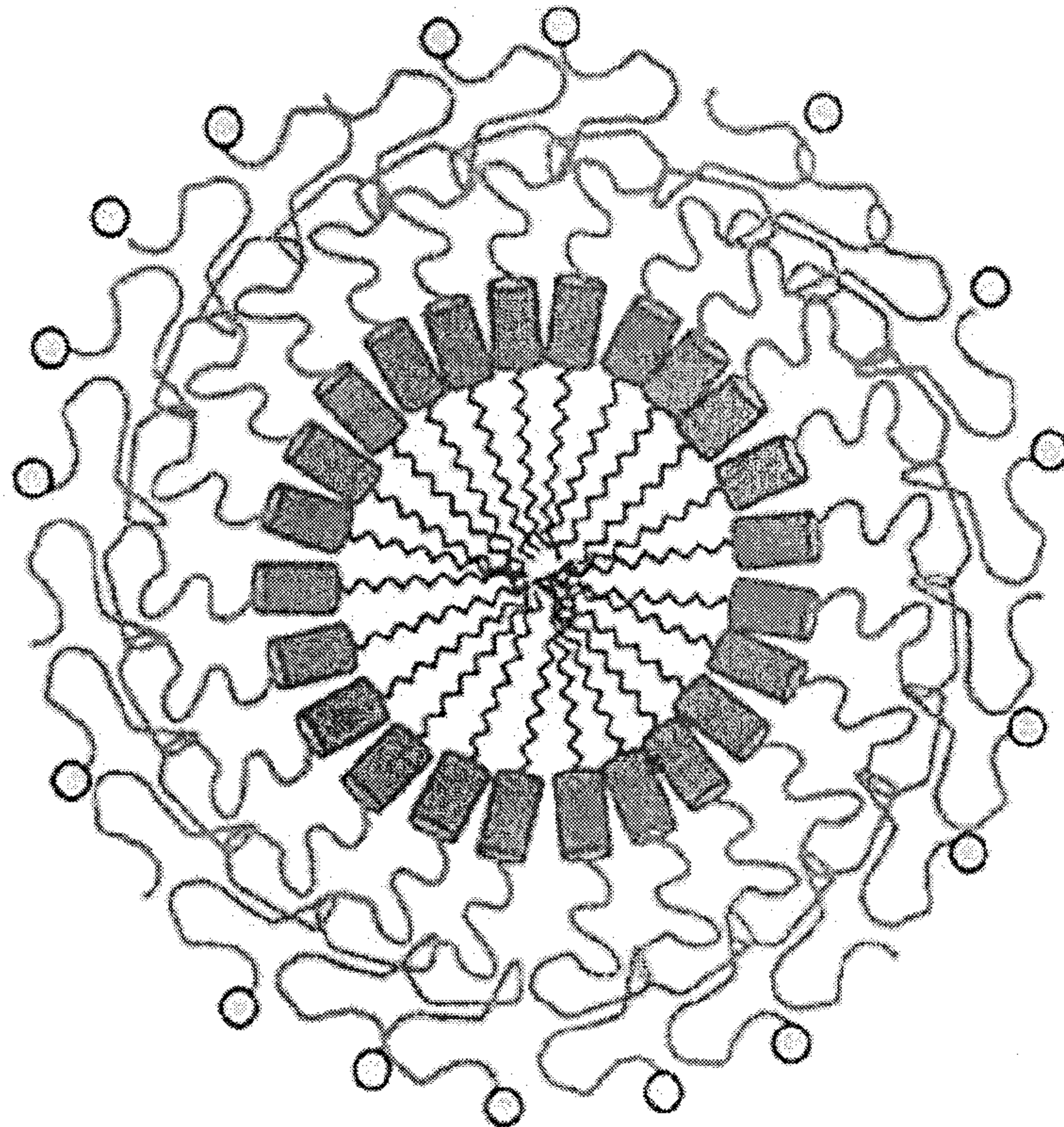
The method according to claim 35, wherein the respiratory diseases is idiopathic pulmonary fibrosis or chronic obstructive pulmonary disease (COPD).

15

Drawings

1/10

Fig. 1



;**Oligonucleotide structure**

~~~~~; **Hydrophobic Material**

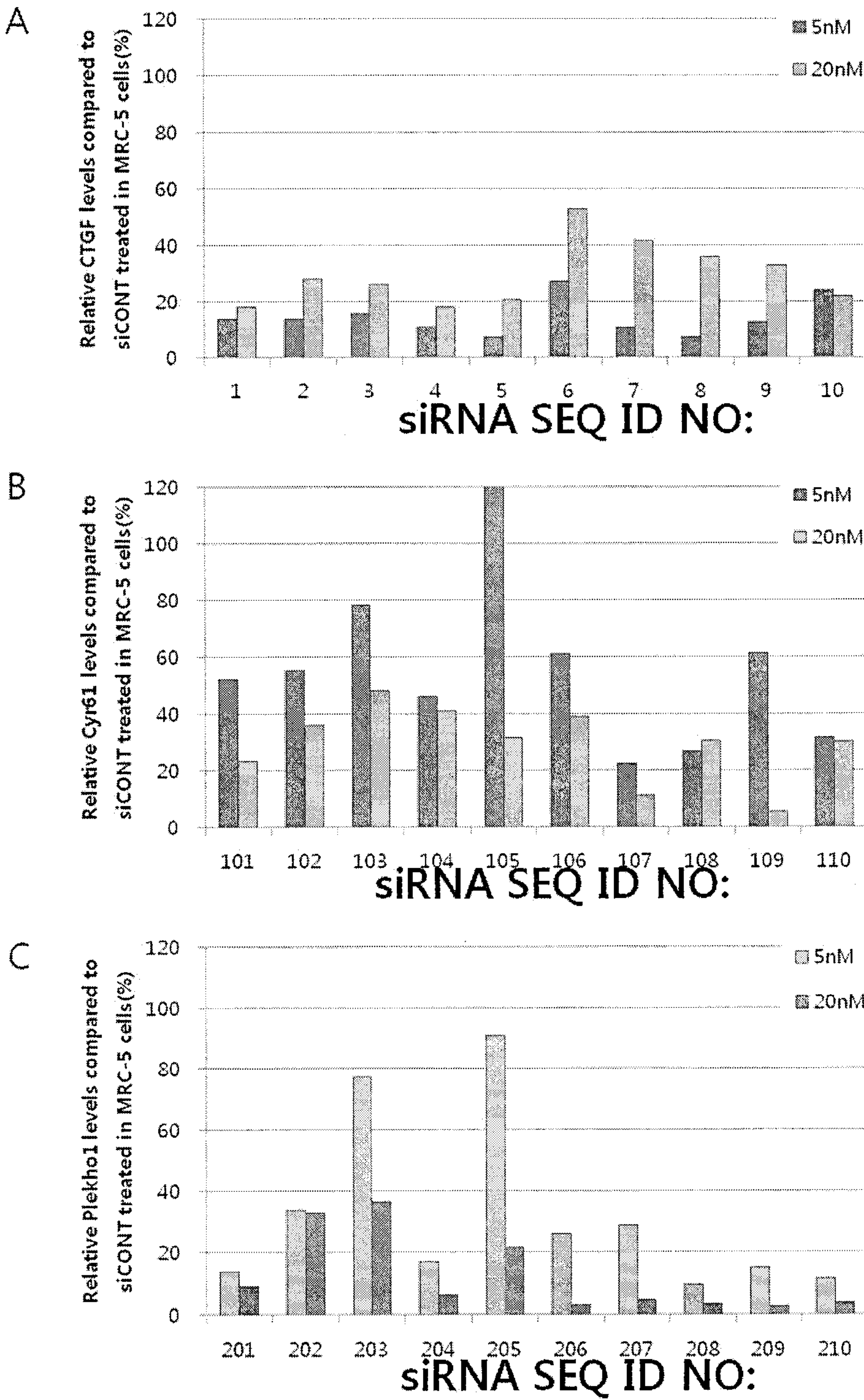
▢; **Oligonucleotide**

~~~~~; **Hydrophilic Material**

○; **Target-Oriented Ligand**

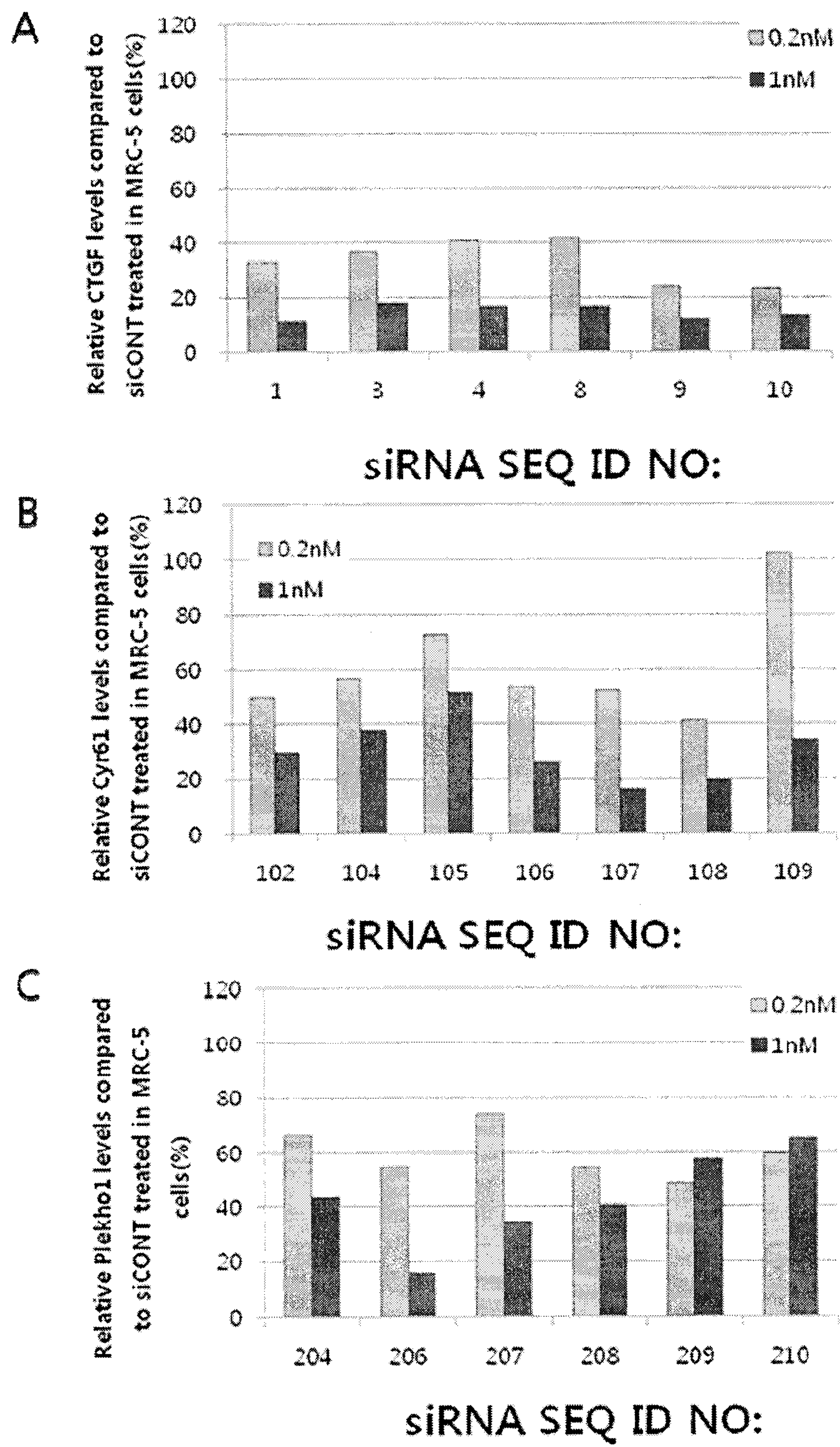
2/10

Fig. 2



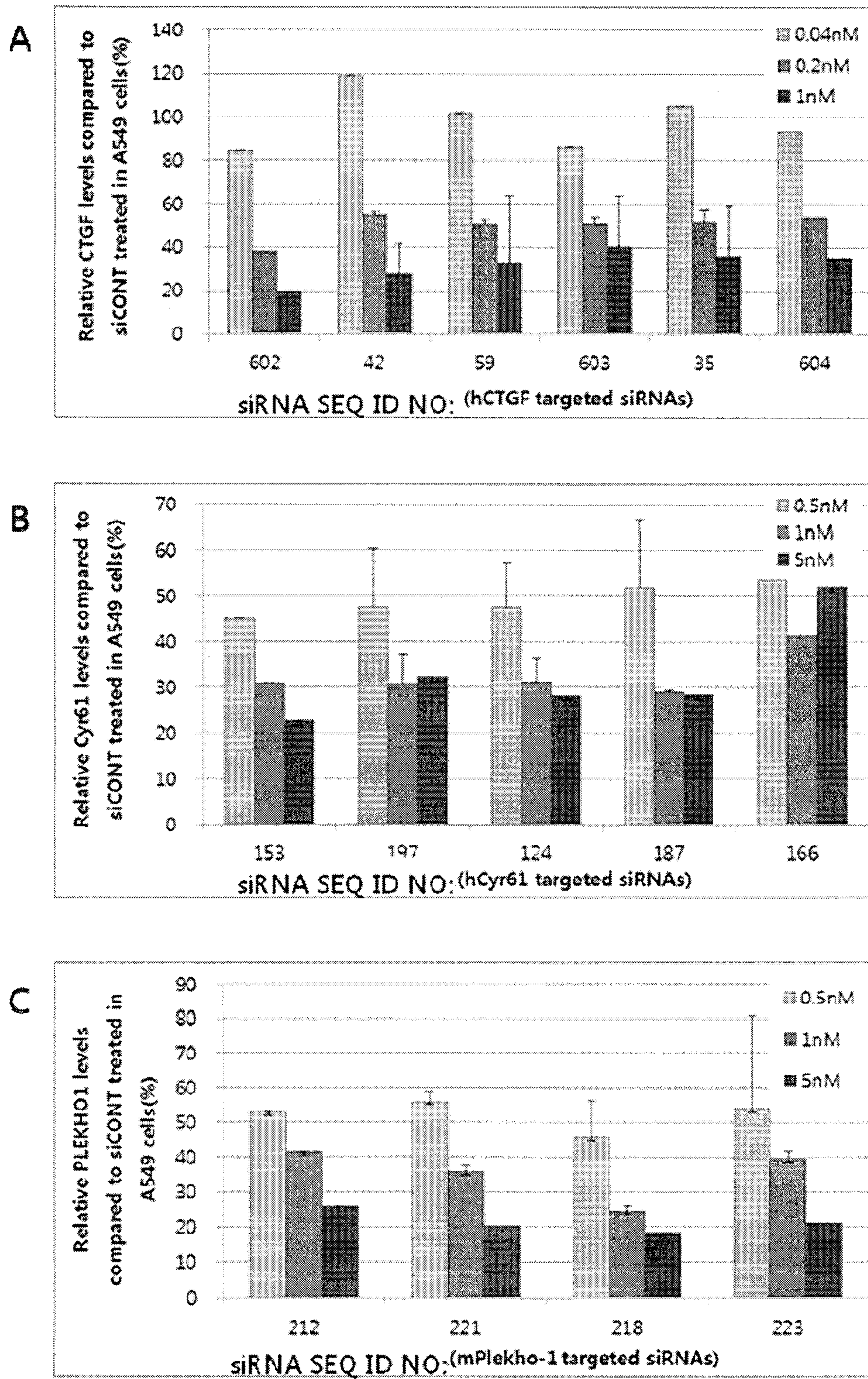
3/10

Fig. 3



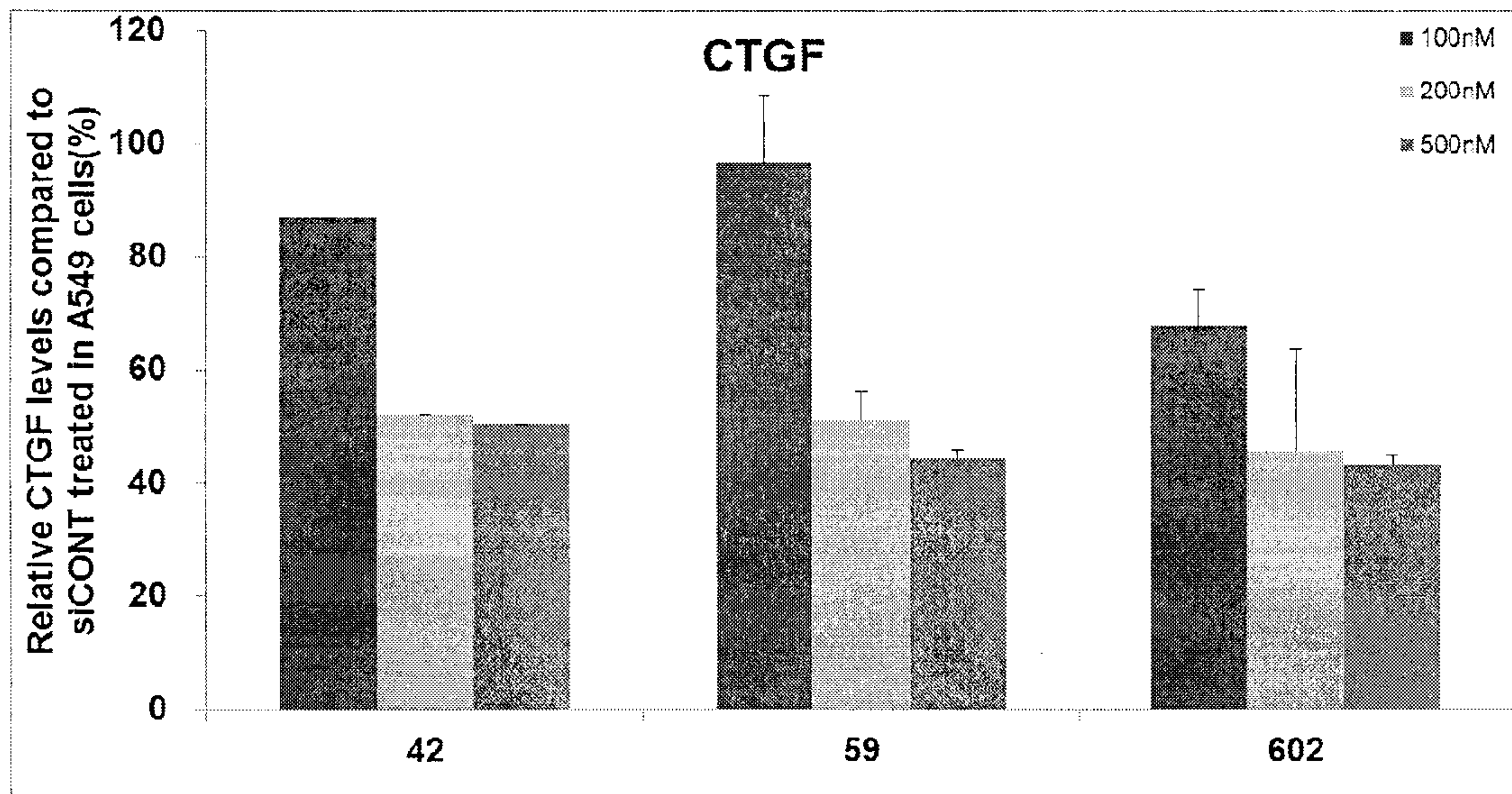
4/10

Fig. 4



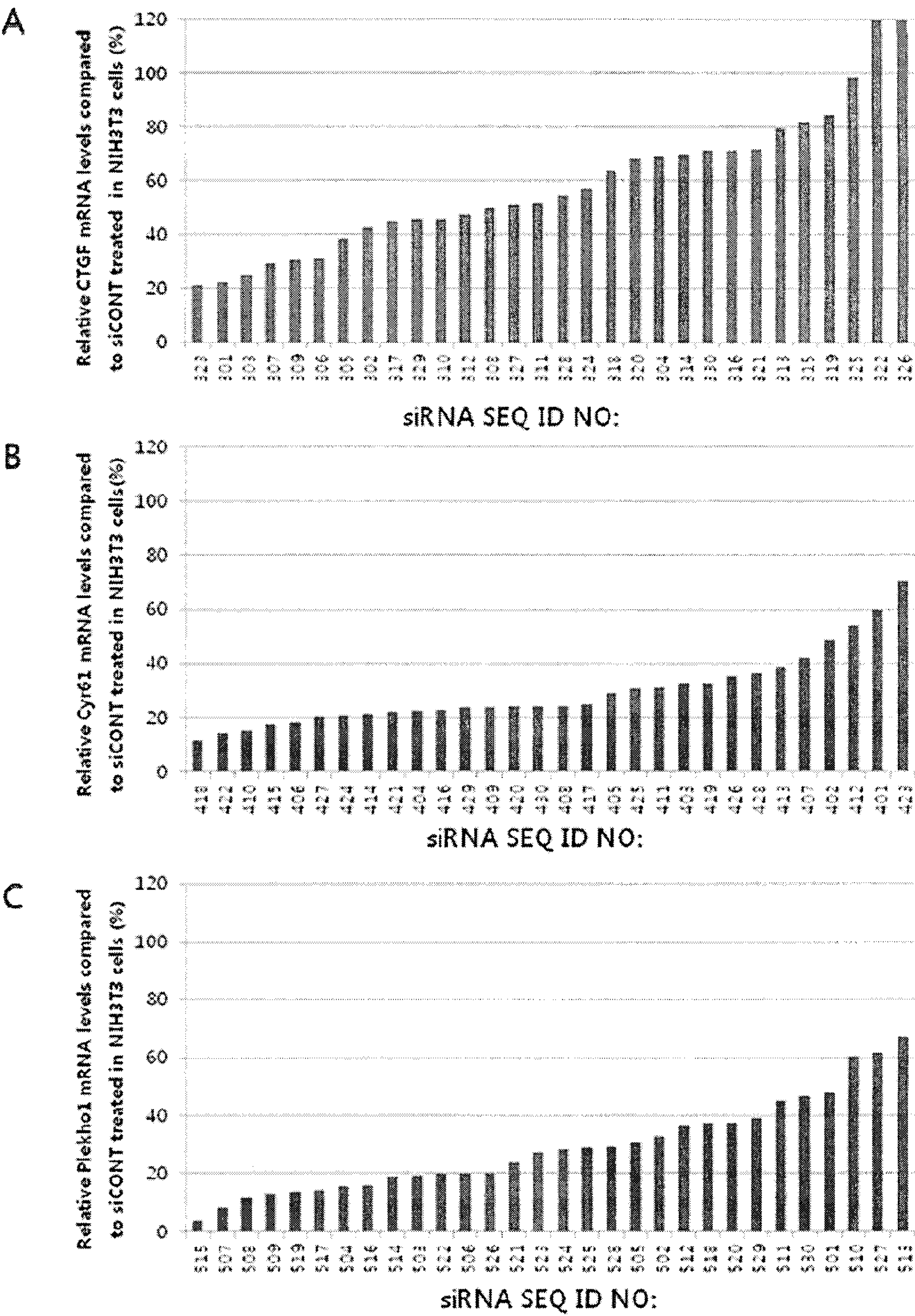
5/10

Fig. 5



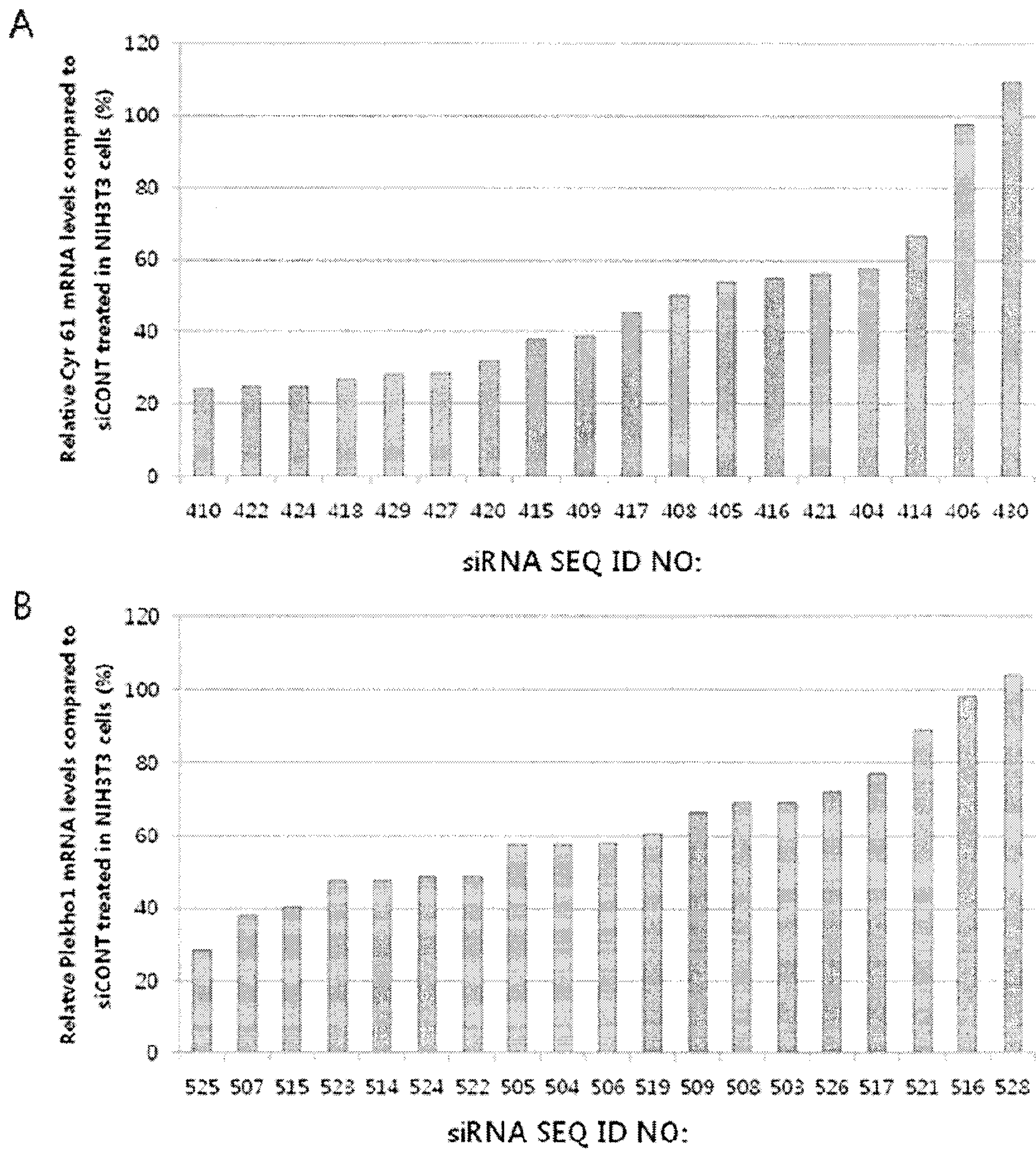
6/10

Fig. 6



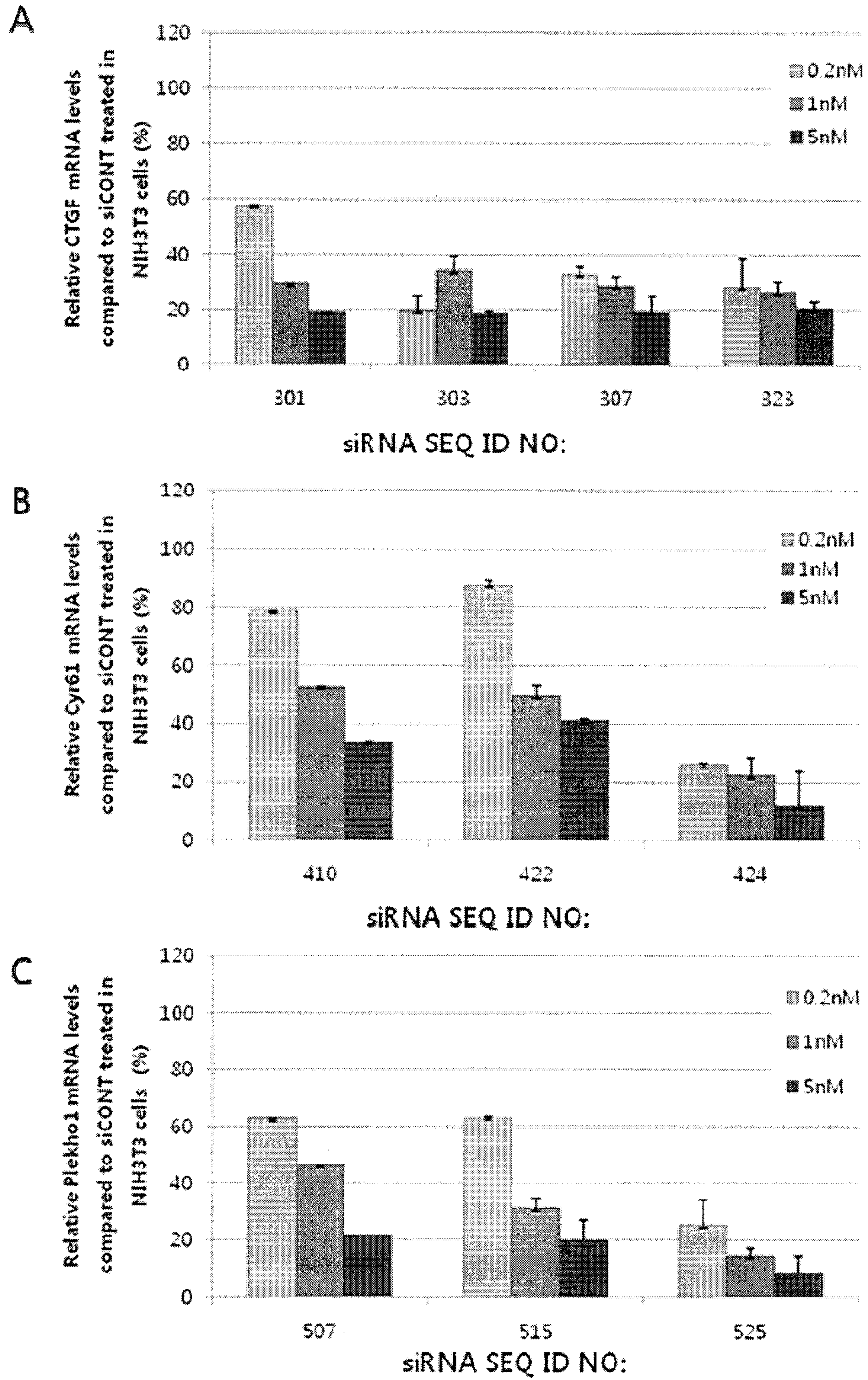
7/10

Fig. 7



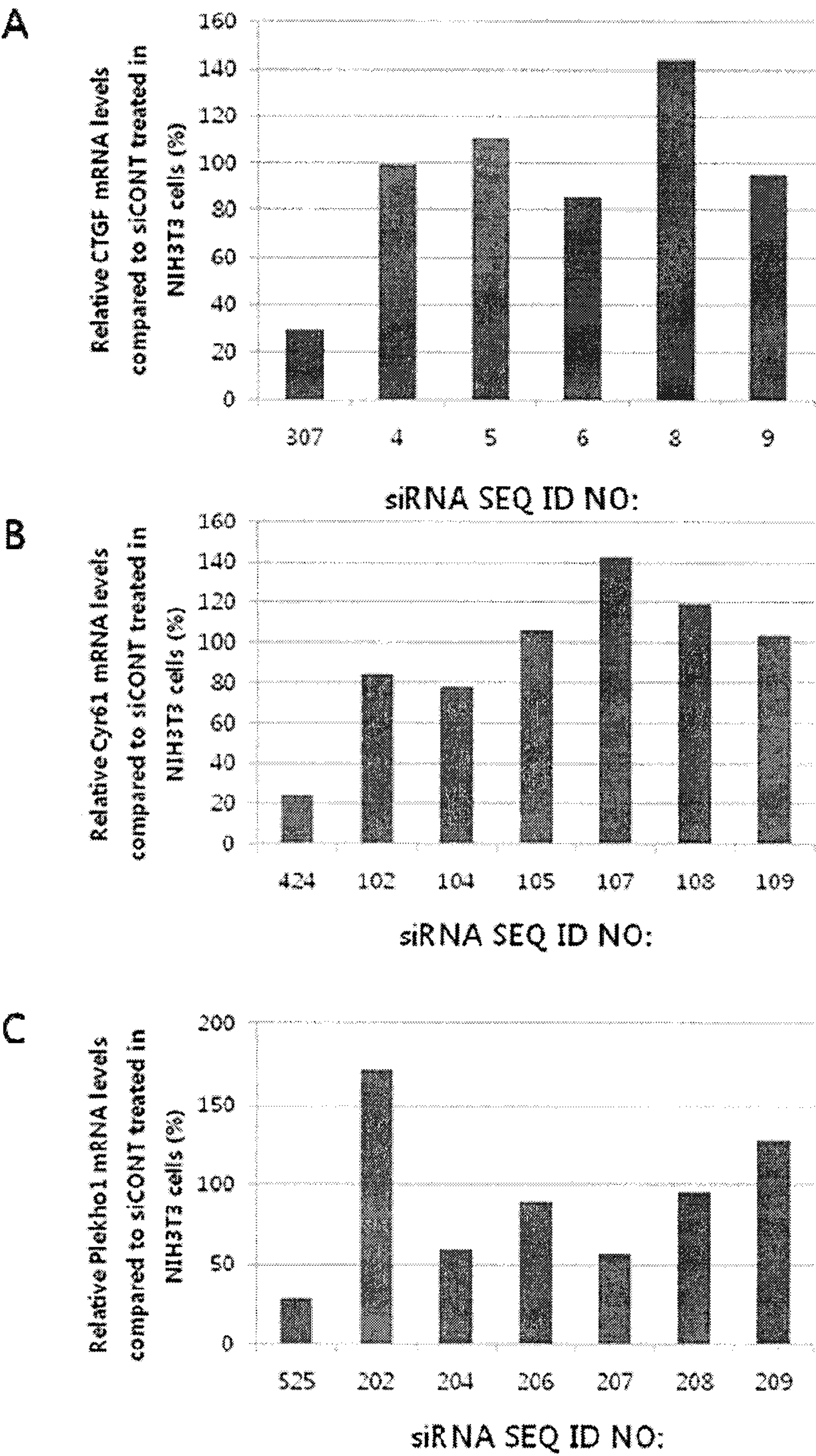
8/10

Fig. 8



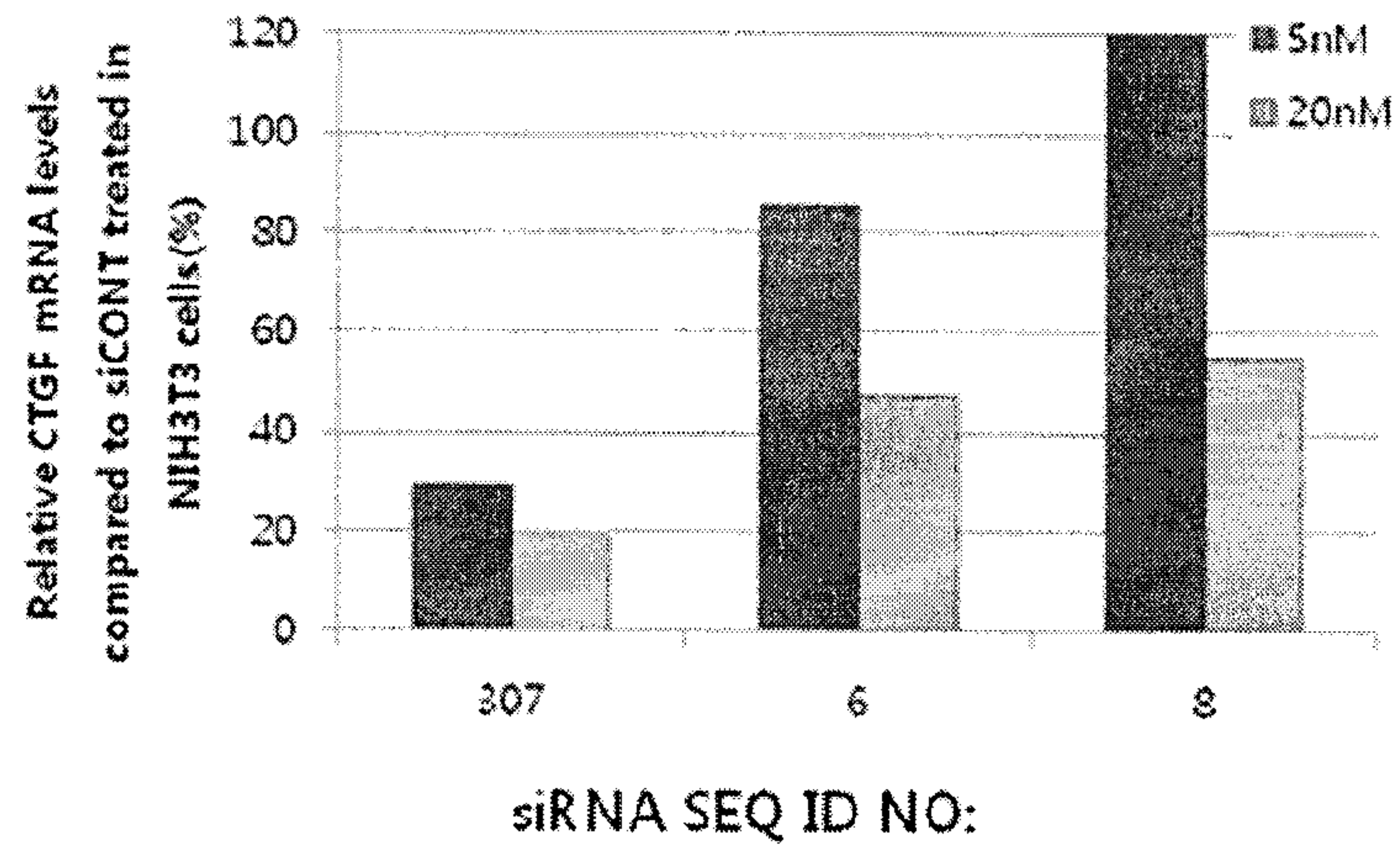
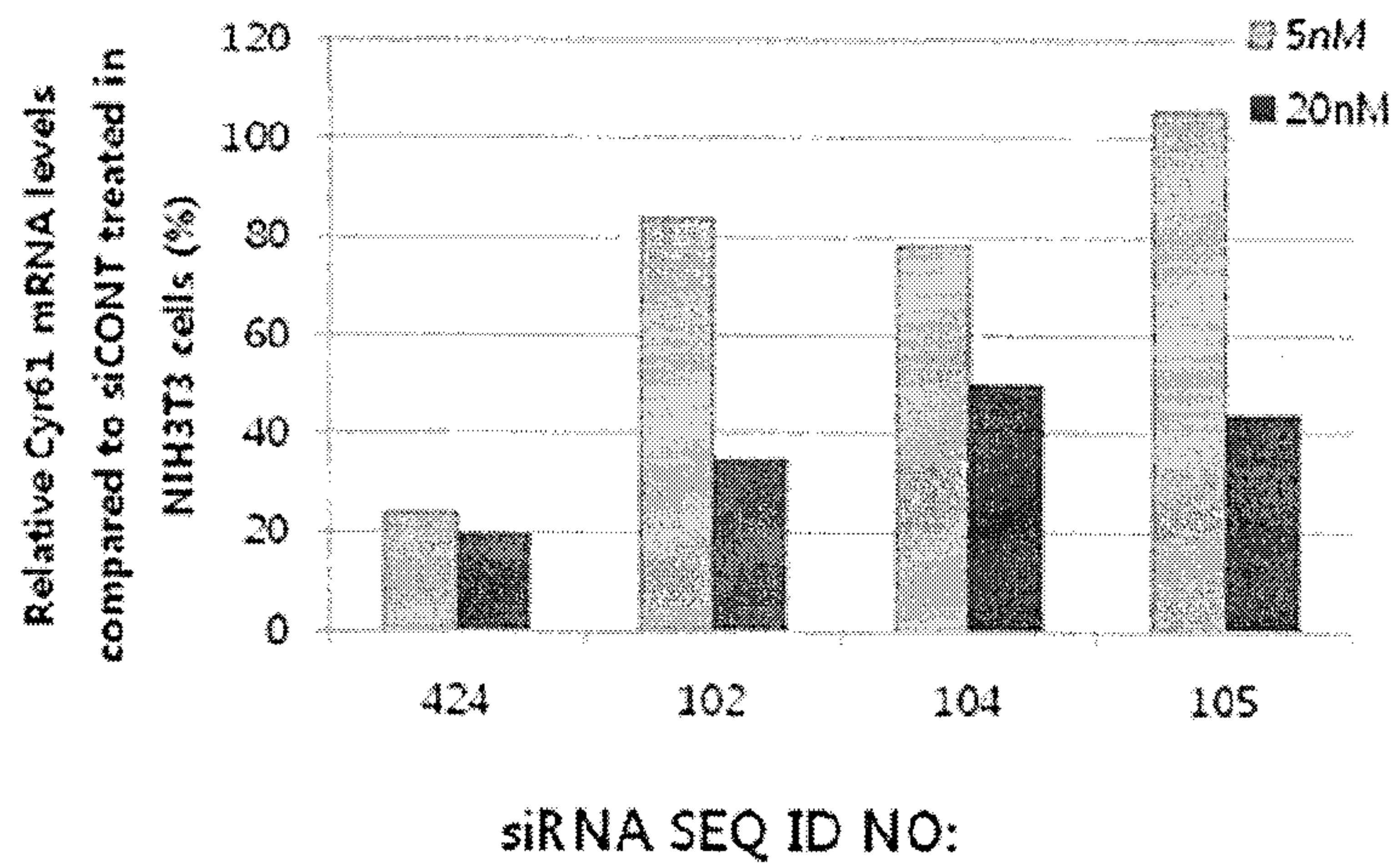
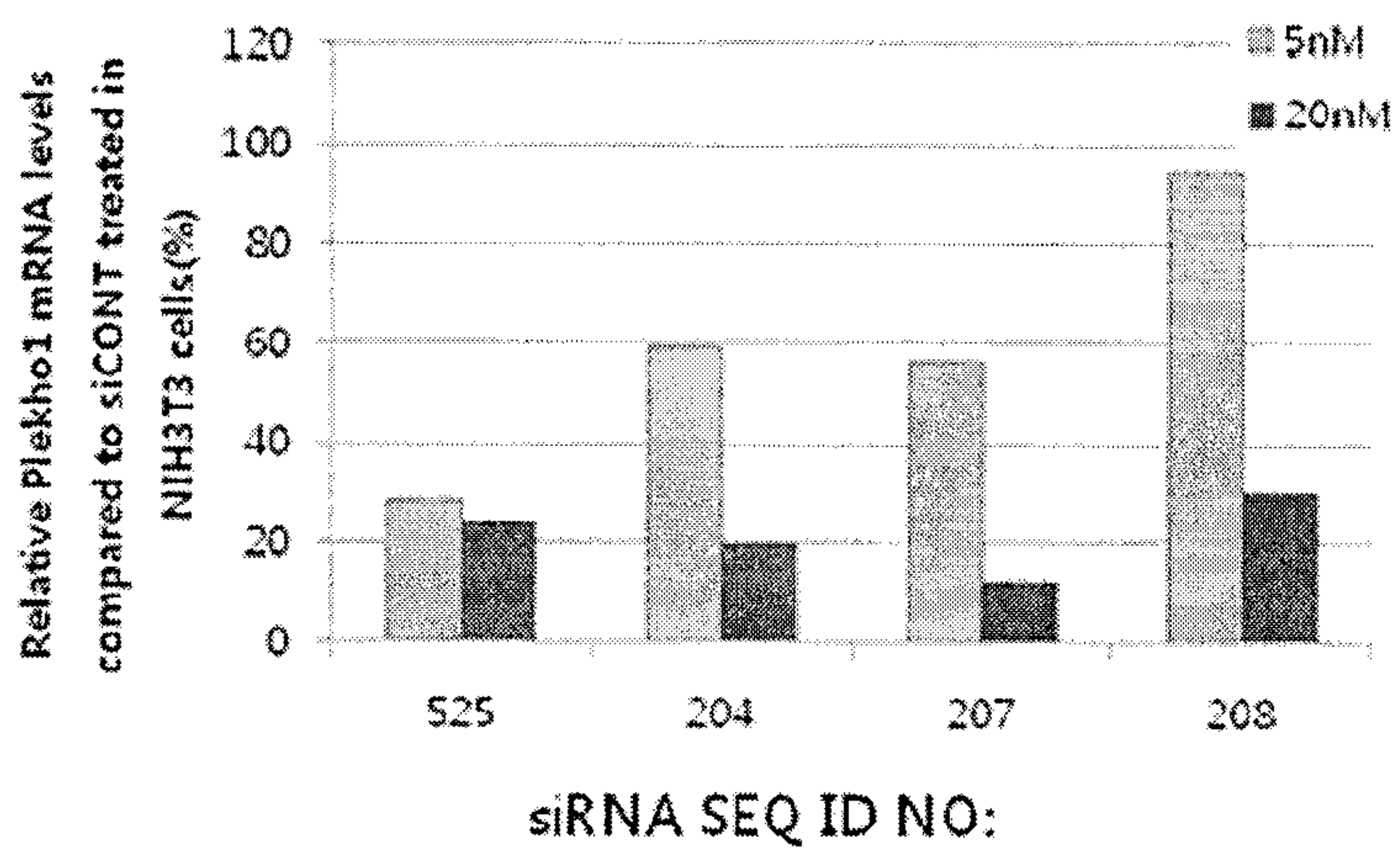
9/10

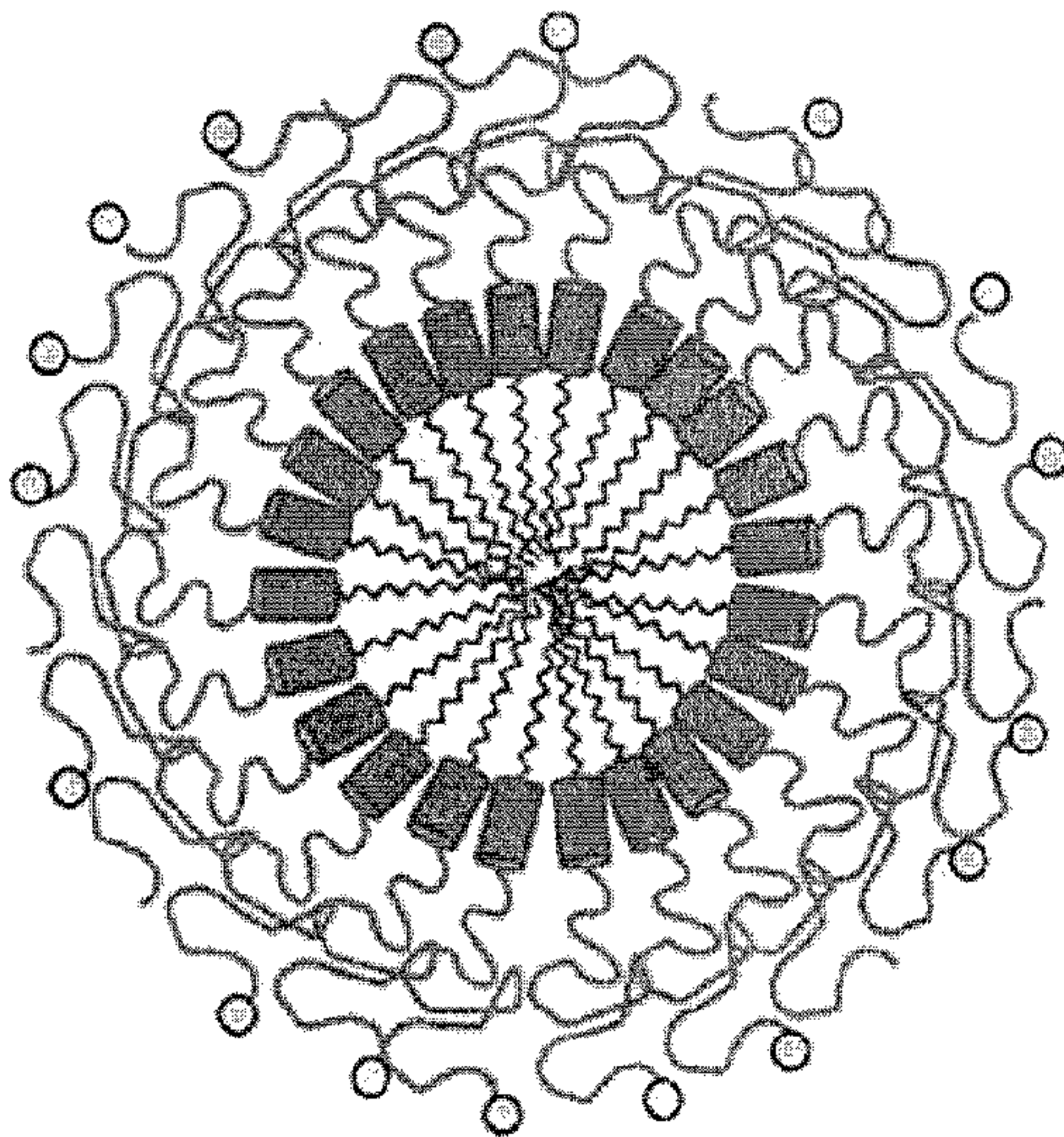
Fig. 9



10/10

Fig. 10

A**B****C**



: **Oligonucleotide structure**

~~~~~ : **Hydrophobic Material**

■ : **Oligonucleotide**

~~~~~ : **Hydrophilic Material**

○ : **Target-Oriented Ligand**