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(54) **Title:** INDUCTION OF EXON SKIPPING IN EUKARYOTIC CELLS

(57) **Abstract:** The present invention provides a method for at least in part decreasing the production of an aberrant protein in a cell, said cell comprising pre-mRNA comprising exons coding for said protein, by inducing so-called exon skipping in said cell. Exon-skipping results in mature mRNA that does not contain the skipped exon which leads to an altered product if said exon codes for amino acids. Exon skipping is performed by providing a cell with an agent capable of specifically inhibiting an exon inclusion signal, for instance an exon recognition sequence, of said exon. Said exon inclusion signal can be interfered with by a nucleic acid comprising complementarity to a part of said exon. Said nucleic acid, which is also herewith provided, can be used for the preparation of a medicament, for instance for the treatment of an inherited disease.

Induction of exon skipping in eukaryotic cells.

Given the rapid advances of human genome research, professionals and the public expect that the near future will bring us - in addition to understanding of disease mechanisms and refined and reliable diagnostics - also therapies for many devastating genetic diseases.

While it is hoped that for some (eg. metabolic) diseases the improved insights will bring easily administrable small-molecule therapies, it is likely that in most cases one or other form of gene therapy will ultimately be required, i.e. the correction, addition or replacement of the defective gene product.

In the past few years, research and development in this field have highlighted several technical difficulties which need to be overcome, eg. related to the large size of many genes involved in genetic disease (limiting the choice of suitable systems to administer the therapeutic gene), the accessibility of the tissue in which the therapeutic gene should function (requiring the design of specific targeting techniques, either physically by restricted injection or biologically, by developing systems with tissue-specific affinities) and the safety to the patient of the administration system. These problems are to some extent interrelated and it can be generally concluded that the smaller the therapeutic agent is, the easier it will become to develop efficient, targetable and safe administration systems.

The present invention addresses this problem by inducing so-called exon-skipping in cells. Exon-skipping results in mature mRNA that does not contain the skipped exon and thus, when said exon codes for amino acids can lead to the expression of an altered product. Technology for exon-skipping is currently directed toward the use of so-called 'Anti-sense Oligonucleotides'(AON's). Much of this work is done in the mdx mouse model for Duchenne muscular dystrophy (DMD). The mdx mouse, which carries a nonsense mutation in exon 23 of the dystrophin gene, has been used as an animal model of Duchenne muscular dystrophy. Despite the mdx mutation, which should preclude the synthesis of a functional dystrophin protein, rare, naturally occurring dystrophin positive fibers have been observed in mdx muscle tissue. These dystrophin-positive fibers are thought to have arisen from an apparently naturally occurring exon-skipping mechanism, either due to somatic mutations or through alternative splicing. AON's directed to, respectively, the 3' and 5' splice sites of introns 22 and 23 in dystrophin pre-mRNA, have been shown to interfere with factors normally involved in removal of intron 23 so that also exon 23 was removed from the mRNA (Wilton, 1999). In a similar study, Dunckley et al (1998) showed that exon skipping using AON's directed to 3' and 5' splice sites can have unexpected results. They observed skipping of not only exon 23 but also of exons 24-29 thus resulting in an mRNA containing an exon 22-exon 30 junction. The underlying mechanism for the appearance of the unexpected 22-30 splicing variant is not known. It could be due to the fact that splice sites contain consensus sequences leading to promiscuous hybridization of the oligo's used to direct the exon skipping. Hybridization of the oligo's to other splice sites than the sites of the exon to be skipped of course could easily interfere with the accuracy of the splicing process. On the other hand the accuracy could be lacking due to the fact that two oligo's (for the 5' and the 3' splice site) need to be used. Pre-mRNA containing one but not the other oligo could be prone to unexpected splicing variants. To overcome these and other problems the present invention provides a method for directing splicing of a pre-mRNA in a system capable of performing a splicing operation comprising contacting said pre-mRNA in said system with an agent capable of specifically inhibiting an exon inclusion signal of at least one exon in said pre-mRNA, said method further comprising allowing splicing of said pre-mRNA. Interfering with an exon inclusion signal (EIS) has the advantage that such elements are located within the exon. By providing an antisense oligo for the interior of the exon to be skipped, it is possible to interfere with the exon inclusion signal thereby effectively masking the exon from the splicing apparatus. The failure of the splicing apparatus to recognize the exon to be skipped thus leads to exclusion of the exon from the final mRNA. The present invention does not interfere directly with the enzymatic process of the splicing machinery (the joining of the exons). It is thought that this allows the method to be more robust and reliable. It is thought that an EIS is a particular structure of an exon that allows splice acceptor and donor to assume a particular spatial conformation. In this concept it is the particular spatial conformation that enables the splicing machinery to recognize the exon. However, the invention is certainly not limited to this model. It has been found that agents capable of binding to an exon can inhibit an EIS. Agents may specifically contact said exon at any point and still be able to specifically inhibit said EIS. Said mRNA may be useful in itself. For instance production of an undesired protein can be at least in part reduced by inhibiting inclusion of a required exon into the mRNA. Preferably, a method of the invention further comprises allowing translation of mRNA produced from splicing of said pre-mRNA. Preferably, said mRNA encodes a functional protein. In a preferred embodiment said protein comprises two or more domains, wherein at least one of said domains is encoded by said mRNA as a result of skipping of at least part of an exon in said pre-mRNA. Exon skipping will typically, though not necessarily be of relevance for proteins in the wild type configuration, having at least two functional domains that each perform a function, wherein said domains are generated from distinct parts of the primary amino-acid sequence. One example are for instance transcription factors. Typically these factors comprise a DNA binding domain and a domain that interacts with other proteins in the cell. Skipping of an exon that encodes a part of the primary amino acid sequence that lies between these two domains can lead to a shorter protein that comprises the same function, at least in part. Thus detrimental mutations in this intermediary region (for instance frame-shift or stop mutations) can be at least in part repaired by inducing exon skipping to allow synthesis of the shorter (partly) functional protein. Using a method of the invention it is also possible to induce partial skipping of the exon. In this embodiment said contacting results in activation of a cryptic splice site in a contacted exon. This embodiment broadens the potential for manipulation of the pre-mRNA leading to a functional protein. Preferably, said system comprises a cell. Preferably said cell is cultured in vitro or in the organism in vivo, typically though not necessarily said organism comprises a human or a mouse.

In a preferred embodiment the invention provides a method for at least in part decreasing the production of an aberrant protein in a cell,

said cell comprising pre-mRNA comprising exons coding for said protein,

the method comprising

providing said cell with an agent capable of specifically inhibiting an exon inclusion signal of at least one of said exons,

the method further comprising allowing translation of mRNA produced from splicing of said pre-mRNA.

Any agent capable of specifically inhibiting an exon exclusion signal can be used for the present invention. Preferably said agent comprise nucleic acid or a functional equivalent thereof. Preferably, but not necessarily said nucleic acid is in single stranded form. Peptide nucleic acid and other molecules comprising the same nucleic acid binding characteristics in kind, not necessarily in amount are suitable equivalents. Nucleic acid or an equivalent may comprise modifications to provide additional functionality. For instance, 2'-O-methyl oligoribonucleotides can be used. These ribonucleotides are more resistant to RNAse action than conventional oligo nucleotides.

In a preferred embodiment of the invention said exon inclusion signal is interfered with by an anti sense nucleic acid directed to an exon recognition sequence (ERS). These sequences are relatively purine rich and can be distinguished by scrutinizing the sequence information of the exon to be skipped (Tanaka et al., 1994 Mol Cell Biol. 14: p. 1347-1354). Exon recognition sequences are thought to aid inclusion into mRNA of so-called weak exons (Achsel et al., 1996; J. Biochem. 120; p.53-60). These weak exons comprise for instance 5' and or 3' splice sites that are less efficiently recognized by the splicing machinery. In the present invention it has been found that exon skipping can also be induced in so-called strong exons. i.e. exons which are normally efficiently recognized by the splicing machinery of the cell. From any given sequence it is (almost) always possible to predict whether the sequence comprises putative exons and to determine whether these exons are strong or weak. Several algorithms for determining the strength of an exon exist. A useful algorithm can be found on the NetGene2 splice site prediction server (Brunak, et al., 1991; J Mol Biol 220: p. 49-65.). Exon skipping by a means of the invention can be induced in (almost) every exon, independent of whether said exon is a weak exon or a strong exon and also independent of whether said exon comprises an ERS. In a preferred embodiment, an exon that is targeted for skipping is a strong exon. In another preferred embodiment an exon targeted for skipping does not comprise an ERS.

Methods of the invention can be used in many ways. In one embodiment a method of the invention is used to at least in part decrease the production of an aberrant protein. Such proteins can for instance be onco-proteins or viral proteins. In many tumors not only the presence of an onco-protein but also it relative level of expression have been associated to the phenotype of the tumor cell. Similarly, not only the presence of viral proteins but also the amount of viral protein in a cell determines the virulence of a particular virus. Moreover, for efficient multiplication and spread of a virus the timing of expression in the life cycle and the balance in the amount of certain viral proteins in a cell determines the whether viruses are efficiently or inefficiently produced. Using a method of the invention it is possible to lower the amount of aberrant protein in a cell such that for instance a tumor cell becomes less tumorigenic (metastatic) and/or a virus infected cell produces less virus.

In a preferred embodiment a method of the invention is used to modify said aberrant protein into a functional protein. In one embodiment said functional protein is capable of performing a function of a protein normally present in a cell but absent in the cells to be treated. Very often even partial restoration of function results in significantly improved performance of the cell thus treated. Due to the better performance, such cells can also have a selective advantage over unmodified cells thus aiding to the effectivity of the treatment.

This aspect of the invention is particularly suited for the restoration of expression of defective genes. This is achieved by causing the specific skipping of targeted exons, thus bypassing or correcting deleterious mutations (typically stop-mutations or frameshifting point mutations, single- or multi-exon deletions or insertions leading to translation termination).

Compared to gene-introduction strategies, this novel form of splice-modulation gene therapy requires the administration of much smaller therapeutic reagents, typically, but not limited to, 14-40 nucleotides. In a preferred embodiment molecules of 14-25 nucleotides are used since these molecules are easier to produce and enter the cell more effectively. The methods of the invention allow much more flexibility in the subsequent design of effective and safe administration systems. An important additional advantage of this aspect of the invention is that it restores (at least some of) the activity of the endogenous gene, which still possesses most or all of its gene-regulatory circuitry, thus ensuring proper expression levels and the synthesis of tissue-specific isoforms.

This aspect of the invention can in principle be applied to any genetic disease or genetic predisposition to disease, in which targeted skipping of specific exons would restore the translational reading frame when this has been disrupted by the original mutation, provided that translation of an internally slightly shorter protein is still fully or partly functional. Preferred embodiments for which this application can be of therapeutic value are: predisposition to second hit mutations in tumor suppressor genes, e.g. those involved in breast cancer, colon cancer, tuberous sclerosis, neurofibromatosis etc., - where (partial) restoration of activity would preclude the manifestation of nullosomy by second hit mutations and thus would protect against tumorigenesis. Another preferred embodiment involves the (partial) restoration of defective gene products which have a direct disease causing effect, e.g., eg. hemophilia A (clotting factor VIII deficiency, some forms of congenital hypothyroidism (due to thyroglobulin synthesis deficiency) and Duchenne Muscular Dystrophy (DMD), in which frameshifting deletions, duplications and stop mutations in the X-linked dystrophin gene cause severe, progressive muscle degradation. DMD is typically lethal in late adolescence or early adulthood, while non-frameshifting deletions or duplications in the same gene cause the much milder Becker muscular dystrophy (BMD), compatible with a life expectancy between 35-40 y to normal. In the embodiment as applied to DMD, the present invention enables exon skipping to extend an existing deletion (or alter the mRNA product of an existing duplication) by as many adjacent exons as required to restore the reading frame and generate an internally slightly shortened, but still functional protein. Based on the much milder clinical symptoms of BMD patients with the equivalent of this induced deletion, the disease in the DMD patients would have a much milder course after AON-therapy.

Many different mutations in the dystrophin gene can lead to a dysfunctional protein. (For a comprehensive inventory see http://www.dmd.nl, the internationally accepted database for DMD and related disorders.) The precise exon to be skipped to generate a functional dystrophin protein varies from mutation to mutation. Table 1 comprises a non-limiting list of exons that can be skipped and lists for the mentioned exons some of the more frequently occurring dystrophin gene mutations that have been observed in humans and that can be treated with a method of the invention. Skipping of the mentioned exon leads to a mutant dystrophin protein comprising at least the functionality of a Becker mutant. Thus in one embodiment the invention provides a method of the invention wherein said exon inclusion signal is present in exon numbers 2, 8, 19, 29, 43, 44, 45, 46, 50, 51, 52 or 53 of the human dystrophin gene. The occurrence of certain deletion/insertion variations is more frequent than others. In the present invention it was found that by inducing skipping of exon 46 with a means or a method of the invention approximately 7% of DMD-deletion containing patients can be treated, resulting in said patients to comprise dystrophin positive muscle fibers. By inducing skipping of exon 51, approximately 15% of DMD-deletion containing patients can be treated with a means or method of the invention. Such treatment will result in the patient having at least some dystrophin positive fibers. Thus with either skipping of exon 46 or 51 approximately using a method of the invention approximately 22% of the patients containing a deletion in the dystrophin gene can be treated. Thus in a preferred embodiment of the invention said exon exclusion signal is present in exon 46 or exon 51. In a particular preferred embodiment said agent comprises a nucleic acid sequence according to hAON#4, hAON#6, hAON#8, hAON#9, hAON#11 and/or one or more of hAON#21-30 or a functional part, derivative and/or analogue of said hAON#. A functional part, derivative and/or analogue of said hAON# comprises the same exon skipping activity in kind, in a method of the invention, not necessarily in amount.

It can be advantageous to induce exon skipping of more than one exon in the pre-mRNA. For instance, considering the wide variety of mutations and the fixed nature of exon lengths and amino acid sequence flanking such mutations, the situation can occur that for restoration of function more than one exon needs to be skipped. A preferred but non-limiting, example of such a case in the DMD deletion database is a 46-50 deletion. Patients comprising a 46-50 deletion do not produce functional dystrophin. However, an at least partially functional dystrophin can be generated by inducing skipping of both exon 45 and exon 51. Another preferred but non-limiting example is patients comprising a duplication of exon 2. By providing one agent capable of inhibiting an EIS of exon 2, it is possible to partly skip either one or both exons two, thereby regenerating the wild-type protein, next to the truncated or double exon two skipped protein. Another preferred but non-limiting example is the skipping of exons 45 through 50. This generates an in frame Becker like variant. This Becker like variant can be generated to cure any mutation localised in exons 45, 46, 47, 48, 49, and/or 50 or combinations thereof. In one aspect the invention therefore provides a method of the invention further comprising providing said cell with another agent capable of inhibiting an exon inclusion signal in another exon of said pre-mRNA. Of course it is completely within the scope of the invention to use two or more agents for the induction of exon skipping in pre-mRNA of two or more different genes.

In another aspect the invention provides a method for selecting the suitable agents for splice-therapy and their validation as specific exon-skipping agents in pilot experiments. Provided is a method for determining whether an agent is capable of specifically inhibiting an exon inclusion signal of an exon, comprising providing a cell having a pre-mRNA containing said exon, with said agent, culturing said cell to allow the formation of an mRNA from said pre-mRNA and determining whether said exon is absent said mRNA. In a preferred embodiment said agent comprises nucleic acid or functional equivalent thereof, said nucleic acid comprising complementarity to a part of said exon. Agents capable of inducing specific exon skipping can be identified with a method of the invention. It is possible to include a prescreen for agents by first identifying whether said agent is capable of binding with a relatively high affinity to exon containing nucleic acid, preferably RNA. To this end a method for determining whether an agent is capable of specifically inhibiting an exon inclusion signal of an exon is provided, further comprising first determining *in vitro* the relative binding affinity of said nucleic acid or functional equivalent thereof to an RNA molecule comprising said exon.

In yet another aspect an agent is provided that is obtainable by a method of the invention. In a preferred embodiment said agent comprises nucleic acid or functional equivalent thereof. Preferably said agent, when used to induce exon skipping in a cell, is capable of at least in part reducing the amount of aberrant protein in said cell. More preferably, said exon skipping results in an mRNA encoding a protein that is capable of performing a function in said cell. In a particularly preferred embodiment said pre-mRNA is derived from a dystrophin gene. Preferably, said functional protein comprises a mutant or normal dystrophin protein. Preferably, said mutant dystrophin protein comprises at least the functionality of a dystrophin protein in a Becker patient. In a particularly preferred embodiment said agent comprises the nucleic acid sequence of hAON#4, hAON#6, hAON#8, hAON#9, hAON#11 and/or one or more of hAON#21-30 or a functional part, derivative and/or analogue of said hAON#. A functional part, derivative and/or analogue of said hAON# comprises the same exon skipping activity in kind, in a method of the invention, not necessarily in amount.

The art describes many ways to deliver agents to cells. Particularly, nucleic acid delivery methods have been widely developed. The artisan is well capable of determining whether a method of delivery is suitable for performing the present invention. In a non-limiting example said method includes the packaging of an agent of the invention into liposomes, said liposomes being provided to cells comprising a target pre-mRNA. Liposomes are particularly suited for delivery of nucleic acid to cells. Antisense molecules capable of inducing exon skipping can be produced in a cell upon delivery of nucleic acid containing a transcription unit to produce antisense RNA. Non-limiting examples of suitable transcription units are small nuclear RNA (SNRP) or tRNA transcription units. The invention therefore further provides a nucleic acid delivery vehicle comprising a nucleic acid or functional equivalent thereof of the invention capable of inhibiting an exon inclusion signal. In one embodiment said delivery vehicle is capable of expressing said nucleic acid of the invention. Of course in case for instance single stranded viruses are used as a vehicle, it is entirely within the scope of the invention when such a virus comprises only the antisense sequence of an agent of the invention. In another embodiment of single strand viruses AONs of the invention are encoded by small nuclear RNA or tRNA transcription units on viral nucleic encapsulated by the virus as vehicle. A preferred single stranded virus is adeno-associated virus.

In yet another embodiment the invention provides the use of a nucleic acid or a nucleic acid delivery vehicle of the invention for the preparation of a medicament. In a preferred embodiment said medicament is used for the treatment of an inherited disease. More preferably, said medicament is used for the treatment of Duchenne Muscular Dystrophy.

Brief description of the drawings

Figure 1. Deletion of exon 45 is one of the most frequent DMD-mutations. Due to this deletion exon 44 is spliced to exon 46, the translational reading frame is interrupted, and a stop codon is created in exon 46 leading to a dystrophin deficiency. Our aim is to artificially induce the skipping of an additional exon, exon 46, in order to reestablish the reading frame and restore the synthesis of a slightly shorter, but largely functional dystrophin protein as found in the much milder affected Becker muscular dystrophy patients affected by a deletion of both exons 45 and 46.

Figure 2. Exon 46 contains a purine-rich region that is hypothesized to have a potential role in the regulation of its splicing in the pre-mRNA. A series of overlapping 2'O-methyl phosphorothioate antisense oligoribonucleotides (AONs) was designed directed at this purine-rich region in mouse dystrophin exon 46. The AONs differ both in length and sequence. The chemical modifications render the AONs resistant to endonucleases and RNaseH inside the muscle cells. To determine the transfection efficiency in our in vitro studies, the AONs contained a 5' fluorescein group which allowed identification of AON-positive cells.

Figure 3. To determine the binding affinity of the different AONs to the target exon 46 RNA, we performed gel mobility shift assays. In this figure, the five mAONs (mAON#4, 6, 8,

9, and 11) with highest affinity for the target RNA are shown. Upon binding of the AONs to the RNA, a complex is formed that exhibits a retarded gel mobility as can be determined by the band shift. The binding of the AONs to the target was sequence-specific. A random mAON, i.e. not-specific for exon 46, did not generate a band shift.

Figure 4. The mouse- and human-specific AONs which showed the highest binding affinity in the gel mobility shift assays were transfected into mouse and human myotube cultures. (A) RT-PCR analysis showed a truncated product, of which the size corresponded to exon 45 directly spliced to exon 47, in the mouse cell cultures upon transfection with the different mAONs#4, 6, 9, and 11. No exon 46 skipping was detected following transfection with a random AON. (B) RT-PCR analysis in the human muscle cell cultures derived from one unaffected individual (C) and two unrelated DMD-patients (P1 and P2) revealed truncated products upon transfection with hAON#4 and hAON#8. In the control this product corresponded to exon 45 spliced to exon 47, while in the patients the fragment size corresponded to exon 44 spliced to exon 47. No exon 46 skipping was detected in the non-transfected cell cultures or following transfection with a random hAON. Highest exon 46 skipping efficiencies were obtained with hAON#8.

Figure 5. Sequence data from the RT-PCR products obtained from patient DL279.1 (corresponding to P1 in Figure 4), whch confirmed the deletion of exon 45 in this patient (upper panel), and the additional skipping of exon 46 following transfection with hAON#8 (lower panel). The skipping of exon 46 was specific, and exon 44 was exactly spliced to exon 47 which reestablishes the translational reading frame.

Figure 6. Immunohistochemical analysis of the muscle cell culture from patient DL279.1 upon transfection with hAON#8. Cells were subject to two different dystrophin antibodies raised against different regions of the protein, located proximally (ManDys-1, ex.-31-32) and distally (Dys-2, ex. 77-79) from the targeted exon 46. The lower panel shows the absence of a dystrophin protein in the myotubes, whereas the hAON#8-induced skipping of exon 46 clearly restored the synthesis of a dystrophin protein as detected by both antibodies (upper panel).

Figure 7:
(A) RT-PCR analysis of RNA isolated from human control muscle cell cultures treated with hAON#23, #24, #27, #28, or #29. A truncated product, with a size corresponding to exon 50 spliced to exon 52 was detected in cells treated with hAON#23 and #28. Sequence analysis of these products confirmed the precise skipping of exon 51 (B). An additional aberrant splicing product was obtained in cells treated with hAON#28 and #29. Sequence analysis revealed the utilization of an in-frame cryptic splice site within exon 51 that is used at a low frequency upon AON treatment. The product generated, included a partial exon 51 which also had a restored reading frame, thereby confirming further the therapeutic value.

Figure 8
(A) Gel mobility shift assays were performed to determine the binding affinity of the different h29AON#'s for the exon 29 target RNA. When compared to non-hybridized RNA (none), h29AON#1, #2, #4, #6, #9, #10, and #11 generated complexes with lower gel mobilities, indicating their binding to the RNA. A random AON derived from dystrophin exon 19 did not generate a complex. (B) RT-PCR analysis of RNA isolated from

human control muscle cell cultures treated with h29AON#1, #2, #4, #6, #9, #10, or #11 revealed a truncated product of which the size corresponded to exon 28 spliced to exon 30. These results indicate that exon 29 can specifically be skipped using AONs directed to sequences either within (h29AON#1, #2, #4, or #6) or outside (h29AON#9, #10, or #11) the hypothesized ERS in exon 29. An additional aberrant splicing product was observed that resulted from skipping of both exon 28 and exon 29 (confirmed by sequence data not shown). Although this product was also present in non-treated cells, suggesting that this alternative skipping event may occur naturally, it was enhanced by the AON-treatment. AON 19, derived from dystrophin exon 19, did not induce exon 29 skipping (C) The specific skipping of exon 29 was confirmed by sequence data from the truncated RT-PCR fragments. Shown here is the sequence obtained from the exon 29 skipping product in cells treated with h29AON#1.

Figure 9

(A) RT-PCR analysis of RNA isolated from mouse gastrocnemius muscles two days post-injection of 5, 10, or 20 μg of either mAON#4, #6, or #11. Truncated products,with a size corresponding to exon 45 spliced to exon 47, were detected in all treated muscles. The samples -RT, -RNA, AD-1, and AD-2 were analyzed as negative controls for the RT-PCR reactions. (B) Sequence analysis of the truncated products generated by mAON#4 and #6 (and #11, not shown) confirmed the precise skipping of exon 46.

EXAMPLES

Example 1

Since exon 45 is one of the most frequently deleted exons in DMD, we initially aimed at inducing the specific skipping of exon 46 (Fig.1). This would produce the shorter, largely functional dystrophin found in BMD patients carrying a deletion of exons 45 and 46. The system was initially set up for modulation of dystrophin pre-mRNA splicing of the mouse dystrophin gene. We later aimed for the human dystrophin gene with the intention to restore the translational reading frame and dystrophin synthesis in muscle cells from DMD patients affected by a deletion of exon 45.

Design of mAONs and hAONs

A series of mouse and human-specific AONs (mAONs and hAONs) was designed, directed at an internal part of exon 46 that contains a stretch of purine-rich sequences and is hypothesized to have a putative regulatory role in the splicing process of exon 46 (Fig.2). For the initial screening of the AONs in the gel mobility shift assays (see below), we used non-modified DNA-oligonucleotides (synthesized by EuroGentec, Belgium). For the actual transfection experiments in muscle cells, we used 2'-O-methyl-phosphorothioate oligoribonucleotides (also synthesized by EuroGentec, Belgium). These modified RNA oligonucleotides are known to be resistant to endonucleases and RNaseH, and to bind to RNA with high affinity. The sequences of those AONs that were eventually effective and applied in muscle cells in vitro are shown below. The corresponding mouse and human-specific AONs are highly homologous but not completely identical.

The listing below refers to the deoxy-form used for testing, in the finally used 2-0-methyl ribonucleotides all T's should be read as U's.

mAON#2: 5' GCAATGTTATCTGCTT
mAON#3: 5' GTTATCTGCTTCTTCC
mAON#4: 5' CTGCTTCTTCCAGCC
mAON#5: 5' TCTGCTTCTTCCAGC
mAON#6: 5' GTTATCTGCTTCTTCCAGCC
mAON#7: 5' CTTTTAGCTGCTGCTC
mAON#8: 5' GTTGTTCTTTTAGCTGCTGC
mAON#9: 5' TTAGCTGCTGCTCAT
mAON#10: 5' TTTAGCTGCTGCTCATCTCC
mAON#11: 5' CTGCTGCTCATCTCC

hAON#4: 5' CTGCTTCCTCCAACC
hAON#6: 5' GTTATCTGCTTCCTCCAACC
hAON#8: 5' GCTTTTCTTTTAGTTGCTGC
hAON#9: 5' TTAGTTGCTGCTCTT
hAON#11: 5' TTGCTGCTCTTTTCC

Gel Mobility Shift Assays

The efficacy of the AONs is determined by their binding affinity for the target sequence. Notwithstanding recent improvements in computer simulation programs for the prediction of RNA-folding, it is difficult to speculate which of the designed AONs would be capable of binding the target sequence with a relatively high affinity. Therefore, we performed gel mobility shift assays (according to protocols described by Bruice et al., 1997). The exon 46 target RNA fragment was generated by in vitro T7-transcription from a PCR fragment (amplified from either murine or human muscle mRNA using a sense primer that contains the T7 promoter sequence) in the presence of 32P-CTP. The binding affinity of the individual AONs (0.5 pmol) for the target transcript fragments was determined by hybridization at 37°C for 30 minutes and subsequent polyacrylamide (8%) gel electrophoresis. We performed these assays for the screening of both the mouse and human-specific AONs (Fig.3). At least 5 different mouse-specific AONs (mAON#4, 6, 8, 9 and 11) and four corresponding human-specific AONs (hAON#4, 6, 8, and 9) generated a mobility shift, demonstrating their binding affinity for the target RNA.

Transfection into muscle cell cultures

The exon 46-specific AONs which showed the highest target binding affinity in gel mobility shift assays were selected for analysis of their efficacy in inducing the skipping in muscle cells in vitro. In all transfection experiments, we included a non-specific AON as a negative control for the specific skipping of exon 46. As mentioned, the system was first set up in mouse muscle cells. We used both proliferating myoblasts and post-mitotic myotube cultures (expressing higher levels of dystrophin) derived from the mouse muscle cell line C2C12. For the subsequent experiments in human-derived muscle cell cultures, we used primary muscle cell cultures isolated from muscle biopsies from one unaffected individual and two unrelated DMD patients carrying a deletion of exon 45. These heterogeneous cultures contained approximately 20-40% myogenic cells. The different AONs (at a concentration of 1 μM) were transfected into the cells using the cationic polymer PEI (MBI Fermentas) at a ratio-equivalent of 3. The AONs transfected in these experiments contained a 5' fluorescein group which allowed us to determine the transfection efficiencies by counting the number of fluorescent nuclei. Typically, more than 60% of cells showed specific nuclear uptake of the AONs. To facilitate RT-PCR analysis, RNA was isolated 24 hours post-transfection using RNAzol B (CamPro Scientific, The Netherlands).

RT-PCR and sequence analysis

RNA was reverse transcribed using C. therm. polymerase (Roche) and an exon 48-specific reverse primer. To facilitate the detection of skipping of dystrophin exon 46, the cDNA was amplified by two rounds of PCR, including a nested amplification using primers in exons 44 and 47 (for the human system), or exons 45 and 47 (for the mouse system). In the mouse myoblast and myotube cell cultures, we detected a truncated product of which the size corresponded to exon 45 directly spliced to exon 47 (Fig.4). Subsequent sequence analysis confirmed the specific skipping of exon 46 from these mouse dystrophin transcripts. The efficiency of exon skipping was different for the individual AONs, with mAON#4 and #11 showing the highest efficiencies. Following these promising results, we focused on inducing a similar modulation of dystrophin splicing in the human-derived muscle cell cultures. Accordingly, we detected a truncated product in the control muscle cells, corresponding to exon 45 spliced to exon 47. Interestingly, in the patient-derived muscle cells a shorter fragment was detected which consisted of exon 44 spliced to exon 47. The specific skipping of exon 46 from the human dystrophin transcripts was confirmed by sequence data. This splicing modulation of both the mouse and human dystrophin transcript was neither observed in non-transfected cell cultures nor in cultures transfected with a non-specific AON.

Immunohistochemical analysis

We intended to induce the skipping of exon 46 in muscle cells from patients carrying an exon 45 deletion, in order to restore translation and the synthesis of a dystrophin protein. To detect a dystrophin product upon transfection with hAON#8, the two patient-derived muscle cell cultures were subject to immunocytochemistry using two different dystrophin monoclonal antibodies (Mandys-1 and Dys-2) raised against domains of the dystrophin protein located proximal and distal of the targeted region respectively. Fluorescent analysis revealed restoration of dystrophin synthesis in both patient-derived cell cultures (Fig.5). Approximately at least 80% of the fibers stained positive for dystrophin in the treated samples.

Our results show, for the first time, the restoration of dystrophin synthesis from the endogenous DMD gene in muscle cells from DMD patients. This is a proof of principle of the feasibility of targeted modulation of dystrophin pre-mRNA splicing for therapeutic purposes.

Targeted skipping of exon 51

Simultaneous skipping of dystrophin exons

The targeted skipping of exon 51. We demonstrated the feasibility of AON-mediated modulation of dystrophin exon 46 splicing, in mouse and human muscle cells in vitro. These findings warranted further studies to evaluate AONs as therapeutic agents for DMD. Since most DMD-causing deletions are clustered in two mutation hot spots, the targeted skipping of one particular exon can restore the reading frame in series of patients with different mutations (see table 1). Exon 51 is an interesting target exon. The skipping of this exon is therapeutically applicable in patients carrying deletions spanning exon 50, exons 45-50, exons 48-50, exons 49-50, exon 52, and exons 52-63, which includes a total of 15% of patients from our Leiden database.

We designed a series of ten human-specific AONs (hAON#21-30, see below) directed at different purine-rich regions within dystrophin exon 51. These purine-rich stretches suggested the presence of a putative exon splicing regulatory element that we aimed to block in order to induce the elimination of that exon during the splicing process. All experiments were performed according to protocols as described for the skipping of exon 46 (see above). Gel mobility shift assays were performed to identify those hAONs with high binding affinity for the target RNA. We selected the five hAONs that showed the highest affinity. These hAONs were transfected into human control muscle cell cultures in order to test the feasibility of skipping exon 51 in vitro. RNA was isolated 24 hrs post-transfection, and cDNA was generated using an exon 53 or 65 specific reverse primer. PCR-amplification of the targeted region was performed using different primer combinations flanking exon 51. The RT-PCR and sequence analysis revealed that we were able to induce the specific skipping of exon 51 from the human dystrophin transcript. We subsequently transfected two hAONs (#23 en 29) shown to be capable of inducing skipping of the exon into six different muscle cell cultures derived from DMD-patients carrying one of the mutations mentioned above. The skipping of exon 51 in these cultures was confirmed by RT-PCR and sequence analysis (fig. 7). More importantly, immunohistochemical analysis, using multiple antibodies raised against different parts of the dystrophin protein, showed in all cases that, due to the skipping of exon 51, the synthesis of a dystrophin protein was restored.

Exon 51-specific hAONs:

hAON#21: 5' CCACAGGTTGTGTCACCAG
hAON#22: 5' TTTCCTTAGTAACCACAGGTT
hAON#23: 5' TGGCATTTCTAGTTTGG
hAON#24: 5' CCAGAGCAGGTACCTCCAACATC
hAON#25: 5' GGTAAGTTCTGTCCAAGCCC
hAON#26: 5' TCACCCTCTGTGATTTTAT
hAON#27: 5' CCCTCTGTGATTTT
hAON#28: 5' TCACCCACCATCACCCT
hAON#29: 5' TGATATCCTCAAGGTCACCC
hAON#30: 5' CTGCTTGATGATCATCTCGTT

Simultaneous skipping of multiple dystrophin exons.
The skipping of one additional exon, such as exon 46 or exon 51, restores the reading frame for a considerable number of different DMD mutations. The range of mutations for which this strategy is applicable can be enlarged by the simultaneous skipping of more than one exon. For instance, in DMD patients with a deletion of exon 46 to exon 50, only the skipping of both the deletion-flanking exons 45 and 51 enables the reestablishment of the translational reading frame.

ERS-independent exon skipping.
A mutation in exon 29 leads to the skipping of this exon in two Becker muscular dystrophy patients (Ginjaar et al., 2000; EJHG, vol. 8, p.793-796). We studied the feasibility of directing the skipping of exon 29 through targeting the site of mutation by AONs. The mutation is located in a purine rich stretch that could be associated with ERS activity. We

designed a series of AONs (see below) directed to sequences both within (h29AON#1 to h29AON#6) and outside (h29AON#7 to h29AON#11) the hypothesized ERS. Gel mobility shift assays were performed (as described) to identify those AONs with highest affinity for the target RNA (Fig. 8). Subsequently, h29AON#1, #2, #4, #6, #9, #10, and #11 were transfected into human control myotube cultures using the PEI transfection reagent. RNA was isolated 24 hrs post-transfection, and cDNA was generated using an exon 31 specific reverse primer. PCR-amplification of the targeted region was performed using different primer combinations flanking exon 29. This RT-PCR and subsequent sequence analysis (Fig. 8 B,C) revealed that we were able to induce the skipping of exon 29 from the human dystrophin transcript. However, the AONs that facilitated this skipping were directed to sequences both within and outside the hypothesized ERS (h29AON#1, #2, #4, #6, #9, and #11). These results suggest that skipping of exon 29 occurs independent of whether or not exon 29 contains an ERS and that therefore the binding of the AONs to exon 29 more likely inactivated an exon inclusion signal rather than an ERS. This proof of ERS-independent exon skipping may extend the overall applicability of this therapy to exons without ERS's.

h29AON#1: 5' TATCCTCTGAATGTCGCATC
h29AON#2: 5' GGTTATCCTCTGAATGTCGC
h29AON#3: 5' TCTGTTAGGGTCTGTGCC
h29AON#4: 5' CCATCTGTTAGGGTCTGTG
h29AON#5: 5' GTCTGTGCCAATATGCG
h29AON#6: 5' TCTGTGCCAATATGCGAATC

h29AON#7: 5' TGTCTCAAGTTCCTC
h29AON#8: 5' GAATTAAATGTCTCAAGTTC
h29AON#9: 5' TTAAATGTCTCAAGTTCC
h29AON#10: 5' GTAGTTCCCTCCAACG

h29AON#11: 5' CATGTAGTTCCCTCC

AON-induced exon 46 skipping in vivo in murine muscle tissue.

Following the promising results in cultured muscle cells, we tested the different mouse dystrophin exon 46-specific AONs in vivo by injecting them, linked to polyethylenimine (PEI), into the gastrocnemius muscles of control mice. With mAON#4, #6, and #11, previously shown to be effective in mouse muscle cells in vitro, we were able to induce the skipping of exon 46 in muscle tissue in vivo as determined by both RT-PCR and sequence analysis (Fig. 9). The in vivo exon 46 skipping was dose-dependent with highest efficiencies (up to 10%) following injection of 20 μg per muscle per day for two subsequent days.

References

Achsel et al., 1996; J. Biochem. 120; p.53-60.

Bruice T.W. and Lima, W.F. (1997) Biochemistry 36(16): pages 5004-5019.

Brunak et al., 1991; J Mol Biol 220: p. 49-65.

Dunckley, MG et al (1998) Human molecular genetics 7: pages 1083-1090.

Ginjaar et al., 2000; EJHG, vol. 8, p.793-796

Mann et al., 2001; PNAS vol. 98, pages 42-47

Tanaka et al., 1994 Mol Cell Biol. 14:p. 1347-1354.

Wilton SD et al (1999) Neuromuscular disorders 9 : pages 330-338.

Details and background on Duchenne Muscular Dystrophy and related diseases can be found on website http://www.dmd.nl

Table 1

Exon to be skipped	Therapeutic for DMD-deletions (exons)	Frequency in http://www.dmd.nl (%)
2	3-7	2
8	3-7	4
	4-7	
	5-7	
	6-7	
43	44	5
	44-47	
44	35-43	8
	45	
	45-54	
45	18-44	13
	46-47	
	44	
	46-48	
	46-49	
	46-51	
	46-53	
46	45	7
50	51	5
	51-55	
51	50	15
	45-50	
	48-50	
	49-50	
	52	
	52-63	

52	51	3
	53	
	53-55	
53	45-52	9
	48-52	
	49-52	
	50-52	
	52	

Table 1 continued

CLAIMS

1. A method for directing splicing of a pre-mRNA in a system capable of performing a splicing operation comprising contacting said pre-mRNA in said system with an agent capable of specifically inhibiting an exon inclusion signal of at least one exon in said pre-mRNA, said method further comprising allowing splicing of said pre-mRNA.

2. A method according to claim 1, further comprising allowing translation of mRNA produced from splicing of said pre-mRNA.

3. A method according to claim 1 or claim 2, wherein said mRNA encodes a functional protein.

4. A method according to any one of claims 1-3, wherein said protein comprises two or more domains, wherein at least one of said domains is encoded by said mRNA as a result of skipping of at least part of an exon in said pre-mRNA.

5. A method according to any one of claims 1-4, wherein said contacting results in activation of a cryptic splice site in a contacted exon.

6. A method for at least in part decreasing the production of an aberrant protein in a cell,

said cell comprising pre-mRNA comprising exons coding for said protein,

the method comprising

providing said cell with an agent capable of specifically inhibiting an exon inclusion signal of at least one of said exons,

the method further comprising allowing translation of mRNA produced from splicing of said pre-mRNA.

7. A method according to any one of claims 1-6, wherein said exon inclusion signal comprises an exon recognition sequence.

8. A method according to any one of claims 1-6, wherein said exon inclusion signal is present in an exon comprising a strong splice donor/acceptor pair.

9. A method according to any one of claims 1-8, wherein said translation results in a mutant or normal dystrophin protein.

10. A method according to claim 9, wherein said mutant dystrophin protein is equivalent to a dystrophin protein of a Becker patient.

11. A method according to claim 9 or claim 10, wherein said exon inclusion signal is present in exon number 2, 8, 43, 44, 45, 46, 50, 51, 52 or 53.

12. A method according to any one of claims 1-11, wherein said agent comprises nucleic acid or a functional equivalent thereof.

13. A method according to claim 12, wherein said nucleic acid contains between 15-25 nucleotides or a functional equivalent thereof.

14. A method according to any one of claims 1-13, further comprising providing said cell with another agent capable of inhibiting an exon inclusion signal present in another exon of said pre-mRNA.

15. A method for determining whether a nucleic acid or functional equivalent thereof, comprising complementarity to a part of an exon, is capable of specifically inhibiting an exon inclusion signal of said exon,
comprising
providing a cell having a pre-mRNA containing said exon, with said nucleic acid, culturing said cell to allow the formation of an mRNA from said pre-mRNA and determining whether said exon is absent from said mRNA.

16. A method according to claim 15 further comprising determining *in vitro* the relative binding affinity of said nucleic acid or functional equivalent thereof to an RNA molecule comprising said exon.

17. A nucleic acid or functional equivalent thereof obtainable by a method according to claim 15 or claim 16.

18. A nucleic acid delivery vehicle comprising a nucleic acid according to claim 17, or the complement thereof.

19. A nucleic acid delivery vehicle capable of expressing a nucleic acid according to claim 17.

20. Use of a nucleic acid according to claim 17 or a nucleic acid delivery vehicle according to claim 18 or claim 19, for the preparation of a medicament.

21. Use of a nucleic acid according to claim 17 or a nucleic acid delivery vehicle according to claim 18 or claim 19, for the preparation of a medicament for the treatment of an inherited disease or predisposition to a disease.

22. Use of a nucleic acid or an equivalent thereof, comprising an exon inclusion signal inhibiting quality for the preparation of a medicament.

23. A non-human animal provided with a nucleic acid according to claim 17.

24. A non-human animal according to claim 23, further comprising a nucleic acid encoding a human protein or a functional equivalent thereof.

25. A non-human animal according to claim 24, further comprising a silencing mutation in the gene encoding an animal homologue of said human protein.

FIGURE 1.

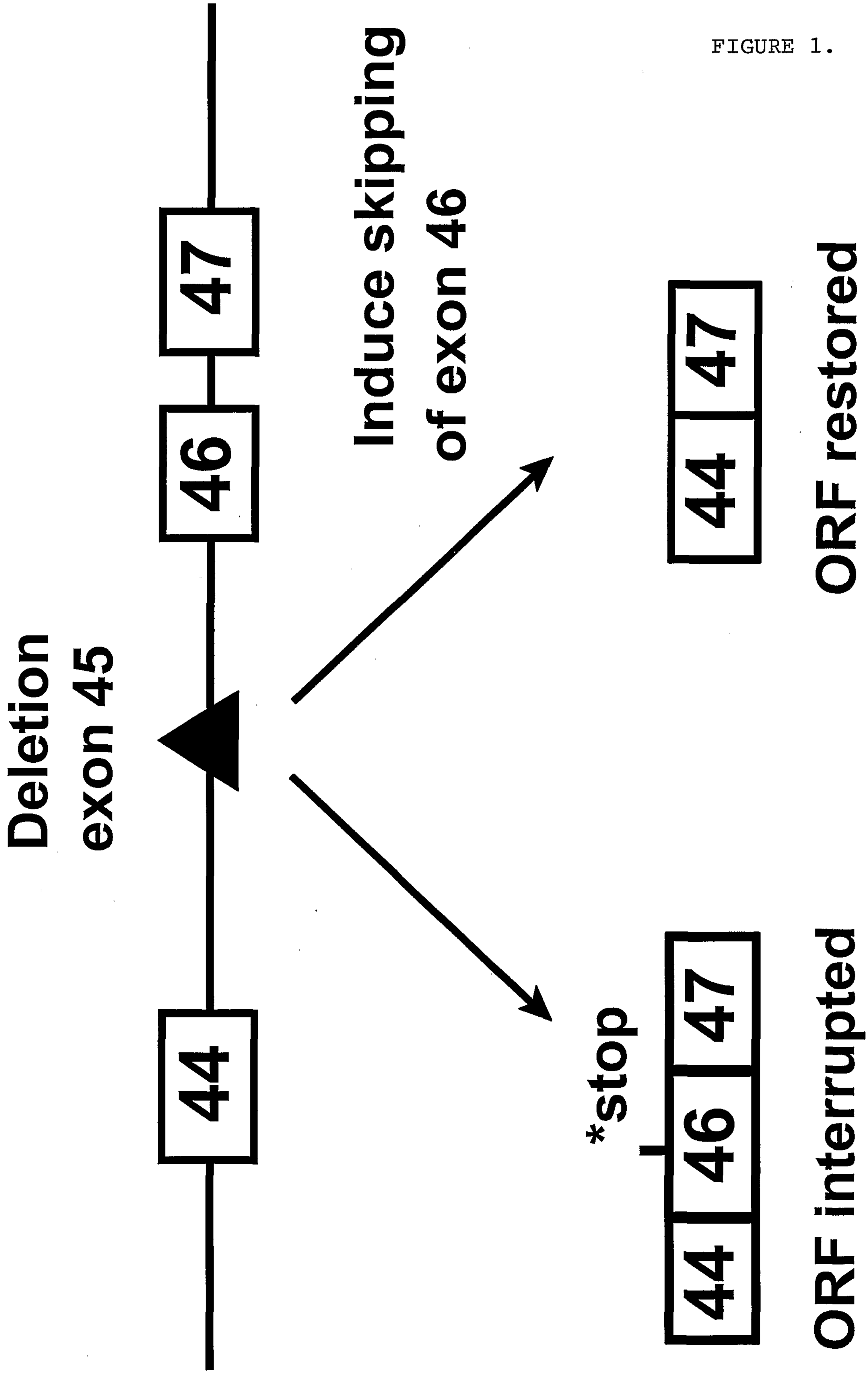

Deletion
exon 45
44
46
47
Induce skipping
of exon 46
*stop
44
46
47
ORF interrupted
44
47
ORF restored

FIGURE 2.

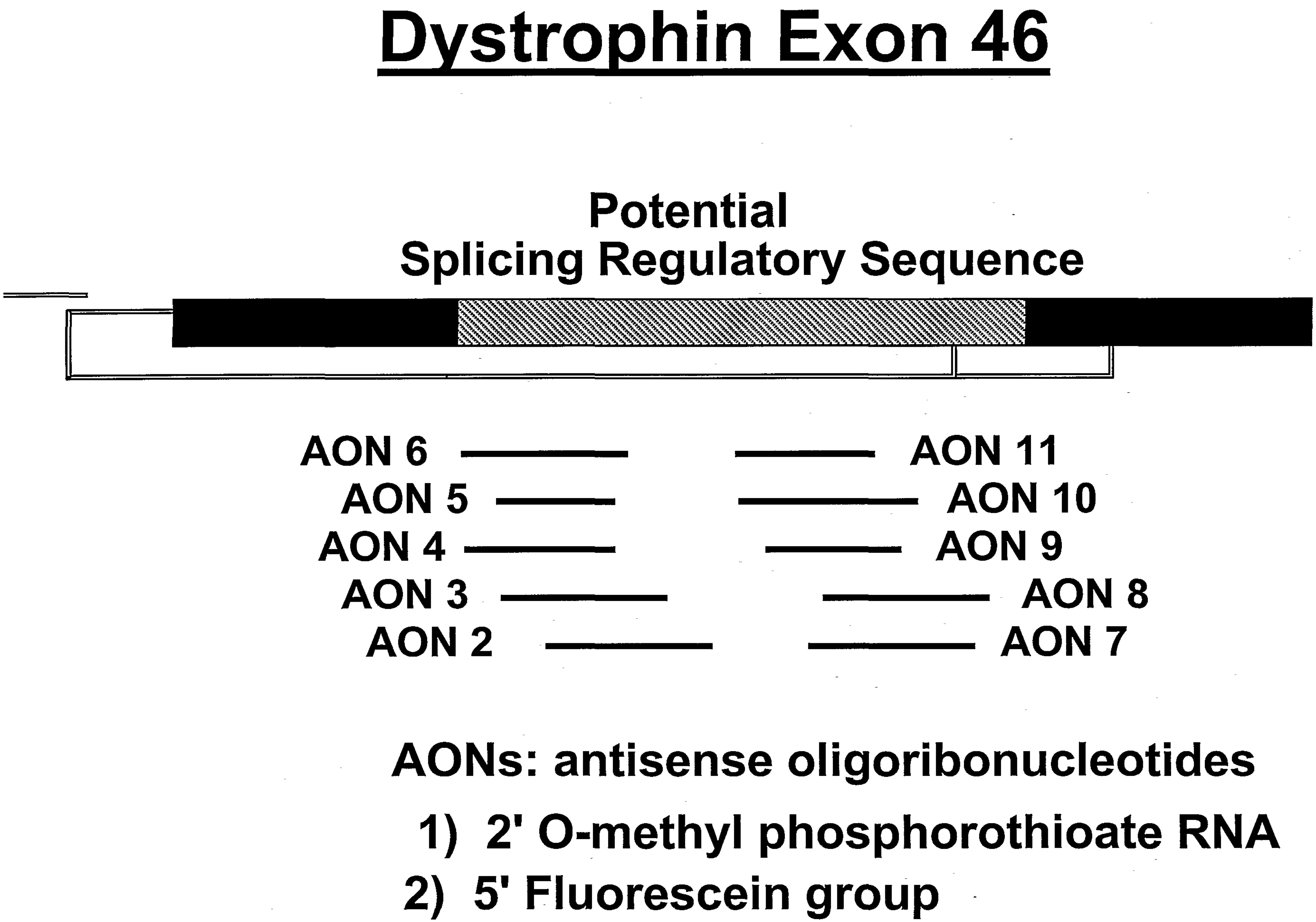

Dystrophin Exon 46
Potential
Splicing Regulatory Sequence
AON 6
AON 5
AON 4
AON 3
AON 2
AON 11
AON 10
AON 9
AON 8
AON 7
AONs: antisense oligoribonucleotides
1) 2' O-methyl phosphorothioate RNA
2) 5' Fluorescein group

FIGURE 3.

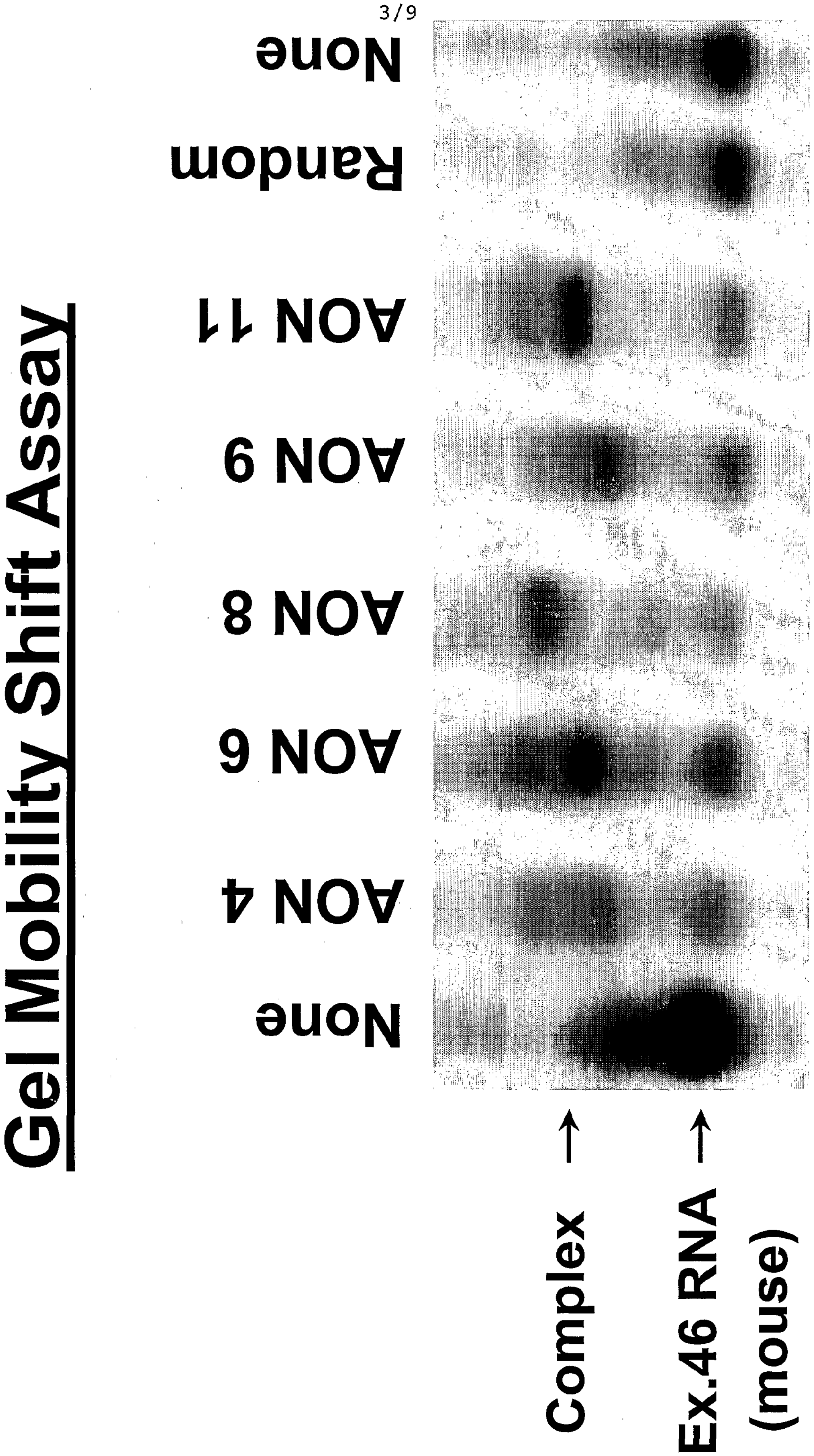
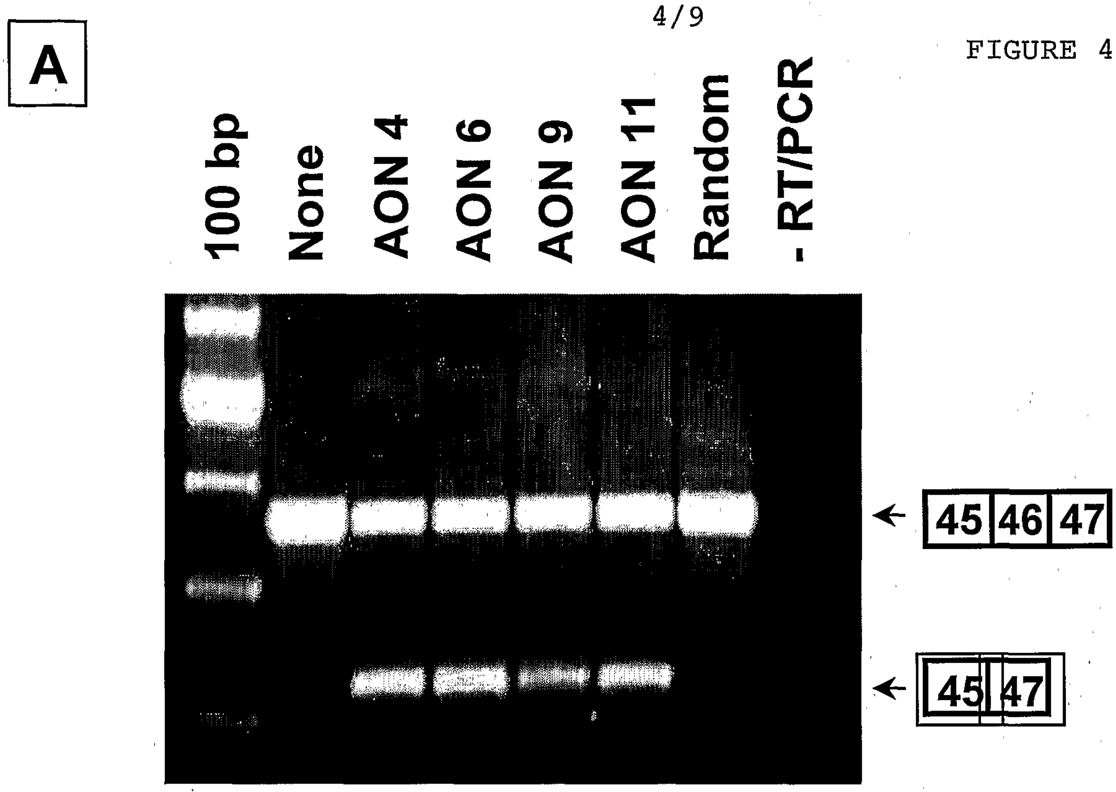

Gel Mobility Shift Assay
None
Random
AON 11
AON 9
AON 8
AON 6
AON 4
None
Complex
Ex.46 RNA
(mouse)

FIGURE 4.


A
100 bp
None
AON 4
AON 6
AON 9
AON 11
Random
- RT/PCR
45 46 47
45 47

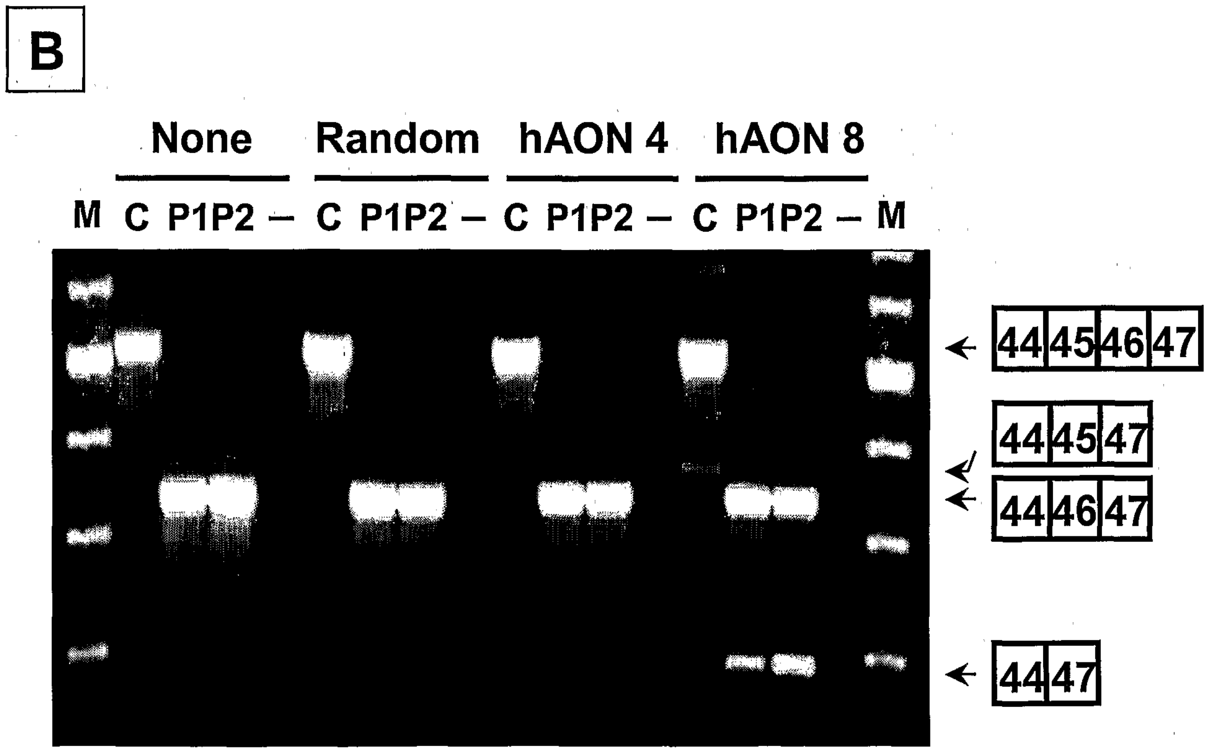
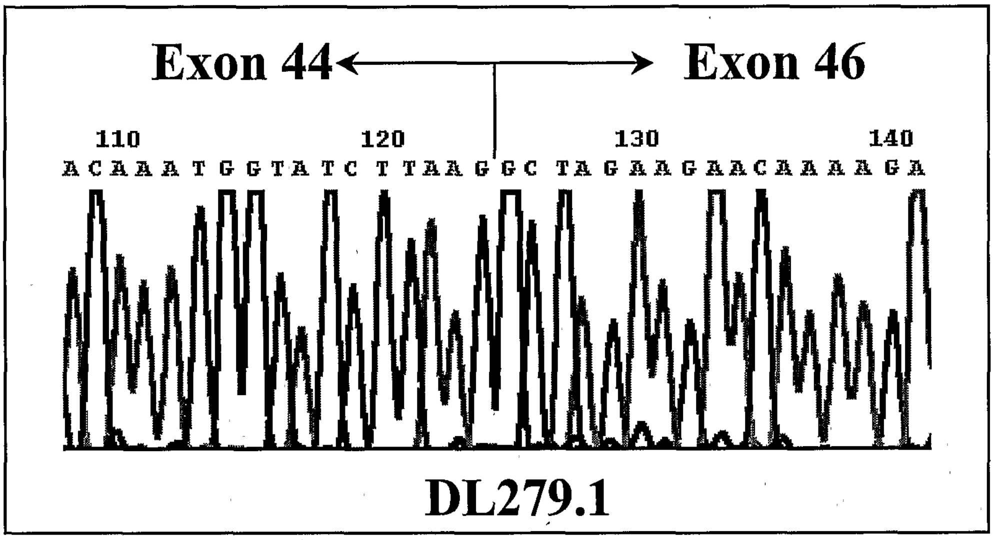

B
None
Random
hAON 4
hAON 8
M C P1P2 – C P1P2 – C P1P2 – C P1P2 – M
44 45 46 47
44 45 47
44 46 47
44 47

FIGURE 5.


Exon 44
Exon 46
110
120
130
140
ACAAATGGTATCTTAAGGCTAGAAGAACAAAAGA
DL279.1

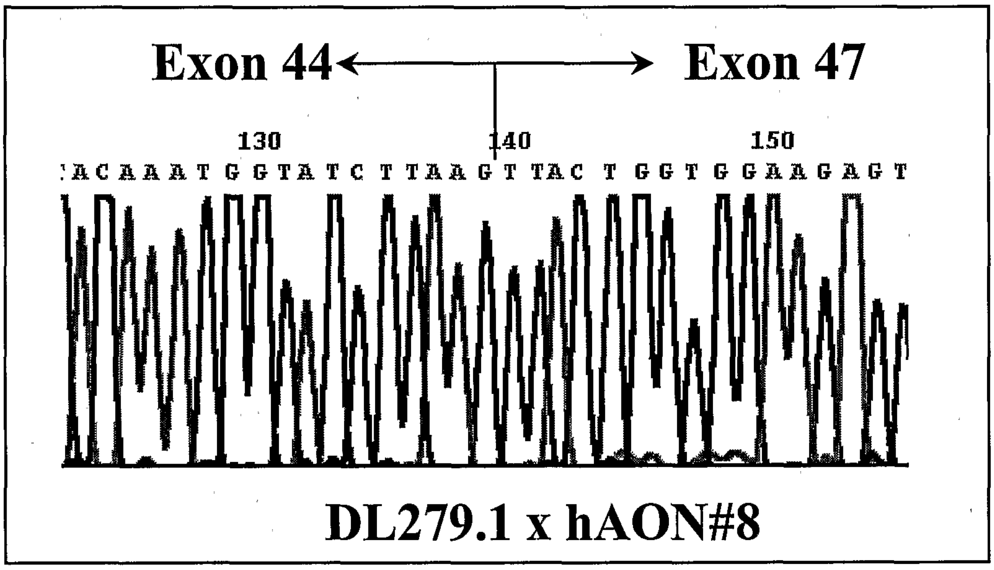
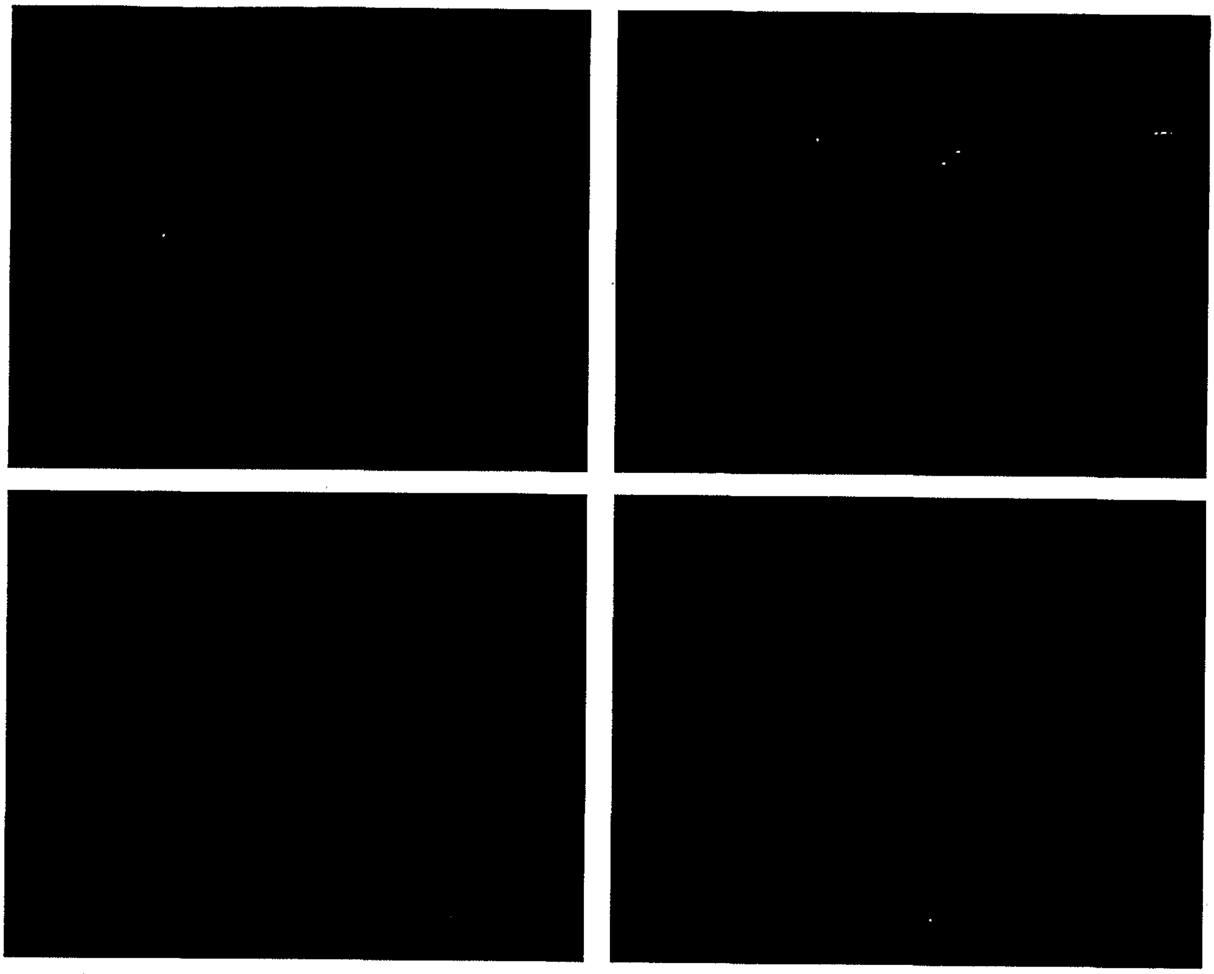
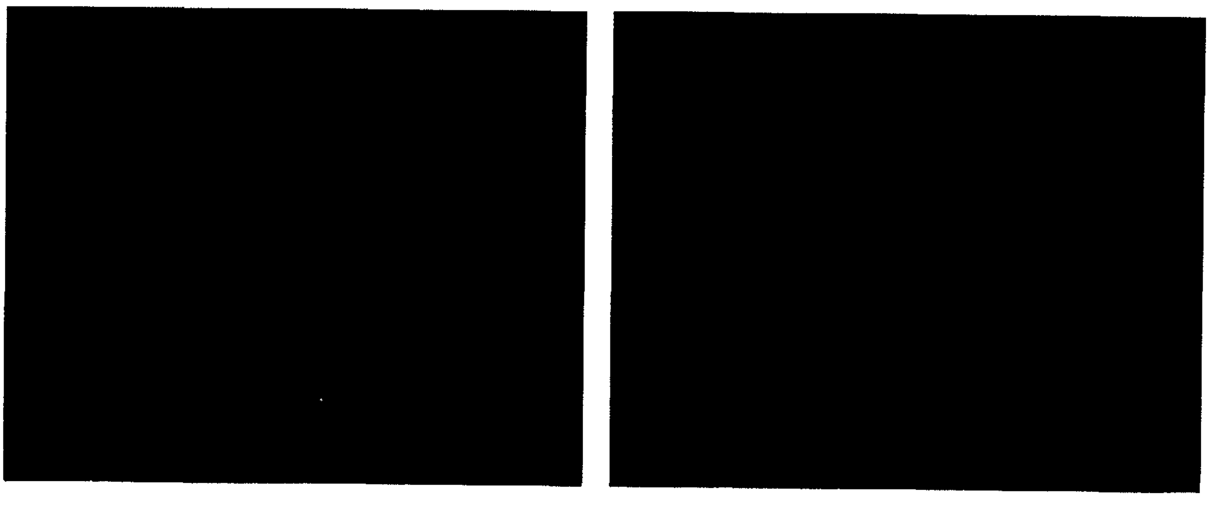

Exon 44
Exon 47
130
140
150
ACAAATGGTATCTTAAGTTACTGGTGGAAGAGT
DL279.1 x hAON#8

FIGURE 6

dystrophin (ex.31-32) dystrophin (ex.77-79)



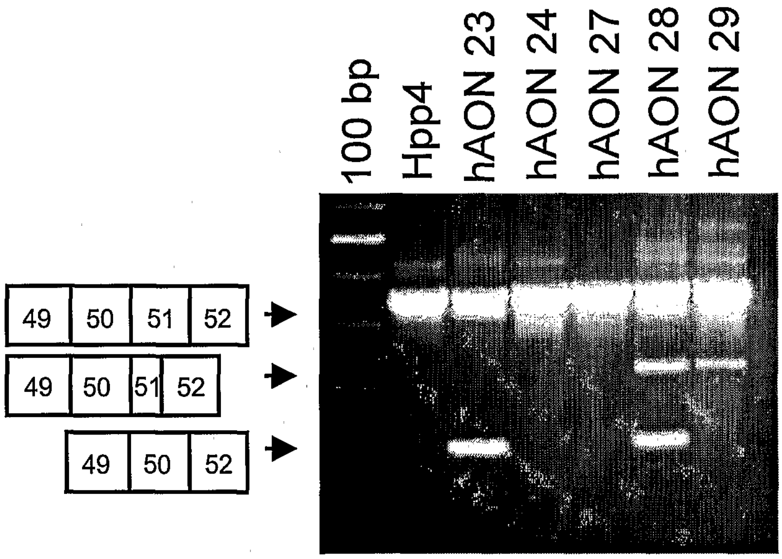
DL279.1 x AON#8



DL279.1

FIGURE 7.

A


100 bp
Hpp4
hAON 23
hAON 24
hAON 27
hAON 28
hAON 29
49 50 51 52
49 50 51 52
49 50 52

B

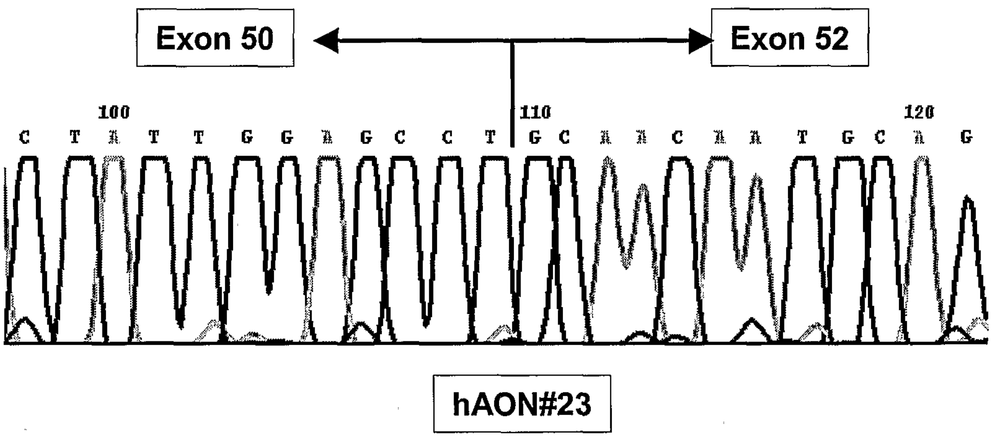

Exon 50
Exon 52
100
110
120
C T A T T G G A G C C T G C A A C A A T G C A G
hAON#23

FIGURE 8.

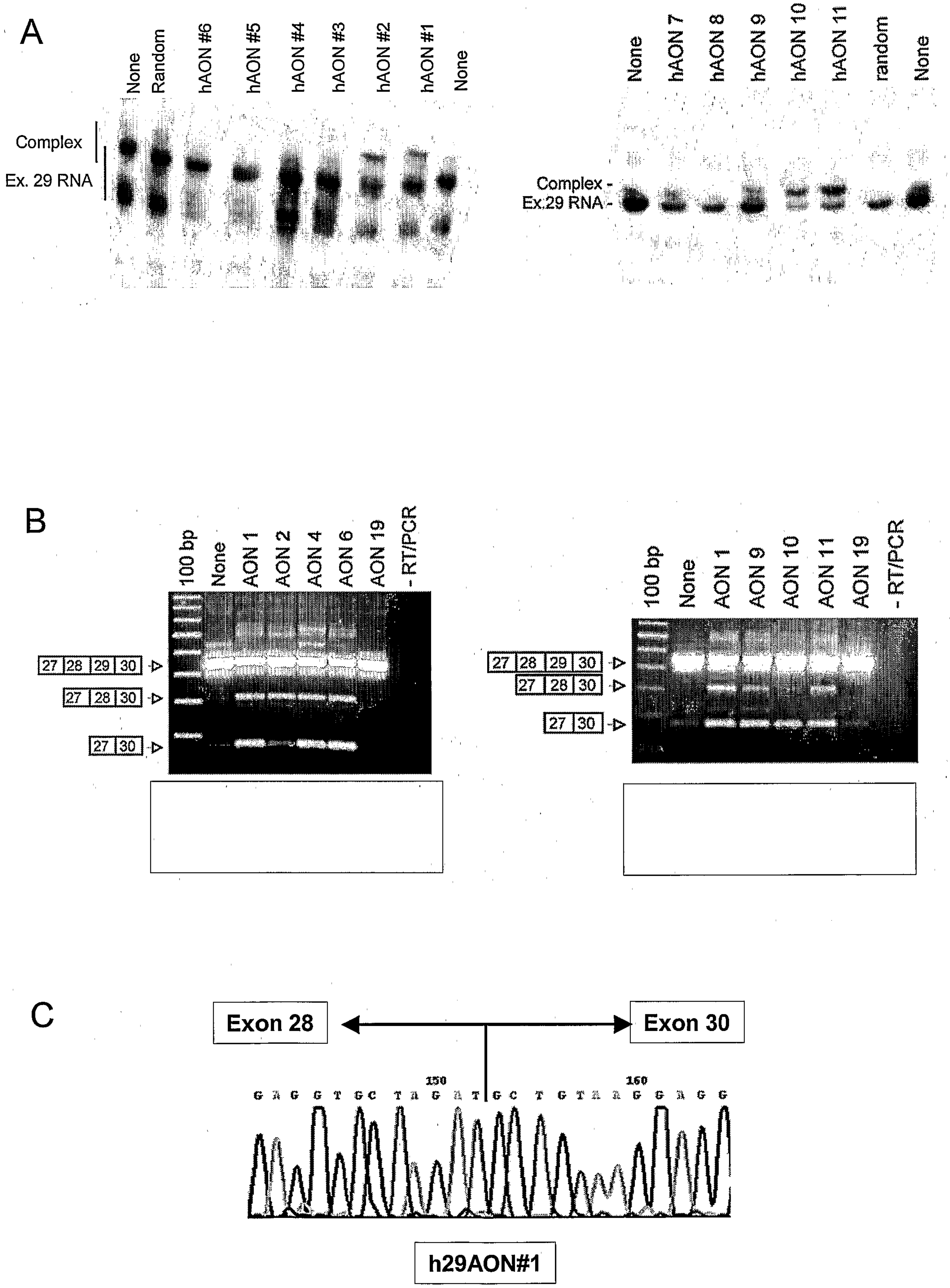
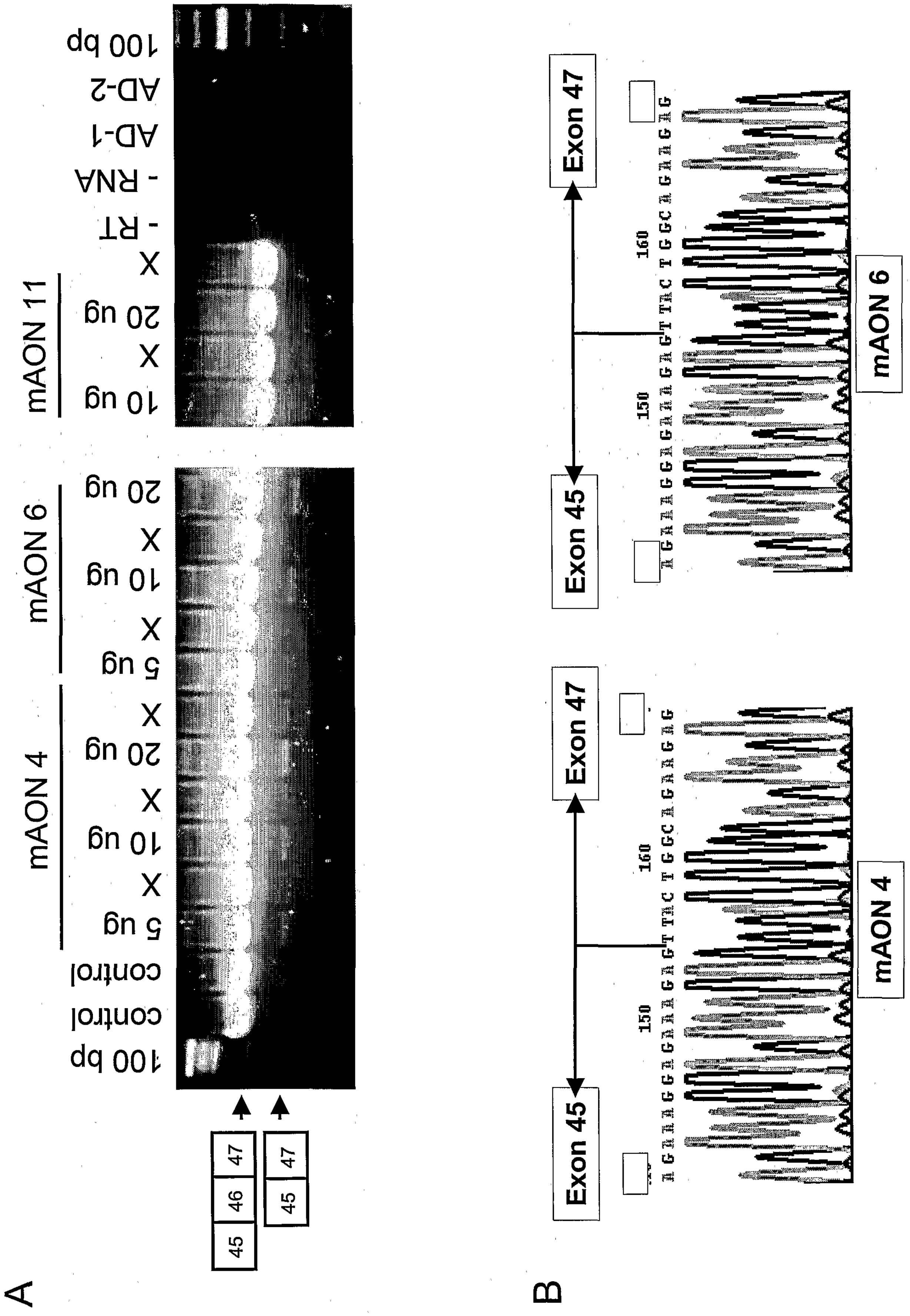

A
None
Random
hAON #6
hAON #5
hAON #4
hAON #3
hAON #2
hAON #1
None
Complex
Ex. 29 RNA
None
hAON 7
hAON 8
hAON 9
hAON 10
hAON 11
random
None
Complex -
Ex.29 RNA -
B
100 bp
None
AON 1
AON 2
AON 4
AON 6
AON 19
- RT/PCR
27 28 29 30
27 28 30
27 30
100 bp
None
AON 1
AON 9
AON 10
AON 11
AON 19
- RT/PCR
27 28 29 30
27 28 30
27 30
C
Exon 28
Exon 30
150
160
G A G G T G C T A G A T G C T G T A A G G A G G
h29AON#1

FIGURE 9.


A
B
mAON 4
mAON 6
mAON 11
100 bp
control
control
5 ug
X
10 ug
X
20 ug
X
5 ug
X
10 ug
X
20 ug
10 ug
X
20 ug
X
- RT
- RNA
AD-1
AD-2
100 bp
45
46
47
45
47
Exon 45
Exon 47
mAON 4
mAON 6
150
160

INTERNATIONAL SEARCH REPORT

International Application No
PCT/NL 01/00697

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/11 A61K48/00 A61K31/7088

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, WPI Data, PAJ, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	*Citation of document, with indication, where appropriate, of the relevant passages*	*Relevant to claim No.*
X	PRAMONO ZACHARIAS ALOYSIUS DWI ET AL: "Induction of exon skipping of the dystrophin transcript in lymphoblastoid cells by transfecting on antisense oligodeoxynucleotide complementary to an exon recognition sequence." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 226, no. 2, 1996, pages 445-449, XP002147077 ISSN: 0006-291X the whole document --- -/--	1-22

[X] Further documents are listed in the continuation of box C.

[ ] Patent family members are listed in annex.

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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 December 2001	21/12/2001

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Nichogiannopoulou, A

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	DUNCKLEY M G ET AL: "Modification of splicing in he dystrophin gene in cultured Mdx muscle cells by antisense oligoribonucleotides" HUMAN MOLECULAR GENETICS,OXFORD UNIVERSITY PRESS, SURREY,GB, vol. 5, no. 1, July 1995 (1995-07), pages 1083-1090, XP000939302 ISSN: 0964-6906 the whole document ---	1-22
Y	MATSUO MASAFUMI: "Duchenne/Becker muscular dystrophy: From molecular diagnosis to gene therapy." BRAIN & DEVELOPMENT, vol. 18, no. 3, 1996, pages 167-172, XP000939335 ISSN: 0387-7604 abstract ---	1-25
Y	DUNCKLEY MATTHEW G ET AL: "Modulation of splicing in the DMD gene by antisense oligoribonucleotides." NUCLEOSIDES & NUCLEOTIDES, vol. 16, no. 7-9, July 1997 (1997-07), pages 1665-1668, XP000973196 ISSN: 0732-8311 the whole document ---	1-25
Y	SHERRATT TIM G ET AL: "Exon skipping and translation in patients with frameshift deletions in the dystrophin gene." AMERICAN JOURNAL OF HUMAN GENETICS, vol. 53, no. 5, 1993, pages 1007-1015, XP000973145 ISSN: 0002-9297 the whole document -----	1-25