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- (71) **Applicant:** MIRRX THERAPEUTICS [DK/DK]; Dip-
lomvej 378, DK-2800 Kongens Lyngby (DK).
- (72) **Inventor:** MOELLER, Thorleif; Over-Holluf-Toften 67,
DK-5220 Odense SOE (DK).
- (74) **Agent:** ORSNES, Henrik; Forskerparken 10, DK-5230
Odense M (DK).
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(54) **Title:** OLIGOMERS WITH IMPROVED OFF-TARGET PROFILE

On-target binding with various oligomer designs

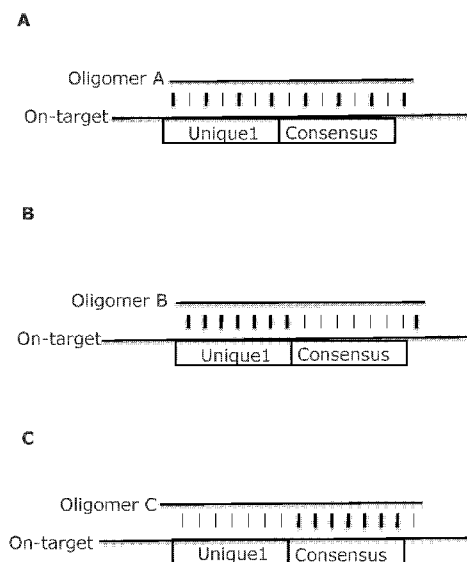


Fig. 1

(57) **Abstract:** The present invention provides oligomers that binds RNA that consists of a lower affinity region and a higher affinity region, wherein the monomers in the higher affinity region increases the melting temperature (i.e. affinity) of the oligomer base paired to RNA more than the monomers used in the lower affinity region, wherein said increase in melting temperature is relatively to the alternative use of DNA monomers of the same (base) sequence. The oligomers of the invention are useful for binding to target RNA such as mRNA and non-coding RNA and have the advantage that they will be less prone to off-target binding via the lower affinity region than via the higher affinity region.

Oligomers with improved off-target profile

Background of the invention

- 5 The present invention relate to oligomers and oligonucleotides that can bind to complementary RNA. Oligonucleotides are useful as reagents in science, research and development e.g. for detection and analysis of cellular RNA or for modulation of the activity of cellular RNA.
- 10 Oligonucleotides are also being developed as therapeutics, where they are typically also intended to bind to and modulate the activity of cellular RNA. Oligonucleotides that bind cellular RNA are herein also termed antisense oligonucleotides.
- 15 Some antisense oligonucleotides act by inducing destabilization of their target RNA e.g. by activating RNase H degradation of the target RNA or by activating the RISC pathway. Such oligonucleotides are typically described as gapmers and siRNAs respectively. Another class of oligonucleotides act as steric blocker and hence prevents the target RNA from interacting with another macromolecule. One
- 20 example is splice switching oligonucleotides that modulate splicing of pre-mRNA. Another example is microRNA inhibitors that bind to microRNA and prevent the microRNA from binding to its mRNA targets. A thorough description of the design, preparation and use of antisense oligonucleotides can be found in "Antisense Drug Technology, Principles, Strategies and Applications, 2nd Edition, Edited by Stanley
- 25 Crooke".

- It is easy to design an antisense oligonucleotide that is complementary to a given target RNA and hence is capable of binding to the target RNA. However, when attempting to develop antisense oligonucleotides as therapeutics,
- 30 complementarity to the target is not enough. The antisense oligonucleotide need to be modified to give it more drug-like properties, e.g. better potency, bioavailability and biostability. Moreover, it has turned out that a problem of many antisense oligonucleotides is off-target binding, i.e. binding to non-intended RNAs,

which may lead to undesirable effects. To minimize off-target binding, it is typically attempted to target unique sequences in the RNA transcriptome. Even so, off-target binding of antisense oligonucleotides is still a problem. One object of the present invention is to provide antisense oligonucleotides, in particular steric block oligonucleotides that have new and desirable characteristics in terms of off-target binding.

Summary of the invention

The present invention provides oligomers that can bind RNA consisting of

- a lower affinity region,
- a higher affinity region,
- wherein the monomers in the higher affinity region increases the melting temperature (i.e. affinity) of the oligomer base paired to RNA more than the monomers used in the lower affinity region, wherein said increase in melting temperature is relatively to the alternative use of DNA monomers of the same (base) sequence.

The oligomers of the invention are useful for binding to target RNA such as mRNA and non-coding RNA and have the advantage that they will be less prone to off-target binding via the lower affinity region than via the higher affinity region.

Brief description of the figures

Figure 1 A show a typical steric block oligomer bound to its intended target (the on-target). The consensus sequence is a sequence that is shared with other RNAs and is preferably part of a binding site for at cellular molecule, .e.g. a microRNA. The sequence adjacent to the consensus sequence is denoted unique 1 and is sequence that differs (also herein termed "specificity sequence") among RNAs sharing the consensus sequence. Base pairs are indicated by lines between the oligomer and the target. The oligomer is uniformly modified with monomer analogues that enhance affinity toward complementary RNA and the position of these modifications is shown by a bold (base pair) line to the target. The oligomer

may e.g. be a BNA/2'O-methyl RNA oligomer and the affinity enhancing analogues is then BNA (bicyclic nucleic acids). The illustrated design could just as well have been affinity enhancing analogues in every third position or even in all positions or any other repeating pattern, which gives a relatively uniform affinity over the
5 length of the oligomer. It is clear that G:C base pairs are stronger than A:U base pairs. However, for the sake of simplicity such sequence specific affinity variations are not considered in the present example.

Figure 1B shows a steric block oligonucleotide of same sequence as oligomer A of
10 figure 1A, but with a non-uniform distribution of affinity increasing modifications bound to its intended target. The affinity of this oligomer toward complementary RNA will not differ dramatically from the oligomer of 1A. Depending on the monomers chosen, the overall affinity may be higher or lower.

15 Figure 1C shows a yet another steric block oligonucleotide of same sequence as oligomer A of figure 1A, but with a non-uniform distribution of affinity increasing modifications bound to its intended target. The affinity of this oligomer toward complementary RNA will not differ dramatically from the oligomer of 1A or 1B. Depending on the monomers chosen, the overall affinity may be higher or lower.

20

In theory, all 3 oligomers have a similar affinity toward complementary RNA and would therefore be expected to have a similar potency, e.g. when used in cells or organisms. However, they have a different off-target profile (binds to a different set of off-targets).

25

Figure 2 shows the same oligomers as illustrated in figure 1, however, bound to an off-target that shares the consensus sequence with the intended target.

The oligomer in 2A will have an intermediate affinity toward the off-target,
30 whereas the oligomer in 2B will have a lowered affinity toward the off-target because the region complementary to the consensus sequence is a "lower affinity region", as seen by the lower density of affinity increasing modifications, such as BNA. I.e. the B oligomer will be less likely bind to off-targets comprising the consensus sequence.

35

On the other hand, the C oligomer will however be more likely to bind to off-targets comprising the consensus sequence, because it does so via its "higher affinity region".

- 5 Figure 3 shows the same oligomers as illustrated in figure 1 and 2, however, bound to an off-target that does not share the consensus sequence. It is seen that oligomer B will do so most potently, because it binds via its higher affinity region, whereas oligomer C will do so least potently because it does so via its lower affinity region. I.e. the increased specificity of oligomer B toward RNA targets
10 that share the consensus sequence is achieved at the expense of decreased specificity toward RNA targets comprising the specificity region.

Disclosure of the invention

The present invention provides oligomers for targeting RNA, e.g. mRNA and non-
15 coding RNA.

A first aspect of the invention is an oligomer of 10-40 monomers that binds RNA comprising (or more preferably consisting of)

- 20
- a lower affinity region,
 - a higher affinity region,
 - wherein the monomers in the higher affinity region (altogether) increases the melting temperature (i.e. affinity) of the oligomer base paired to complementary RNA more than the monomers used in the lower affinity
25 region (altogether), wherein said increase in melting temperature is relatively to the alternative use of DNA monomers of the same (base) sequence,
 - and wherein the lower affinity region or higher affinity region is of 5-12 contiguous monomers, such as 5-10, 5-9, 5-8, 6-10, 7-10, 8-10, 6-9 or 6-
30 8 contiguous monomers and wherein the other region is either contiguous or consists of two sub regions flanking the region of 5-12 monomers.

It should be understood that when referring to *"the monomers in the higher affinity region.."* and *"the monomers used in the lower affinity region"* in the above, reference is to the monomers altogether in the region and not to the monomers individually. Thus, not every monomer in the higher affinity region
5 does necessarily increase the melting temperature more than individual monomers used in the lower affinity region.

Preferably, the monomers in the higher affinity region (altogether) increases the melting temperature (i.e. affinity) of the oligomer base paired to RNA at least 5
10 degrees Celsius more than the monomers used in the lower affinity region, such as at least 5 degrees, 10 degrees, 15 degrees, 20 degrees, 25 degrees, 30 degrees, 35 degrees, 40 degrees Celsius more than the monomers used in the lower affinity region, wherein said increase in melting temperature is relatively to the alternative use of DNA monomers of the same sequence.

15

When referring to the melting temperature (also herein termed t_m or t_m value) of the oligomer base paired to RNA, the temperature is preferably measured in 100 mM NaCl, 0.1 mM EDTA, 10 mM NaH_2PO_4 , 5 mM Na_2HPO_4 , pH 7.0), using 1.0 μM concentrations of both oligomer and complementary RNA.

20

In a preferred embodiment, the monomers in the higher affinity region on average (per monomer) increase the melting temperature more than the monomers in the lower affinity region. I.e. the increase in t_m of the lower and higher affinity region is divided by the number of monomers in the lower and higher affinity
25 region, respectively. It should be noted that the increase in t_m of the lower affinity region may be negative, which is the case when the t_m is decreased relatively to the alternative use of DNA monomers of the same sequence.

Preferably, the monomers in the higher affinity region on average (per monomer)
30 increase the melting temperature at least 2 degrees Celsius, such as 3, 4, 5, 6, 7 or 8 degrees Celsius more than the monomers in the lower affinity region.

The oligomer is typically an oligonucleotide and preferably comprise at least two different types of monomers, e.g. selected from the group consisting of DNA,
35 RNA, BNA (in particular 2',4'-bicyclic nucleic acids (2'4'-BNA) such as ENA and

LNA (2'-O,4'-C-methylene-beta-D-ribofuranosyl and analogues thereof e.g., amino-LNA, thio-LNA, alfa-L-ribo-LNA, beta-D-xylo-LNA, S-cMOE (2',4'-constrained MOE), R-cMOE, cEt (2',4'-constrained ethyl), morpholino, phosphoramidate, FANA, PNA, CENA, 2'MOE, 2'F, 2'O-methyl.

5

It is particular preferred that the higher affinity region comprises 2',4'-bicyclic nucleic acids (2'4'-BNA).

In another embodiment, the lower affinity region comprises only two types of
10 monomers, preferably selected from the group consisting of DNA, RNA, morpholino, phosphoramidate, FANA, PNA, UNA, 2'MOE, 2'F and 2'O-methyl.

In another embodiment, the lower affinity region comprises only one type of monomer, preferably selected from the group consisting of morpholino,
15 phosphoramidate, FANA, PNA, UNA, 2'MOE, 2'F, and 2'O-methyl.

As is known to the skilled man, different monomers generally have different effects on t_m . E.g. BNAs have a strong effect on t_m and 2'-modifications have a moderate effect. Some modifications like e.g. UNA even decrease t_m , i.e. have a
20 negative effect.

As used in the present context, 2',4'-bicyclic nucleic acids are herein classified as monomers that have a strong effect on t_m . Morpholino, phosphoramidate-, FANA, PNA, CENA, 2'MOE, 2'F, 2'O-methyl monomers are herein classified as monomers
25 that have a moderate effect on t_m . Monomers that decrease t_m are e.g. UNA (unlocked nucleic acid). DNA and RNA monomers are herein classified as neutral monomers with regard to t_m (DNA monomers are reference monomers).

In a preferred embodiment, the lower affinity region has a lower density (number
30 of affinity increasing monomers/total number of monomers in the given region) of monomers that have a strong and/or moderate effect on t_m than does the higher affinity region. This feature can usually be used to easily identify oligomers of the invention, e.g. by identifying the lower affinity region within the oligomer.

It follows that oligomers with a uniform distribution of high affinity/and or moderate monomers are not part of the scope of this invention, because they do not comprise a lower affinity region. Also oligomers with slight deviations from a uniform distribution are not part of the scope of this invention, as slight deviations
5 are not enough to create a region of lower affinity that differ substantially in affinity (as expressed in the melting temperature of the oligonucleotide) from the rest of the oligomer.

In many embodiments, the oligomer comprises one or more phosphorothioate
10 linkages. The oligomer may e.g. be fully modified with phosphorothioate linkages or e.g. one, two or three phosphorothioate linkages at each end. Phosphorothioate linkages generally decrease melting temperature. However, this may be counteracted e.g. by the use of 2'4' BNA monomers. I.e. the higher affinity region may very well comprise phosphorothioate linkages.

15

Length and affinity of the oligomer

The overall affinity (as expressed by the melting temperature) of the oligomer toward complementary RNA depends on the length of the oligomer as well as the content of affinity increasing (and sometimes decreasing) monomers. It is an
20 object of the invention to design the oligomer such that it has sufficient affinity toward its intended target, while displaying improved selectivity and/or potency toward its intended target over other targets sharing an identical sequence (which is hence a shared sequence).

25 The length of the oligomer is preferably between 10 and 40 monomers. In other embodiments, the length is between 10 and 35 monomers, between 10 and 30 monomers, between 10 and 25 monomers. Even more preferably, the length of the oligomer is between 10 and 20 monomers, such as between 11 and 19 monomers or between 12 and 18 monomers.

30

When using shorter lengths, it is necessary to use a higher density of monomers that increase the affinity of the oligomer. Particular preferred are 2',4'-bicyclic nucleic acids (2'4'-BNA) that have a strong effect on affinity. Hence, in a preferred embodiment, at least 30 % of the monomers are 2'4'-BNA monomers, e.g.

selected from the group consisting of: LNA (2'-O,4'-C-methylene-beta-D-ribofuranosyl and analogues thereof e.g., amino-LNA, thio-LNA, alfa-L-ribo-LNA, beta-D-xylo-LNA, S-cMOE (2',4'-constrained MOE), R-cMOE, cEt (2',4'-constrained ethyl). More preferably, at least 35 %, such as least 40%, 45%, 50%,
5 55% or 60 % are 2'4'-BNA monomers.

The melting temperature of the oligomer base paired to RNA should preferably be at least 60 degrees Celsius. In other embodiments, it is preferred that the t_m of the oligomer is at least 65 degrees Celsius, at least 70 degrees Celsius, at least 75
10 degrees Celsius, at least 80 degrees Celsius, at least 85 degrees Celsius, at least 90 degrees Celsius or at least 95 degrees Celsius.

It is even more preferred that the t_m is at least 75 degrees Celsius, such as 80, 85, 90 or 95 degrees Celsius.
15

In one embodiment, the lower affinity region is shorter than the higher affinity region. In another region, the lower affinity region is longer than the higher affinity region.

20 *The lower and higher affinity regions*

As mentioned above, it is preferred that the lower affinity region has a lower density of monomers that have a strong and/or moderate effect on t_m than does the higher affinity region.

25 When the oligomer comprise 2'4'-BNA monomers, the density of these may e.g. 100 % in the higher affinity region (full modification), 50% (mixmer with 1 BNA per 1 other monomer, e.g. 1 BNA monomer in every second position), 33 % (1 BNA per 2 other monomers, e.g. in every third position), 25 % etc. The BNAs need not necessarily be evenly dispersed the high affinity region. At any rate, the
30 lower affinity region is easily identified by the lower density of 2'4'-BNA monomers. When the higher affinity region comprises 2'4' BNA monomers, it typically contains at least 1 BNA per 4 non-BNA monomers and also typically does not contain 4 or 5 contiguous non-BNA monomers.

The amount of 2'4'-BNA monomers in the higher affinity region is preferably at least 2 fold, or even more preferably 3, 4 or 5 fold higher than in the lower affinity region of the oligomer.

- 5 In a preferred embodiment, the lower affinity region does not comprise any affinity enhancing monomers selected from the group consisting of 2'4'-BNA, PNA, 2'MOE and 2'F.

More preferably, the lower affinity region does not comprise any 2'4'-BNA
10 monomers.

In another embodiment, the lower affinity region comprise at least 5 contiguous monomers, such as 6 or 7 contiguous monomers which are not 2'4'BNA
15 monomers.

In yet another embodiment, the lower affinity region comprise at least 5 contiguous monomers, such as 6 or 7 contiguous monomers which are not DNA
monomers.

- 20 In yet another embodiment, neither the 5'end of the lower affinity region nor the 3'end of the lower affinity region is a BNA monomer. Even more preferably, neither the two monomers at the 5'end of the lower affinity region nor the two monomers at the 5'end of the monomer are BNA monomers. This feature further helps define the lower affinity region within an oligomer of the invention.

25 Preferably, the melting temperature of the lower affinity region toward complementary RNA is less than 70 degrees Celsius, such as less than 65, 60, 55, 50, 45, 40 and 35 degrees Celsius. The melting temperature in this embodiment may be determined by measuring the t_m against a truncated RNA with a length
30 corresponding to the lower affinity region, i.e. where the truncated RNA cannot base pair to the higher affinity region of the oligomer. It is even more preferred that the melting temperature of the lower affinity region toward complementary RNA is less than 60 degrees Celsius, such as less than 55, 50, 45, 40 and 35 degrees Celsius.

35

Preferably, the lower affinity region is contiguous and of 5-12 monomers, such as 5-10, 5-9, 5-8, 6-10, 7-10, 8-10, 6-9 or 6-8 contiguous monomers. Even more preferred is a lower affinity region of 6-10 contiguous monomers. I.e. in a preferred embodiment, the lower affinity region of the oligomer can be identified
5 as a region with none or just 1 BNA monomers over a region of 6-10 monomers, wherein the density of BNA monomers in the remaining part of the oligomer has a higher density of BNA monomers, and hence the remaining part of the oligomer is the higher affinity region.

10 Uses and advantages - selectivity

The oligomers of the invention are useful for binding to target RNA such as mRNA and non-coding RNA and have the advantage that they will be less prone to off-target binding via the lower affinity region than via the higher affinity region.

15

Consider e.g. two RNA sequences of 10-40 monomers (within RNA targets such as mRNA or non-coding RNA) that have identical sequences in one region and differ e.g. by 1, 2 or 3 nucleotides over a length of between 5 and 10 nucleotides in sequence in an adjacent region. The region that differs may be termed the
20 "specificity region", whereas the identical region may be referred to as the "shared region". There could just as well be multiple target RNAs that share the shared sequence and differ in the adjacent specificity region.

When the goal is to design an oligomer that preferentially bind one RNA sequence
25 (the intended target, herein also termed the on-target) over the other target (the off-target), it is obvious that the oligomer should be complementary to the intended target. However, before the present invention, it was not obvious to design and use an oligomer comprising a higher affinity region and a lower affinity such that the higher affinity region of the oligomer should be complementary to
30 the specificity region of the (intended) on-target and the lower affinity region should be complementary to the shared region (shared between the off-targets and the on-target). In this way, off-target binding via the shared region will be minimized because of a lower affinity as expressed in t_m , while still maintaining high affinity to the intended target.

On the other hand, if a certain degree of off-target binding is acceptable or even desirable, the higher affinity region of the oligomer should be complementary to the shared region and the lower affinity region should be complementary to the
5 specificity sequence. In this way, off-target binding via the shared region will be increased.

It is to be understood that oligomers of the invention do not necessarily overall have less or more binding to off-targets in the transcriptome of a cell when
10 compared to a uniformly modified oligomer of the same sequence.
However, they will have decreased binding to off-targets sharing the same shared sequence (because the lower affinity region is complementary to the shared sequence). Potentially, this may be achieved at the expense of more off-target binding via the higher affinity region. At any rate, the oligomers of the invention
15 have a different off-target profile as compared to uniformly modified oligomers of the same sequence.

Hence, the oligomers of the invention can be designed to have less off-target binding among off-targets of interest or more off-target binding among off-targets
20 of interest compared to a uniformly modified oligomer of the same sequence and similar T_m value.

It should be understood that the oligomer will preferably have perfect complementarity to its intended target.

25 The non-obvious characteristics and uses of the oligomer of the invention will be further described below.

Activity/mechanism of action of the oligomer of the invention – steric block

30 The oligomers of the invention are typically steric blockers, i.e. they bind to target RNA without mediating degradation of the target RNA. Steric block oligonucleotides are well described in the art and are e.g. used as splice switching oligonucleotides and microRNA inhibitors. As is known by the skilled man, many monomers can be used in the design of steric block oligonucleotides, since most

artificial nucleotide monomers do not allow recruitment of RNase H. See e.g. Antisense Drug Technology, Principles, Strategies and Applications, 2nd Edition, Edited by Stanley Crooke, page 93, which mentions 2-O-Me, 2-O-methoxyethyl (MOE), and 2-O-aminopropyl, phosphoramidate, and methylphosphonate derivatives, as well as locked nucleic acid (LNA/2'4'-BNA), peptide nucleic acid (PNA), and morpholino based oligomers. Also mixtures of these monomers do not allow RNase H recruitment. RNase H recruitment generally requires at least 5 contiguous DNA monomers and most often 6, 7 or 8 contiguous monomers are used. Therefore, in a preferred embodiment, the oligomer of the invention does not comprise contiguous DNA monomers, such as 5, 6, 7 or 8 contiguous DNA monomers.

In one embodiment, the oligomer does not comprise a Morpholino monomer
In another embodiment, the oligomer does not comprise a FANA monomer.
15 In another embodiment, the oligomer does not comprise a PNA monomer.
In another embodiment, the oligomer does not comprise a CENA monomer.
In another embodiment, the oligomer does not comprise a 2'MOE monomer.
In another embodiment, the oligomer does not comprise a 2'F monomer.
In another embodiment, the oligomer does not comprise a 2'O-methyl monomer.
20 In yet another embodiment, the oligomer does not comprise a phosphoramidate monomer.

Preferred target RNAs and sequences

25 Binding sites for cellular macromolecules such as RNA binding proteins and RNA (e.g. mRNA or microRNA) often comprise a sequence which is shared among other binding sites of the same cellular macromolecule. Such sequences are herein referred to as consensus sequences. As described above, it is one objective of the present invention to provide oligomers that have improved (or reduced) selectivity
30 in terms of targeting an intended target (RNA) over other RNAs that share a sequence with the intended target. In a preferred embodiment, the shared sequence is a binding site for an RNA binding protein or RNA or and the shared sequence may be represented by a consensus sequence.

One way to avoid or reduce off-target binding to other RNAs sharing the same (consensus) sequence could be to avoid the consensus sequence as target, i.e. not included a sequence complementary to the consensus region in the oligomer. However, when the oligomer is intended to block a binding site, this may reduce
5 the activity of the oligomer, since the binding site is then not completely blocked. Most often it will be desirable to indeed target the consensus sequence as well as adjacent sequence(s).

Oligomers with increased selectivity are most preferred. In these embodiments,
10 the lower affinity region is preferably complementary to a consensus sequence. The length of the lower affinity region is preferably the same as the length of the consensus sequence or 1, 2, 3 or 4 monomers longer. The additional monomers may be added to the 5'end of the lower affinity region, the 3'end of the lower affinity region or both.

15

Preferred consensus sequences are microRNA binding sites in mRNA of a given microRNA, which typically share complementarity to position 2-7 (the so-called seed sequence) of the microRNA, but differ in sequence outside of this region. I.e. in this instance the consensus sequence of the binding site is a sequence that is
20 complementary to the seed sequence of the microRNA.

Another preferred consensus sequence is the seed sequence shared among microRNA families that typically differ outside of the seed sequence.

25 Hence, in a preferred embodiment, the oligomer of the invention comprise a lower affinity region that can bind to a RNA sequence that is complementary to position 1-7, 2-7, 1-8 or 2-8 of any of SEQ ID NOs: 1-2042 or a lower affinity region that can bind to a RNA sequence that comprise position 1-7, 2-7, 1-8 or 2-8 of any SEQ ID NOs: 1-2042, wherein the positions are counted from the 5' end. The
30 region capable of binding to the consensus sequence may be referred to as the anti-consensus sequence, which is hence comprised within the lower affinity region of the oligomer or is identical to the lower affinity region of the oligomer. In this embodiment, the oligomer improves selectivity, when targeting one microRNA over other microRNA in the same family or when targeting one microRNA binding
35 site over other binding sites of the same microRNA.

Likewise, the oligomers may also be used for decreasing selectivity. In this embodiment, the oligomer of the invention comprise a higher affinity region can bind to a RNA sequence that is complementary to position 1-7, 2-7, 1-8 or 2-8 of any of SEQ ID NOs: 1-2042 or a lower affinity region that can bind to a RNA sequence that comprise position 1-7, 2-7, 1-8 or 2-8 of any SEQ ID NOs: 1-2042, wherein the positions are counted from the 5' end.

Oligomers with increased selectivity are most preferred.

10

Table 1. Human microRNA sequences

NO	Sequence (5' to 3')	ID and accession
1	AAGAUGUGGAAAAAUUGGAAUC	>hsa-miR-576-3p MIMAT0004796
2	CAGUGGUUUUACCCUAUGGUAG	>hsa-miR-140-5p MIMAT0000431
3	CAGGCAGUGACUGUUCAGACGUC	>hsa-miR-2682-5p MIMAT0013517
4	AAGAAGAGACUGAGUCAUCGAAU	>hsa-miR-5197-3p MIMAT0021131
5	CUCUAGAGGGAAGCGCUUUCUG	>hsa-miR-522-5p MIMAT0005451
6	UUUCUGUCUUUUCUGGUCCAG	>hsa-miR-4743-3p MIMAT0022978
7	GUUUGCACGGGUGGGCCUUGUCU	>hsa-miR-557 MIMAT0003221
8	AAAGACCGUGACUACUUUUGCA	>hsa-miR-548ao-3p MIMAT0021030
9	AAAAGUACUUGCGGAUUU	>hsa-miR-548av-5p MIMAT0022303
10	UGUAAACAUCCCCGACUGGAAG	>hsa-miR-30d-5p MIMAT0000245
11	UGGGCGAGGGGUGGGCUCUCAGAG	>hsa-miR-4649-5p MIMAT0019711
12	ACCAGGAGGCUGAGGCCCCU	>hsa-miR-665 MIMAT0004952
13	CUCUAGAGGGAAGCACUUUCUG	>hsa-miR-518d-5p MIMAT0005456
14	AGGACUGAUCCUCUCGGGCAGG	>hsa-miR-4740-5p MIMAT0019869
15	UCACCUGAGCUCCCGUGCCUG	>hsa-miR-3622b-3p MIMAT0018006
16	ACUGGGGGCUUUCGGGCUCUGCGU	>hsa-miR-637 MIMAT0003307
17	AGAAGGCCUUUCCAUCUCUGU	>hsa-miR-4493 MIMAT0019028
18	CAGGCACGGGAGCUCAGGUGAG	>hsa-miR-3622a-5p MIMAT0018003
19	AAAGUGCUUCCUUUUAGAGGG	>hsa-miR-520b MIMAT0002843
20	ACCUGGACCCAGCGUAGACAAAG	>hsa-miR-3690 MIMAT0018119
21	UAGGCAGUGUCAUUAGCUGAUUG	>hsa-miR-34b-5p MIMAT0000685
22	UAUACAAGGGCAAGCUCUCUGU	>hsa-miR-381-3p MIMAT0000736
23	UUGAAGAGGAGGUGCUCUGUAGC	>hsa-miR-4709-3p MIMAT0019812

24	GAAAGCGCUUCCCUUUGCUGGA	>hsa-miR-518a-3p MIMAT0002863
25	UGAGGCUAAUGCACUACUUCAC	>hsa-miR-3975 MIMAT0019360
26	UCUAGGCUGGUACUGCUGA	>hsa-miR-645 MIMAT0003315
27	CUUAGCAGGUUGUAUUAUCAU	>hsa-miR-374b-3p MIMAT0004956
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1795	GGGUGGGGAUUUGUUGCAUUAC	>hsa-miR-92a-2-5p MIMAT0004508
1796	GAGGCUGAUGUGAGUAGACCACU	>hsa-miR-3929 MIMAT0018206
1797	AGGCAUUGACUUCUCACUAGCU	>hsa-miR-1256 MIMAT0005907
1798	UCAA AUGCUCAGACUCCUGUGGU	>hsa-miR-105-5p MIMAT0000102
1799	AGCCAGGCUCUGAAGGGAAAGU	>hsa-miR-4755-3p MIMAT0019896
1800	AUGAUCCAGGAACCUGCCUCU	>hsa-miR-640 MIMAT0003310
1801	AGACCUGGCCCAGACCUCAGC	>hsa-miR-631 MIMAT0003300
1802	ACAGUAGUCUGCACAUUGGUUA	>hsa-miR-199a-3p MIMAT0000232
1803	CCCCACCUCUCUCUCCUCAG	>hsa-miR-1224-3p MIMAT0005459
1804	UCUCUGAGUACCAUAUGCCUUGU	>hsa-miR-3921 MIMAT0018196
1805	UCUGGUAUGUAGUAGGUAAUAA	>hsa-miR-4774-5p MIMAT0019929
1806	CUUUCAGUCAGAUGUUUGCUGC	>hsa-miR-30d-3p MIMAT0004551
1807	ACGGGUUAGGCUCUUGGGAGCU	>hsa-miR-125b-1-3p MIMAT0004592
1808	UGAU AUGUUUGAUUAUUAGGU	>hsa-miR-190a MIMAT0000458
1809	CAAUUUAGUGUGUGUGAUUUU	>hsa-miR-32-3p MIMAT0004505
1810	UCGACCGGACCUCGACCGGCU	>hsa-miR-1307-5p MIMAT0022727
1811	UGAGGUAGUAGUUUCUU	>hsa-miR-4500 MIMAT0019036
1812	AUGGCCAGAGCUCACACAGAGG	>hsa-miR-4435 MIMAT0018951
1813	CUAGGAGGCCUUGGCC	>hsa-miR-4266 MIMAT0016892
1814	GUGUUCUCUGAUGGACAG	>hsa-miR-4273 MIMAT0016903
1815	GAAGGCGCUUCCCUUUAGAGCG	>hsa-miR-525-3p MIMAT0002839
1816	AAGGAGCUUACAAUCUAGCUGGG	>hsa-miR-708-5p MIMAT0004926
1817	UUGAAAGGCUAUUUCUUGGUC	>hsa-miR-488-3p MIMAT0004763
1818	GGGUGCGGGCCGGCGGGG	>hsa-miR-4466 MIMAT0018993
1819	AGCAGAGGCAGAGAGGCUCAGG	>hsa-miR-2467-3p MIMAT0019953
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1822	AAAAGUAAUCACUGUUUUUGCC	>hsa-miR-548y MIMAT0018354
1823	AAGGAACCAGAAAAUGAGAAGU	>hsa-miR-3914 MIMAT0018188
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1830	GGGACCCAGGGAGAGACGUAAG	>hsa-miR-711 MIMAT0012734
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1832	UGUUGGGAUUCAGCAGGACCAU	>hsa-miR-4425 MIMAT0018940
1833	ACGGAGACGACAAGACUGUGCUG	>hsa-miR-5091 MIMAT0021083
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1844	UCAGAUGAUCUAAAGGCCUAUA	>hsa-miR-1245b-3p MIMAT0019951
1845	ACGCCCUUCCCCCCCUCUUCA	>hsa-miR-1249 MIMAT0005901
1846	GAAGAUGGUGCUGUGCUGAGGAA	>hsa-miR-4647 MIMAT0019709
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1848	ACUCCAAGAAGAAUCUAGACAG	>hsa-miR-5695 MIMAT0022488
1849	AGGUGGAUGCAAUGUGACCUCA	>hsa-miR-3165 MIMAT0015039
1850	UGAGGCAGUAGAUUGAAU	>hsa-miR-1827 MIMAT0006767
1851	CAAAAAUCUCAAUUACUUUUGC	>hsa-miR-548c-3p MIMAT0003285
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1854	AUGGGUGAUGGGUGUGGUGU	>hsa-miR-4701-3p MIMAT0019799
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1856	GGCUGGUCAGAUGGGAGUG	>hsa-miR-6131 MIMAT0024615
1857	GCUGCACCGGAGACUGGGUAA	>hsa-miR-3130-3p MIMAT0014994
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1864	UCAUUUAUCUGUUGGGAAGCUA	>hsa-miR-4729 MIMAT0019851
1865	GAAUAUGGGUAUAUUAGUUUGG	>hsa-miR-5583-3p MIMAT0022282
1866	AGAGGCUUUGUGCGGAUACGGGG	>hsa-miR-3188 MIMAT0015070
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1870	UCUAGUGCGGGCGUUCGGG	>hsa-miR-6080 MIMAT0023705
1871	UGGAAGACUAGUGAUUUUGUUGU	>hsa-miR-7-5p MIMAT0000252
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1873	ACAGGAGUGGGGUGGGACAU	>hsa-miR-4433-3p MIMAT0018949
1874	CUGACUGAAUAGGUAGGGUCAUU	>hsa-miR-3136-5p MIMAT0015003
1875	UCUACAAAGGAAAGCGCUUUCU	>hsa-miR-1283 MIMAT0005799
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1878	GUUCUCCCAACGUAAGCCCAGC	>hsa-miR-629-3p MIMAT0003298
1879	AGCAUACACCUGUAGUCCUAGA	>hsa-miR-5689 MIMAT0022481
1880	UUUCCCUUCCAUCUGGCAG	>hsa-miR-5006-3p MIMAT0021034
1881	AGCAGACUUGACCUACAAUUA	>hsa-miR-4771 MIMAT0019925
1882	CAGUGCAAUGAUGAAAGGGCAU	>hsa-miR-130b-3p MIMAT0000691
1883	CAAAAACCGCAAUACUUUUGCA	>hsa-miR-548z MIMAT0018446
1884	AUAAUACAUGGUUAACCUCUUU	>hsa-miR-655 MIMAT0003331
1885	CAAAGCGCUUCCCUUUGGAGC	>hsa-miR-518d-3p MIMAT0002864
1886	AUCACACAAAGGCAACUUUUGU	>hsa-miR-377-3p MIMAT0000730
1887	UCCUGAGCAAAGCCAC	>hsa-miR-4319 MIMAT0016870
1888	UGCAACGAACCUGAGCCACUGA	>hsa-miR-891a MIMAT0004902
1889	AUAAUACAACCUGCUAAGUGCU	>hsa-miR-374c-5p MIMAT0018443
1890	UUCACAUUGUGCUACUGUCUGC	>hsa-miR-130a-5p MIMAT0004593
1891	UUAUUGCUUAAGAAUACGCGUAG	>hsa-miR-137 MIMAT0000429
1892	ACAGUAGUCUGCACAUUGGUUA	>hsa-miR-199b-3p MIMAT0004563
1893	CAGCAGGAGGUGAGGGGAG	>hsa-miR-6165 MIMAT0024782

1894	UCACUCUCACCUUGCUUUGC	>hsa-miR-4639-3p MIMAT0019698
1895	UAGUGCAAUAUUGCUUAUAGGGU	>hsa-miR-454-3p MIMAT0003885
1896	GCCCCUGGGCCUAUCCUAGAA	>hsa-miR-331-3p MIMAT0000760
1897	UAGUACUGUGCAUAUCAUCUAU	>hsa-miR-1278 MIMAT0005936
1898	UCGUGUCUUGUGUUGCAGCCGG	>hsa-miR-187-3p MIMAT0000262
1899	CUGGGGAGAUCUCGAGGUUGG	>hsa-miR-3150a-3p MIMAT0015023
1900	CGCGCCUGCAGGAACUGGUAGA	>hsa-miR-6720-3p MIMAT0025851
1901	AGAGUCUUGUGAUGUCUUGC	>hsa-miR-924 MIMAT0004974
1902	GAACGCGCUUCCCUAUAGAGGGU	>hsa-miR-523-3p MIMAT0002840
1903	UGACUUCUACCUCUCCAAAG	>hsa-miR-6505-3p MIMAT0025467
1904	UAGAUAAAAUAUUGGUACCUG	>hsa-miR-577 MIMAT0003242
1905	GAAGUUGUUCGUGGUGGAUUCG	>hsa-miR-382-5p MIMAT0000737
1906	UGAGAUGACACUGUAGCU	>hsa-miR-4770 MIMAT0019924
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1908	ACCGUGCAAAGGUAGCAUA	>hsa-miR-1973 MIMAT0009448
1909	GGGGGGGGGGGGGGGGGGGCCG	>hsa-miR-1234-5p MIMAT0022944
1910	AUGGUUCCGUCAAGCACCAUGG	>hsa-miR-218-1-3p MIMAT0004565
1911	AAACUAAUCUCUACACUGCUGC	>hsa-miR-3129-3p MIMAT0019202
1912	GACUGACACCUCUUUGGGUGAA	>hsa-miR-888-3p MIMAT0004917
1913	AUAUGGGUUUACUAGUUGGU	>hsa-miR-3115 MIMAT0014977
1914	CCGUCCCCAGGAGAACCUGCAGA	>hsa-miR-4746-5p MIMAT0019880
1915	AGCAGCAUUGUACAGGGCUAUC	>hsa-miR-107 MIMAT0000104
1916	UUUUGUGUCUCCCAUUCUCCAG	>hsa-miR-5010-3p MIMAT0021044
1917	UCACAACAACCUUGCAGGGUAGA	>hsa-miR-5003-5p MIMAT0021025
1918	UUGGACGGUAAGGUUAAGCAA	>hsa-miR-4804-5p MIMAT0019984
1919	GUAGAUUCUCCUUCUAUGAGUA	>hsa-miR-376a-5p MIMAT0003386
1920	UAUACAAGGGCAGACUCUCUCU	>hsa-miR-300 MIMAT0004903
1921	CAUCCCUUGCAUGGUGGAGGG	>hsa-miR-188-5p MIMAT0000457
1922	GAAGAAUAGGAGGGACUUUGU	>hsa-miR-6507-5p MIMAT0025470
1923	UCCGUACAAACUCUGCUGUG	>hsa-miR-3678-5p MIMAT0018102
1924	CCACCAGGUCUAGCAUUGGGAU	>hsa-miR-4733-3p MIMAT0019858
1925	UUAAUUUUUUGUUUCGGUCACU	>hsa-miR-4775 MIMAT0019931
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1928	AAACAAACAUGGUGCACUUCUU	>hsa-miR-495-3p MIMAT0002817
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1930	GUGAGUGUGGAUCCUGGAGGAAU	>hsa-miR-4658 MIMAT0019725
1931	UGUGCGCAGGGAGACCUCUCCC	>hsa-miR-933 MIMAT0004976
1932	CAGCCUGACAGGAACAG	>hsa-miR-4293 MIMAT0016848
1933	GGGAGAAGGGUCGGGGC	>hsa-miR-4516 MIMAT0019053
1934	CAAGGGACCAAGCAUUCAUUUAU	>hsa-miR-4475 MIMAT0019002
1935	CAAAGCGCUUCUCUUUAGAGUGU	>hsa-miR-518c-3p MIMAT0002848
1936	AACGGGAAUGCAGGCUGUAUCU	>hsa-miR-4681 MIMAT0019766
1937	GAAUGUUGCUCGGUGAACCCCU	>hsa-miR-409-3p MIMAT0001639
1938	UUCCCUUUGUCAUCCUAUGCCU	>hsa-miR-204-5p MIMAT0000265
1939	GUGAGUCUCUAAGAAAAGAGGA	>hsa-miR-627 MIMAT0003296
1940	CAUACAAUCUGACAUGUAUUU	>hsa-miR-4666a-3p MIMAT0019742
1941	CAGCCCGGAUCCCAGCCCACUU	>hsa-miR-3940-3p MIMAT0018356
1942	GAUGCGCCGCCACUGCCCCGCGC	>hsa-miR-4787-3p MIMAT0019957
1943	UUCUGCUGCCGGCCAAGGC	>hsa-miR-6071 MIMAT0023696
1944	CAUGGUUCUGUCAAGCACCGCG	>hsa-miR-218-2-3p MIMAT0004566
1945	ACUGAUUAUCUUAACUCUCUGA	>hsa-miR-3920 MIMAT0018195
1946	UAAAUUUCACCUUUCUGAGAAGA	>hsa-miR-513c-3p MIMAT0022728
1947	ACCUUGGCUCUAGACUGCUUACU	>hsa-miR-212-5p MIMAT0022695
1948	CUCUAGAGGGAAGCGCUUUCUG	>hsa-miR-519b-5p MIMAT0005454
1949	AAAAACUGCAAUCACUUUUGC	>hsa-miR-548az-3p MIMAT0025457
1950	CUGUAAUAUAAAUUUAAUUAUU	>hsa-miR-2054 MIMAT0009979
1951	UAUGGCACUGGUAGAAUUCACU	>hsa-miR-183-5p MIMAT0000261
1952	AUUCUGCAUUUUUAGCAAGUUC	>hsa-miR-544a MIMAT0003164
1953	CAGGCCAUAAUUGUGCUGCCUCA	>hsa-miR-15a-3p MIMAT0004488
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1955	UAGCCUUCAGAUCUUGGUGUUUU	>hsa-miR-3614-3p MIMAT0017993
1956	AAAGGUAAUUGCAGUUUUUCCC	>hsa-miR-548ai MIMAT0018989
1957	UUGGACAGAAAACACGCAGGAA	>hsa-miR-4520a-3p MIMAT0019057
1958	AAUGCACCCGGGCAAGGAUUCU	>hsa-miR-501-3p MIMAT0004774
1959	UGAGUGUGUGUGUGUGAGUGUGU	>hsa-miR-574-5p MIMAT0004795
1960	CAGGAGGCAGUGGGCGAGCAGG	>hsa-miR-4695-5p MIMAT0019788
1961	CAAUGUUUCCACAGUGCAUCAC	>hsa-miR-33a-3p MIMAT0004506

1962	UGAGUGCCGGUGCCUGCCCUG	>hsa-miR-1909-5p MIMAT0007882
1963	AAAACUGUAAUACUUUUGUAC	>hsa-miR-548g-3p MIMAT0005912
1964	CACAUAGAAGUGAGCCAGCAC	>hsa-miR-5580-3p MIMAT0022274
1965	UCAGGCAGUGUGGGUAUCAGAU	>hsa-miR-4692 MIMAT0019783
1966	GAUUGAGACUAGUAGGGCUAGGC	>hsa-miR-4461 MIMAT0018983
1967	UCAUAGCCCUGUACAAUGCUGCU	>hsa-miR-103b MIMAT0007402
1968	AGAAGUAACUACGGUUUUUGCA	>hsa-miR-548ao-5p MIMAT0021029
1969	GUGAGGGCAUGCAGGCCUGGAUGGGG	>hsa-miR-1226-5p MIMAT0005576
1970	AAUGUGGAAGUGGUCUGAGGCAU	>hsa-miR-4657 MIMAT0019724
1971	AGCAGGUGCGGGGCGGCG	>hsa-miR-3665 MIMAT0018087
1972	GAAUCGGAAAGGAGGCGCCG	>hsa-miR-3610 MIMAT0017987
1973	UUACAGGCGUGAACCACCGCG	>hsa-miR-5095 MIMAT0020600
1974	CGCGGGCGCUCCUGGCCGCCGCC	>hsa-miR-4767 MIMAT0019919
1975	GAGGGUUGGGUGGAGGCUCUCC	>hsa-miR-296-3p MIMAT0004679
1976	GAAGGCGCUUCCCUUUGGAGU	>hsa-miR-524-3p MIMAT0002850
1977	AUAGGCACCAAAAAGCAACAA	>hsa-miR-4423-3p MIMAT0018936
1978	ACAGCAGGCACAGACAGGCAGU	>hsa-miR-214-3p MIMAT0000271
1979	CUCUAGAGGGAAGCGCUUUCUG	>hsa-miR-519c-5p MIMAT0002831
1980	UCCUCUUCUCCCUCCUCCAG	>hsa-miR-877-3p MIMAT0004950
1981	UAGGACACAUGGUCUACUUCU	>hsa-miR-1197 MIMAT0005955
1982	UGAGGCGGGGGGCGAGC	>hsa-miR-6087 MIMAT0023712
1983	CCUGUGCUCUCCAGGGCCUCGC	>hsa-miR-5008-3p MIMAT0021040
1984	GAGGGCGGGUGGAGGAGGA	>hsa-miR-3141 MIMAT0015010
1985	UGUCUGCCCGCAUGCCUGCCUCU	>hsa-miR-346 MIMAT0000773
1986	UUCACAGUGGCUAAGUUCUGC	>hsa-miR-27b-3p MIMAT0000419
1987	UAGCUUAUCAGACUGAUGUUGA	>hsa-miR-21-5p MIMAT0000076
1988	UUCACCACCUUCUCCACCCAGC	>hsa-miR-197-3p MIMAT0000227
1989	AAAGUGCUGCGACAUUUGAGCGU	>hsa-miR-372 MIMAT0000724
1990	AAACCUGUGUUGUUCAAGAGUC	>hsa-miR-649 MIMAT0003319
1991	CCUCUGGGCCCUUCCUCCAG	>hsa-miR-326 MIMAT0000756
1992	UAAAACUUUAAGUGUGCCUAGG	>hsa-miR-5582-3p MIMAT0022280
1993	UGAGACCAGGACUGGAUGCACC	>hsa-miR-4786-5p MIMAT0019954
1994	GAUUUCAGUGGAGUGAAGUUC	>hsa-miR-205-3p MIMAT0009197
1995	UGCCUACUGAGCUGAAACACAG	>hsa-miR-24-2-5p MIMAT0004497

1996	UGCAAAAGUAAUUGCAGUUUUUG	>hsa-miR-548g-5p MIMAT0022722
1997	AUAUACAGGGGGAGACUCUUUAU	>hsa-miR-1185-1-3p MIMAT0022838
1998	UUCUCAAGGAGGUGUCGUUUUAU	>hsa-miR-513c-5p MIMAT0005789
1999	AUCAUGAUGGGCUCCUCGGUGU	>hsa-miR-433 MIMAT0001627
2000	GGAGGUUGGGAAGGGCAGAG	>hsa-miR-6086 MIMAT0023711
2001	AGUGGACCGAGGAAGGAAGGA	>hsa-miR-4800-5p MIMAT0019978
2002	GUCCAGUUUUCCCAGGAUCCCU	>hsa-miR-145-5p MIMAT0000437
2003	GCAGUGGCUCUGAAAUGAACUC	>hsa-miR-5693 MIMAT0022486
2004	UACACAAGAAAACCAAGGCUCA	>hsa-miR-4801 MIMAT0019980
2005	ACCCUUGAGCCUGAUCCCUAGC	>hsa-miR-4780 MIMAT0019939
2006	UGUAGAUACGAGCACCAGCCAC	>hsa-miR-3935 MIMAT0018350
2007	GACACGGGCGACAGCUGCGGCCC	>hsa-miR-602 MIMAT0003270
2008	AACAACAAAUCACUAGUCUCCA	>hsa-miR-3529-3p MIMAT0022741
2009	AACUAGCUCUGUGGAUCCUGAC	>hsa-miR-4661-5p MIMAT0019729
2010	AUCCCCAGAUACAAUGGACAA	>hsa-miR-2355-5p MIMAT0016895
2011	UAAAACCCACAAUUAUGUUUGU	>hsa-miR-548as-3p MIMAT0022268
2012	GGCCACUGAGUCAGCACCA	>hsa-miR-4252 MIMAT0016886
2013	AGGAGCUAUCCACUCCAGGUGUCC	>hsa-miR-6500-5p MIMAT0025454
2014	CCAGGAGAUCCAGAGAGAAU	>hsa-miR-4768-3p MIMAT0019921
2015	ACGGUGCUGGAUGUGGCCUUU	>hsa-miR-1250 MIMAT0005902
2016	AUACCCAUAGCUUAGCUCCCA	>hsa-miR-5591-3p MIMAT0022302
2017	UAGGCACACUUAAGUUUAUAGC	>hsa-miR-5582-5p MIMAT0022279
2018	UAGCAGCACGUAAAUUUGGCG	>hsa-miR-16-5p MIMAT0000069
2019	GGGAAAAGGAAGGGGGAGGA	>hsa-miR-6124 MIMAT0024597
2020	GAGCUUGGUCUGUAGCGGUU	>hsa-miR-4453 MIMAT0018975
2021	CUGGGAGGUGUGAUUUGUGGU	>hsa-miR-3689b-3p MIMAT0018181
2022	UAGGAUUACAAGUGUCGGCCAC	>hsa-miR-3159 MIMAT0015033
2023	UUGGGACAUACUUAUGCUAAA	>hsa-miR-1302 MIMAT0005890
2024	GGCUACAACACAGGACCCGGGC	>hsa-miR-187-5p MIMAT0004561
2025	UGAGCUGCUGUACCAAAAU	>hsa-miR-558 MIMAT0003222
2026	AUUGACACCUCUGUGAGUGGA	>hsa-miR-514b-3p MIMAT0015088
2027	AGGAAUGUCCUUCUUUGCC	>hsa-miR-613 MIMAT0003281
2028	UGGGUGGUCUGGAGAUUUGUGC	>hsa-miR-1293 MIMAT0005883
2029	AGAGUCGGCGACGCCGCCAGC	>hsa-miR-4785 MIMAT0019949

2030	UGGGGGAGCCAUGAGAUAAAGAGCA	>hsa-miR-4723-5p MIMAT0019838
2031	AUCAAUAAGGACUAGUCUGCA	>hsa-miR-3671 MIMAT0018094
2032	CGCCCCUCCUGCCCCCACAG	>hsa-miR-4749-3p MIMAT0019886
2033	UGAGCCCCUGUGCCGCCCCCAG	>hsa-miR-1225-3p MIMAT0005573
2034	GCUGAUGAUGAUGGUGCUGAAG	>hsa-miR-4502 MIMAT0019038
2035	GGGAGUCUACAGCAGGG	>hsa-miR-4294 MIMAT0016849
2036	CACUCAGCCUUGAGGGCACUUUC	>hsa-miR-512-5p MIMAT0002822
2037	GACACAUGACCAUAAAUGCUGAA	>hsa-miR-4643 MIMAT0019703
2038	UAAGUGCUUCCAUGUUUGAGUGU	>hsa-miR-302d-3p MIMAT0000718
2039	UGCACGGCACUGGGGACACGU	>hsa-miR-3177-3p MIMAT0015054
2040	CCUCCUGCCCUCUUGCUGU	>hsa-miR-1976 MIMAT0009451
2041	CAACGGAAUCCCAAAGCAGCUG	>hsa-miR-191-5p MIMAT0000440
2042	CAGCCCUCCUCCGCACCCAAA	>hsa-miR-4687-5p MIMAT0019774

In one embodiment, the oligomer does not comprise a lower affinity region that can bind to a RNA sequence that is complementary to position 2-7 of SEQ ID NO:1051.

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In yet another embodiment, the oligomer is not complementary to any of SEQ ID NOs: 1-2041 (over its full length).

Particular preferred oligomers of the invention have a length of 10-20 monomers, and consists of

- a higher affinity region that comprise at least 25% BNA monomers
- a lower affinity region of 6-10 contiguous monomers that comprise less than 25% BNA monomers and wherein the two monomers at the 5' end of the lower affinity region and the two monomers at the 3'end of the lower affinity region are non-BNA monomers
- and wherein the oligomer does not comprise a region of 5 contiguous DNA monomers

In this embodiment, different affinities of the higher affinity region and the lower affinity region (as defined above) is ensured by a higher density of BNA

monomers in the higher affinity region as compared to the density of BNA monomers in the lower affinity region.

It is preferred that the higher affinity region consist of at least 4 monomers, more preferably, at least 5, 6, 7 or 8 monomers.

Preferably, the density of BNA monomers in the higher affinity region is at least 2-fold higher than the density of BNA monomers in the lower affinity region. Even more preferably, the density is at least 3-fold higher such as 4 or 5 fold higher.

10

In a preferred embodiment, the lower affinity region does not comprise any BNA monomers at all.

The higher affinity region preferably comprise at least 33% (1 BNA monomer/3 monomers in the higher affinity region), 50% (1 BNA/2 monomers), 67% (2 BNA/3 monomers), (3 BNA/4 monomers) 75 % or 100 % BNA monomers.

Preferably, at least one internucleotide linkage is a phosphorothioate linkage. In another embodiment, all internucleotide linkages are phosphorothioate linkages.

20

In a related embodiment, the oligomer the lower affinity region consists of 8-10 contiguous monomers and the remaining monomers of the oligomer are BNA monomers.

25 Typically, both the 5'end of the oligomer and the 3'end of the oligomer is a BNA monomer.

The oligomer may even be of 12-18 monomers or 13-17 monomers.

30 Preferably, the lower affinity region can base pair to the seed sequence of a microRNA or can base pair to the RNA complement of the seed sequence of a microRNA. Human microRNAs are preferred.

Examples

Example 1

In the present example, the affinity of various oligomers toward an intended target, as well as to an off-target RNA was measured. Finally, the affinity of the
5 oligomers toward a target RNA consisting of the consensus sequence was measured.

The employed target RNA first was:

10

(135-Hcvtarg) 5'GAUGGGGGCGGACACUCCACCAUGAAU

wherein a consensus sequence is underlined.

15 The sequence of the oligomers complementary to this target RNA:

CUGUGAGGUGGUAC-5'

And when bound to each other:

20

Target: 5'GAUGGGGGCGGACACUCCACCAUGAAU

. | | | | | | | | | | | | | |

HCV Oligomer CUGUGAGGUGGUAC5'

25 First, the following oligomers were employed, wherein lower affinity regions are underlined:

(123-HCVtm, uniformly modified)

ICIAmUmGIGmUIGIGmAIGmUmGITIC

(124-HCVtm, lower affinity region complementary to consensus sequence)

30 ICIAITIGIGITmGmGmAmGmUmGIUC

(125-HCV, tm lower affinity region complementary to consensus sequence)

ICIAITIGIGmUmGmGmAmGmUmGmUIC

(126-HCVtm, lower affinity region complementary to consensus sequence)

ICIAITIGIGmUmGmGuAmGmUmGmUIC

(127-HCVtm, lower affinity region complementary to consensus sequence)

ICIAmUmGIGmUmGmGmAmGmUmGITIC

(128-HCVtm, higher affinity region complementary to consensus sequence)

5 mCmAmUmGmGITIGIGIAIGITIGITmC

m indicates 2'O-methyl RNA

I indicate LNA (BNA)

u indicate unlocked Nucleic Acid (UNA)

10

The melting temperatures were measured in in medium salt concentration, i.e. 100 mM NaCl, 0.1 mM EDTA, 10 mM NaH₂PO₄, 5 mM Na₂HPO₄, pH 7.0), using 1.0 µM concentrations of both oligomer and complementary RNA and in low salt concentration, i.e. in 10 mM NaCl instead of 100 mM NaCl.

15

Table 2:

Oligomer	Tm, 100 mM NaCl	Tm, 10 mM NaCl
123-HCVtm	>90	86
124-HCVtm	>90	84
125-HCVtm	>90	80
126-HCVtm	79	65
127-HCVtm	>90	79
128-HCVtm	>85	83

For the measurements in high salt, only 126HCVtm sticks out with a lower tm
20 value, which is in line with the presence of a UNA monomer that decreases affinity.

For the measurements in low salt, the tm values correlate well with the content of
LNA monomer and again it is seen that one UNA monomer decreases affinity
25 significantly.

Next, the affinity of another oligomer sequence (Aldo A) toward the same target RNA was measured. This other oligomer is complementary to the same consensus sequence of the target RNA, but differs in the remaining part of the sequence:

5 Target: 5' GAUGGGGGCGACACUCCACCAUGAAU

|1|1|1|1|1|1|1|

Aldo Oligomer: GUUGUGAGGUCCGG

1 indicate a potential G:U base pair.

10 The oligomers used in these measurements were:

Lower affinity regions are underlined

(129-Aldo, uniformly modified)

lG1GmC1CmU1GmG1AmGmU1GmU1T1G

15 (130-Aldotm, lower affinity region complementary to consensus sequence)

lG1G1C1C1TmGmGmAmGmUmG1T1T1G

(131-Aldotm, lower affinity region complementary to consensus sequence)

20 lG1G1C1C1CmUmGmGmAmGmUmGmU1T1G

(133-Aldotm, higher affinity region complementary to consensus sequence)

mGmGmCmC1T1G1G1A1G1T1G1TmUmG

25 Table 3:

Oligomer	Tm, 100 mM NaCl
129-Aldotm	77
130-Aldotm	70
131-Aldotm	66
133-Aldotm	83

In this set of measurements, the HCV target may be seen as an off-target that shares the consensus target with the intended target of the oligomer. Again the melting temperature correlates overall with the content of LNA. Moreover, it is

seen that affinity increases when the content of LNA increases in the complementary region. When the LNA density is higher in the non-complementary region, the melting temperature decreases, see oligomer 131.

5

Next, the affinity of the oligomers toward a complementary 8 nucleotide consensus RNA was measured. The affinity of the oligomers toward this 8 nucleotide consensus RNA may be seen as a measure of the affinity of the
10 oligomer toward to off-targets comprising the consensus sequence, but which are not complementary to the oligomer in the regions adjacent to the consensus sequence.

The consensus RNA was:

15 5'ACACUCCA

Table 4:

Oligomer	T _m , 100 mM NaCl
123-HCVtm	77
124-HCVtm	59
125-HCVtm	48
126-HCVtm	No transition
127-HCVtm	60
128-HCVtm	82
129-Aldotm	73
130-Aldotm	66
131-Aldotm	55
132-Aldotm	84

As seen, less off-target binding (more specific oligomers) can be designed by
20 reducing the LNA content in the complementary region.

If the same design principles are used to design antisense oligomers toward other target sequences comprising a consensus sequence, generally improved specificity can be achieved.

- 5 Thus, the teachings of the present invention, including the findings in the above experiments, should be generally applicable and not limited to certain sequences/targets.

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Claims

1. An oligomer of 10-20 monomers that binds RNA that consists of
 - 5 • a higher affinity region that comprise at least 25% BNA monomers
 - a lower affinity region of 6-10 contiguous monomers that comprise less than 25% BNA monomers and wherein the two monomers at the 5' end of the lower affinity region and the two monomers at the
10 3'end of the lower affinity region are non-BNA monomers
 - and wherein the oligomer does not comprise a region of 5 contiguous DNA monomers
- 15 2. The oligomer of claim 1, wherein the density of BNA monomers in the higher affinity region is at least 3 fold higher than the density of BNA monomers in the lower affinity region.
3. The oligomer of claim 1, wherein the lower affinity region does not
20 comprise any BNA monomers.
4. The oligomer of any of the preceding claims, wherein the higher affinity region comprise at least 50 % BNA monomers.
- 25 5. The oligomer of any of the preceding claims, wherein at least one internucleotide linkage is a phosphorothioate linkage
6. The oligomer of any of the preceding claims, wherein the lower affinity region consists of 8-10 contiguous monomers and wherein the remaining
30 monomers of the oligomer are BNA monomers.
7. The oligomer any of the preceding claims, wherein both the 5'end of the oligomer and the 3'end of the oligomer is a BNA monomer.
- 35 8. The oligomer of any of the preceding claims consisting of 12-18 monomers.

9. The oligomer of any of the preceding claims, wherein the lower affinity region can base pair to the seed sequence of a microRNA or can base pair to the RNA complement of the seed sequence of a microRNA.

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10. The microRNA of any of the preceding claims, wherein the microRNA is a human microRNA.

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On-target binding with various oligomer designs

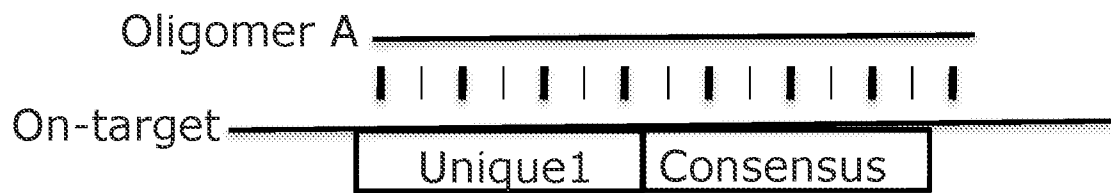
A**B****C**

Fig. 1

2/3

Off-target binding to competing consensus sequence

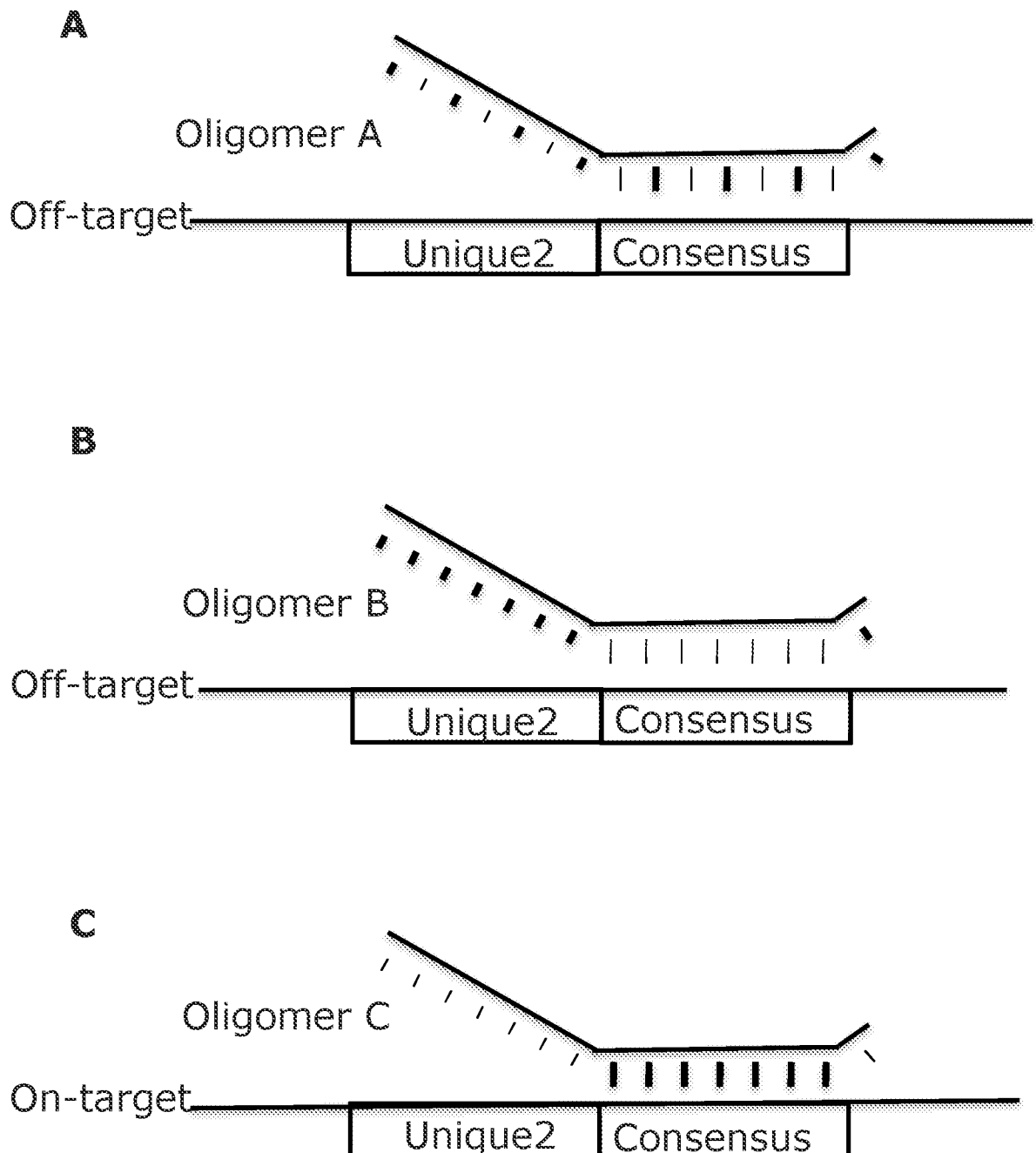


Fig. 2

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Off-target binding to non-consensus target

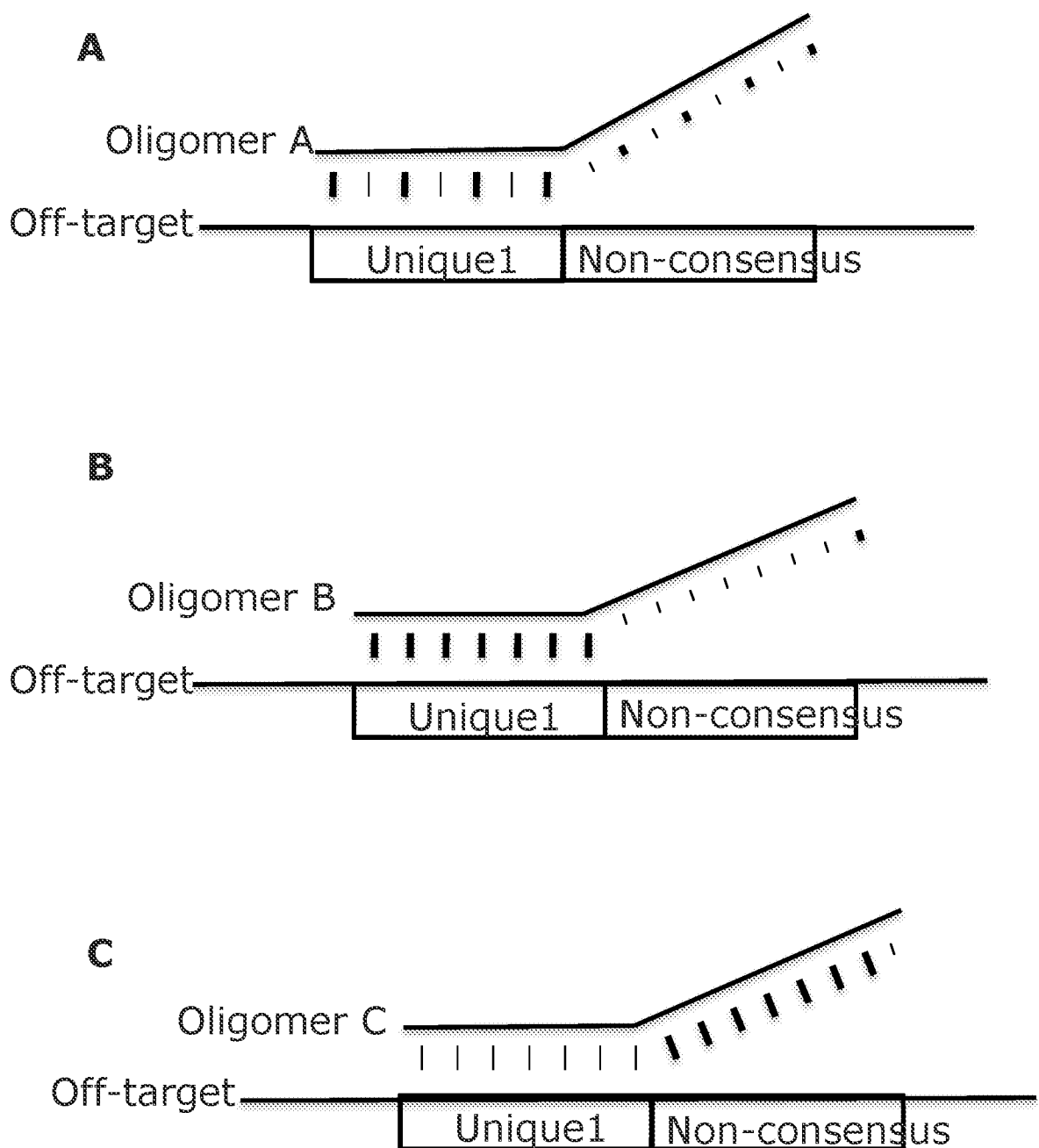


Fig. 3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK2013/050308

A. CLASSIFICATION OF SUBJECT MATTER

C12N 15/113 (2010.01), C07H 21/00 (2006.01)

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&CPC: C12N, C07H

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

DK, NO, SE, FI: Classes as above.

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

EPODOC, WPI, MEDLINE, CHEMICAL ABSTRACTS, BIOSIS, EMBASE, ELSEVIER (XPESP)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	TAKAGI-SATO, M. et al.: "Fine-Tuning of ENA [®] Gappers as Antisense Oligonucleotides for Sequence-Specific Inhibition", OLIGONUCLEOTIDES, 2007, Vol. 17, No. 3, pages 291-301 Abstract; page 298, left column, paragraph 1; table 2; figure 4	1-4, 6-8
X	WO 2007/031081 A2 (SANTARIS PHARMA A/S (DK)) 22/03/2007 Page 18, paragraph 7 – page 19, paragraph 1; page 19, paragraph 6; page 20, paragraph 3; claim 20	1-5, 8
A	WO 2011/117353 A1 (MIRRX THERAPEUTICS A/S (DK)) 29/09/2011 Page 19, paragraph 3; page 26, paragraph 1; page 26, paragraph 5	-
A	WO 2008/061537 A2 (QUERDENKER APS (DK)) 29/05/2008 Abstract; page 5, paragraph 2; page 37, paragraph 4 – page 38, paragraph 1; page 46, paragraph 3; page 47, paragraph 2; claim 18	-
A	MORITA, K. et al.: "Inhibition of VEGF mRNA by 2'-O,4'-C-ethylene-bridged nucleic acids (ENA [®]) antisense oligonucleotides and their influence on off-target gene expressions", NUCLEOSIDES, NUCLEOTIDES AND NUCLEIC ACIDS, 2006, Vol. 25, No. 4-6, pages 503-521 Figures 2-4, 6	-

☒ Further documents are listed in the continuation of Box C.☒ See patent family annex.

* Special categories of cited documents:

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"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

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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

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Name and mailing address of the ISA

Nordic Patent Institute

Helgeshøj Allé 81

DK - 2630 Taastrup, Denmark.

Facsimile No. + 45 43 50 80 08

Authorized officer

Peter Elsner

Telephone No. +45 43 50 83 30

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK2013/050308

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2005/061710 A1 (SANTARIS PHARMA A/S (DK)) 07/07/2005 Page 20, paragraph 7; claims 1 and 8	-
A	WO 2008/151639 A2 (QUERDENKER APS (DK)) 18/12 2008	-
A	WO 2011/115818 A1 (ISIS PHARMACEUTICALS INC (US)) 22/09/2011	-
A	WO 2009/090182 A1 (SANTARIS PHARMA A/S (DK)) 23/07/2009	-

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK2013/050308

Patent document cited in search report / Publication date		Patent family member(s) / Publication date	
WO 2005061710 A1	2005.07.07	CA 2550258 A1	2005.07.07
		AU 2004303464 A1	2005.07.07
		AU 2004303464B B2	2009.10.01
		US 2005203042 A1	2005.09.15
		US 7622453 B2	2009.11.24
		EP 1706489 A1	2006.10.04
		EP 1706489 B1	2010.05.12
		KR 20070006709 A	2007.01.11
		CN 1918292 A	2007.02.21
		CN 100569945C C	2009.12.16
		BRPI 0418104 A	2007.04.17
		JP 2007515175 A	2007.06.14
		JP 4642775B B2	2011.03.02
		NZ 548254 A	2008.09.26
		RU 2377301 C2	2009.12.27
		RU 2006126643 A	2008.01.27
		AT 467679T T	2010.05.15
		ES 2344566T T3	2010.08.31
		DK 1706489T T3	2010.09.13
WO 2007031081 A2	2007.03.22	WO 2007031081 A3	2007.05.18
		CA 2622583 A1	2007.03.22
		AU 2006291836 A1	2007.03.22
		AU 2006291836B B2	2012.02.23
		NO 20081307 A	2008.03.12
		EP 1931778 A2	2008.06.18
		KR 20080068019 A	2008.07.22
		CN 101292034 A	2008.10.22
		EA 200800823 A1	2008.10.30
		JP 2009507499 A	2009.02.26
		US 2009118213 A1	2009.05.07
		BRPI 0616250 A2	2011.06.14
WO 2011117353 A1	2011.09.29	EP 2550360 A1	2013.01.30
		US 2013079505 A1	2013.03.28
WO 2008061537 A2	2008.05.29	WO 2008061537 A3	2009.02.19
		CA 2681568 A1	2008.05.29
		AU 2007323469 A1	2008.05.29
		EP 2097527 A2	2009.09.09
		US 2010021914 A1	2010.01.28
		CN 101641440 A	2010.02.03
WO 2008151639 A2	2008.12.18	JP 2010509923 A	2010.04.02
		WO 2008151639 A3	2009.07.23
		CA 2690643 A1	2008.12.18

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK2013/050308

Patent document cited in search report / Publication date		Patent family member(s) / Publication date	
		AU 2008261404 A1	2008.12.18
		CN 101821390 A	2010.09.01
		JP 2010529847 A	2010.09.02
		US 2010256223 A1	2010.10.07
WO 2011115818 A1	2011.09.22	US 2013041144 A1	2013.02.14
WO 2009090182 A1	2009.07.23	NONE	