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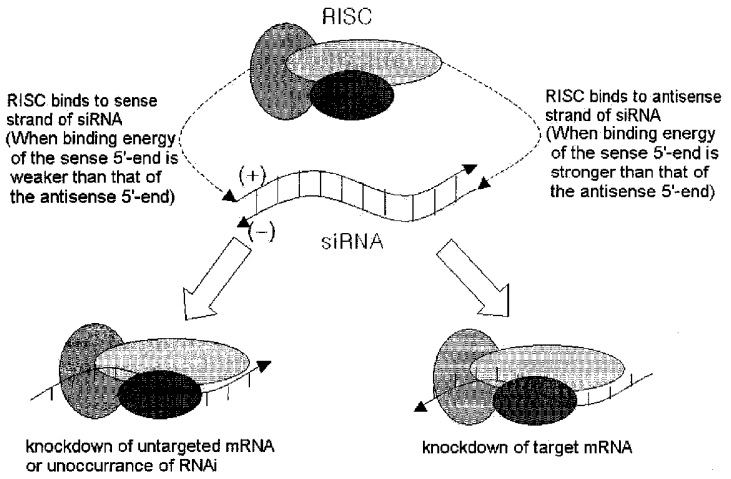

(57) Abstract: A inhibition method of target mRNA expression includes: (a) obtaining binding energy of a double combination section on a dsRNA sequence of all combination comprising complementary nucleotides to a random target mRNA; (b) dividing the binding energy into four sections on the dsRNA sequence of each combination to obtain a difference of the mean binding energy between each section and convert into a score of a relative combination energy pattern; (c) selecting siRNA whose inhibition efficiency to target mRNA is expected to be high by applying the converted score to the dsRNA sequence with other factors that affect the efficiency of siRNA; and (d) inhibiting target mRNA expression using the selected siRNA. As a result, a researcher or an experimenter can analyze patterns of a relative binding energy on base sequences of unknown siRNA without actual experiments to determine whether the siRNA is effective or ineffective rapidly, thereby design and production efficiency of siRNA can be maximized and target mRNA can be effectively inhibited with efficient siRNA to the target mRNA.

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METHOD OF INHIBITING EXPRESSION OF TARGET MRNA USING SIRNA CONSISTING OF NUCLEOTIDE SEQUENCE COMPLEMENTARY TO SAID TARGET mRNA

Technical Field

The present invention generally relates to a inhibition method of target mRNA expression using small interfering RNA (hereinafter, referred to as "siRNA"), and more specifically, to a inhibition method of target mRNA expression using siRNA comprising the steps of selecting complementary siRNA predicted to show the maximal target inhibition efficiency by analyzing a relative binding energy pattern between adjacent and nonadjacent portions of nucleotide sequence of candidate siRNAs and inhibiting target mRNA expression by treating said selected siRNA.

Background of the Invention

RNA interference (hereinafter, referred to as "RNAi") refers to a phenomenon of decomposing target mRNA in a cytoplasm by double-stranded RNA (hereinafter, referred to as "dsRNA") having complementary nucleotide sequence of the target mRNA. After first discovered in *C. elegans* by Fire and Mello in 1998, RNAi phenomenon has been reported to occur in Drosophila, Trypanosoma (a kind of Mastigophora) and vertebrates (Tabara H, Grishok A, Mello CC, Science, 282(5388), 430-1, 1998). In case of human, it was difficult to obtain RNAi effect due to the induction of antiviral interferon pathway upon dsRNA introduction. In 2001, Elbashir and Tuschl et al., reported that the introduction of small dsRNA of 21 nucleotides length into human cells did not cause the interferon pathway but specifically decomposed complementary target mRNA (Elbashir, S.M., Harborth, J., Lendeckel, W., Yalcin, A., Weber, K., Tuschl, T., Nature, 411, 494-

498, 2001; Elbashir, S.M., Lendeckel, W., Tuschl, T., Genes & Dev., 15, 188-200, 2001; Elbashir, S.M., Martinez, J., Patkaniowska, A., Lendeckel, W., Tuschl, T., EMBO J., 20, 6877-6888, 2001). Thereafter, dsRNA of 21nt length has been spotlighted as a tool of new functional genomics and named as small interfering RNA (hereinafter, referred to as "siRNA"). The small interfering RNA (siRNA and microRNA) was granted to the No. 1 of Breakthrough of the Year of the Science Journal in 2002 year (Jennifer Couzin, BREAKTHROUGH OF THE YEAR: Small RNAs Make Big Splash, Jennifer Couzin, Science 20 December 2002: 2296-2297).

siRNA has some advantages as a tool of therapeutics and functional genomics over conventional antisense RNA. First, while antisense RNA requires to synthesize many kinds of antisense RNAs and to perform experiments with a lot of times and costs so as to obtain an effective target sequences, the efficiency of siRNA can be predicted using some algorithms so that more efficient siRNA may be selected through the smaller number of experiments. Second, siRNA has been known to inhibit the expression of genes effectively at a lower concentration than antisense RNA. It means that a smaller amount of siRNA can be used for study and higher therapeutic effect can be expected. Third, inhibition of gene expression by RNAi is a natural mechanism in a body and its action is very specific.

Generally, RNAi experiment includes siRNA design (target site selection), cell culture experiment (cell culture assay, target mRNA degradation rate, the most effective siRNA selection), animal experiment (stability, modification, delivery, pharmacokinetics, toxicology) and clinical test. Of these experiments, the most important step is selecting effective siRNA sequence(s) and delivering selected siRNA into a target tissue (drug delivery). The selection of siRNA sequence having high efficiency is important because different siRNAs show different efficiency and only a siRNA having high efficiency

results in an accurate experimental result and can be used for therapy. The efficient nucleotide sequence can be selected by a computer-aided scoring method and an experimental method. The experimental method is directed to select nucleotide sequences that combine well with target mRNA synthesized by *in vitro* transcription. However, the mRNA structure obtained from *in vitro* transcription may be different from that of the mRNA in a cell, and various proteins may be bonded to the mRNA in a cell so that a result obtained from the experiment using mRNA obtained by *in vitro* transcription may not reflect an actual result. Therefore, developing an algorithm for searching an effective siRNA sequence is important and this can be done by considering various elements that influence the effectiveness of siRNA sequence.

Generally, conventional siRNA design has been performed according to the Tuschl rule which considers 3'overhang type, GC ratio, repetition of specific nucleotide, SNP (single nucleotide polymorphism) in a sequence, secondary structure of RNA, homology with un-targeted mRNA sequence (S.M. Elbashir, J. Harborth, W. Lendeckel, A. Yalcin, Klaus Weber, T. Tuschl, Nature, 411, 494-498, 2001a; S.M. Elbashir, W. Lendeckel, T. Tuschl, Genes & Dev., 15, 188-200, 2001b; S.M. Elbashir, J. Martinez, A. Patkaniowska, W. Lendeckel, T. Tuschl, EMBO J., 20, 6877-6888, 2001c). However, binding energy status in a double-stranded part of siRNA has recently been considered in the siRNA design (Khvorova, A., Reynolds, A., Jayasena, S.D., Cell, 115(4), 505, 2003; Reynolds, A., Leake, D., Boese, Q., Scaringe, S., Marshall, W.S., Khvorova, A., Nat. Biotechnol., 22(3), 326-330, 2004). For example, considering that the efficiency of siRNA could be affected critically by which strand of double-stranded siRNA is bonded with RISC (RNAi-induced silencing complex), siRNA efficiency could be predicted by calculating the energy differences between 5'-end and 3'-end of candidate siRNA (Schwarz DS, Hutvagner G, Du T, Xu Z, Aronin N, Zamore PD., Cell, 115(2), 199-208,

2003, see Fig. 1).

The present inventors have studied the relationship between the efficiency of siRNA and the binding energy status of the entire double-stranded parts of siRNA more accurately and precisely using statistical method. Until now, said relationship has only been reported for the partial parts of the siRNA. As a result, we have found that the inhibition efficiency of candidate siRNA on target mRNA can be predicted through pattern analysis of the relative binding energy of the candidate siRNA, and that the expression of target mRNA can be effectively inhibited using the selected siRNA.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is directed to provide a method of effectively inhibiting the expression of target mRNA using siRNA selected by analyzing a relative binding energy pattern of candidate siRNA without any experiment.

According to an embodiment of the present invention, an inhibition method of target mRNA expression using siRNA comprises:

(1) obtaining all combinations of dsRNA sequences each of which consists of n numbers of nucleotides complementary to a predetermined target mRNA (n is an integer);

(2) obtaining E_A, E_B, E_C and E_D with respect to each dsRNA, which are mean binding energy values of 1^{st}-2^{nd} (A), 3^{rd}-7^{th} (B), 8^{th}-15^{th} (C) and 16^{th}-18^{th} (D) in the base sequence of the dsRNA,

(3) allotting $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ to each section of (A) through (D) according to the following equation for each of the combination of dsRNA sequence,

for the section (A-B),

i) if $E_{f(A-B)} - 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}} < X_{(A-B)} < E_{f(A-B)} + 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}}$, then $Y_{(A-}$

$_{B)}$ = 10 point,

ii) if $E_{n(A-B)} - 1.96\sqrt{\frac{S_{n(A-B)}}{N_n}} < X_{(A-B)} < E_{n(A-B)} + 1.96\sqrt{\frac{S_{n(A-B)}}{N_n}}$, then $Y_{(A-B)}$ = 0 point,

iii) if $X_{(A-B)}$ does not belong to said ranges, then $Y_{(A-B)}$ = 5 point,

in the same way, allotting $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ for the sections (B-C), (C-D) and (A-D),

wherein E_i(A-B) is a mean value of the difference of mean energy value for each section (A-B),

S_i(A-B) is a distribution value of the E_i(A-B),

N_i is the number of experimental data of siRNA,

$X_{(A-B)}$ is a value corresponding to a difference between mean binding energy E_A of the section (A) and mean binding energy E_B of the section (B), and the same goes for $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$;

(4) allotting a relative binding energy Y value by the following Equation 4 with respect to each dsRNA:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

wherein $W_{(A-B)}$ is weight for the section (A-B);

(5) allotting Z value by the following Equation 5 with respect to each dsRNA:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer representing a factor affecting siRNA's inhibition

efficiency on the target mRNA, at least one of which is the relative binding energy of the siRNA,

Z_i is a point given to each factor, provided that $Z_1 = Y$, representing a relative binding energy of step (4),

M_i is a predetermined maximum value allotted to each factor, and

W_i is a predetermined weight allotted to each factor based on W_1;

(6) arranging Z values obtained from the step (5) in a descending order with respect to each dsRNA to select predetermined top % of dsRNAs; and

(7) applying the selected dsRNAs to inhibit the target mRNA expression.

The siRNA is dsRNA comprising 21~23, preferably 21 nucleotides and has the structure of double stranded central region consisting of 19 nucleotides and an overhanging 1~3, preferably 2 nucleotides at both 3′ ends of the double stranded central region (see Fig. 3).

In order to optimize the design of siRNA for target mRNA by analyzing relative binding energy pattern of candidate siRNAs which inhibits the expression of the target mRNA, the present inventors have scored and systematized the siRNAs depending on the relative binding energy pattern of the double-stranded region of the siRNAs.

In order to find out the inhibition efficiency of a certain siRNA to target mRNA, the present inventors have examined the correlation between the binding energy status and the inhibition efficiency of the siRNA. The present inventors have focused not on an absolute binding energy value of specific regions of the double-stranded siRNA but on a variation of the relative binding energy between adjacent and nonadjacent parts of the siRNA (see Fig. 2).

According to one embodiment of the present invention, gene expression inhibition data using siRNA are collected from two papers. The one is from Khvorova's

paper (Khvorova A, Reynolds A, Jayasena SD, Cell, 115(4), 505, 2003) and the other is from Amarzguioui's paper (Amarzguioui M, Prydz H, Biochem. Biophys. Res. Commun., 316(4), 1050-8, 2004). Khvorova's paper discloses a nucleotide sequence represented by the SEQ. ID. NO:1 corresponding to 193-390 nucleotide sequence of human cyclophilin gene (hCyPB), a nucleotide sequence represented by the SEQ. ID. NO:2 corresponding to 1434-1631 nucleotide sequence of firefly luciferase gene (pGL3), and siRNAs for inhibiting the genes. Amarzguioui's paper discloses siRNAs for inhibiting various genes (AA). From the collected data, the base sequence of siRNA used in data analysis and the inhibition effect of gene expression of the siRNA are obtained. Table 1 shows a part of experimental data obtained from Khvorova's paper. INN-HB nearest neighbor model renders information of the base sequences into data on the binding energy (Xia T, SantaLucia J Jr, Burkard ME, Kierzek R, Schroeder SJ, Jiao X, Cox C, Turner DH, Biochemistry, 37(42), 14719-35, 1998, see Figs. 3 and 4).

[Table 1]

Gene	Position	Sequence*	SEQ ID NO.	Knockdown %
hCyPB	5(+192)	CAAAAACAGTGGATAATTT	3	>90
M60857	27(+192)	GGCCTTAGCTACAGGAGAG	4	>90
	35(+192)	CTACAGGAGAGAAAGGATT	5	>90
	41(+192)	GAGAGAAAGGATTTGGCTA	6	>90
	43(+192)	GAGAAAGGATTTGGCTACA	7	>90
	45(+192)	GAAAGGATTTGGCTACAAA	8	>90
	65(+192)	ACAGCAAATTCCATCGTGT	9	>90
	69(+192)	CAAATTCCATCGTGTAATC	10	>90
	95(+192)	TCATGATCCAGGGCGGAGA	11	>90
	99(+192)	GATCCAGGGCGGAGACTTC	12	>90
	131(+192)	GCACAGGAGGAAAGAGCAT	13	>90
	139(+192)	GGAAAGAGCATCTACGGTG	14	>90
	159(+192)	GCGCTTCCCCGATGAGAAC	15	>90

	7(+192)	AAAACAGTGGATAATTTTG	16	<50
	9(+192)	AACAGTGGATAATTTTGTG	17	<50
	11(+192)	CAGTGGATAATTTTGTGGC	18	<50
	17(+192)	ATAATTTTGTGGCCTTAGC	19	<50
	23(+192)	TTGTGGCCTTAGCTACAGG	20	<50
	31(+192)	TTAGCTACAGGAGAGAAAG	21	<50
	51(+192)	ATTTGGCTACAAAAACAGC	22	<50
	61(+192)	AAAAACAGCAAATTCCATC	23	<50
	63(+192)	AAACAGCAAATTCCATCGT	24	<50
	73(+192)	TTCCATCGTGTAATCAAGG	25	<50
	97(+192)	ATGATCCAGGGCGGAGACT	26	<50
	101(+192)	TCCAGGGCGGAGACTTCAC	27	<50
	103(+192)	CAGGGCGGAGACTTCACCA	28	<50
	113(+192)	ACTTCACCAGGGGAGATGG	29	<50
	115(+192)	TTCACCAGGGGAGATGGCA	30	<50
	119(+192)	CCAGGGGAGATGGCACAGG	31	<50
	149(+192)	TCTACGGTGAGCGCTTCCC	32	<50
	151(+192)	TACGGTGAGCGCTTCCCCG	33	<50
	171(+192)	TGAGAACTTCAAACTGAAG	34	<50
	173(+192)	AGAACTTCAAACTGAAGCA	35	<50
	179(+192)	TCAAACTGAAGCACTACGG	36	<50

* represents a base sequence described as SEQ ID NO:1 from a designated position to 21th nucleotide.

Referring to Fig. 3, the siRNA includes 18 binding energy patterns. The correlation between the 18 binding energy patterns of siRNA having a specific base sequence obtained from the step (a) and the inhibition efficiency of gene expression is determined depending on how the 18 binding energy patterns are divided into sections to grasp the entire pattern of the binding energy. As a result, the present inventors calculated the mean of each binding energy pattern from the 1st through 18th positions in 140 experimental data sets for siRNA inhibition of gene expression obtained from (a), and

then showed a graph having an axis x from the 1st to 18th positions and an axis y of the binding energy (-ΔG) as shown in Fig. 5.

The present inventors set sections to have a phenomenon where a difference of the mean binding energy between one section and its adjacent section is most largely reversed between effective siRNA (over 90% gene inhibition) and ineffective siRNA (below 50% gene inhibition). That is, when the 18 binding energy locations are divided into a plurality of sections, preferably four sections A, B, C and D, and each mean energy is defined E_A, E_B, E_C and E_D, and sections are set such that a difference of the mean binding energy in each section of the effective siRNA and the ineffective siRNA, that is, E_A-E_B, E_B-E_C, E_C-E_D, is the farthest from 0 to show the largest change.

To do so, the experimental data of siRNA gene expression inhibition are divided into an effective group and an ineffective group. A null hypothesis that there is no difference between the two groups in the 1st~18th binding energy locations was verified through a t-test. That is, the binding energy location having a p-value of less than 0.05 has a difference of the binding energy around a significance level of 5% in the two groups. Fig. 6 is a graph illustrating a result in an axis x of the binding energy location and an axis y of the p-value, and Fig. 7 is a graph with a smooth curved line in an axis x of the binding energy location and an axis y of the t-value obtained by the following Equation 1.

[Equation 1]

$$(t-value)=\frac{\overline{X}-\overline{Y}}{\sqrt{\frac{S_x}{N_x}+\frac{S_y}{N_y}}}$$

herein, $\overline{X}$: the mean binding energy of the effective group;

$\overline{Y}$: the mean binding energy of the ineffective group;

S_x : the distribution of the effective group;

S_y : the distribution of the ineffective group;

N_x : the number of variation of the effective group;

N_y : the number of variation of the ineffective group.

Three kinds of data sets are used in the preferred embodiment of the present invention. The two data sets extracted from Khvorova's paper include experimental results of gene inhibition on pGL3 and hCyPB that are classified into the efficient group (over 90% inhibition) and the inefficient group (below 50% inhibition). The one data set extracted from Amarzguioui's paper includes experimental results on various kinds of genes (AA) that are compositely classified into the effective group (over 70% inhibition) and the ineffective group (below 70% inhibition). Khvorova's paper includes 40 effective results and 20 ineffective results on gene firefly luciferase (pGL3), and 13 efficient results and 21 inefficient results on human cyclophilin (hCyPB). Amarzguioui's paper includes 21 effective results and 25 ineffective results on various kinds of genes (AA).

The present inventors noticed that the t-value change type of the three data sets was shown in the same pattern as shown in Fig. 7. As it was expected that the division of the effective and ineffective groups in the data set obtained from Amarzguioui's paper is more ambiguous than that in the rest data sets, the data set obtained from Amarzguioui's paper was shown to have a smaller change width of the t-value than that of the rest data sets. It means that there is a specific division of the binding energy pattern between the effective siRNA and the ineffective siRNA.

The t-value has a maximum or minimum value, or the p-value becomes close to 0 where a difference of the binding energy between the effective siRNA group and the ineffective siRNA group is extremely large. That is, if a neighboring area with this part

as the center is set as one section, the deviation of the binding energy between the neighboring sections can be maximized. Even though the t-value has a maximum or minimum value, where the deviation of the maximum and minimum values of the t-value is not large, that is, the p-value is not considered as being discriminative, and they may be excluded in designation of sections.

In the preferred embodiment of the present invention, locations which are the center of the section are designated using the p-value of Fig. 6. Here, the following standards are applied.

① where the p-value of one or more of the two data sets of Khovorova is 0.1 or less

② where all of the two data sets of Khovorova are 0.4 or less

The location suitable for standard ① and ② includes the 1^{st} binding energy location, $5\sim6^{th}$ binding energy location, 14^{th} binding energy location and $17\sim18^{th}$ binding energy location.

Hereinafter, only the two data sets of Khovorova are used because the group division standard in the data sets of Amarzoguioui is different from that of the two data sets of Khovorova, and also performance is to be tested after a method for evaluating the efficiency of siRNA according to the present invention is established.

Next, a section is determined with the above four locations as the center. The base of the determination of the section is to maximize the change of the difference between the mean binding energy of the determined section and the binding energy of the other adjacent section. Preferably, the subsequent process can be divided into the following two cases.

(1) when the process is set to be continuously performed without any vacant space between the adjacent sections

(2) when the process is set to be discontinuously performed with a vacant space between the adjacent sections

The above two cases have both merits and demerits. The case (1) degrades the prediction due to a partially undistinguished section although the status of all binding energy can be examined. On the other hand, the case (2) cannot evaluate the location although the undistinguished section is excluded to maximize the prediction.

Preferably, the section (1) is set as follows.

The section (a) is divided into four sections A, B, C and D to include four locations set based on the standards ① and ② respectively and also include locations of all binding energy without invading regions of other locations, thereby obtaining 20 combinations as shown in Table 2.

Table 2

Section A	Section B	Section C	Section D	Section A	Section B	Section C	Section D
1~2	3~7	8~14	15~18	1~3	4~7	8~14	15~18
1~2	3~8	9~14	15~18	1~3	4~8	9~14	15~18
1~2	3~9	10~14	15~18	1~3	4~9	10~14	15~18
1~2	3~10	11~14	15~18	1~3	4~10	11~14	15~18
1~2	3~11	12~14	15~18	1~3	4~11	12~14	15~18
1~2	3~7	8~15	16~18	1~3	4~7	8~15	16~18
1~2	3~8	9~15	16~18	1~3	4~8	9~15	16~18
1~2	3~9	10~15	16~18	1~3	4~9	10~15	16~18
1~2	3~10	11~15	16~18	1~3	4~10	11~15	16~18
1~2	3~11	12~15	16~18	1~3	4~11	12~15	16~18

Here, the number of effective siRNAs is N_f and the number of ineffective siRNAs is N_n, the efficiency is i ('f' in case of siRNA of the effective group, 'n' in case of siRNA of the ineffective group). The mean binding energy per one binding energy that the jth (to have a number of 1~N_f or 1~N_n as a value) siRNA has in a section k (one of A, B, C and D) is defined as E_{ijk}. That is, the mean energy per one binding energy is represented as E_{f3B} in the section B of the 3rd siRNA of the effective group. Each E_{ijk} is

obtained using experimental data.

The variation of the mean binding energy which becomes a representative among sections A~B($E_{i(A-B)}$), B~C($E_{i(B-C)}$), C~D($E_{i(C-D)}$) is obtained using each E_{ijk} depending on the following Equation 2.

[Equation 2]

$$E_{i(A-B)} = E_{iA} - E_{iB} = \frac{1}{N_i}\sum_j (E_{ijA} - E_{ijB})$$

$E_{i(B-C)}$ and $E_{i(C-D)}$ may be obtained using the Equation 2. Here, $E_{f(A-B)}$ is a value that represents binding energy per one binding energy location in the sections A and B of siRNAs of the effective group, and $E_{n(A-B)}$ is that of the ineffective group. That is, if a section is taken to increase an absolute value of $E_{f(A-B)}$ - $E_{n(A-B)}$, a difference of the mean binding energy between the effective siRNA group and the ineffective siRNA group in the sections A and B becomes larger. As a result, a section can be selected using the above-described characteristic. The same goes for B~C and C~D. The present inventors selected only combinations of sections having an absolute value of 0.1 or more in $E_{f(A-B)}$ - $E_{n(A-B)}$, $E_{f(B-C)}$ - $E_{n(B-C)}$ and $E_{f(C-D)}$ - $E_{n(C-D)}$. In the preferred embodiment of the present invention, four sections are selected, and Table 3 shows information on the selected sections.

Table 3

Section A	Section B	Section C	Section D
1~2	3~7	8~15	16~18
1~2	3~8	9~15	16~18
1~3	4~7	8~15	16~18
1~3	4~8	9~15	16~18

The t-test is performed among $E_{f(A-B)}$ and $E_{n(A-B)}$, $E_{f(B-C)}$ and $E_{n(B-C)}$, and $E_{f(C-D)}$ and $E_{n(C-D)}$ in the selected four sections to obtain a t-value and a p-value. Through this process, one section for distinguishing the effective siRNA group and the ineffective

siRNA group is determined in p-value < 0.05, t-value > 2 of all sections of gene hCyPB, pGL3. The sections are A(1~2), B(3~7), C(8~15) and D(16~18), and Fig. 8 shows information on these sections.

Preferably, the section (2) is set as follows:

The same procedure of the section (1) is basically repeated, except that a different method is used to set a width of the section since the sections are allowed to be discontinuous and overlapped with each other.. Table 4 shows combinations of all sections in the 2 binding energy location including 4 binding energy locations set based on the standards ① and ②.

Table 4

Section A	1	1~2	1~3						
Section B	3~6	4~6	5~6	3~7	4~7	5~7	3~8	4~8	5~8
Section C	12~14	13~14	14	12~15	13~15	14~15	12~16	13~16	14~16
Section D	15~18	16~18	17~18						

If one of the sections A, B, C and D is selected in Table 4, a combination of the necessary section is performed. As a result, 729 (=3 X 9 X 9 X 3) kinds of combinations are possible. Since it is almost impossible to select only one combination of one section through the method of the equation 2 and the t-test in the 729 combinations, a new variable R (abbreviation of robustness) is preferably introduced. R is a figure that represents how many bonding energies are located in the section excluding 4 bonding energies set by the standards ① and②. For examples, if the section A is set as 1~2 and the section B is set as 4~7, the R value of the section A is 1 and the R value of the section B is 2. When the R value of the two sections like (1) $E_{f(A-B)}$ of the section A(1~2) and the section B(4~7) is under consideration, each R value of the two sections are added so that the R value in the section A~B is set as 3.

The E_{ijk} mentioned in (1) is respectively obtained in all combinations of the sections A, B, C and D shown in Table 4. The values $E_{i(A-B)}$, $E_{i(B-C)}$ and $E_{i(C-D)}$ calculated

from the equation 2 are obtained in all combinations through Table 4 , and the t-test is performed to obtain respective t-value and p-value. Here, the above-mentioned R value is applied. Fig. 9 is a graph illustrating a ratio of combination with p-values of 0.05 less in total combinations having a specific R value of the sections A~B, B~C and C~D. As the R value becomes larger, the p-value tends to decrease. As a result, the R value before radical decrease of the p-value is calculated to obtain a section including the largest range having a desired p-value. Referring to Fig. 9, when the R value is 3 or 4 or less, the ratio of the section of p-value < 0.05 is shown to be higher. Therefore, only the sections having R=3 or 4 are included in proposed sections in the preferred embodiment of the present invention.

The final sections are determined through the R value and the t-test results. Since the R value is required to be 3 or 4 in the two sections, two binding energy locations are added in the sections B and C where a section is added in both sides, and one binding energy location is added in the sections A and D where a section is added in one side. As a result, R=3 in A~B, R=4 in B~C and R=3 in C~D. After all combinations of sections satisfying this condition are made, the t-test is performed on these combinations to select one section combination having an extremely low p-value. The selected sections are A(1~2), B(3~6), C(14~16) and D(16~18). Table 5 shows information on these sections.

Table 5

		Section A-B	Section B-C	Section C-D
		1~2	3~6	14~16
		3~6	14~16	16~18
hCyPB	t-value	3.175553	-3.4246	5.915552
	p-value	0.00165	0.000853	0.000001

pGL3	t-value	2.68004	-2.32939	3.217273
	p-value	0.004783	0.011671	0.001059
AA	t-value	1.887835	-0.89566	1.266718
	p-value	0.032827	0.18765	0.10596

In the preferred embodiment of the present invention, the two sections set through (1) and (2) (see Fig. 10) are selected by distinguishing a relative binding energy pattern with the adjacent section. However, since there is a sufficient difference of the binding energy between non-adjacent sections, the t-test is performed on six combinations of A-B, B-C, C-D, A-C, A-D and B-D obtained by the difference of the four sections A, B, C and D. Table 6 shows the t-test results.

Table 6

Section A	Section B	Section C	Section D				
1~2	3~7	8~15	16~18				
		Section A-B	Section B-C	Section C-D	Section A-C	Section A-D	Section B-D
hCyPB	t-value	3.15303	-2.25399	3.27599	1.38792	5.40182	1.00611
	p-value	0.00175	0.01559	0.00127	0.08737	0.00000	0.16095
pGL3	t-value	2.42243	-2.40223	2.13573	0.42633	2.31082	-0.15585
	p-value	0.00928	0.00976	0.01847	0.33572	0.01221	0.42834
AA	t-value	1.87483	-1.02960	1.09863	1.41229	1.94585	0.22186
	p-value	0.03373	0.15441	0.13895	0.08245	0.02904	0.41273
Section A	Section B	Section C	Section D				
1~2	3~6	14~16	16~18				
			Section A-B	Section B-C	Section A-C	Section A-D	Section B-D
hCyPB	t-value	3.16461	-3.42274	5.92078	0.65134	5.40182	0.82726
	p-value	0.00340	0.00172	0.00000	0.51948	0.00001	0.41421

pGL3	t-value	2.69174	-2.32867	3.20424	0.17064	2.31082	-0.32109
	p-value	0.00464	0.01169	0.00110	0.43255	0.01221	0.37465
AA	t-value	1.89671	-0.91889	1.27660	1.29998	1.94585	0.16337
	p-value	0.03222	0.18158	0.10422	0.10019	0.02904	0.43549

As shown in Table 6, there is no big difference in the sections A-C and B-D. The combination of A-D satisfies the condition of p-value <0.05 in the non-adjacent section. Here, the fact that a difference of binding energy between the section A of 5′ end and the section B of 3′ end affects the efficiency of siRNA has been well known in other experimental results (Schwarz, D.S., Hutvagner, G., Du, T., Xu, Z., A ronin, N., Zamore, P.D., Cell, 115(2), 199-20, 2003).

The present inventors used the collected experimental data and selected sections for calculating the relative binding energy of unknown siRNA. For establishing a scoring system, the two data sets extracted from the Khvorova's paper, that is the experimental results on firefly luciferase (pGL3) and human cyclophilin (hCyPB) are included in the collected data to obtain a larger data set. One data set extracted from the Amarzguioui's paper obtained by dividing the set on a basis of 70% inhibition efficiency of gene expression was excluded in the data for establishing the scoring system since the classification standard was different from that of the data of the Khvorova's paper that regarded 90% or more as effective and 50% or less as ineffective. The obtained data were classified into the effective group (inhibition efficiency of gene expression of 90% or more: functional or f) and the ineffective group (inhibition efficiency of gene expression of 50% less; nonfunctional or n).

The obtained data are divided into the sections obtained by the above-described process to obtain $E_{i(A-B)}$, $E_{i(B-C)}$, $E_{i(C-D)}$ and $E_{i(A-D)}$ from the equation 2. These values mean energy values obtained by averaging values on difference of the average energy in

eachgroup. In this process, each value has distribution values which are $S_{i(A-B)}$, $S_{i(B-C)}$, $S_{i(C-D)}$ and $S_{i(A-D)}$. The number of siRNA experimental data is defined as N_i. Table 7 shows values $E_{i(A-B)}$, $E_{i(B-C)}$, $E_{i(C-D)}$, $E_{i(A-D)}$, values $S_{i(A-B)}$, $S_{i(B-C)}$, $S_{i(C-D)}$, $S_{i(A-D)}$, N_i, and t-values and p-values through the t-test.

Table 7

Section A	Section B	Section C	Section D		
1~2	3~7	8~15	16~18		
		Section A-B	Section B-C	Section C-D	Section A-D
	mean(Ef)	0.18	-0.15	0.18	0.22
effective	distribution(Sf)	0.55	0.28	0.41	0.32
Nf=53	Standard deviation	0.74	0.53	0.64	0.57
	Nf	53	53	53	53
	mean(Ef)	-0.42	0.25	-0.28	-0.45
ineffective	distribution(Sf)	0.49	0.43	0.4	0.53
Nn=41	Standard deviation	0.7	0.65	0.63	0.73
	Nn	41	41	41	41
	T	4.026342	-3.16981	3.489798	4.826898
	P	0.000058	0.001036	0.000372	0.000003
Section A	Section B	Section C	Section D		
1~2	3~6	14~16	16~18		
		Section A-B	Section B-C	Section C-D	Section A-D
	mean(Ef)	0.2	-0.21	0.23	0.22
effective	distribution(Sf)	0.56	0.57	0.34	0.32
Nf=53	Standard deviation	0.75	0.75	0.59	0.57
	Nf	53	53	53	53
	mean(Ef)	-0.42	0.3	-0.33	-0.45
ineffective	distribution(Sf)	0.47	0.45	0.21	0.53
Nn=41	Standard deviation	0.69	0.67	0.46	0.73
	Nn	41	41	41	41
	T	4.166805	-3.49839	5.207057	4.826898

	P	0.000035	0.000362	0.000001	0.000003

As shown in Table 7, since the data set is p-value < 0.05 in all sections, it can be used in the scoring system for dividing the effective siRNA and the ineffective siRNA.

If the mean binding energy difference between the sections A and B of a specific siRNA in the effective siRNA group is $X_{f(A-B)}$, X ranges according to the equation 3 in the significance level of p-value < 0.05.

[Equation 3]

$$E_{f(A-B)} - 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}} < X_{f(A-B)} < E_{f(A-B)} + 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}}$$

The equation 3 can be applied to all of $X_{i(A-B)}$, $X_{i(B-C)}$, $X_{i(C-D)}$ and $X_{i(A-D)}$, and also each range of values $X_{i(A-B)}$, $X_{i(B-C)}$, $X_{i(C-D)}$ and $X_{i(A-D)}$ can be obtained as shown in Fig. 11.

The efficiency of unknown siRNA is scored through the relative binding energy pattern under consideration of the results by:

1) obtaining the average binding energy values, that is, $X_{(A-B)}$, $X_{(B-C)}$, $X_{(C-D)}$ and $X_{(A-D)}$, in the sections A-B, B-C, C-D and A-D of unknown siRNA

2) determining which range the value of $X_{(A-B)}$ belongs to and give a score as follows:

i) if $E_{f(A-B)} - 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}} < X_{(A-B)} < E_{f(A-B)} + 1.96\sqrt{\frac{S_{f(A-B)}}{N_f}}$, 10 points are given;

ii) if $E_{n(A-B)} - 1.96\sqrt{\frac{S_{n(A-B)}}{N_n}} < X_{(A-B)} < E_{n(A-B)} + 1.96\sqrt{\frac{S_{n(A-B)}}{N_n}}$, 0 point is given;

iii) when the range does not belong to i) or ii), 5 points are given.

In the same way, scores are given to $X_{(B-C)}$, $X_{(C-D)}$ and $X_{(A-D)}$.

Each score is defined as $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$.

Referring to Fig. 11, in the continuous section, if $-0.02 < X_{(A-B)} < 0.38$, $-0.29 < X_{(B-C)} < -0.01$, $0.00 < X_{(C-D)} < 0.35$, $0.07 < X_{(A-D)} < 0.37$, then $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 10 points, and if $-0.63 < X_{(A-B)} < -0.21$, $0.05 < X_{(B-C)} < 0.44$, $-0.47 < X_{(C-D)} < -0.09$, $-0.67 < X_{(A-D)} < -0.23$, then $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 0 point, and $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 5 points when $X_{(A-B)}$, $X_{(B-C)}$, $X_{(C-D)}$ and $X_{(A-D)}$ do not belong to said ranges.

In the discontinuous section, if $0.00 < X_{(A-B)} < 0.40$, $-0.41 < X_{(B-C)} < -0.01$, $0.07 < X_{(C-D)} < 0.39$, $0.07 < X_{(A-D)} < 0.37$, then $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 10 points, and if $-0.63 < X_{(A-B)} < -0.21$, $0.10 < X_{(B-C)} < 0.51$, $-0.47 < X_{(C-D)} < -0.19$, $0.67 < X_{(A-D)} < -0.23$, then $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 0 point, and $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are individually given 5 points when $X_{(A-B)}$, $X_{(B-C)}$, $X_{(C-D)}$ and $X_{(A-D)}$ do not belong to said ranges.

3) when weighting factors of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ are defined as $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$, the score Y of the relative binding energy pattern is converted based on full mark 100 points using the equation 4:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

The binding energy pattern of siRNA is scored depending on how the weighting factors $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ in each section are set. In order to optimize the combination of the weighting factors, the t-value between the effective siRNA group and the ineffective siRNA is examined as each weighting factor is increased from 0 to 1 by 0.01. Fig. 12 shows distribution of combinations depending on each weighting factor value among the upper 100 t-values which are arranged in a descending order. Referring to the distribution of Fig. 12, a location for maximizing a t-value, that is, a location for

maximizing a difference of the binding energy variation between the effective siRNA group and the ineffective siRNA group can be found. The combination of $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ for maximizing the t-value between the two groups is ranging from 0.90 to 1.00, 0.2 to 0.4, 0.2 to 0.3 and 0.7 to 0.9, preferably, 1.00, 0.37, 0.20, 0.90 in the continuous section, and ranging from 0.5 to 0.7, 0.3 to 0.5, 0.3 to 0.5 and 0.9 to 1.0, preferably, 0.65, 0.48, 0.48 and 0.90 in the discontinuous section. If it is set beyond a threshold value in each case, the t-value is rapidly decreased even to insignificant level for discriminating in the scoring method.

Finally, the present inventors considered how the relative binding energy pattern can be combined with other factors (GC content, T_m, absolute scores of binding energy, homology with other mRNA, secondary structure of RNA) to obtain a system for predicting the overall efficiency of siRNA. The following linear equation basically the same way of scoring the relative binding energy pattern is used as a scoring method.

$$S_t = \sum_i W_i S_i$$

If the score given to each factor is defined as $Z_i(Z_1, Z_2, Z_3, \ldots, Z_n)$, the full mark of each factor is defined as $M_i(M_1, M_2, M_3, \ldots, M_n)$, and the efficiency of each factor, that is, the weighting factor of each score is defined as $W_i(W_1, W_2, W_3, \ldots, W_n)$, then the score Z that represents the efficiency of siRNA can be expressed based on full mark 100 points according to the equation 5:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer ranging from 1 to n, Z_i comprising various factors for affecting inhibition of target mRNA includes the relative binding energy as an essential

factor and one or more factors selected from the group comprising the number of A/U in 5 bases of 3′-end, the presence of G/C at 1st position, the presence of A/U at 19th position, the content of G/C, T_m, secondary structure of RNA, the homology with other mRNA and the like as an optional factor. The optional factors are not necessarily included in allotting the Z value but factors for inducing better prediction with the relative binding energy can be included without limitation. Also, there is no specific limitation in combination of factors. In the preferred embodiment of the present invention, the following factors are selected as Z_i: Z_1 – the score (Y) of the relative binding energy, Z_2 – the number of A/U in 5 bases of 3′-end, Z_3 – the presence of G/C at 1st position, Z_4 – the presence of A/U at 19th position, Z_5 – the score of G/C content. The respective value of M_i is as follows: $M_1 = 100$, $M_2 = 5$, $M_3 = 1$, $M_4 = 1$, $M_5 = 10$.

In the preferred embodiment of the present invention, Z_1 is the calculated score Y, Z_2 is the number of A/U in 5 bases of 3′-end, Z_3 is 1 when the base of 5′ end is G/C or 0 when it isn't, Z_4 is 1 when the base of 3′ end is A/U or 0 when it isn't, and Z_5 is 10 when the content of G/C ranges from 36 to 53% and 0 when it does not belong within the range.

Fig. 13 is a graph for optimizing the weighting factor W_i on each score in the same way of the scoring the relative binding energy pattern as in Fig. 12. The combination of W_1, W_2, W_3, W_4 and W_5 optimized through this process ranges from 0.9 to 1.0, from 0.0 to 0.2, from 0.1 to 0.3 and from 0.0 to 0.2, preferably, 0.90, 0.07, 0.15, 0.19 and 0.11.

The Z value obtained through the above process can be an index for distinguishing which relative binding energy pattern unknown siRNA has. As a result, only the analysis of the base sequence enables evaluation of the binding energy, thereby maximizing the design and production efficiency of siRNA.

According to the present invention, it is possible to predict the inhibition efficiency of unknown siRNA to target mRNA. As a result, the expression of target mRNA can be effectively inhibited by applying a selected siRNA having an excellent inhibition efficiency, preferably a selected siRNA having a Z value within upper 10% to the target mRNA using the above-described method. The above numerical value can be any value and may be flexibly applied depending on sample size of a candidate siRNA group, experimental conditions and the like.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a diagram illustrating inhibition efficiency of gene expression of siRNA changes depending on combination patterns of RISC enzyme.

Fig. 2 is a diagram illustrating a method for scoring the relationship between the inhibition efficiency of gene expression and the binding energy of siRNA.

Fig. 3 is a diagram illustrating binding energydistribution of binding energy of siRNA in INN-HB nearest neighbor model.

Fig. 4 illustrates binding energy values in INN-HB nearest neighbor model.

Fig. 5 is a graph illustrating the mean of the binding energy in each location of collected siRNA data:

axis X; from the 1^{st} to 18^{th} positions,

axis Y; mean of the binding energy ($-\Delta G$),

solid line; when the inhibition efficiency of gene expression is 90% or more,

dotted line; when the inhibition efficiency of gene expression is below 50%.

Fig. 6 is a graph illustrating t-test result of the binding energy in each location of collected siRNA data:

axis X; from the 1^{st} to 18^{th} positions, axis Y; p-value,

solid line; pGL3 gene, dotted line; hCyPB gene

dash-dot line; complex gene extracted from Amarzguioui's paper.

Fig. 7 is a graph illustrating t-test result of the binding energy in each location of collected siRNA data:

axis X; from the 1st to 18th positions, axis Y; t-value,

solid line; pGL3 gene, dotted line; hCyPB gene

dash-dot line; complex gene extracted from Amarzguioui's paper.

Fig. 8 is a graph illustrating various information on sections A(1~2), B(3~7), C(8~15) and D(16~18) obtained by analyzing binding energy data through the process (1).

Fig. 9 is a graph illustrating ratio distribution where the p-value is less than 0.05 among the combination of A~B, B~C and C~D having a specific R value.

Fig. 10 is a diagram illustrating a section selected through the processes (1) and (2).

Fig. 11 illustrates a graph (A) that shows a reliable section of a relative difference between the mean binding energy of ineffective siRNA and effective siRNA in the sections A~B, B~C, C~D and A~D selected through the process (1) and a graph (B) that shows a reliable section between a relative difference of the mean binding energy of ineffective siRNA and effective siRNA in the sections A~B, B~C, C~D and A~D selected through the process (2).

Fig. 12 is a graph illustrating the relationship between weighting factor and the t-value in the score of relative binding energy pattern, wherein the combination of weighting factors are arranged in a descending order depending on the t-value to show the number of the weighting factors of the upper 100 combinations in each section. Here, A is distribution of the weighting factors in the continuous section, and B is distribution of weighting factors in the discontinuous section.

Fig. 13 shows a graph for optimizing the weighting factor W_i on each score in the same way of scoring the relative binding energy pattern as shown in Fig. 12.

Preferred Embodiments

The present invention will be described in detail by referring to examples below, which are not intended to limit the present invention.

<Example 1> Comparison with conventional mehod of siRNA design

In order to test the performance of the siRNA design optimizing method using the relative binding energy pattern according to the present invention, the siRNA design optimizing method was compared with the scoring method of the siRNA design disclosed in Patent No. WO2004/045543 (Functional and Hyperfunctional siRNA, published on June 3, 2004). The scoring method of siRNA efficiency disclosed in many algorithms of the Patent No. WO2004/045543 was performed according to the following equation 6:

[Equation 6]

Relative functionality of siRNA = $-(GC/3) + (AU_{15\text{-}19}) - (Tm_{20°C})*3 - (G_{13})*3 - (C_{19}) + (A_{19})*2 + (A_3) + (U_{10}) + (A_{13}) - (U_5) - (A_{11})$

Of the three data sets obtained from Khvorova's paper and Amarzguioui's paper, one data set extracted from the Amarzguioui's paper except the two data sets extracted from the Khvorova's paper used in scoring the relative binding energy pattern was used as a test set to compare prediction of two scoring methods. First, each score of siRNA included in the effective/ineffective groups was calculated using the two scoring methods. Through LDA (Linear discriminant analysis) and QDA (Quadratic discriminant analysis), decision on whether a random siRNA was effective or ineffective was calculated. Preferably, the above value can be obtained using a statistical program R (http://www.R-project.org) ([1] Richard A. Becker, John M. Chambers, and Allan R. Wilks. The New S

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Unlike that of the Khvorova's paper, the dataset extracted from the Amarzguioui's paper divide the effective/ineffective groups on a basis of 70% inhibition efficiency of the expression. That is, the difference is expected to be shown more precisely in comparison with the success rate of prediction of the two scoring method in

this data set. Table shows the results.

Table 8

	Relative binding energy pattern	Dharmacon
LDA	0.652	0.586
QDA	0.657	0.521

Referring to Table 8, the success rate of prediction is shown to be higher by 10% in the scoring method binding energyaccording to the present invention using the relative binding energy pattern than in the conventional scoring method of siRNA efficiency in both cases of LDA and QDA.

<Example 2> Inhibition experiment of Survivin gene expression

Through the siRNA design optimizing method according to the present invention using the relative binding energy pattern, 36 siRNAs for inhibiting surviving gene expression were designed, and then the inhibition experiment of the surviving gene expression was performed. The resultant data set was divided into effective/ineffective groups on a basis of 75% inhibition efficiency of expression. Here, the three data sets obtained from the Khvorova's paper and the Amarzguioui's paper were used as train sets, and the survivin data set was used as a test set. In the same way of Example 1, the score of siRNA was marked, and the success rate of prediction of the efficiency of siRNAs was calculated through LDA (Linear discriminant analysis) and QDA (Quadratic discriminant analysis) using the statistical program R. As a result, the sucess rate of prediction was 0.64 in both cases of LDA and QDA to show almost the same results of Example 1 (see Table 9).

Table 9

NO	Exp. ID number	Sequence (3′ overhang: TT)	SEQ ID NO:	Knock Down(%)	Z score	Precise prediction
1	570(D)	GCAAUGUCUUAGGAAAGGA	37	>90	62.83	0
2	1106(D)	AGAAUAHCACAAACUACAA	38	>90	53.31	0

3	1189(D)	GAGACAGAAUAGAGUGAUA	39	>90	72.15	0
4	1212(Q)	GCGUCUGGCAGAUACUCCU	40	>90	68.48	0
5	299(AS)	UGCGCUUUCCUUUCUGUCA	41	75-90	40.89	
6	319(G)	GAAGCAGUUUGAAGAAUUA	42	75-90	64.37	0
7	574(Q)572	UGUCUUAGGAAAGGAGAUC	43	75-90	50.92	0
8	783(Q)	GGCAGUGUCCCUUUUGCUA	44	75-90	57.52	0
9	1099(AS)	AAUUCACAGAAUAGCACAA	45	75-90	46.80	
10	1133(D)	AAGCACAAAGCCAUUCUAA	46	75-90	53.35	0
11	1305(Q)	GGCAGUGGCCUAAAUCCUU	47	75-90	69.63	0
12	1480(G)	GGCUGAAGUCUGGCGUAAG	48	75-90	50.20	0
13	1481(G)	GCUGAAGUCUGGCGUAAGA	49	75-90	45.91	
14	1585(G)	CGGCUGUUCCUGAGAAAUA	50	75-90	72.72	0
15	92(D)	AAGGACCACCGCAUCUCUA	51	50-75	41.57	0
16	94(Q)92	GGACCACCGCAUCUCUACA	52	50-75	71.82	
17	294(G)	CCGGUUGCGCUUUCCUUUC	53	50-75	44.18	0
18	693(D)	GCUGCUUCUCUCUCUCUCU	54	50-75	63.54	
19	1021(G)	GUGAUGAGAGAAUGGAGAC	55	50-75	57.86	
20	1188(G)	GGAGACAGAAUAGAGUGAU	56	50-75	57.44	
21	1394(Q)	CCUUCACAUCUGUCACGUU	57	50-75	57.48	
22	1546(G)	GAUUGUUACAGCUUCGCUG	58	50-75	57.37	
23	90(AS)	UCAAGGACCACCGCAUCUC	59	<50	29.75	0
24	95(G)	GACCACCGCAUCUCUACAU	60	<50	55.86	
25	294(Q)282	AAGCAUUCGUCCGGUUGCG	61	<50	18.86	0
26	289(D)	UUCGUCCGGUUGCGCUUUC	62	<50	39.01	0
27	428(Q)426	ACUGCGAAGAAAGUGCGCC	63	<50	23.96	0
28	780(Q)778	GAAGGCAGUGUCCCUUUUG	64	<50	56.04	
29	807(G)	GACAGCUUUGUUCGCGUGG	65	<50	43.89	0
30	846(Q)	UGUGUCUGGACCUCAUGUU	66	<50	47.41	0
31	1130(Q)	ACUAAGCACAAAGCCAUUC	67	<50	47.75	0
32	1141(Q)	AGCCAUUCUAAGUCAUUGG	68	<50	33.49	0
33	1142(Q)	GCCAUUCUAAGUCAUUGGG	69	<50	37.58	0
34	1236(D)	CACUGCUGUGUGAUUAGAC	70	<50	35.92	0
35	1325(D)	UUAAAUGACUUGGCUCGAU	71	<50	52.86	
36	1390(G)	CCAACCUUCACAUCUGUCA	72	<50	63.50	
		Total success rate of prediction (23/36) =64%				23

Industrial Applicability

As described above, according to the method of the present invention, a researcher or an experimenter can analyzes patterns of a relative binding energy on base sequences of unknown siRNA without actual experiments to determine whether the siRNA is effective or ineffective rapidly, thereby design and production efficiency of siRNA can be maximized and target mRNA expression can be effectively inhibited with efficient siRNA to the target mRNA.

SEQUENCE LIST

Attached

What is Claimed is:

1. A method of inhibiting target mRNA expression using siRNA, comprising the steps of:

(1) obtaining all combinations of ds (double strand) RNA sequences each of which consists of n numbers of nucleotides complementary to a predetermined target mRNA (n is an integer);

(2) obtaining E_A, E_B, E_C and E_D with respect to each dsRNA, which are mean binding energy values of 1^{st}-2^{nd} section (A), 3^{rd}-7^{th} section (B), 8^{th}-15^{th} section (C) and 16^{th}-18^{th} section (D) in the base sequence of the dsRNA, respectively;

(3) allotting $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ to each section of (A) through (D) according to the following equation,

i) in case of $-0.02 < E_A - E_B < 0.38$, $-0.29 < E_B - E_C < -0.01$, $0.00 < E_C - E_D < 0.35$, $0.07 < E_D - E_A < 0.37$, then each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 10 point,

ii) in case of $-0.63 < E_A - E_B < -0.21$, $0.05 < E_B - E_C < 0.44$, $-0.47 < E_C - E_D < -0.09$, $-0.67 < E_D - E_A < -0.23$, each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 0 point,

iii) in case of $E_A - E_B$, $E_B - E_C$, $E_C - E_D$ and $E_D - E_A$ being out of range defined in (i) and (ii), each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 5 point;

(4) allotting a relative binding energy value Y value with respect to each dsRNA according to the following Equation 4:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

wherein $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are weights for sections (A-B), (B-C), (C-D) and (A-D) which ranges from 0.90 to 1.00, 0.2 to 0.4, 0.2 to 0.3 and 0.7 to 0.9, respectively;

(5) allotting Z value with respect to each dsRNA according to the following Equation 5:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer representing a factor affecting siRNA's inhibition efficiency on the target mRNA, at least one of which is the relative binding energy of the siRNA,

Z_i is a point given to each factor, provided that $Z_1 = Y$, representing a relative binding energy,

M_i is a predetermined maximum value allotted to each factor, and

W_i is a predetermined weight allotted to each factor based on W_1;

(6) arranging Z values obtained from the step (5) in a descending order with respect to each dsRNA to select predetermined top % of dsRNAs; and

(7) applying the selected dsRNAs to inhibit the target mRNA expression.

2. The method according to claim 1, wherein the siRNA is double strand RNA of 21 nucleotides where n is 21.

3. The method according to claim 1 or 2, wherein the siRNA has an overhang structure of 1 to 3 nucleotide at the dsRNA portion and both side 3′-ends of 19 nucleotides.

4. The method according to claim 1, wherein the weighting factors $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are individually 1.00, 0.37, 0.20 and 0.90.

5. The method according to claim 1, wherein the factor that affects inhibition efficiency of siRNA to target mRNA in the step (5) includes a relative binding energy as an essential factor, and one or more factors selected from the group comprising the number of A/U in 5 bases of 3′-end, the presence of G/C at 1st position, the presence of A/U at 19th position, the content of G/C, T_m, secondary structure of RNA, homology with other mRNA as an optional factor.

6. The method according to claim 1 or 5, wherein the Equation 5 of the step (5) is characterized in that I = 5; Z_1 = relative binding energy point (Y), Z_2 = point allotted to the number of A/U in 5 bases of 3′-end, Z_3 = point allotted to the presence of G/C at 1st position, Z_4 = point allotted to the presence of A/U at 19th position, and Z_5 = point allotted to the content of G/C; M_1-M_5 are individually 100, 5, 1, 1, 10; W_1-W_5 are individually 0.90, 0.07, 0.15, 0.19, 0.11.

7. The method according to claim 1, wherein the predetermined % of the step (5) is upper 10%.

8. A method of inhibiting target mRNA expression using siRNA, comprising the steps of:

(1) obtaining all combination of ds (double strand) RNA sequences each of which consists of n numbers of nucleotides complementary to a predetermined target

mRNA (n is an integer);

(2) obtaining E_A, E_B, E_C and E_D with respect to each dsRNA, which are mean binding energy values of 1^{st}-2^{nd} section (A), 3^{rd}-6^{th} section (B), 14^{th}-16^{th} section (C) and 16^{th}-18^{th} section (D) in the base sequence of the dsRNA, respectively;

(3) allotting $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ to each section of (A) through (D) according to the following equation

i) in case of $0.00 < E_A - E_B < 0.40$, $-0.41 < E_B - E_C < -0.01$, $0.07 < E_C - E_D < 0.39$, $0.07 < E_D - E_A < 0.37$, then each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 10 point,

ii) in case of $-0.63 < E_A - E_B < -0.21$, $0.10 < E_B - E_C < 0.51$, $-0.47 < E_C - E_D < -0.19$, $-0.67 < E_D - E_A < -0.23$, each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 0 point,

iii) in case of $E_A - E_B$, $E_B - E_C$, $E_C - E_D$ and $E_D - E_A$ being out of range defined in (i) and (ii), each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 5 point;

(4) allotting a relative binding energy Y value with respect to each dsRNA according to the following Equation 4:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

wherein $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are individually weights for sections (A-B), (B-C), (C-D) and (A-D) which ranges from 0.5 to 0.7, 0.3 to 0.5, 0.3 to 0.5 and 0.9 to 1.0, respectively;

(5) allotting Z value with respect to each dsRNA according to the following Equation 5:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer representing a factor affecting siRNA's inhibition efficiency on the target mRNA, at least one of which is the relative binding energy of siRNA,

Z_l is a point given to each factor, provided that Z_i = Y, representing a relative binding energy point,

M_i is a predetermined maximum value allotted to each factor, and

W_i is a predetermined weight allotted to each factor based on W_1;

(6) arranging Z values obtained from the step (5) in a descending order with respect to each dsRNA to select predetermined top % of dsRNAs; and

(7) applying the selected dsRNAs to inhibit the target mRNA expression.

9. The method according to claim 8, wherein the siRNA is double strand RNA of 21 nucleotides where n is 21.

10. The method according to claim 8 or 9, wherein the siRNA has an overhang structure of 1 to 3 nucleotide at the dsRNA portion and both side 3′-ends of 19 nucleotides.

11. The method according to claim 8, wherein the weighting factors $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are individually 0.65, 0.48, 0.48 and 0.90.

12. The method according to claim 8, wherein the factor that affects inhibition efficiency of siRNA to target mRNA in the step (5) includes a relative binding

energy as an essential factor, and one or more factors selected from the group comprising the number of A/U in 5 bases of 3′-end, the presence of G/C at 1st position, the presence of A/U at 19th position, the content of G/C, T_m, secondary structure of RNA, homology with other mRNA as an optional factor.

13. The method according to claim 8 or 12, wherein the Equation 5 of the step (5) is characterized in that i = 5; Z_1 = relative binding energy point (Y), Z_2 = point allotted to the number of A/U in 5 bases of 3′-end, Z_3 = point allotted to the presence of G/C at 1st position, Z_4 = point allotted to the presence of A/U at 19th position, and Z_5 = point allotted to the content of G/C; M_1-M_5 are individually 100, 5, 1, 1, 10; and W_1-W_5 are individually 0.90, 0.07, 0.15, 0.19, 0.11.

14. The method according to claim 8, wherein the predetermined % of the step (5) is upper 10%.

15. A method of optimizing siRNA design, comprising the steps of;

(1) obtaining all combinations of ds (double strand) RNA sequences each of which consists of n numbers of nucleotides complementary to a predetermined target mRNA (n is an integer);

(2) obtaining E_A, E_B, E_C and E_D with respect to each dsRNA, which are mean binding energy values of 1st-2nd section (A), 3rd-7th section (B), 8th-15th section (C) and 16th-18th section (D) in the base sequence of the dsRNA, respectively;

(3) allotting $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ to each section of (A) through (D) according to the following equation,

i) in case of $-0.02 < E_A - E_B < 0.38$, $-0.29 < E_B - E_C < -0.01$, $0.00 < E_C -$

$E_D < 0.35$, $0.07 < E_D - E_A < 0.37$, then each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 10 point,

ii) in case of $-0.63 < E_A - E_B < -0.21$, $0.05 < E_B - E_C < 0.44$, $-0.47 < E_C - E_D < -0.09$, $-0.67 < E_D - E_A < -0.23$, each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 0 point,

iii) in case of $E_A - E_B$, $E_B - E_C$, $E_C - E_D$ and $E_D - E_A$ being out of range defined in (i) and (ii), each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 5 point;

(4) allotting a relative binding energy value Y value with respect to each dsRNA according to the following Equation 4:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

wherein $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are weights for sections (A-B), (B-C), (C-D) and (A-D) which ranges from 0.90 to 1.00, 0.2 to 0.4, 0.2 to 0.3 and 0.7 to 0.9, respectively;

(5) allotting Z value with respect to each dsRNA according to the following Equation 5:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer representing a factor affecting siRNA's inhibition efficiency on the target mRNA, at least one of which is the relative binding energy of the siRNA,

Z_i is a point given to each factor, provided that $Z_1 = Y$, representing a relative binding energy,

M_i is a predetermined maximum value allotted to each factor, and

W_i is a predetermined weight allotted to each factor based on W_1; and

(6) arranging Z values obtained from the step (5) in a descending order with respect to each dsRNA to select predetermined top % of dsRNAs.

16. A method of optimizing siRNA design, comprising the steps of:

(1) obtaining all combination of ds (double strand) RNA sequences each of which consists of n numbers of nucleotides complementary to a predetermined target mRNA (n is an integer);

(2) obtaining E_A, E_B, E_C and E_D with respect to each dsRNA, which are mean binding energy values of 1^{st}-2^{nd} section (A), 3^{rd}-6^{th} section (B), 14^{th}-16^{th} section (C) and 16^{th}-18^{th} section (D) in the base sequence of the dsRNA, respectively;

(3) allotting $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ to each section of (A) through (D) according to the following equation

i) in case of $0.00 < E_A - E_B < 0.40$, $-0.41 < E_B - E_C < -0.01$, $0.07 < E_C - E_D < 0.39$, $0.07 < E_D - E_A < 0.37$, then each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 10 point,

ii) in case of $-0.63 < E_A - E_B < -0.21$, $0.10 < E_B - E_C < 0.51$, $-0.47 < E_C - E_D < -0.19$, $-0.67 < E_D - E_A < -0.23$, each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 0 point,

iii) in case of $E_A - E_B$, $E_B - E_C$, $E_C - E_D$ and $E_D - E_A$ being out of range defined in (i) and (ii), each of $Y_{(A-B)}$, $Y_{(B-C)}$, $Y_{(C-D)}$ and $Y_{(A-D)}$ is 5 point;

(4) allotting a relative binding energy Y value with respect to each dsRNA according to the following Equation 4:

[Equation 4]

$$Y = \frac{W_{(A-B)}Y_{(A-B)} + W_{(B-C)}Y_{(B-C)} + W_{(C-D)}Y_{(C-D)} + W_{(A-D)}Y_{(A-D)}}{10(W_{(A-B)} + W_{(B-C)} + W_{(C-D)} + W_{(A-D)})} \times 100$$

wherein $W_{(A-B)}$, $W_{(B-C)}$, $W_{(C-D)}$ and $W_{(A-D)}$ are individually weights for sections (A-B), (B-C), (C-D) and (A-D) which ranges from 0.5 to 0.7, 0.3 to 0.5, 0.3 to 0.5 and 0.9 to 1.0, respectively;

(5) allotting Z value with respect to each dsRNA according to the following Equation 5:

[Equation 5]

$$Z = 100 \times \frac{\sum_i W_i \frac{Z_i}{M_i}}{\sum_i W_i}$$

wherein i is an integer representing a factor affecting siRNA's inhibition efficiency on the target mRNA, at least one of which is the relative binding energy of siRNA,

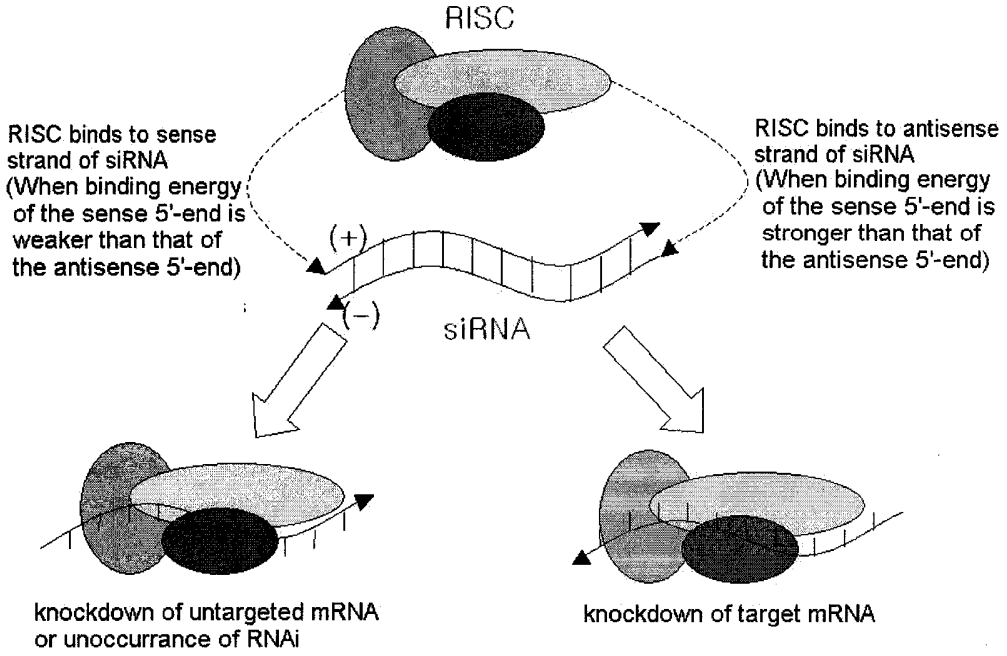
Z_1 is a point given to each factor, provided that Z_i = Y, representing a relative binding energy point,

M_i is a predetermined maximum value allotted to each factor, and

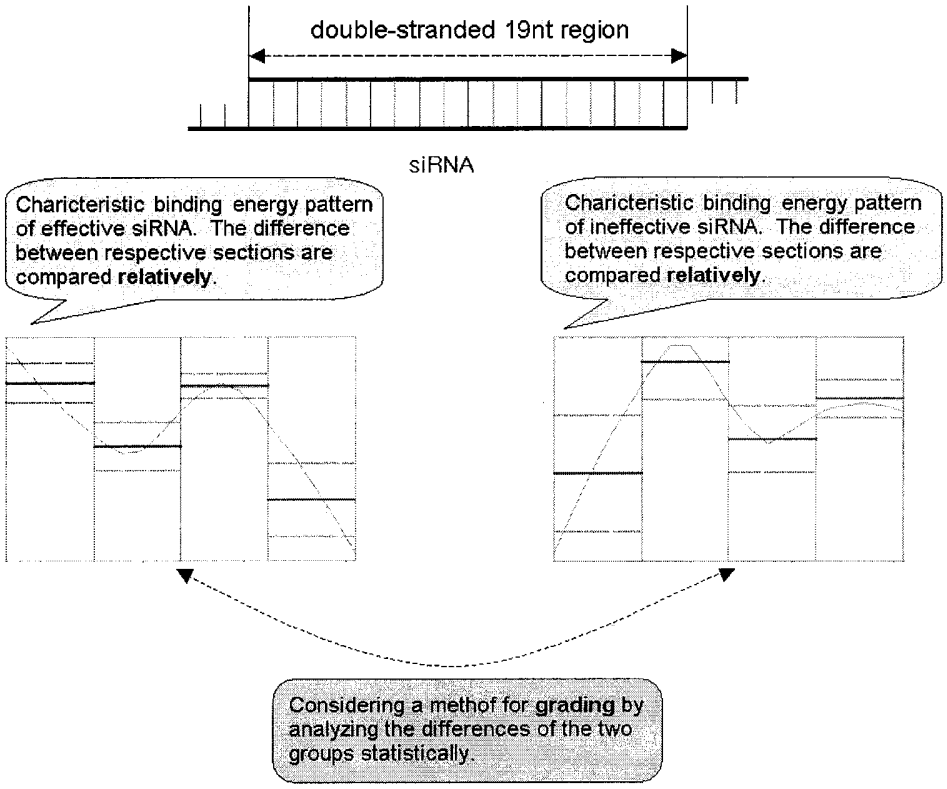
W_i is a predetermined weight allotted to each factor based on W_1; and

(6) arranging Z values obtained from the step (5) in a descending order with respect to each dsRNA to select predetermined top % of dsRNAs.

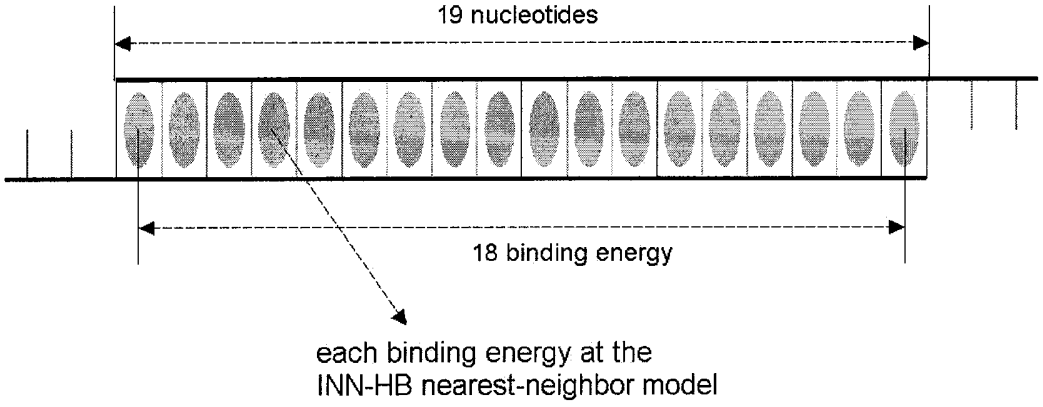
[Fig. 1]


RISC
RISC binds to sense strand of siRNA (When binding energy of the sense 5'-end is weaker than that of the antisense 5'-end)
RISC binds to antisense strand of siRNA (When binding energy of the sense 5'-end is stronger than that of the antisense 5'-end)
(+)
(-)
siRNA
knockdown of untargeted mRNA or unoccurrance of RNAi
knockdown of target mRNA

[Fig. 2]


double-stranded 19nt region
siRNA
Charicteristic binding energy pattern of effective siRNA. The difference between respective sections are compared relatively.
Charicteristic binding energy pattern of ineffective siRNA. The difference between respective sections are compared relatively.
Considering a methof for grading by analyzing the differences of the two groups statistically.

[Fig. 3]



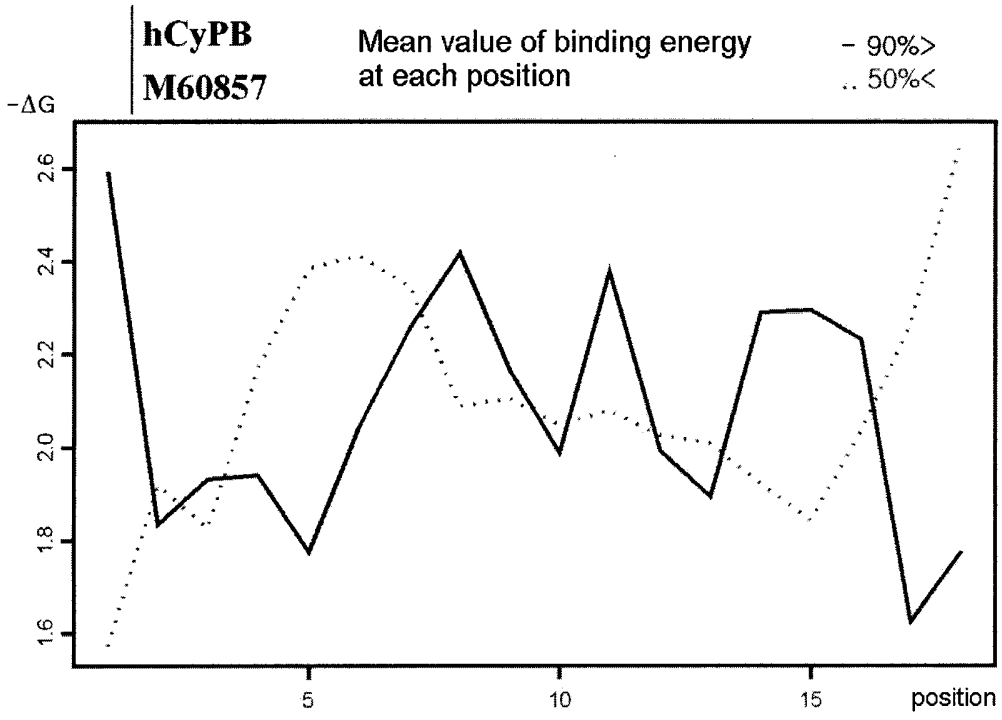
[Fig. 4]

RNA Thermodynacic Parameters for INN-HB Nearest-Neighbor Model, 1 M NaCl, pH 7[a]

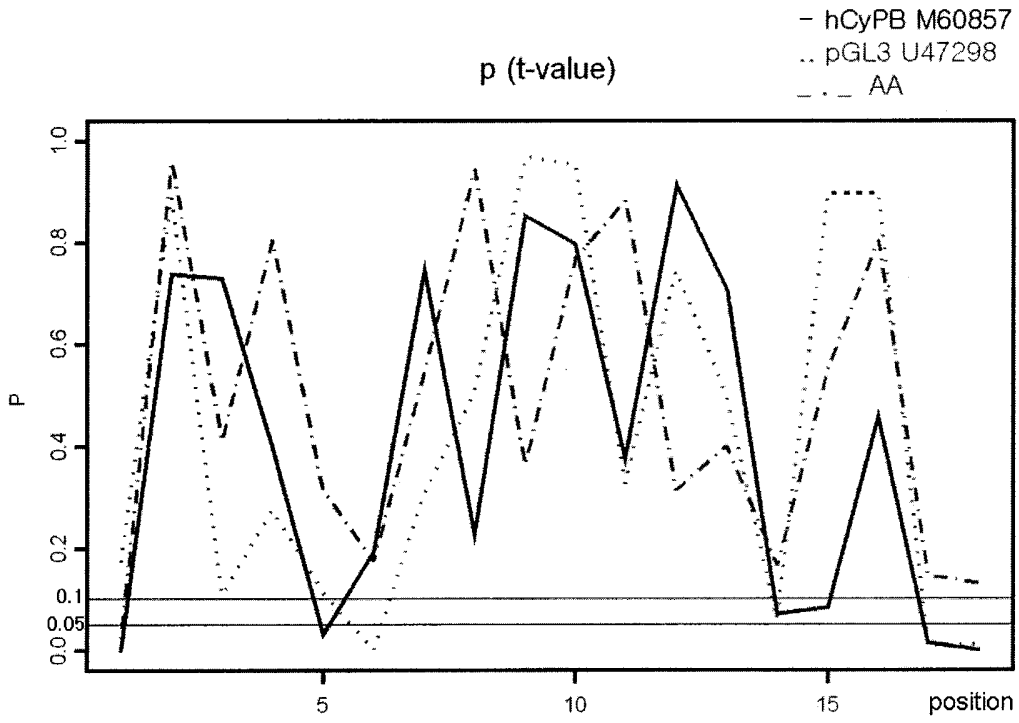
parameters	ΔG°_{37} (kcal/mol)	ΔH° (kcal/mol)	ΔS^{ob} (eu)
5'AA3' 3'UU5'	-0.93(0.03)	-6.82(0.09)	-19.0(2.5)
5'AU3' 3'UA5'	-1.10(0.08)	-9.38(1.68)	-26.7(5.2)
5'UA3' 3'AU5'	-1.33(0.09)	-7.69(2.02)	-20.5(6.3)
5'CU3' 3'GA5'	-2.08(0.06)	-10.48(1.24)	-27.1(3.8)
5'CA3' 3'GU5'	-2.11(0.07)	-10.44(1.28)	-26.9(3.9)
5'GU3' 3'CA5'	-2.24(0.06)	-11.40(1.23)	-29.5(3.9)
5'GA3' 3'CU5'	-2.35(0.06)	-12.44(1.20)	-32.5(3.7)
5'CG3' 3'GC5'	-2.36(0.09)	-10.64(1.65)	-26.7(5.0)
5'GG3' 3'CC5'	-3.26(0.07)	-13.39(1.24)	-32.7(3.8)
5'GC3' 3'CG5'	-3.42(0.08)	-14.88(1.58)	-36.9(4.9)
initiation[c]	4.09(0.22)	3.61(4.12)	-1.5(12.7)
per terminal AU[d]	0.45[d](0.04)	3.72[d](0.83)	10.5[d](2.6)
symmetry correction (self-complementary)	0.43	0	-1.4
symmetry correction (non-self-complementary)	0	0	0

[a]Numbers in parentheses are uncertainties for parameters.
[b]Calculated from nearest-neighbor parameters for ΔG°_{37} and ΔH°.
[c]Includes potential GC end effects.
[d]Parameter is per terminal AU pair.

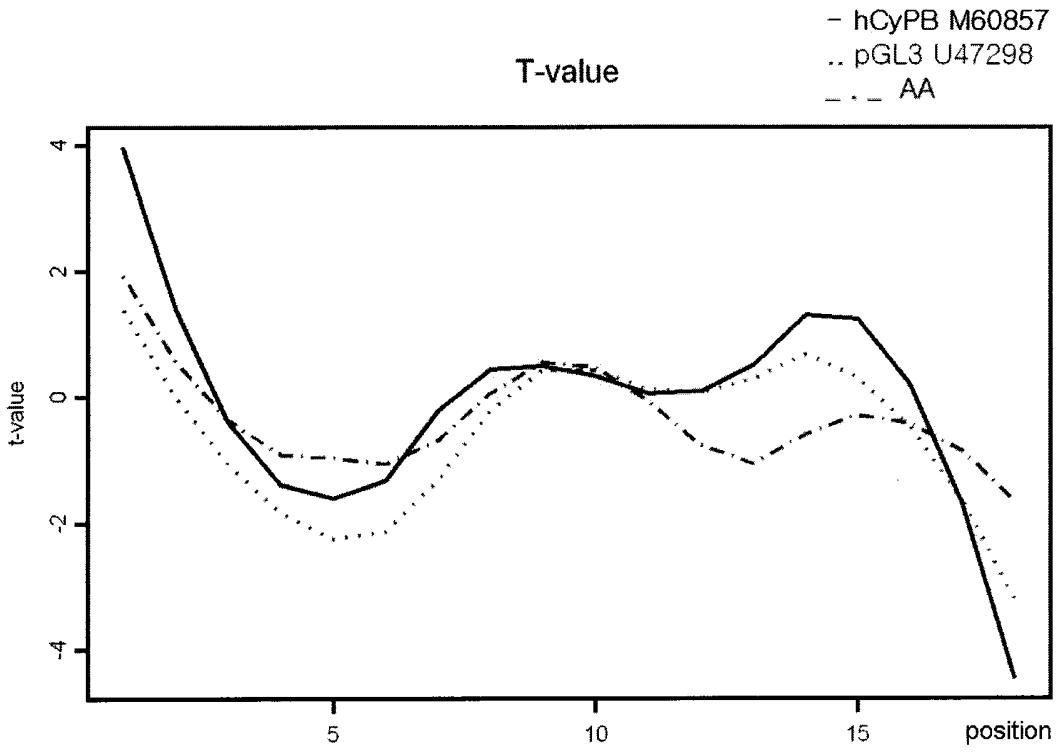
[Fig. 5]


hCyPB
M60857
Mean value of binding energy
at each position
- 90%>
.. 50%<
-ΔG
2.6
2.4
2.2
2.0
1.8
1.6
5
10
15
position

[Fig. 6]

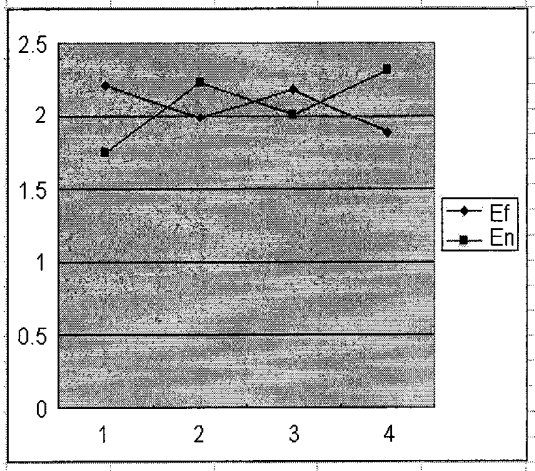

- hCyPB M60857
.. pGL3 U47298
_ . _ AA
p (t-value)
P
1.0
0.8
0.6
0.4
0.2
0.1
0.05
0.0
5
10
15
position

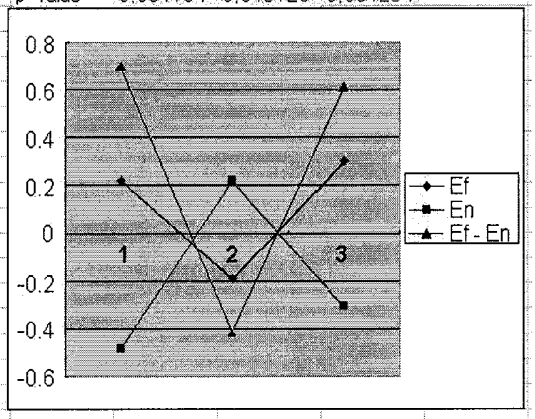
[Fig. 7]


T-value
- hCyPB M60857
.. pGL3 U47298
_ . _ AA
t-value
4
2
0
-2
-4
5
10
15
position

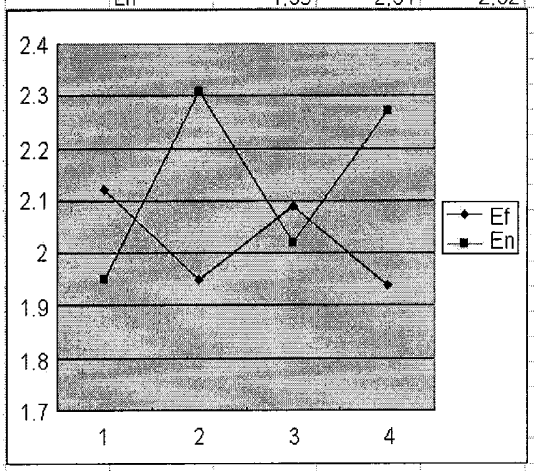
[Fig. 8]

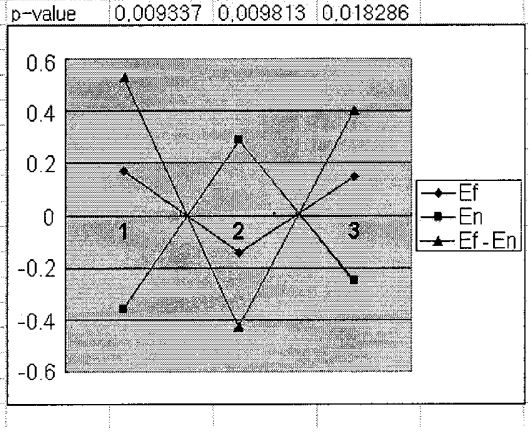
Genes		section A	section B	section C	section D		A-B	B-C	C-D
		1 ~ 2	3 ~ 7	8 ~ 15	16 ~ 18				
hCyPB	Ef	2,21	1,99	2,18	1,88		0,22	-0,19	0,3
	En	1,75	2,23	2,01	2,32		-0,48	0,22	-0,31
						Ef - En	0,7	-0,41	0,61
						t-value	3,15	-2,25	3,28
						p-value	0,001764	0,015728	0,001254



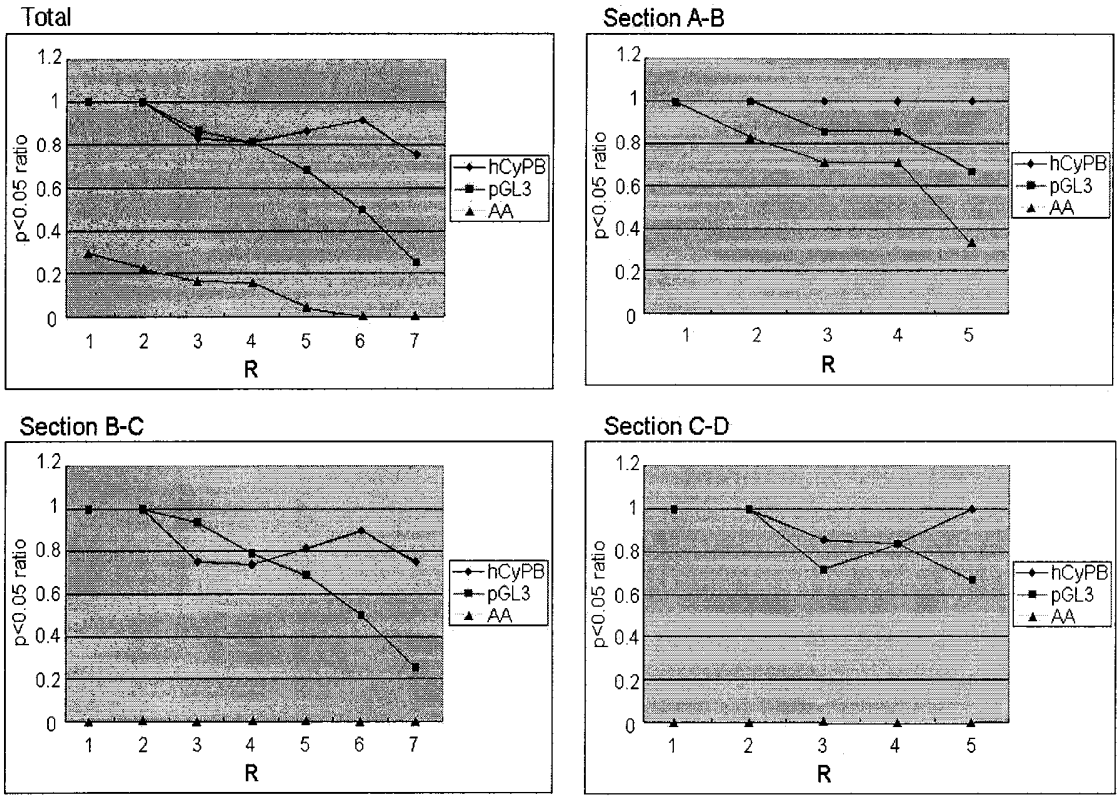


pGL3	Ef	2,12	1,95	2,09	1,94		0,17	-0,14	0,15
	En	1,95	2,31	2,02	2,27		-0,36	0,29	-0,25
						Ef - En	0,53	-0,43	0,4
						t-value	2,42	-2,40	2,14
						p-value	0,009337	0,009813	0,018286



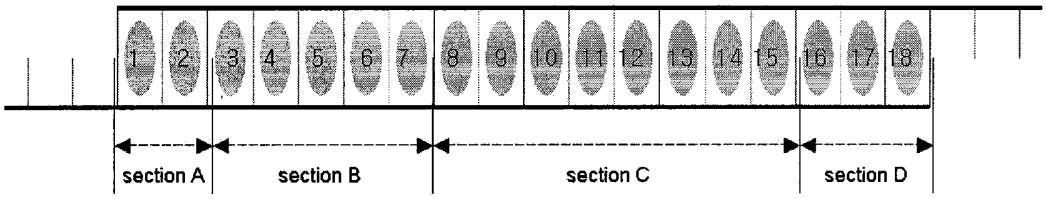


[Fig. 9]

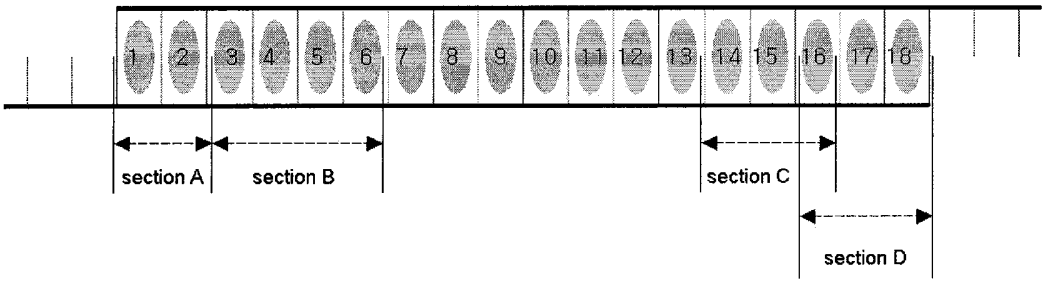

Relationship between R and p<0.05 ratio
Total
Section A-B
Section B-C
Section C-D
p<0.05 ratio
R
hCyPB
pGL3
AA

[Fig. 10]

Continuously divided sections



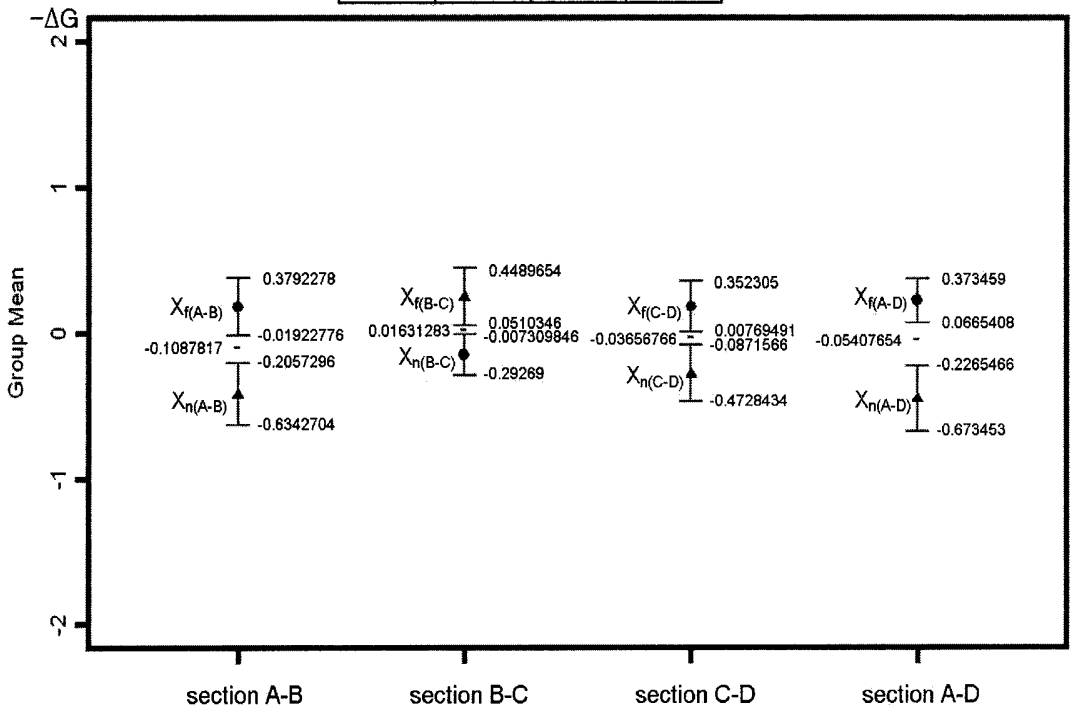
Discontinuously divided sections



[Fig. 11]

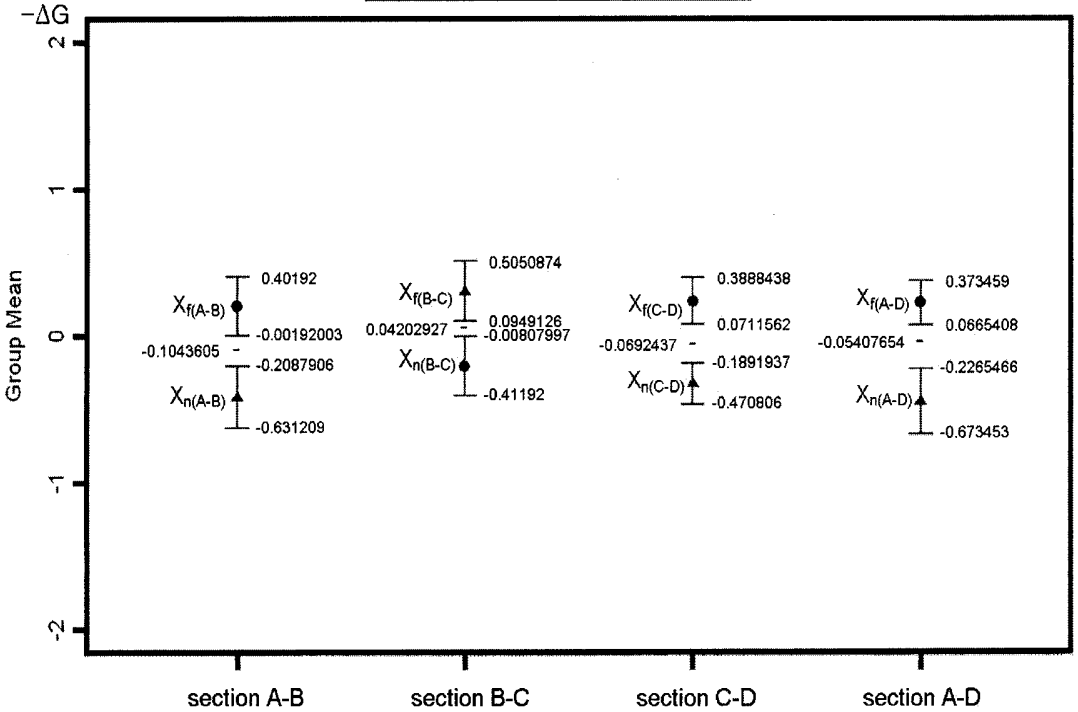
A hCyPB+pGL3

section 1	section 2	section 3	section 4
1-2	3-7	8-15	16-18
section 1-2	section 2-3	section 3-4	section 1-4

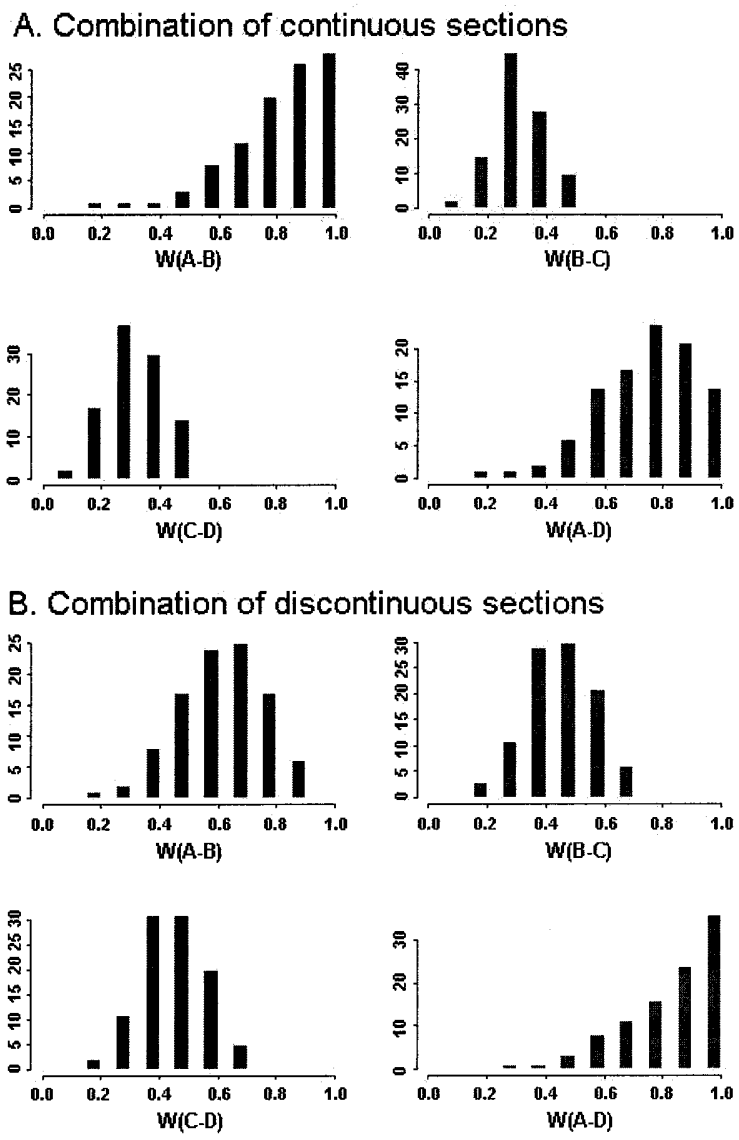


B hCyPB+pGL3

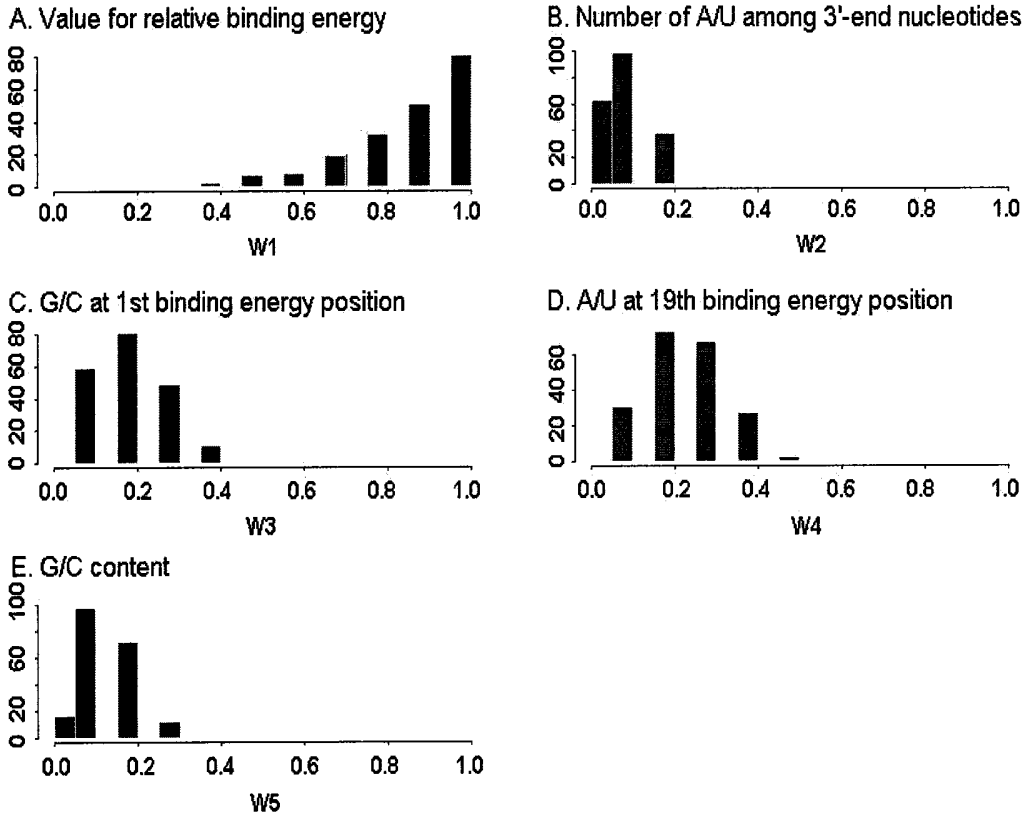
section 1	section 2	section 3	section 4
1-2	3-6	14-16	16-18
section 1-2	section 2-3	section 3-4	section 1-4



[Fig. 12]


A. Combination of continuous sections
W(A-B)
W(B-C)
W(C-D)
W(A-D)
B. Combination of discontinuous sections
W(A-B)
W(B-C)
W(C-D)
W(A-D)

[Fig. 13]


A. Value for relative binding energy
0 20 40 60 80
0.0 0.2 0.4 0.6 0.8 1.0
W1
B. Number of A/U among 3'-end nucleotides
0 20 60 100
0.0 0.2 0.4 0.6 0.8 1.0
W2
C. G/C at 1st binding energy position
0 20 40 60 80
0.0 0.2 0.4 0.6 0.8 1.0
W3
D. A/U at 19th binding energy position
0 20 40 60
0.0 0.2 0.4 0.6 0.8 1.0
W4
E. G/C content
0 20 60 100
0.0 0.2 0.4 0.6 0.8 1.0
W5

Sequence Listing

<110> BIONEER CORPORATION

<120> Method of Inhibiting Expression of Target mRNA Using siRNA Consisting of Nucleotide Sequence Complementary to Said Target mRNA

<160> 72

<170> KopatentIn 1.71

<210> 1
<211> 208
<212> DNA
<213> Homo sapiens

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gttccaaaaa cagtggataa ttttgtggcc ttagctacag gagagaaagg atttggctac 60

aaaaacagca aattccatcg tgtaatcaag gacttcatga tccagggcgg agacttcacc 120

aggggagatg gcacaggagg aaagagcatc tacggtgagc gcttccccga tgagaacttc 180

aaactgaagc actacgggcc tggctggg 208

<210> 2
<211> 200
<212> DNA
<213> Drosophila sp.

<400> 2
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cgtggattac gtcgccagtc aagtaacaac cgcgaaaaag ttgcgcggag gagttgtgtt 120

tgtggacgaa gtaccgaaag gtcttaccgg aaaactcgac gcaagaaaaa tcagagagat 180

cctcataaag gccaagaagg 200

Sequence Listing

<210> 3
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 3
caaaaacagt ggataattt 19

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 27 position of Seq. ID. No. 1

<400> 4
ggccttagct acaggagag 19

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 35 position of Seq. ID. No. 1

Sequence Listing

<400> 5
ctacaggaga gaaaggatt 19

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 41 position of Seq. ID. No. 1

<400> 6
gagagaaagg atttggcta 19

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 43 position of Seq. ID. No. 1

<400> 7
gagaaaggat ttggctaca 19

<210> 8
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at

Sequence Listing

45 position of Seq. ID. No. 1

<400> 8
gaaaggattt ggctacaaa 19

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
acagcaaatt ccatcgtgt 19

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 10
caaattccat cgtgtaatc 19

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

Sequence Listing

<220>
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<400> 11
tcatgatcca gggcggaga 19

<210> 12
<211> 19
<212> DNA
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<220>
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<400> 12
gatccagggc ggagacttc 19

<210> 13
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 131 position of Seq. ID. No. 1

<400> 13
gcacaggagg aaagagcat 19

<210> 14

Sequence Listing

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 139 position of Seq. ID. No. 1

<400> 14
ggaaagagca tctacggtg 19

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> functional siRNA sequence for human cyclophilin gene starting at 159 position of Seq. ID. No. 1

<400> 15
gcgcttcccc gatgagaac 19

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 16
aaaacagtgg ataattttg 19

Sequence Listing

<210> 17
<211> 19
<212> DNA
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<220>
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<400> 17
aacagtggat aattttgtg 19

<210> 18
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 18
cagtggataa ttttgtggc 19

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 17 position of Seq. ID. No. 1

Sequence Listing

<400> 19
ataattttgt ggccttagc 19

<210> 20
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 23 position of Seq. ID. No. 1

<400> 20
ttgtggcctt agctacagg 19

<210> 21
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 31 position of Seq. ID. No. 1

<400> 21
ttagctacag gagagaaag 19

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

Sequence Listing

<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 51 position of Seq. ID. No. 1

<400> 22
atttggctac aaaaacagc 19

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 61 position of Seq. ID. No. 1

<400> 23
aaaaacagca aattccatc 19

<210> 24
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 63 position of Seq. ID. No. 1

<400> 24
aaacagcaaa ttccatcgt 19

<210> 25
<211> 19
<212> DNA

Sequence Listing

<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 73 position of Seq. ID. No. 1

<400> 25
ttccatcgtg taatcaagg 19

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 97 position of Seq. ID. No. 1

<400> 26
atgatccagg gcggagact 19

<210> 27
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 101 position of Seq. ID. No. 1

<400> 27
tccagggcgg agacttcac 19

Sequence Listing

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 103 position of Seq. ID. No. 1

<400> 28
cagggcggag acttcacca 19

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 113 position of Seq. ID. No. 1

<400> 29
acttcaccag gggagatgg 19

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 115 position of Seq. ID. No. 1

<400> 30

Sequence Listing

ttcaccaggg gagatggca 19

<210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 119 position of Seq. ID. No. 1

<400> 31
ccaggggaga tggcacagg 19

<210> 32
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 149 position of Seq. ID. No. 1

<400> 32
tctacggtga gcgcttccc 19

<210> 33
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 151 position of Seq. ID. No. 1

Sequence Listing

<400> 33
tacggtgagc gcttccccg 19

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 171 position of Seq. ID. No. 1

<400> 34
tgagaacttc aaactgaag 19

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 173 position of Seq. ID. No. 1

<400> 35
agaacttcaa actgaagca 19

<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

Sequence Listing

<220>

<223> nonfunctional siRNA sequence for human cyclophilin gene starting at 179 position of Seq. ID. No. 1

<400> 36

tcaaactgaa gcactacgg 19

<210> 37

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> siRNA specific for survivin mRNA

<400> 37

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<210> 38

<211> 19

<212> RNA

<213> Artificial Sequence

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<400> 38

agaauagcac aaacuacaa 19

<210> 39

<211> 19

<212> RNA

<213> Artificial Sequence

Sequence Listing

<220>
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<400> 39
gagacagaau agagugaua 19

<210> 40
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
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<400> 40
gcgucuggca gauacuccu 19

<210> 41
<211> 19
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<220>
<223> siRNA specific for survivin mRNA

<400> 41
ugcgcuuucc uuucuguca 19

<210> 42
<211> 19
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<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 42
gaagcaguuu gaagaauua 19

<210> 43
<211> 19
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<220>
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<400> 43
ugucuuagga aaggagauc 19

<210> 44
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
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<400> 44
ggcagugucc cuuuugcua 19

<210> 45
<211> 19
<212> RNA
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Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 45
aauucacaga auagcacaa 19

<210> 46
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<213> Artificial Sequence

<220>
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<400> 46
aagcacaaag ccauucuaa 19

<210> 47
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<213> Artificial Sequence

<220>
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<400> 47
ggcaguggcc uaaauccuu 19

<210> 48
<211> 19
<212> RNA
<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 48
ggcugaaguc uggcguaag 19

<210> 49
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 49
gcugaagucu ggcguaaga 19

<210> 50
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 50
cggcuguucc ugagaaaua 19

<210> 51
<211> 19
<212> RNA
<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 51
aaggaccacc gcaucucua 19

<210> 52
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 52
ggaccaccgc aucucuaca 19

<210> 53
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 53
ccgguugcgc uuuccuuuc 19

<210> 54
<211> 19
<212> RNA
<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 54
gcugcuucuc ucucucucu 19

<210> 55
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 55
gugaugagag aauggagac 19

<210> 56
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 56
ggagacagaa uagagugau 19

<210> 57
<211> 19
<212> RNA
<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 57
ccuucacauc ugucacguu 19

<210> 58
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 58
gauuguuaca gcuucgcug 19

<210> 59
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> siRNA specific for survivin mRNA

<400> 59
ucaaggacca ccgcaucuc 19

<210> 60
<211> 19
<212> RNA
<213> Artificial Sequence

Sequence Listing

<220>
<223> siRNA specific for survivin mRNA

<400> 60
gaccaccgca ucucuacau 19

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/KR2005/004207

A. CLASSIFICATION OF SUBJECT MATTER

C12Q 1/68(2006.01)i

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)

IPC8 C12Q 1/68

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

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

NCBI PubMed, e-KIPASS, delphion "siRNA, design, mRNA, binding energy, etc."

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Wenwu Cui, et al., 'OptiRNAi, an RNAi design tool', In: Computer Methods and Programs in Biomedicine, Vol.75(1), pp.67-73 (2004)	1 - 16
A	WeiPing Chen, et al., '3Si: A computer program for the optimal design of short interfering RNA(siRNA) for gene silencing', In: Proceedings of the 17th IEEE Symposium on Computer-Based Medical Systems (CBMS'04), pp.335-342 (24-25 June 2004)	1 - 16
A	WeiPing Chen, et al., 'Identification of highly significant sequence patterns in siRNAs for the optimal design of siRNA', In: Proceedings of the 17th IEEE Symposium on Computer-Based Medical Systems (CBMS'04), pp.343-350 (24-25 June 2004)	1 - 16
A	Ola Snove Jr., et al., 'Designing effective siRNAs with off-target control', In: Biochemical and Biophysical Research Communications, Vol.325, pp.769-773 (online 06 Nov. 2004)	1 - 16
A	Angela Reynolds, et al., 'Rational siRNA design for RNA interference', In: Nature Biotechnology, Vol.22(3), pp.326-330 (Mar. 2004) cited in the application	1 - 16
A	Anastasia Khvorova, et al., 'Functional siRNAs and miRNAs exhibit strand bias', In: Cell, Vol.115, pp.209-216 (10 Oct. 2003)	1 - 16

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of 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
"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
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"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
31 MARCH 2006 (31.03.2006)	**31 MARCH 2006 (31.03.2006)**

Name and mailing address of the ISA/KR
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Republic of Korea
Facsimile No. 82-42-472-7140

Authorized officer
SHIN, Kyeong A
Telephone No. 82-42-481-5589

INTERNATIONAL SEARCH REPORT

International application No.
PCT/KR2005/004207

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of :

   a. type of material
      - [x] a sequence listing
      - [x] table(s) related to the sequence listing

   b. format of material
      - [x] on paper
      - [x] in electronic form

   c. time of filing/furnishing
      - [x] contained in the international application as filed
      - [x] filed together with the international application in electronic form
      - [ ] furnished subsequently to this Authority for the purposes of search

2. [ ] In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments: