



(54)

- -

, Canlon - Canlon DNA, cDNA, . Canlon , , .

1

, Canlon ( , ) 5'- 3'- Canlon . Canlon .

가 가 (CNS) 가 가 , CNS .

CNS . CNS . CNS . Diagnosis Statistical Manual of Mental Di sorder fourth edition(DSM- )

CNS 가 가 .

2000 . Na+ - Ca+ -1 . Na+ Ca+ 가 ( -2, , 2 ) Ca+ -1 ( ) 4 ( ) 4 K+ - 1:1 K+

(Terlau et al., Naturwissenschaften 85: 437-444 (1998)).  
 Williams, et al. Science 257: 389-395 (1992); Mori, et al., Nature 350: 398-402 (1991)  
 ; Koch, et al., J.Biol.Chem. 265 (29): 17786-17791 (1990) . Canlon  
 Ca+ Na+ Lee et al., FEBS Lett. 445 231:236 (1999)

(spanning) 6 -  
 4  
 24 - ( , ) ,  
 가 , , 4  
 .가 , -1 7 ( )  
 1 A H ) -1  
 -1A -1B , -1A가 -1B  
 (neuromuscular junction) , -1A가  
 (Schwann cell) -1B -1A가 -1E  
 (Purkinje cell) 가  
 -1C -1D  
 /  
 : L-, N-, P-, Q- (HVA); (IVA, R- ); - (L  
 VA, T- )(Morena et al., Annals NY Acad. Sci. 102-117(1999)).

( -1)  
 (Zhang et al., Neuropharmacology 32(11): 1075-1088(1993). , -1 -1

-1 ;  
 가 ,  
 -1  
 (Hell et al., Annals N.Y. Acad. Sci. 747: 282-293(1994)).

QT  
 Bulman et al., Hum. M  
 A ( )  
 Ca+  
 ol. Gen. 6(10) 1679-1685(1997)  
 Moreno, supra).

A

가	-1A	
2	-1A	
6	-1A	
(Tottering) (Learner)	-1A	
-	-1A, -1B	
	-1S	
	-1S	
Zucker	-1C; -1D	
	-4	
	-2/	
가 (Stargazer)		

NS  
 가  
 가  
 가

Canlon  
 Canlon  
 (5' ) (3' )  
 Canlon  
 cDNA  
 Canlon  
 cDNA  
 DNA  
 가  
 Canlon  
 Canlon

Canlon  
 Canlon  
 Canlon  
 가 , Canlon

SEQ ID NO 1 4 6  
 SEQ ID NO 4 50  
 Canlon  
 SEQ ID NO 5  
 Canlon

(address)가  
 가  
 가  
 Canlon  
 Canlon  
 Canlon

Canlon  
Canlon

가

가

(knock out)

Canlon

SEQ ID NO 5

a)

가  
; b)

; c)

Canlon

-Canlon

Canlon

가

, Canlon

Canlon

Canlon

;

ii)  
; b)

Canlon

a) i)

가

RNA

Canlon

가

-Canlon

Canlon

가

; b)

a)

Canlon

Canlon

Canlon

가 가

Canlon

Canlon

Canlon

가

; b)

a)

C

anlon

Canlon

a)

가

가

Canlon

; b)

Canlon

가

Canlon









50%, 60 75% 가 5  
 0%, 60 90%, 95%, 가 99% w/w  
 가 HPLC 가  
 ) (DNA, RNA  
 %, 90%, 95%, 96%, 96%, 98%, 99%, 100% 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80  
 ( , 99.995% 90% 100% 1/1000  
 w/w 1/1000 %

( , - ),

2 , 가 ( , , , , )

(folding) 가  
 Fab, Fab', F(ab)<sub>2</sub>, F(ab')<sub>2</sub>  
 Canlon  
 3 6  
 8-10 ; 2- ; Geysen et al. 1984; PCT WO 84/03564; PCT  
 WO 84/03506 ; Pepscan

가 DNA RNA ( , 4  
 ) RNA, DNA, RNA/DNA RNA, DNA, RNA/DNA

(a) , (b) , (c)  
 (d) '가 ( : WO95/04064).  
 , *ex vivo*

RNA 가 가 가 가

가 , 가 가 , 가 ,  
CNS ; , ,

(heterozygosity rate)  
 $2P_a(1-P_a)$  가  $P_a$  가

Canlon (genotyping)

1% DNA

ymorphic) 2 가 2 가 (pol 가

가 가 가 가

20% ( 0.32 가 30% ), 가 1% 30% ( 0.42 가 10% )

가 3' 5'

1 2 가 1 5 가 2 가 4 가

3' 5' 가 0 1 가 0 3 , 1 2 가 0 5 , 2 1

가 0 7 , 3 , 5' , DNA 2 (Str

Watson amp; Crick , 3 ,

yer, L., Biochemistry, 4<sup>th</sup> edtion, 1995)

Watson amp; Crick 가

A T( A U), C G . 2 가 , , ,

Canlon

SEQ ID No 1 4 95%

SEQ ID No 1 4 12 99%

SEQ ID No 1 4 12 99.5%

가 99.8% , 가 , 가 , 가

Canlon 가

Canlon Canlon A17 가 A1 가 A1

(free-standing)',

8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 1000 A1 A17

가 Canlon

2-\_\_\_\_\_

Canlon  
 가 - 가  
 ; 3) Canlon 가 ( , Ca  
 ) ; 4) 가 Canlon, Ca  
 nlon (preprotein)  
 Canlon  
 가 ' 가 ' 가 ' 가 '  
 (hydropathic)  
 가 : (1) Ala,  
 Pro, Gly, Glu, Asp, Gln, Asn, Ser, Thr; (2) Cys, Ser, Tyr, Thr; (3) Val, Ile, Leu, Met, Ala, Phe; (4) Lys, Arg, H  
 is; (5) Phe, Tyr, Trp, His.

Canlon -C  
 ONH- (CH2NH) , (NHCO) , (CH2-O) , (C  
 H2-S) , (CH2CH2) , (CO-CH2) , (CHOH-CH2) , (C  
 (N-N) , E- -CH=CH 가 , ,  
 가 Canlon  
 가 (free-standing)',  
 55 5, 6, 7, 8, 9, 10 15, 10 20, 15 40, 30  
 , Canlon

' %' ' %'  
 2  
 가 ( , ) % ( 가 ) 가  
 가 100  
 가 TBLASTN, BLASTIP, FASTA, TFASTA, CLUSTALW (Pearson  
 and Lipman, 1988; Altschul et al., 1990; Thompson et al., 1994; Higgins et al., 1996; Altschul et al., 1990; Al  
 tschul et al., 1993)  
 Basic Local Alignment Tool('BLAST') 가 (Karlin and Altschul, 1990; Altschul  
 et al., 1990 1993, 1997).

, 5 BLAST :  
 (1) BLASTP BLAST3 ;  
 (2) BLASTN ;  
 (3) BLASTX ( 가 ) 6 - ;

(4) TBLASTN 6 ( 가 )

(5) TBLASTX 6 - 6 -

BLAST

가 ( , )  
 BLOSUM62 (Gonnet et al., 1992; Henikoff and Henikoff, 1993) , P  
 AM PAM250 (Schwartz and Dayhoff, eds., 1978). BLAST  
 가 , 가 -  
 % Karlin  
 (Karlin and Altschul, 1990) 가 .

BLAST 가 .

6 x SSC , 5 x , 0.5% SDS, 100µg/Mℓ DNA 65

4가 :

- 2 x SSC 0.1% SDS 65 5 2 ;
- 2 x SSC 0.1% SDS 65 30 1 ;
- 2 x SSC 0.1% SDS 65 10 1 .

20

. 가 , Hames Higgins(1985)

Canlon

Canlon , Canlon 가 , SEQ ID No 1 3 Ca  
 , SEQ ID No 1 3 70, 75, 80, 85, 90 95%  
 가 , SEQ ID No 1 3  
 가 Canlon , Canlon  
 SEQ ID No 1 3 ,  
 Canlon Canlon  
 Canlon Canlon  
 , 500 1000 SEQ ID No 1 3 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250 가 .

B

엑손	SEQ ID No 1에서 위치		인트론	SEQ ID No 1에서 위치	
	시작	종결		시작	종결
1	2001	2026	1	2027	19187
2	19188	19334	2	19335	22995
3	22996	23178	3	23179	39730
4	39731	39814	4	39815	41336
5	41337	41476	5	41477	41564
6	41565	41693	6	41694	73012
7	73013	73167			

엑손	SEQ ID No 2에서 위치		인트론	SEQ ID No 2에서 위치	
	시작	종결		시작	종결
8	43726	43868	7	43869	43997
9	43998	44102	8	44103	52092
10	52093	52179	9	52180	77567
11	77568	77699	10	77700	98225
12	98226	98393	11	98394	106566
13	106567	106758	12	106759	144108
14	144109	144246	13	144247	159793
15	159794	159868	14	159869	191291
16	191292	191428	15	191429	192966
17	192967	193108	16	193109	211539
18	211540	211613	17	211614	225005
19	225006	225107	18	225108	225543
20	225544	225613	19	225614	228449
21	228450	228541	20	228542	228629
22	228630	228752	21	228753	231288
23	231289	231345	22	231346	231588
24	231589	231709	23	231710	231812
25	231813	231944	24	231945	232899
26	232900	233067	25	233068	235354
27	235355	235459			

엑손	SEQ ID No 3에서 위치		인트론	SEQ ID No 3에서 위치	
	시작	종결		시작	종결
28	3895	4001	26	4002	9610
29	9611	9731	27	9732	9815
30	9816	9914	28	9915	15775
31	15776	15869	29	15870	16381
32	16382	16488	30	16489	16696
33	16697	16771	31	16772	17933
34	17934	18053	32	18054	23643
35	23644	23712	33	23713	24927
36	24928	25076	34	25077	25912
37	25913	26006	35	26007	30766
38	30767	30899	36	30900	31560
39	31561	31676	37	31677	34043
40	34044	34201	38	34202	37492
41	37493	37643	39	37644	39651
42	39652	39801	40	39802	41562
43	41563	41680	41	41681	44130
44	44131	45841			

Canlon 44 가 Canlon 2  
 SEQ ID No 1 3  
 5' 3'  
 1 1 2 A  
 Canlon 43 가  
 Canlon Canlon 2

**Canlon cDNA**

Canlon 가 mRNA SEQ ID No 4  
 SEQ ID No 4  
 Canlon cDNA가 SEQ ID No 4  
 SEQ ID No 4  
 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, 1000 (s)  
 pan) 가  
 A12 A16 Canlon-  
 SEQ ID No 4 95% 99%  
 99.5% 가 99.8%  
 SEQ ID No 4  
 SEQ ID No 5 6 Canlon  
 SEQ ID No 5  
 277, 338, 574, 678, 680, 683, 691, 692, 695, 696, 894, 1480, 1481, 1483, 1484, 1485, 1630, 1631, 1632, 1636, 1660, 1667, 1707, 1709 1, 2, 3, 5 10 SEQ ID No 5  
 SEQ ID No 5  
 80, 85, 90, 95, 98, 99, 99.5 99.8% Canlon

가

SEQ ID No 4 cDNA SEQ ID No 4 1 65  
5'-UTR . SEQ ID No 4 cDNA 5283 6799  
3'-UTR

Canlon cDNA 5'UTR

Canlon cDNA 3'UTR

Canlon cDNA

Canlon

2

Canlon SEQ ID No 4 cDNA mRNA Canlon  
(CDS) SEQ ID No 4 66 (ATG ) 5282  
(TGA ) SEQ ID No 5 6  
8 10 12, 15, 20, 25, 30, 40, 50, 100

Canlon

Canlon

/

Canlon

Canlon

44

Canlon

5-

3-

5' 3'  
1

Canlon

Canlon

5'

가

SEQ ID No 1  
( , )  
rook et al.(Sambrook, 1989)

)

SEQ ID No 1

Samb

EP-1  
(Promega)

(Clontech);

Canlon  
pSEAP-Basic, pSEAP-Enhancer, p gal-Basic, p gal-Enhancer, pEG  
pGL2-Basic, pGL3-Basic - 가 ,

Canlon

가

가

가

DNA

DNA

(nested) 5' / 3'

III

가

(Coles et al.(19

98)).





(ii) 5' 95%

(iii) 5'

(iv) ( ), ( ), ( )

b) (a) 가 ;

c) , 3'- Canlon 3'-

Canlon cDNA 5'- (5'-UTR),

Canlon cDNA 3'- (3'-UTR),

5'- (5'-UTR)

5'- 가

3'- (3'-UTR)

3'- 가

. Canlon

SEQ ID No 5

( , )

Canlon

RNA

Canlon

2

Canlon

DNA

Canlon

Canlon cDNA

SEQ ID No 1

4 Canlon

가

DNA 5'-

, Canlon

가

가

SEQ ID No 4

Canlon cDNA 가 Canlon cDNA

, Canlon  
A1 A17 가 , Canlon  
가  
'Canlon ' , 'Canlon cDNA ' , '  
DNA Gossen et al.(1992, 1995) Furth et al.(1994) Canlon  
( *E. Coli* ) Tn10 tet (tetop) , tet  
DNA Tn10 7 Canlon  
5'- Canlon  
가 DNA 가 HCMVIE1 /  
MMTV-LTR (rTA) VP16 (t  
TA) DNA , tet  
tTA rTA  
DNA rTA  
가 DNA :  
DNA 5'- 3'- : (a) Canlon  
1 ; (b) (positive) , (neo)  
; (c) Canlon (a) Canlon 2  
DNA (a) (c) (tk) (Thomas et al., 198  
6), (Te Riele et al., 1990), hprt (Van der Lugt et al., 1991; Reid et al., 1990)  
A (Dt-A) (Nada et al., 1993; Yagi et al. 1990)  
Canlon Canlon  
Thomas et al.(1986; 1987); Mansour et al.,(988); Koller et al.(1992)  
1 2 (a) (c) Canlon , , ,  
/ 50kb, 1 10kb, 2 6kb, 가 2 (a) (c) 1  
가 DNA : Cre-LoxP  
DNA P1 P1 34 loxP  
Cre 2 (recombinase) . loxP 8bp  
13bp DNA 2 (Hoess et al., 1986). 2 loxP Cre  
Cre-loxP Gu et al.(1993, 1994)  
2 loxP  
( Cre ) (a) Araki et al.(1995) Cre  
Baubonis et al.(1993)  
; (b)  
가 Cre  
; (c) Gu et al.(1993) Sauer et al.(1988)  
가 Cre  
Gu et al.(1994)

xP가 , Canlon 가 lo  
가 , Cre , 2 가 : Canlon  
Cre-loxP Zou et al.(1994)

DNA 5'- 3'- : (a) Canlon  
1 ; (b) loxP 2  
Canlon 가 , ; (c) Canlon (a)  
2

loxP (b) , 2 loxP  
가

DNA loxP 가 Gu et al.(1994)  
가 , - 가 Cre

Cre Gu et al.(1994) 1 2  
가 loxP Cre Canlon- 2

Cre - Graham(1995) Kanegae et al.(1995) Cre  
in vivo , Cre 가

DNA Canlon cDNA Canlon Canlon cDNA , 가  
) Canlon Canlon cDNA DNA 1 (

DNA

lon SEQ ID No 4 Canlon Canlon  
Sczakiel et al.(1995)

WO 95/24223 Canlon mRNA 5' (15-200bp)

mRNA ATG Canlon Canlon mRNA

3' Liu et al.(1994) 가- RNA II 3' poly(A)가 , Ec  
Canlon

kner et al.(1991) 3'-5'

Canlon , SEQ ID No 1 4 6 ,  
 , 1 .

60, 70, 80, 90, 100, 150, 200, 500, 1000 SEQ ID No 1 3 12, 15, 18, 20, 25, 30, 35, 40, 50, 2000  
 , A1 A17 , ,

SEQ ID No 4 , , ,  
 , , Canlon cDNA , SEQ ID 4  
 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, 1000 , 2000, 3000, 4000, 5000  
 6000

SEQ ID 4 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, 1000 , 2000, 3000, 4000, 5000 6000  
 A1 A17 , ,

SEQ ID 6 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 300 400 ,  
 , SEQ ID No 6 , A18 ,

SEQ ID No 1 3 Canlon ,  
 , ,

SEQ ID No 1 4 6 가 8 50  
 가 , Canlon-  
 , Canlon- A1 A18 35 ,  
 25 3' 3' ; , 3' ,  
 3' ; , 3' ,  
 : P1 P18 .

SEQ ID No 1 4 8 50  
 가 , Canlon- 3'  
 20 3' ; , Canlon- A1 A18 3'  
 , Canlon- ; , ; ,  
 : D1 D18 E1 E18 1 .

가 : B1 B17 C1 C17 ,  
 , , SEQ ID No 1 4 6 Canlon-  
 ,  
 SEQ ID No 1 4 6 Canlon-  
 가 .  
 ,  
 Canlon- ,  
 , Canlon-

25, 35, 40, 50, 60, 70, 80, 90, 100, 250, 500, 1000  
8, 10, 15, 20 30 100, 10 50, 15 30  
8 1000 , , 12, 15, 18, 20,

가-  
가 가  
E18 1, 2, 3 P1 P18 , B1 B17, C1 C17, D1 D18, E1

C DNA (Tm) . Tm , G+  
G+C , G:C 3  
A:T 2 GC 10 75%,  
35 60%, 40 55% .

Narang et al.(1979)

, Brown et al.(1979)

, Beaucage et al.(1981)

, EP 0 707 592

WO 92/20702

가 가 , 5, 185,44; 5,034,506, 5,142,047 . dNTP가  
가 가 ' - 가 ' . - 가 , 3'  
3' , 가 , 3'  
(U.S. Patent No. 07/049,061, filed April 19, 1993).

( , <sup>32</sup> P, <sup>35</sup> S, <sup>3</sup> H, <sup>125</sup> I),

( , 5-

3' 5'

No. FR-7810975,

Urdea et al(1988); Sanchez- Pescador et al.(1988)

Urdea et al.(1991) EP 0 225

807 (Chiron)

DNA

DNA

(

DNA

가 , 가,

가

가

. DNA

DNA

PCR

Canlon

mRNA

Canlon

( , 가 ), ( ) , (duracyte)

가 , ( ) ,

가

. 가

( )

가

가 , , , , ( ) , , 2, 5, 8, 10, 12, 15, 20 25

SEQ ID No 1 4 6,

a) SEQ ID No 1 4 6 , ;

b)

SEQ ID No 1 4 6,

a) SEQ ID No 1 4 6, ;

b)

가

C17, D1 D18, E1 E18 , P1 P18 , B1 B17, C1 , A1 A18

Canlon

, Canlon

가 (addressable) ,  
가

가

가 Genechips™ , US Patent 5,143,854; PCT WO 90/15070 92/10092

or et al., 1991). 'Very Large Scale Immobilized Polymer Sy  
nthesis'(VLSIPS™) 가 US Patent 5,143,854; 5,412,087; PCT WO 90/15070; WO 92/10092; WO 9  
VLSIPS™ 5/11995

가 PCT WO 94/12305; WO 94/11530; WO 97 /29212; WO 97/31256

Canlon

( , 가)  
 n et al.(1996) Canlon Huang et al.(1996) Sams  
 Canlon DNA DNA  
 Canlon DNA cDNA  
 Canlon  
 4L (tiled) 4 (A, C, G, T), 15  
 L 4L 가 . 15-mer  
 (footprint)'가 Chee et al.(1996)

2  
 P1 P18, B1 B17, C1 C17, D1 D18, E1 E18,  
 8, 10, 12, 15, 18, 20, 25, 30 40 가 A1 A18  
 P1 P18, B1 B17, C1 C17, D1 D18, E1 E18,  
 8, 10, 12, 15, 18, 20, 25, 30 40 가 A1 A18  
 2가

**Canlon**

'Canlon 가  
 SEQ ID No 5 Canlon Canlon  
 SEQ ID No 1 4 6  
 SEQ ID No 5 6 8 10  
 12, 15, 20, 25, 30, 40, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 1200, 1400, 1600 1700  
 가  
 Canlon 가,  
 SEQ ID No 5 6 8 10  
 12, 15, 20, 25, 30, 40, 50, 100, 150, 200, 300, 400, 500, 700, 1000, 1200, 1400, 1600 1700  
 가  
 277, 338, 574, 678, 680, 683, 691, 692, 695, 696, 894, 1480, 1481, 1483, 148  
 4, 1485, 1630, 1631, 1632, 1636, 1660, 1667, 1707, 1709 1, 2, 3, 5 10  
 , SEQ ID No 5 277 ; 338 ; 574 ; 678  
 ; 680 ; 683 ; 691 ; 692  
 ; 695 ; 696 ; 894 ; 1480  
 ; 1481 ; 1483 ; 1484 ; 1485  
 ; 1630 ; 1631 ; 1632 ; 1  
 636 ; 1660 ; 1667 가 ; 1707  
 ; 1709



SEQ ID No 5

70, 75, 80, 85, 90, 95, 98 99%

가

Canlon

가

Canlon

가

(chaotropic)

가

SEQ ID No 4 on

Canlon cDNA

Canlon

Canlon

Canlon

Canlon 가

Genetics Institute(Cambridge, MA), Stratagenen(La Jolla, California), Promega (Madison, Wisconsin), Invitrogen (San Diego, California)

(U.S. Patent No. 5,082,767).

cDNA

A

Canlon cDNA

가

Canlon

1

Canlon cDNA

A

가

BglI Sall

, Ca

pSG5(Stratagene)

가 pXT1

LRT

A

Moloney

pXT1(Stratagene)

LTR

가

ID No 5

Canlon cDNA

5'

Canlon

Pst I

cDNA 3'

5'

SEQ Bgl

, Canlon cDNA

PCR

Canlon

A

PCR

Pst I

Bgl

Bgl

A

pXT1

(Life Technologies, Inc., Grand Island, New York)

NIH 3T3 (Sigma, St. Louis, Missouri)

(transfectant)

600ug/M $\ell$  G418

가

Canlon

Canlon

가

Canlon

Canlon

, Canlon

가

가

Canlon

Canlon

가

Canlon

가 , Canlon

Canlon

Canlon

pSG5(Stratagene) ,

II

가

Davis et al.,(19 Promega

86) 가 , Stratagene, Life Technologies, Inc., In vitro Express™ Translation Kit(Stratagene)

Canlon

Canlon

Canlon

SEQ ID No 5 Canlon

1

ELISA, RIA

. Canlon Canlon

2

Canlon

1

5%, 10%, 15%, 20%, 25%, 50% Canlon

100%

SEQ ID No 5

6

8

10

12, 15, 20, 25, 30, 40, 50, 100, 200, 300, 400, 500, 700

1000

SEQ ID No 5

277, 338, 574, 678, 680, 683, 691, 692, 695, 69

6, 894, 1480, 1481, 1483, 1484, 1485, 1630, 1631, 1632, 1636, 1660, 1667, 1707, 1709

1, 2, 3, 5

10

Canlon

Canlon

3

6

8-10

3

50

PROTEAN Jameson-Wolf

(Version 4.0 Windows, DNAST

AR, Inc., 1228 South Park Street Madison, WI)

Canlon

Canlon

Canlon

10

1

Canlon

Canlon

( , Canlon )

. Canlon

Canlon

가,

10 30

Canlon

가

anlon lon 가 Canlon C Can

Canlon

a) SEQ ID No 5 Canlon

b) Canlon

a) SEQ ID No 5 Canlon

b) 가 가

gG2, IgG3, IgG4 T- (TCR) IgG(IgG1, I

vs(sdFv), V<sub>L</sub> Fab, Fab', F(ab)2, F(ab')2, Fd, Fvs(scFv), F

가 가 , CH1, CH2, CH3 , CH1, CH2, CH3

가

( : WO 93/17715; WO 92/08802; WO 91/00 360; WO 92/05793; Tutt, A. et al.(1991) J. Immunol. 147:60-69; US 5,573,920, 4,474,893, 5,601,819, 4, 714,681, 4,925,648; Kostelny, S.A. et al.(1992) J. Immunol. 148:1547-1553).

N- C-

가

(ortholog)

95% , 90% , 85% , 80% , 75% , 70% , 65% , 60% , 55% , 50%  
( )

가  
(Kd)가  $5 \times 10^{-6} M$ ,  $10^{-6} M$ ,  $5 \times 10^{-7} M$ ,  $10^{-7} M$ ,  $5 \times 10^{-8} M$ ,  $10^{-8} M$ ,  $5 \times 10^{-9} M$ ,  $10^{-9} M$ ,  $5 \times 10^{-10} M$ ,  $10^{-10} M$ ,  $5 \times 10^{-11} M$ ,  $10^{-11} M$ ,  $5 \times 10^{-12} M$ ,  $10^{-12} M$ ,  $5 \times 10^{-13} M$ ,  $10^{-13} M$ ,  $5 \times 10^{-14} M$ ,  $10^{-14} M$ ,  $5 \times 10^{-15} M$ ,  $10^{-15} M$

가 ,  
(Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

N- C-  
( )  
가 ,  
(WO 92/08495; WO 91/14438; WO 89/12624; US Patent 5,314,995; EP 0 396 387).

가 ,  
(folding)  
3

가  
(Harlow et al.(1988); Hammerling, et. al.(1981)). Fab F(ab')2  
(Fab ) (F(ab')2 )

DNA 가 ,  
( , )  
III VII Fab, Fv Fv  
fd M13

Brinkman U. et al.(1995); Ames, R.S. et al.(1995); Kettleborough, C.A.. et al. (1994); Persic, L. et al.(1997); Burton, D.R. et al.(1994); PCT/GB91/01134; WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; US Patents 5,698,426, 5,223,409, 5,403,484, 5,580,717, 5,427,908, 5,750,753, 5,821,047, 5,571,698, 5,427,908, 5,516,637, 5,780,225, 5,658,727, 5,733,743

가 , Fab, Fab'F(ab)2, F(ab')2  
(WO 92/22324; Mullinax, R.L. et al.(1992); Sawai, H. et al.(1995); Better, M. et al.(1988)).

Fvs U.S. Patents 4,946,778 5,258,498; Huston et al.(1991); Shu, L. et al.(1993); Skerra, A. et al.(1988)

(Morrison(1985);  
Oi et al.,(1986); Gillies, S.D. et al.(1989); US Patent 5,807,715). CDR- ( )  
EP 0 239 400; WO 91/09967; US Patent 5,530,101; 5,585,089), (veneering) (resurfacing)(EP 0 592 106; EP 0 519 596; Padlan E.A.,(1991); Studnicka G.M. et al.(1994); Roguska M.A. et al.(1994)),  
(shuffling)(US Patent 5,565,332)

(US Patents 4,444,887, 4,716,111, 5,545,806, 5,814,318;

WO 98/46645; WO 98/50433; WO 98/24893; WO 96/34096; WO 96/33735; WO 91/10741).

가 (가 ,  
 ) 가 .  
 가 .  
 (Harbor et al. supra  
 and WO 93/21232; EP 0 430 095; Naramura M. et al.(1994); US Patent 5,474,981; Gillies, S.O. et al.(1992);  
 Fell, H.P. et al.(1991)).

가 , Fc , CH1 , CH2 , CH3 , 가  
 Fc , 가 , Fc  
 Fc IgA IgM  
 (US Patents 5,336,603, 5,622,929, 5,359,046, 5,349,053, 5,447,851, 5,112,  
 946; EP 0 307 434, EP 0 367 166; WO 96/04388, WO 91/06570; Ashkenazi A. et al.(1991); Zheng, X.X. et al.  
 (1995); Vil, H. et al.(1992)).

가 ,  
 가  
 /  
 가 . ( , )  
 가  
 가  
 가  
 (WO 96/40281;  
 US Patent 5,811,097; Deng B. et al.(1998); Chen, Z. et al.(1998); Harrop J.A. et al.(1998); Zhu, Z. et al.(1998  
 ); Yoon, D.Y. et al.(1998); Prat, M. et al.(1998); Pitard, V. et al.(1997); Liautard, J. et al.(1997); Carlson, N.G.  
 et al.(1997); Taryman, R.E. et al.(1995); Muller, Y.A. et al(1998); Bartunek, P. Et al.(1996)).

(Greenspan and Bona, (1989); Nissinoff, (1991)). 가 ,  
 (multimerization)

**Canlon-**

Canlon-	RFLP( )	VNTR( )
1 RFLP (microsatellite) 5-50	2 가 가	RFLP VNTR (minisatelli) 0.1 20 Kilobase DNA 가 , 10 <sup>4</sup> VNTR
가, RELP VNTR		

가 . SNP 3x10<sup>9</sup> , RELP VNTR 가 , SNP RFLP VNTR 가 10<sup>7</sup>

가 , 2 , (genotyping) 가 가

가 (polygenic) ( ) 가

가 가 , Canlon

**Canlon-**

Canlon- 'Canlon- ' Ca A1

Canlon- Canlon-

가 2 1 4 6 가

가 Canlon 2 1

17 Canlon- , A1 A17 Canlon A1

2 A16 Canlon A18 Canlon

Canlon- /

Q ID 1 4 6, A1 A18, SE

8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 60, 70, 80, 100, 250, 500, 1000

1 2 가 6, 5, 4, 3, 2, 1 3'

3' 가 3'

, SEQ ID 1 4 8 1000



SEQ ID 1 4 6,

8

50  
3'

3'

3'

Canlon-

B1

B17

C1

C17

. Canlon

1

3'

4

Canlon-

A1

A18

A1

A17

Canlon-

A12 A16

D1

D18

E1

E18

가

1

2

가

6, 5, 4, 3, 2, 1

P1

P18

가

가

2, 5, 8, 10, 12, 15, 20

가

25

가

가

가

Canlon-

가

가

**De Novo**

DNA

DNA

DNA

DNA

(pooling)

DNA

가

가.

가

, DNA

가



가 (informativeness) 가 10%

(penetrance) 가

DNA

가 DNA 가 , 1000 , 50 200 가 100 DNA

DNA

marrow aspirate) DNA (bone marrow aspirate) DNA 1

DNA

DNA

DNA DNA

DNA

2), (PCR, RT-PCR), (LCR(EP-A-320 308, WO 9320227, EP-A 439 18 (NASBA) (Guatelli J.C., et al.(1990); C ompton J.(1991), Q- ( No 4544610), 가 (Walker et al.(1996); EP A 684 315) (PCT WO 9322461)

LCR Gap LCR 가 (LCR) , DNA 가 DNA 가 ( 3 4) 가 , 2 ( 1 2) 가 1 2 5' -3' 가 2 , 1 2 , 가 2 가 2 , 1 2 , 2 , 3( ) 1 가 4( ) 가 , 3 4 가 , 가 , 가 , 3 4 가 , LCR 가 (WO 9320227). Gap LCR(GLCR) 가 , 2 3 LCR LCR

mRNA , mRNA cDNA ( RT-PCR), ( 5,322,770), Gap LCR(RT-AGLCR) (Marsshall et al.(1994)) . AGLCR RNA GLCR

PCR PCR (White(1997); 'PCR M methods and Application', 1991, Cold Spring Harbor laboratory Press). PCR , Pfu , Vent PCR dNTP , Taq , , , , . P

CR 4,683,195; 4,683,202; 4,965,188

PCR PCR 2 PCR

SEQ ID 4 cDNA 가 PCR Canlon , SEQ ID No 1 3 :

a) ;

b) ,

A , Canlon , SEQ ID No 1 3 : SEQ ID 4 cDN

a) Canlon ;

b) ,

1 E18 , B1 B17, C1 C17, D1 D18, E

DNA DNA 500 bp 500 bp

Canlon , 가 ,

2, 1 B1 B17 C1 C17

DNA

(Sanger ) Maxam-Gilbert DNA

DNA Sambrook et al.(1989) 가 DNA Chee et al.(1996)

, DNA (dye terminator cycle sequencing protocol)

fact) , 2 , 2 DNA 가 (background noise) (arti

가 , 2 , 100

0.1 , (pooling) 90%

0.25 , 0.9 ,

0.1 0.8 , 0.18 , 0.32 , 0.3 0.42

0.7 ,

0.1 DNA ,

가

가

1

1

가

5-6

가

1

3

가

(false negative)

가

가 2

가

가

( Bona fide )

(haplotyping),

가

가

가

가

가

가

1

20

50

가

100

가

가 30

%

(haplotyping),

가

Canlon

DNA

Canlon-

Canlon-

A1  
Ca

A18

nlon-

A1

A17

Canlon-

A12

A16

가

PCR, LCR,

가

DNA RNA

DNA

가

DNA

DNA

가

DNA  
DNA

DNA

가

가

DNA

가

DNA

가

가

2

DNA

가

가

25 bp  
100-600 bp

35 bp

25-3000 bp,

50-1000 bp,  
DNA

가

DNA

가

DNA

(DGGE),  
t al.(1992), Grompe et al.(1989 1993))

4,656,127

(SSCP)(Orita et al.(1989)),  
(Sheffield et al.(1991), White e

1)

PCR

DNA

DNA

DNA

DNA

가

2)

DNA  
 가  
 3' )  
 ddNTP( 1  
 83 , , ABI377 ddNTP EP 412 8  
 4  
 ddNTP  
 Chen and Kwok(1997) Chen et al.(1997) Taq 5'-  
 NA 1 2가  
 MALDI-TOF  
 (Haff and Smirnov, 1997).  
 가  
 가  
 5' 가  
 가  
 1  
 가  
 가  
 가  
 DNA (microtitratio  
 n)  
 ddNTP (Syvanen, 1994) (Livak and Hainer, 1994).  
 ddNTP  
 (chromogenic) ( , p- )  
 : (DNP) ddNTP -DNP  
 가 (Harju et al., 1993), ( 92/15712).  
 yren et al.(1993) (ELIDA) DNA , N  
 Pastinen et al.(1997)  
 가 (DNA ) DNA  
 가  
 D1 D18 E1 E18 4  
 , 3' 4  
 , 8, 12, 15, 20, 25, 30, 40 50  
 ( )  
 3' 가

3)

가

가 , / 가  
 가 , 가 , DNA 2가 3' (paring) 3'  
 , DNA DNA ,  
 ,  
 2가 , ,  
 nlon 가 2가 가 , Ca  
 , 2가 ,  
 , 가 3' , 3'  
 /  
 ' (OLA) 가 가 , 가 가 2가  
 , Nickerson et al.(1990)  
 가 PCR DNA , PCR DNA ,  
 , PCR DNA OLA  
 Gap LCR(GLCR) . LCR 2 가 LCR( 가 ), 'DNA '  
 - 가 , LCR 가 가 가  
 , 가 가  
 , 가  
 , dNTP(DNA 가  
 ), (WO 90/01069). ,  
 가 / - Genetic Bit Analysis ™  
 , 가  
 4)  
 , 가 , 가 가  
 , (Sambrook et al., 1989)  
 , 가  
 2가 가 가  
 가 가 ,  
 가 ,  
 ,

가 , 가  
 (Sambrook et al., 1989).  
 (Tm) 5 가 pH  
 DNA ,  
 DNA  
 가 ,  
 DNA ,  
 2가 (Landegren U. et al.  
 , 1998). TaqMan Taq DNA 5  
 TaqMan (advancing) TaqMan (quenching)  
 가 2가 (Livak et al., 1995).  
 (molecular beacon)가 (Tyagi et al., 1998).  
 8 50  
 1  
 가 25  
 4 1  
 10, 15, 20 , 25, 30, 40, 47 8  
 P1 P8 50  
 4, 3, 2, 1 , 5,  
 가 가  
 5) 가  
 DNA ( , ) DNA  
 BRCA1 HIV -1 ( *S. cerevisiae* )  
 al., 1996; Kozal et al., 1996). (Hacia et al., 1996; Shoemaker et  
 Chip <sup>TM</sup> ), Hyseq(HyChip and HyGnostics), Protogene Laboratories Affymetrix(Gene

(tiling) 가 PCR 95/11955 가  
 가  
 U) ) 5 (A, T, G, C( (cross-  
 hybridization)

(scanning) PCR WO 92/10092 WO 95/11955; 5,424,186 가  
 15 가  
 1 8 10, 15, 20  
 25, 30, 40, 47 50  
 P1 P8 5, 4, 3, 2, 1  
 5, 6, 7, 8 2, 3, 4,

가  
 6)

PCR 5,589,136  
 PCR  
 가 (moving part)가

가 (Lander and Schork, 1994). - 2가  
 : 가 (cosegregation)

(Khoury et al., 1993). (parametric) -

가 가

WO 98/20165



가 (codegregation)

---

가 (recombinant fraction)

가 (Weir, 1996). (lod) (Morton, 1955; Ott, 1991). lod ( ) . 가

2 20 Mb 가 (resolution) 5,000 600 kb

(penetrance)( a )

가, 2Mb 20Mb 가 (resolution)

(lod) 가 (Risch and Merikangas. (1996)).

---

heritance) (allele sharing)' (polygenic in 2)

가 (IBS) (IBD)

(affected sib pair analysis)

가 IBD- IBS-

(Zhao et al., 1998).

Canlon 가 가

가,

가 가

가,

)  
 . 가  
 . 가 가 가, (fine-  
 scale mapping) . 가  
 ,  
 가

---

DNA  
 , , (counting)  
 ) , ; b)  
 (proportional representation)  
 n- ; A1 A18 ; A1 A17 ; a  
 Canlon- ; Canlon- ; Canlo  
 A16 ; ; A12  
 ; Canlon-

---

가 가 가 가  
 . 가 가 (Perlin et al., 1994). 가 가 가  
 . 가 가 가 가  
 CR . 가 PCR (Newton et al, 1989; Wu et al., 1989) P  
 (Ruano et al., 1990) 가 가 가,  
 Sarkar, G. and Sommer S. S., 1991). PCR ( 가 가 )  
 , Clark, A.G.(1990) 가  
 PCR- DNA . 가 가  
 , 가 가  
 , 1 가 가 가 가  
 , Hardy-Weinberg (

(random mating) 가  
- (expectation-maximization)(EM)  
5). EM 가 /

(maximum likelihood estimate)  
(Exocoffier L. and Slatkin M., 199  
. EM

가  
, : a) 1 Canlo  
n- ; b)  
; c) a) b)  
; d)  
18 Canlon- A1 A  
Canlon-  
A1 A17  
Canlon- A12 A16  
PCR , Clark , - PCR ,

2  
(Ajioka R.S. et al., 1997).

가 ( ),  
:  
가 가 가  
가 가 가  
가 가

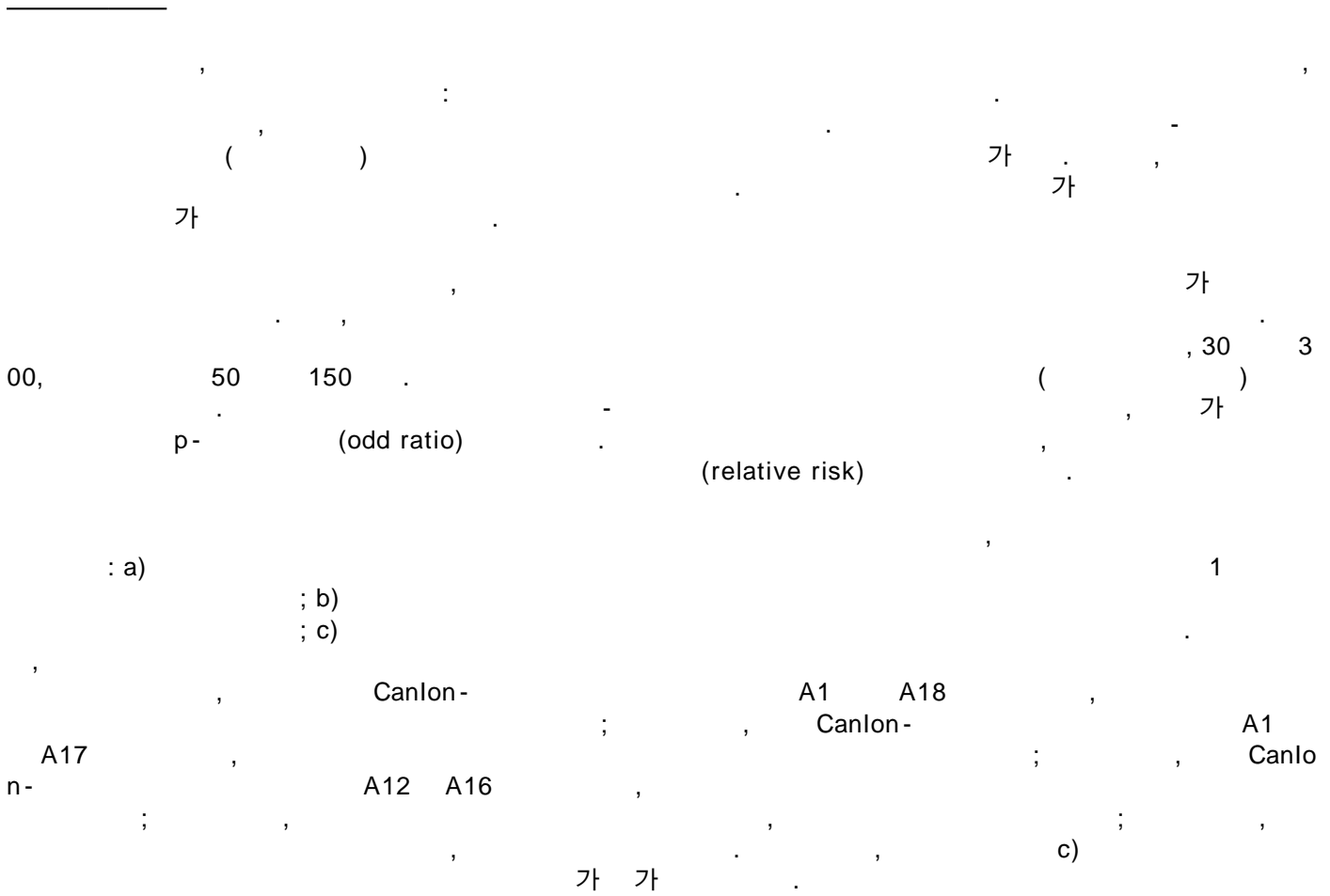
(linkage disequilibrium)

가 ( ) ,  
, ( , ) 가  
가 가  
가 ( , - ) 가  
가 ( , - ) - 가

( )  
 가 ( ) ( , )  
 (confusion factor)  
 , 2가  
 (Lander and Schork, 1994).  
 , 4가 : , 가 ,  
 ( , ) 가  
 1 98%, 1 80%, 1 50%, 1 30  
 %, 가 1 20% , 가 가  
 , 2가 가 가  
 , 50 300 , 100

\_\_\_\_\_ ) , , 1 Canlon- : a  
 ; b) Canlon-  
 ; c) 가 Canlon-  
 , Canlon- A1 A18 , A1  
 A17 , Canlon- ; , Canlon-  
 A12 A16 , , a) b  
 ) ; , ; , a  
 ) b) (subsample) ; , a

( )  
 가 가 가 가 가  
 ( , 가 가 ) , 가 가  
 가 ( ) 가  
 가 가  
 , 2가 , 가 , Canlon  
 가 ,



(stratification) TDT( / TDT ) TDT (subpopulation)

(Spielmann S. et al., 1993; Schaid D.J. et al., 1996, Spielmann S. and Ewens W.J., 1998).

1) (Terwilliger J.D. and Ott J., 1994; Ott J., 1991).

2)

가 , 가 (Lange K., 1997; Weir, B.S., 1996) (expectation-maximization)(EM) (Dempster et al., 1977; Exocoffier L. and Slatkin M., 1995).

APLO (Hawley M. E. et al., 1994) EM Arlequin (Schneider et al., 1997) EM-H EM

$K$  가  $N$  가  $F$  (  $K$  , 가  $H=2$   $K$  ,  $H$ 가 ) .

$C_j$ 가  $j$

$$P_j = \sum_{i=1}^{c_j} P(\text{genotyp}(i)) = \sum_{i=1}^{c_j} P(h_k, h_l) \quad \text{방정식 1}$$

$P_j$   $j$  th ,  $P(h_k, h_l)$   $h_k$   $h_l$   $j$  th (Hardy-Weinberg Equilibrium) ,  $P(h_k, h_l)$  :

$$\begin{aligned} P(h_k, h_l) &= P(h_k)^2 \text{ for } h_k = h_l, \\ P(h_k, h_l) &= 2P(h_k)P(h_l) \text{ for } h_k \neq h_l. \end{aligned} \quad \text{방정식 2}$$

E-M

$$P_1^{(0)}, P_2^{(0)}, P_3^{(0)}, \dots, P_H^{(0)}$$

$(1), \dots, P_H^{(1)}$  가

$s$  th

$$P_1^{(1)}, P_2^{(1)}, P_3^{(1)}$$

$$P(h_k, h_l)^{(s)} = \frac{n_j}{N} \left[ \frac{P_j(h_k, h_l)^{(s)}}{P_j} \right], \quad \text{방정식 3}$$

$n_j$   $j$  th (counting) ,  $P(h_k, h_l)^{(s)}$   $j$   $h_k, h_l$  (Smith, Ann. Hum. Genet., 21:254-276, 1957) 가 :

$$P_i^{(s+1)} = \frac{1}{2} \sum_{j=1}^F \sum_{i=1}^{c_j} \delta_{ij} P_j(h_k, h_l)^{(s)} \quad \text{방정식 4}$$

$it$   $t$  가  $l$  th ;  $it = 0, 1, 2$  .

E-M (MLE)  $j$  (multi-nomial distribution) 가  $s$  , (likelihood function)  $L$  . 2 가 ,  $10^{-7}$  .

3)

$M_i$                        $(a_i/b_i)$                        $M_j$                        $(a_j/b_j)$   
 $(M_i, M_j)$                       가                      :                      Piazza  
 $(a_i, a_j; a_i, b_j; b_i, a_j; b_i, b_j)$

$$a_i a_j = 4 - (4 + 3)(4 + 2),$$

$$4 = \dots = M_i \quad a_i \quad M_j \quad a_j \quad ;$$

$$3 = \dots = M_i \quad a_i \quad M_j \quad a_j \quad ;$$

$$2 = \dots = M_i \quad a_i \quad M_j \quad a_j \quad .$$

Weir B. S., 1996                      ,                      (                      )                      (MLE)  
 $(a_i, a_j; a_i, b_j; b_i, a_j; b_i, b_j)$                       (M<sub>i</sub>, M<sub>j</sub>)                      (LD)  
 MLE                      :

$$D_{iaj} = (2n_1 + n_2 + n_3 + n_4/2)/N - 2(\text{pr}(a_i) \cdot \text{pr}(a_j))$$

$$, n_1 \quad (a_i/a_i, a_j/a_j), n_2 \quad (a_i/a_i, a_j/b_j), n_3 \quad (a_i/b_i, a_j/a_j), n_4 \quad (a_i/b_i, a_j/b_j), N$$

가                      ,                      가                      가가

$b_j)$                       Hardy-Weinberg                      ,                      ,  $M_i(a_i/b_i)$                        $M_j(a_j/b_j)$   
 가                      .

$$D_{iaj} = \text{pr}((a_i, a_j)) - \text{pr}(a_i) \cdot \text{pr}(a_j).$$

$$, \text{pr}(a_j) \quad a_i \quad \text{pr}(a_j) \quad a_j \quad , \text{pr}(a_i) \cdot \text{pr}(a_j)$$

$M_i \quad M_j$                       가                      (measure of disequilibrium)

$$D'_{aij} = D_{aij} / \max(-\text{pr}(a_i) \cdot \text{pr}(a_j), -\text{pr}(b_i) \cdot \text{pr}(b_j)) \text{ with } D_{aij} < 0$$

$$D'_{aij} = D_{aij} / \max(\text{pr}(b_i) \cdot \text{pr}(a_j), \text{pr}(a_i) \cdot \text{pr}(b_j)) \text{ with } D_{aij} > 0$$

(heterozygosity rate)                      50                      100 ,  
 75                      200 ,                      100

4)

가 ( ) , 가  
 1 (degree of freedom) (chi-square test) P-  
 (P- 가 )

가  
 10<sup>-2</sup> , 1 x 10<sup>-6</sup> , 1 x 10<sup>-4</sup> , 2 p 1 x 10<sup>-3</sup> , 1 x

가  
 (permutation)

1 , 가  
 .2 가 , 1  
 100 10000

가  
 'Methods, software and apparati for identifying genomic re-  
 gions harboring a gene associated with a dectable trait'(60/107,986; 1998.11.10 )

5) 가  
 (odds ratio) (RR) 가 P(R+)가 R P(R-)가 가

RR= P(R+)/P(R-)  
 (measure) 가

$$OR = \left[ \frac{F^+}{1-F^+} \right] / \left[ \frac{F^-}{1-F^-} \right]$$

$$OR = (F^+ / (1-F^+)) / (F^- / (1-F^-))$$

F + , F - , F + F -  
 가... 가

(AR) 가  
 가 . AR

(relevance)



:

$$AR = P_E (RR - 1) / (P_E (PR - 1) + 1)$$

AR ; RR . P<sub>E</sub>

가 , 가 , 가 , 가 , 가 ; (a) ; (b) ; (c) ; (d) . (b) (c)

A1 A18 가

가 Canlon Canlon , Canlon , Canlon , Canlon Ca nlon (manifestation)

- Canlon DNA ; - ; - DNA ; - -

A1 A18

가



CNS

Diagnosis Statistical Manual of Mental Disorder fourth edition(DSM- )

DNA

RNA

-가

가

Canlon

/

Canlon

cDNA

Canlon

'Canlon

'Canlon cDNA

SEQ ID No 1

3

6

Canlon

Canlon cDNA,

SEQ ID No 4

cDNA

가

Canlon

Canlon

가

가

/ 가

가

Canlon

SEQ ID No 5

Canlon

Canlon

SEQ ID No

4

Canlon-

A1

A18

a)

DNA

/ c)

DNA

DNA

( )

, b)

/

가

: (a)

(i)

; (ii)

/

; (iii)

; (b)

, , : (a) (i) ; (ii) / ; (iii) ; (b)

(i) : (a) ; (ii) / ; (iii) ; (b) ; c)

, 가 : (i) ; (ii) DNA / ; (iii) 가 DNA

( 6,054,288; 6,048,729; 6,048,724; 6,048,524; 5,994,127; 5,968,502; 5,965,125; 5,869,239; 5,817,789; 5,783,385; 5,733,761; 5,641,670; 5,580,734; P CT WO 96/29411, WO 94/12650; Koller et al. Proc, 1994, Natl. Acad. Sci. USA 86:8932-8935 (1989)).

1.

YAC( ), BAC( DNA ), DNA

(1) 가 10 300bp DNA cis-

(2) mRNA 가 (1)

(3) N- 가 가 (periplasmic space)

DNA SV40 , 5'- - . SV40

SEQ ID No 5 Canlon Canlon

SEQ ID No 2 Canlon

2.

가

CAT( ) , pKK232-8 pCM7

LacI, LacZ, T3 T7 RNA , gpt, PR, PL, tr  
 p (EP 0036776), Smith et al., 1983; O'Reilly et al., 1992), PR trc p10 (Kit Novagen)(

CMV, HSV , SV40, LTR,

-L . 가 , Sambrook et al.(1989) Fuller et al.(1996)

cDNA

SV40

3.

가 가 가

; ( *S. cerevisiae* ) TRP1; ( *E. coli* )  
 ( *mycobacteria* )

4.

가 가 pBR322(ATCC 37017) pKK22

3-2(Pharmacia, Uppsala, Sweden) GEM1(Promega Biotec, Madison, WI, USA)

가 가 가

: pQE70, pQE60, pQE-9(Qiagen), pbs, pD10, phagescript, psiX174 pbluescript SK, pbsks, pNH8A, pNH16A, pNH18A, pNH46A(Stratagene); ptrc99a pKK223-3, pKK233-3, pDR540, pRIT5(Pharmacia); pWLNEO, pSV2 CAT, pOG44, pXT1, pSG(Stratagene); pSVK3 pBPV, pMSG, pSVL(Pharmacia); pQE-30(QIAexpress).

P1 80 100kb

P1 p158 p158/neo8 Stemberg(1992, 1994) Canlon  
 P1 40kb (Linto  
 n et al., 1993). P1 DNA McCormick et al.(1994)  
 ( *E. coli* ) ( NS3529) 25µg/Ml  
 ) P1 DNA Qiagen Plasmid Maxi kit(Qiagen, Chatsworth, CA USA  
 ( *E. coli* ) P1 DNA 2 Qiagen-tip 500  
 , DNA 70% DNA TE(10 mM Tris-HCL, pH 7.4, 1mM EDTA) DNA  
 , DNA 가

Canlon P1  
 P1 (Sfil, NotI Sall) 가 P1 DNA P1 DNA  
 et al. 1993a; Peterson et al., 1993) 가 YAC DNA (Schedl  
 DNA Millipore Ultrafree-MC Filter Unit(Millipore Bedford, MA USA -30,000 )  
 (type VS, 0.025 µm, Millipore) 100mM NaCl, 30 µ M , 70 µ M  
 (10mM Tris-HCl, pH 7.4, 250µm EDTA) P1 DNA  
 (intactness) 1% 가 (Sea Kem GTG: FMC Bio-products) -  
 가

SEQ ID No 5 Canlon  
 erda ) SF9 (ATCC N ° CRL 1711) ( *Spodoptera frugip*  
 (Pharmingen) pVL1392/1393

SEQ ID No 5 Canlon  
 Chai et al.(1993), Vlasak et al.(1983), Lenhard et al.(1996) 가

n Steg(1996) Ohno et al.(1994) Feldma  
 2 5 (Ad2, Ad 5) (French N ° FR-9  
 3.05954)

DNA

Mink-Cell  
 4070A 1504A , Abelson(  
 ATCC No VR-999), Friend(ATCC No VR-245), Gross(ATCC No VR-590), Rauscher(ATCC No VR-998), Mo  
 loney (ATCC No VR-190; PCT WO 94/24298)가  
 Bryan high titer(ATCC Nos VR-334, VR-657, VR-726, VR-659, VR-728)가  
 Roth et al.(1996), PCT WO 93/25234, PCT WO 94/06920 Roux et al., 198  
 9, Julan et al., 1992, Neda et al., 1991

(AAV)  
 (Muzyczka et al., 1992). DNA -  
 (Flotte et al., 1992; Samulski et al., 1989; McLau

ghlin et al., 1989). AAV

(primary cell)

BAC

*coli*) (BAC) (Shizuya et al., 1992) DNA (100-300kb) ( *E.*  
 Kim et al.(1996) pBeloBAC11  
 Bam HI Hind  
 T7 SP6 RNA  
 BAC DNA BAC DNA  
 BAC Not 가  
 DNA cosN 가 , pBeloBAC11  
 (termi  
 nase) BAC 가 DNA BAC

5.

가 ,  
 (Graham et al., 1973; Chen et al., 1987), DEAE- (Gopal, 1985),  
 (Tur-Kaspa et al., 1986; Potter et al., 1984), (Harland et al., 1985), DNA-  
 (Nicolau et al., 1982; Fraley et al., 1979), (Wu and Wu, 1987; 1988)

가 (cognate) ( DNA ) 가  
 가 가

PCT WO 90/11092(Vical Inc.  
 ), PCT WO 95/11307(Institut Pasteur, INSERM, Universite d'Ottawa), Tacson et al.(1996), Huygen et al.  
 (1996)

DNA가 ( 가 DNA-  
 (Klein et al.(1987)).  
 (Ghosh and Bacchawat, 1991; Wong et al  
 ., 1980; Nicolau et al., 1987).

가 Canlon 가

0.1 100µg

Canlon

SEQ ID No 1

4 Canlon

Canlon

( )

(

nlon cDNA

'Canlon

'Ca

A1 A18

a) : (*Escherichia coli*)(I.E.DH5- ), (*Bacillus subtilis*),  
 ( *Salmonella typhimurium* ) ( *Pseudomonas* ), ( *Streptomyces* ),  
 ( *Staphylococcus* ) ;

b) : HeLa (ATCC N ° CCL2; N ° CCL2.1; N ° CCL2.2), Cv 1 (ATCC N ° CCL70), COS  
 (ATCC N ° CRL1650; N ° CRL1651), Sf-9 (ATCC ° CRL1711), C127 (ATCC N ° CRL-1804); 3T3(  
 ATCC N ° CRL-6361), CHO(ATCC N ° CCL-61), 293(ATCC N ° 45504; N ° CRL-1573), BHK(ECAC  
 C N ° 84100501; N ° 84111301);

c)

Canlon

Canlon  
DNA

cDNA

Canlon

DNA 가 , 가 ,  
 7.4, 250µm EDTA 1 ng/Mℓ(BAC ) 3ng/µℓ(P1 ) 10mM Tris-HCl, pH  
 A DNA가 DNA  
 (Schedl et al.(1993b)).

ES DNA (ES)  
 . ES (inner cell mass)  
 ES : ES-E14TG2a(ATCC n ° CRL-1821), ES-D3(ATCC n ° CRL1  
 934, n ° CRL-11632), YS001(ATCC n ° CRL-11776), 36.5(ATCC n ° CRL-11116). ES  
 ES  
 Robertson(1987) Abbondanzo et al.(1993)  
 Pease Williams(1990)가 LIF  
 13 14





SV40 T *onc* - (C  
hou(1989), Shay et al.(1991))

Canlon

Canlon  
, Canlon

Canlon

Canlon 가 Canlon  
가,  
( ) - ( ) 가  
( , , ) CNS ( , ,  
) Caslon  
. 가 , Canlon

Canlon  
( ),  
(patch clamping)  
L, N, T  
(end-point radiotracer),  
(Denyer et al., D  
rug Disc. Today 3(7):323-332(1998).

( , ), ( , ), ( , ) ;  
FPL-64176 BAYK 8644가 ;  
, U-54494A((+/-)-cis-3,4- -N- -N-[2-(1- )- ]-  
)가 Canlon

a) (i) Canlon (ii) Canlon ;

b) ;

c) ;

d) Canlon .

Canlon , Canlon  
 Canlon ( , Ca<sup>2+</sup> Na<sup>+</sup>)  
 Canlon 가 Canlon .

Canlon , Canlon  
 가 Ca<sup>2+</sup> Na<sup>+</sup> , K<sup>+</sup> 가

Canlon  
 Canlon-  
 ( , Ca<sup>2+</sup> Na<sup>+</sup>)  
 (sorting)

i) Canlon ,

ii) Canlon , Canlon  
 Canlon 가 가 ,  
 Canlon Ca<sup>2+</sup> / Na<sup>+</sup> 가 .

Canlon Canlon  
 +, Na<sup>+</sup>, K<sup>+</sup>) / Denyer et al.(supra) (Ca<sup>2+</sup> ,

Canlon -

Canlon (voltage stimulation) . Ca<sup>2+</sup> , Ca  
 , Na<sup>+</sup> K<sup>+</sup> K<sup>+</sup> ( )

Ca<sup>2+</sup> (Fluo-3, -1, Molecular Probes, OR, U.S.A)가 가 . Ca  
 Na<sup>+</sup>  
 20 60 Denyer et al.(  
 supra) 22Na<sup>+</sup> 14C- Na<sup>+</sup> 4  
 5Ca<sup>2+</sup> Ca<sup>2+</sup> . Denyer et al.(supra) Canlon  
 Cytostar -T (Amersham International, U.K.)가 .

가 Ca<sup>2+</sup>  
 가

가 가 가 ,

FRET -  
ay 4(9): 431-439(1999).

(Auora Biosciences, CA, USA; Gonzalez et al., Drug Disc. Tod

가 .가 , - K+ ( *Saccharomyces cerev*  
*isiae* ) K+ K  
+ (Anderson et al., Symp. Soc. Exp. Biol. 48: 85-97(1994)). Ca2+  
Na+ Canlon  
Na+ Na+/K+ Na+ 가  
Na+ Na+ .  
(Manger et al., Anal. Biochem. 214: 190-194(1993)).

(*electrophysiology*)

가 (Hamil, Pflugers Arch. 391, 85-100(1  
981)).  
(Neurosearch A/S, Glostrup, Denmark; Olesen et al., Voltage gated ion channel modulators, 7-8 Dec  
ember, Philadelphia PA, USA(1995); Denyer et al., supra).

**Canlon**

Canlon , Canlon,  
Canlon , Canlon  
Canlon Canlon  
가 , SEQ ID No 5 6 , 8 10 ,  
12, 15, 20, 25, 30, 40, 50 100  
, HPLC Canlon  
(Bush et al.(1997)) (Wang et al.(1997))

, SEQ ID No 5 6 , 8 10 ,  
12, 15, 20, 25, 30, 40, 50 100 Canlon  
가 , 가  
Canlon Canlon

Canlon Canlon  
Canlon Canlon  
Canlon Canlon

a) SEQ ID No 5 6 , 8 10 ,  
12, 15, 20, 25, 30, 40, 50 100 Canlon

- b) ;
- c) ;
- d) .

, Canlon ,  
 a) SEQ ID No 5 6 , 8 10 ,  
 12, 15, 20, 25, 30, 40, 50 100 Canlon ;

b) , Canlon ,  
 , Canlon ,  
 Canlon 가 가 .  
 가 가 - cDNA  
 , Canlon ,  
 , Canlon ,  
 , Canlon ,

**A.**

, DNA (Parmley and S  
 mith, 1988). 가 DNA 8 20  
 (Oldenburg K.R. et al., 1992; Valadon P., et al., 1996; Lucas A.H., 1994; Westerink M.A.J.  
 , 1995; Felici F. et al., 1991). Canlon  
 , Canlon Canlon

가 , Canlon ,  
 ( pH) (가 , ( *E. coli* ) -Canlon (over-infection)  
 , 2-4 , -

**B.**

, SEQ ID No 5 6 , 8 10 ,  
 12, 15, 20, 25, 30, 40, 50 100 Canlon ,  
 , Canlon Canlon  
 가 가 가 Canlon . Canlon  
 가 , Canlon 가 가  
 가 Canlon 가 Canlon

C.

SEQ ID No 5 6 8 10 1  
 2, 15, 20, 25, 30, 40, 50 100  
 Canlon  
 가 Affi Gel  
 Canlon S (GST) 가 Canlon  
 Ramunsen et al.(1997) 2-D

D.

SEQ ID No 5 6 8 10 1  
 2, 15, 20, 25, 30, 40, 50 100  
 Canlon  
 (Edwards and Leatherbarrow(1997), Szabo et al.(1995)).  
 가 ( , )  
 (SPR) SPR  
 SPR Canlon Canlon  
 Canlon Canlon Canlon  
 Canlon Canlon Canlon  
 가

E.

-  
 Gal4 DNA (Fields and Song 1989),  
 ,173(Fields et al.) 5,667,973 5,283

- Harper et al.(1993), Cho et al.(1998) F  
 romont-Racine et al.(1997)

SEQ ID No 5 6 8 10  
 12, 15, 20, 25, 30, 40, 50 100 Canlon  
 , Canlon GAL4 DNA  
 pAS2 pM3  
 cDNA cDNA 가 GAL4  
 cDNA pACT  
 가 DNA CAT Gal  
 4 가 , pG5EC

, 2가 가 , 2가 :

- Y190, (MATa, Leu2-3, 112 ura3-12, trpl-901 his3-D200 ade2-101, gal4Dgal80D URA3 GAL-LacZ, LYS GAL-HIS3, cyh) ;

- Y187, (MATa gal4 gal80 his3 trpl-901 ade2-101 ura3-52 leu2-3, -112 URA3 GAL-lacZmet) , Y190 (mating type) .

, 20µg pAS2/Canlon 20µg pACT-cDNA Y190 -  
 3-AT(50mM)  
 (lift)  
 ( His + , beta-gal + )  
 (10mg/Ml) pAS2/Canlon pACT-cDNA  
 Y190 Gal4 Canlon ;  
 B, SNF1 Y187 [Harper et al.(1993), Bram et al.(Bram  
 RJ et al., 1993)], (lift) Gal4  
 beta-gal 가 (false positive) .

Hybrid System 2(Catalog No. K1604-1, Clontech) 가 Two  
 Hybrid System 2(Catalog No. K1604-1, Clontech) , Canlon  
 DNA cDNA, cDNA GAL4 DNA  
 HIS3 GAL4 DNA GAL4  
 lacZ Canlon GAL4 lacZ  
 cDNA

**Canlon**

Canlon  
 Canlon 5' 3'  
 가  
 Matchmaker One-Hybrid System kit(Catalog Ref. n ° K1603-1, Clontech)  
 가 DNA ( Saccharomyces cer  
 evisiae ) Canlon  
 cDNA GAL4  
 Canlon  
 cDNA  
 Canlon  
 DNase  
 Canlon  
 (Fried and Crothers(1981); Garner and Revzin(1981); Dent and Latchman(1993)).  
 DNA DNA  
 Canlon

**Canlon**

Canlon

a) Canlon ;

b) ;

c) Canlon .

A16 , Canlon 가 A12

DNA , DNA Canlon 5'

Canlon mRNA ELISA RIA Canlon

, Canlon mRNA Canlon cDNA PCR Canlon-

Canlon 가 Canlon

Canlon

:

가

5'

;

;

가

, 5'

ID No 4 Canlon cDNA 5'UTR 가 SEQ

가

(CAT)

가

(GFP),

Canlon

5'

가

가  
가

Canlon

:

a) , SEQ ID No 4 Canlon cDNA 5'UTR

, 가 5'UTR ;

b) ;

c) 가

, SEQ ID No 4 Canlon cDNA 5'UTR ,  
Canlon 5'UTR



, SEQ ID No 4 Canlon cDNA 5'UTR ,  
Canlon 5'UTR

A12 A16 , SEQ ID No 4 Canlon cDNA 5'UTR

Canlon  
SEQ ID No 4 Canlon cDNA 5'UTR ,  
가

Canlon WO 97/05277  
A Canlon cDNA Canlon DNA (T3, T7 or SP6) RN  
DNA cDNA 100 RNA , Canlon  
( , -UTP DIG-UTP)  
RNA mRNA  
(40-50 , 16 , 80% , 0.4M NaCl pH 7.8)  
RNA ( , RNases CL3, T1, Phy M, U2 A)  
-UTP 가  
. DIG -DIG ELISA 가

Canlon mRNA  
n cDNA 가 , Canlon 가 DNA, Canlo  
A1 A17 가 , 15  
25  
50 100 , 500

가 , Canlon DNA (Sचना et al.(1995 and  
1996)). Canlon cDNA PCR , 96- 가  
1 0.2% SDS 1 , 1 2 , 5 1 2  
5 95 2 1 0.2% SDS 2

mRNA 1 60  
14 x 14mm 1cm<sup>2</sup> 6-12 . 25  
10 (1 x SSC/0.2% SDS) 5 , (0.1 x SSC/0.2% SDS)  
0.1 x SSC 2

Canlon DNA Canlon cDNA  
(Pietu et al.(1996)). Canlon cDNA PCR , mRNA mRN  
A mRNA (phosphoimaging) 가 , m  
RNA

, Canlon DNA, Canlon cDNA (Lockhart et al.(1996); Sosnowsky et al.(1997)). Canlon DNA Canlon cDNA ,  
가 가 A1 A17  
(Lockhart et al. supra), 15-50  
(Sosnowski et al., supra), 20

50 100  
(Lockhart et al., supra)  
cDNA  
Canlon cDNA mRNA  
(Sosnowsky et al., 1997)  
cDNA  
Canlon mRNA

Canlon

Canlon Canlon Canlon  
A1 A17 가

Sczakiel et al.(1995)

Canlon mRNA 5' (15-200bp)

ATG

Canlon mRNA

Canlon mRNA

가  
Green

et al., (1986); Izant and Weintraub, (1984)

Canlon

T7 SP6 가  
DNA

가 Canlon

Rossi et al.(1991);  
EP 0 572 287 A2

WO 94/23026, WO 95/04141, WO 92/18522;

가 RNA ( , ' ) RNA  
(1) 가 ; (3)  
( 30 )

Sczakiel et al.(1995)

Canlon DNA Canlon

Canlon DNA 가 Canlon  
groove) , Canlon DNA (major

, Canlon DNA  
10-mer 20-mer  
, Canlon

Canlon

Canlon  
가

, DEAE-

PCR , RNase

Canlon  
Canlon

가 ( ) (anomer)  
3'  
Griffin et al.(1989)

Canlon-

Canlon

Canlon

Canlon  
가

Canlon-

, Canlon

가

Canlon

Canl  
Ca

on-  
nlon

Canlon

Canlon

, Canlon

[Diagnosis and Statistical Manual of Mental Disorders(DSM- )].  
Canlon

'Remington's Pharmaceutical Sciences,'(Mack Publishing Co. Easton, PA)

(Medtronic, Inc., Minneapolis, MN)

/

가

(penetrant)가 ( )

가 /

가 가 가

가 가

가 가 가 가

100

가

가

1



1000 (Sun Microsystems, Palo Alto, CA) (100) Sun Enterprise  
 (105) III(Intel Corpo  
 ration), (Sun, Motorola, Compaq International Business Machines)  
 가 (100) (105), (110),  
 105) (100) (115)(, RAM) ( 가  
 (118) 가 (100) (110)  
 (118) (110) (control logic) / 가 (100)  
 00) (100) (125a-c) (120) (100) (1  
 ( , , , ) (115)  
 가 (100) 가 가  
 / (peptidomimetics), (100) 가 . 가 ,  
 가 가 ,  
 3 (200)  
 T (100) 가 GENBANK, PIR SWISSPRO  
 (100) (200) (201) (202) RAM ,  
 (200) (204) 가 ,  
 2 (210) 가 , 2  
 (feature)  
 가 (210) (210)  
 (200) ,  
 (200) (214)

(200) (218) ,  
 (200) (220) 가 , (2  
 (224) ,  
 (212) (200) (218)  
 가 ,  
 가 ,  
 가 ,  
 2, 5, 10, 15, 20, 2  
 5, 30 50

BLAST2N  
 가  
 2, 5, 10,  
 15, 20, 25, 30 50

4 (252) (254) (250) (250)  
 (256) 가 (250) (260) 가  
 (262) A, T, C, G( U)가  
 가  
 (264) 가 (250) (268)  
 가 (250) 가 (loop)  
 가 (250) (274)  
 가 (250) (276)  
 100  
 100%가 가

가  
 가 (SNP)





(feature)

10, 15, 20, 25, 30, 50

2, 5,

.가 ,

DB2, SYBASE ORACLE ASCII  
가 ,

: MacPattern(EMBL), DiscoveryBase(Molecular Applications Group), GeneMine(Molecular Applications Group), Look(Molecular Applications Group), MacLook(Molecular Applications Group), BLAST BLAST 2(NCBI), BLASTN BLASTX(Altschul et al, 1990), FASTA(Pearson and Lipman, 1988), FASTDB(Brutlag et al., 1990), Catalyst(Molecular Simulations Inc.), Catalyst/SHAPE(Molecular Simulations Inc.), Cerius<sup>2</sup>.DBAccess(Molecular Simulations Inc.), HypoGen(Molecular Simulations Inc.), Insight II(Molecular Simulations Inc.), Discover(Molecular Simulations Inc.), CHARMM(Molecular Simulations Inc.), Felix(Molecular Simulations Inc.), DelPhi(Molecular Simulations Inc.), QuanteMM(Molecular Simulations Inc.), Homology(Molecular Simulations Inc.), Modeler(Molecular Simulations Inc.), ISIS(Molecular Simulations Inc.), Quanta/Protein Design(Molecular Simulations Inc.), WebLab(Molecular Simulations Inc.), WebLab Diversity Explorer(Molecular Simulations Inc.), Gene Explorer(Molecular Simulations Inc.), SeqFold(Molecular Simulations Inc.), the EMBL/Swissprot, MDL Available Chemicals Directory, MDL Drug Data Report, Comprehensive Medicinal Chemistry, Derwents's World Drug Index, BioByteMaster File, Genbank, Genseqn

(zoppers), - -

(homeobox),

(acidic stretch),

**1: - DNA**

. 100

DNA

30 Mℓ

EDTA

(50 Mℓ

( ) 2000 rpm 10 : 10 mM Tris pH 7.6; 5 mM MgCl<sub>2</sub>; 10 mM NaCl)

(10 , 2000 rpm)

3.7 Mℓ

42

- 3 Mℓ TE 10-2(Tris-HCl 10 mM, EDTA 2 mM)/NaCl 0.4 M

- 200  $\mu\ell$  SDS 10%

- 500  $\mu\ell$  K- (2 mg K- /TE 10-2/NaCl 0.4 M)

, 1 Ml NaCl(6M)(1/3.5 v/v) 가 , 10000 rpm 20

DNA , 2 100% 가 , 2000 rpm 30

. DNA 70% 3 2000 rpm 20  
 37 1 Ml TE 10-1 1 Ml . DNA 260 nm OD 가  
 (1 OD = 50  $\mu\text{g}/\text{Ml}$  DNA).

DNA , OD 260/OD 280 . 1.8 2 OD 260/OD 280  
 DNA

(pool) DNA

2: : PCR DNA

1 DNA DNA (pool) , 50

PCR :

25 $\mu\ell$

DNA 2 ng/ $\mu\ell$

MgCl<sub>2</sub> 2 mM

dNTP( ) 200  $\mu$  M

( ) 2.9 ng/ $\mu\ell$

Ampli Taq Gold DNA 0.05 unit/ $\mu\ell$

PCR (10x = 0.1 M TrisHCl pH 8.3 0.5M KCl) 1x

1) Canlon 가 20 OSP (Hilier amp; Green, 199  
 1 PU RP

1:

애플리콘	SEQ ID 1에서 애플리콘의 위치 범위		프라이머 이름	SEQ ID 1에서 애플리콘의 위치 범위		프라이머 이름	상보적인 위치 range of amplification of amplification 프라이머 in SEQ ID No 1	
99-62626	12343	12810	B1	12343	12363	C1	12793	12810
99-62632	13814	14296	B2	13814	13832	C2	14279	14296
99-62633	24863	25396	B3	24863	24881	C3	25378	25396
99-62611	69198	69650	B4	69198	69218	C4	69632	69650
99-62605	73005	73483	B5	73005	73022	C5	73466	73483
99-62635	79808	80334	B6	79808	79826	C6	80314	80334
애플리콘	SEQ ID 2에서 애플리콘의 위치 범위		프라이머 이름	SEQ ID 2에서 증폭 프라이머의 위치 범위		프라이머 이름	SEQ ID 2에서 증폭 프라이머의 상대적 위치 범위	
99-79335	51031	51559			51031		51051	
99-79336	60925	61374		60925	60945		61354 61374	
99-79338	80271	80720		80271	80290		80700 80720	
99-79339	91037	91486		91037	91056		91466 91486	
99-79314	100285	100784		100285	100305		100764 100784	
99-79316	106568	107020		106568	106585		107000 107020	
99-79322	165864	166401		165864	165884		166381 166401	
99-79306	235713	236210		235713	235732		236190 236210	
애플리콘	SEQ ID 3에서 애플리콘의 위치 범위		프라이머 이름	SEQ ID 3에서 증폭 프라이머의 위치 범위		프라이머 이름	SEQ ID 3에서 증폭 프라이머의 상대적 위치 범위	
99-79310	31618	32100		B15	31618		31635	C15
99-79311	42324	42723	B16	42324	42344	C16	42704 42723	
애플리콘			프라이머 이름	SEQ ID 6에서 증폭 프라이머의 위치 범위		프라이머 이름	SEQ ID 6에서 증폭 프라이머의 상보적 위치 범위	
99-62617				B17	1		20	C17

PU 가 PU 5' : TGTAACGACGGCCAGT ; RP RP 5  
 : CAGGAAACAGCTATGACC 가 PU 5' SEQ ID No 7  
 가 RP 5' SEQ ID No 8

GENSET UFPS 24.1 (phosphoramidite)

DNA Genius II . 95 10 가 , 40  
 :95 30 , 54 1 , 72 30 , 72 10  
 (intercalant agent) Picogreen(Molecular Probes)

96- 가

3: - DNA

2 DNA ABI  
 (dye terminator cycle sequencing protocol)

(ABI Prism DNA

(2.1.2))

가 가

17 , 18

가

2

2:

앰플리콘	BM	마커 이름	다형성		SEQ ID에서 BM 위치	
			all1	all2	No 1	No 4
99-62626	A1	99-62626-168	A	T	12642	
99-62632	A2	99-62632-275	A	G	14088	
99-62633	A3	99-62633-409	A	T	24981	
99-62611	A4	99-62611-51	A	C	69248	
99-62605	A5	99-62605-56	A	G	73428	
99-62635	A6	99-62635-443	A	G	80250	
앰플리콘	BM	마커 이름	다형성		SEQ ID에서 BM 위치	
			all1	all2	No 2	No 4
99-79335	A7	99-79335-60	C	T	51090	
99-79336	A8	99-79336-369	A	G	61293	
99-79338	A9	99-79338-332	C	T	80602	
99-79314	A10	99-79314-201	G	T	100485	
99-79314	A11	99-79314-225	A	G	100509	
99-79316	A12	99-79316-158	C	T	106725	1658
99-7932	A13	99-79322-224	G	T	166087	
99-79322	A14	99-79322-473	A	G	166336	
99-79306	A15	99-79306-182	C	T	235894	
앰플리콘	BM	마커 이름	다형성		SEQ ID에서 BM 위치	
			all1	all2	No 3	No 4
99-79310	A16	99-79310-29	A	C	31646	4481
99-79311	A17	99-79311-50	G	C	42373	
앰플리콘	BM	마커 이름	다형성		SEQ ID에서 BM 위치	
			all1	all2	No 6	
99-62617	A18	99-62617-105	G	C	105	

BM ' ' . all1 all2 , 1 2

3:

BM	마커 이름	SEQ ID No 1에서 프로브의 위치 범위		프로브
A1	99-62626-168	12630	12654	P1
A2	99-62632-275	14076	14100	P2
A3	99-62633-409	24969	24993	P3
A4	99-62611-51	69236	69260	P4
A5	99-62605-56	73416	73440	P5
A6	99-62635-443	80238	80262	P6
BM	마커 이름	SEQ ID No 2에서 프로브의 위치 범위		프로브
A7	99-79335-60	51078	51102	P7
A8	99-79336-369	61281	61305	P8
A9	99-79338-332	80590	80614	P9
A10	99-79314-201	100473	100497	P10
A11	99-79314-225	100497	100521	P11
A12	99-79316-158	106713	106737	P12
A13	99-79322-224	166075	166099	P13
A14	99-79322-473	166324	166348	P14
A15	99-79306-182	235882	235906	P15
BM	마커 이름	SEQ ID No 3에서 프로브의 위치 범위		프로브
A16	99-79310-29	31634	31658	P16
A17	99-79311-50	42361	42385	P17
BM	마커 이름	SEQ ID No 6에서 프로브의 위치 범위		프로브
A18	99-62617-105	93	117	P18

4:

3

1

가  
DNA

DNA  
PCR

PCR ( 1)

가 19

4

4:

마커 이름	대립 유전자 마커	Mis. 1	SEQ ID No 1에서 마이크로서열분석 프라이머 mis 1의 위치 범위	Mis. 2	SEQ ID No 1에서 마이크로서열분석 프라이머 mis 2의 위치 범위
99-62626-168			12623 - 12641		12643 - 12661
99-62632-275			14069 - 14087		14089 - 14107
99-62633-409			24962 - 24980		24982 - 25000
99-62611-51			69229 - 69247		69249 - 69267
99-62605-56		"	73409 - 73427		73429 - 73447
99-62635-443			80231 - 80249		80251 - 80269
마커 이름	대립 유전자 마커	Mis. 1	SEQ ID No 2에서 마이크로서열분석 프라이머 mis 1의 위치 범위	Mis. 2	SEQ ID No 2에서 마이크로서열분석 프라이머 mis 2의 위치 범위
99-79335-60			51071 - 51089		51091 - 51109
99-79336-369			61274 - 61292		61294 - 61312
99-79338-332			80583 - 80601		80603 - 80621
99-79314-201			100466 - 100484		100486 - 100504
99-79314-225			100490 - 100508		100510 - 100528
99-79316-158			106706 - 106724		106726 - 106744
99-79322-224			166068 - 166086		166088 - 166106
99-79322-473			166317 - 166335		166337 - 166355
99-79306-182			235875 - 235893		235895 - 235913
마커 이름	대립 유전자 마커	Mis. 1	SEQ ID No 3에서 마이크로서열분석 프라이머 mis 1의 위치 범위	Mis. 2	SEQ ID No 3에서 마이크로서열분석 프라이머 mis 2의 위치 범위
99-79310-29			31627 - 31645		31647 - 31665
99-79311-50			42354 - 42372		42374 - 42392
마커 이름	대립 유전자 마커	Mis. 1	SEQ ID No 6에서 마이크로서열분석 프라이머 mis 1의 위치 범위	Mis. 2	SEQ ID No 6에서 마이크로서열분석 프라이머 mis 2의 위치 범위
99-62617-105			86 - 104		106 - 124

Mis1 Mis2 , Canlon - 가 Canlon 가

:

, 10 pmol  
 , 1U Thermosequenase(Amersham E79000G), 1.25µl Thermosequenase (260 mM Tris HCl pH 9.5, 65 mM MgCl<sub>2</sub>)  
 ddNTP(Perkin Elmer, Dye Terminator Set 401095) 20 µl 가 .94 4 , Tetrad  
 PTC-225 (MJ Research) 55 15 , 72 5 , 94 10 PCR 20  
 -EDTA

ABI PRISM 377 DNA , 95 2 가 CanlonScan (Perkin Elmer)

가

가

가

가

가

(height ratio)

.2

Canlon

Canlon

Amicon

mg/Ml

A. \_\_\_\_\_

Canlon

Kohler, G. and Milstein, C.,(1975)  
(Harlow, E. and D. Lane. 1988 ).

mg Canlon

(HAT )

가  
ELISA(Engvall,(1980))

Davis,

L. et al. Basic Methods in Molecular Biology Elsevier, New York. Section 21 -2

B. \_\_\_\_\_

Canlon

Canlon

, Canlon 가

( , RIBI )

가  
(mBSA), (BSA), B

(KLH)

(ng ) 가  
(Mayer and Walker(1987)).

Vaitukaitis, J

. et al.(1971)

가  
(Ouchterlony, O. et al.(1973)).

Ml 0.1 0.2mg( 12 μ M)  
(Fisher, D.,(1980))

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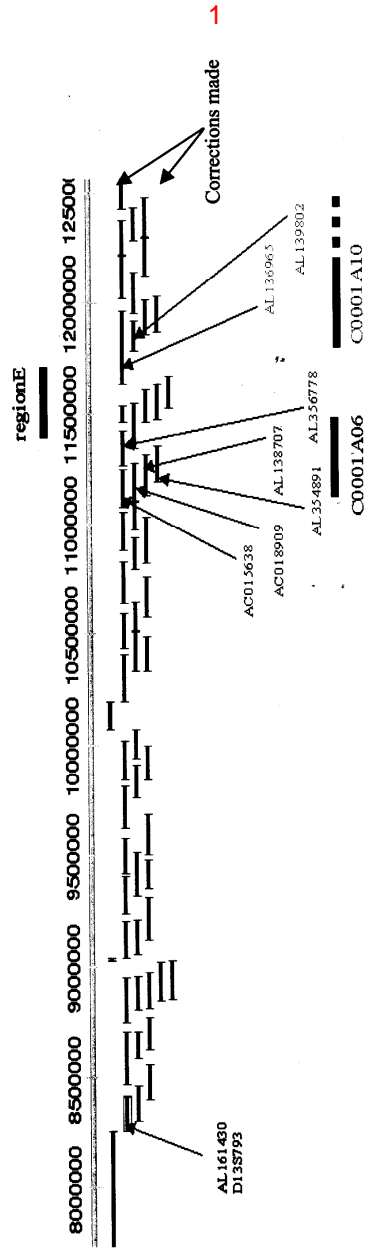
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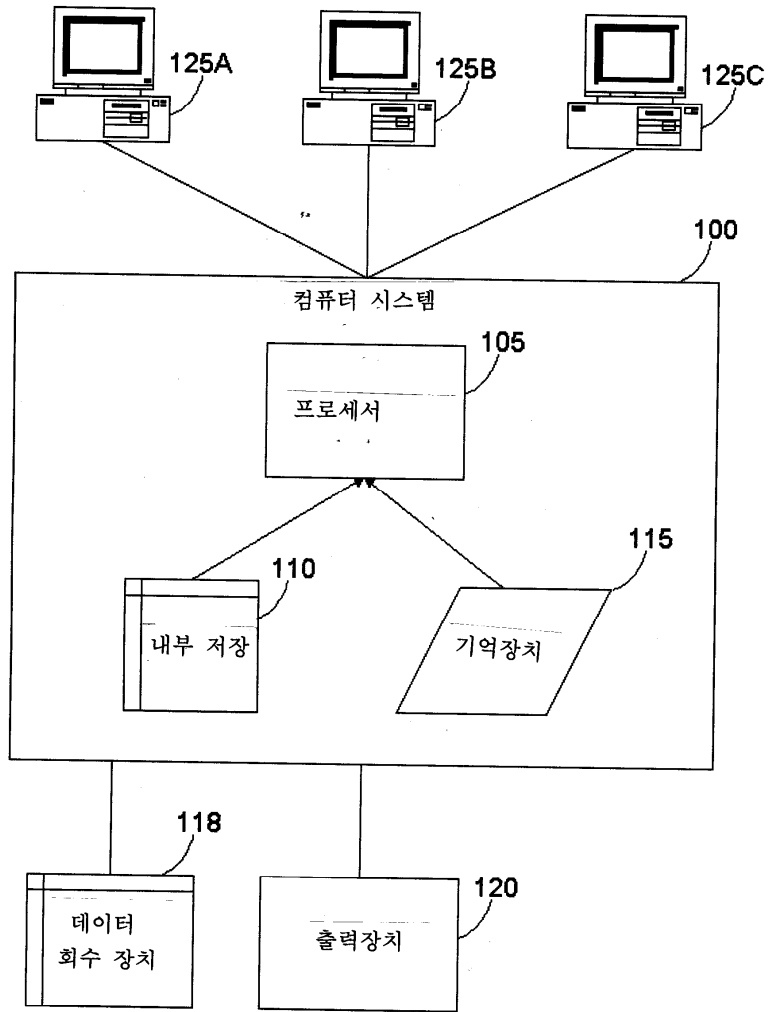
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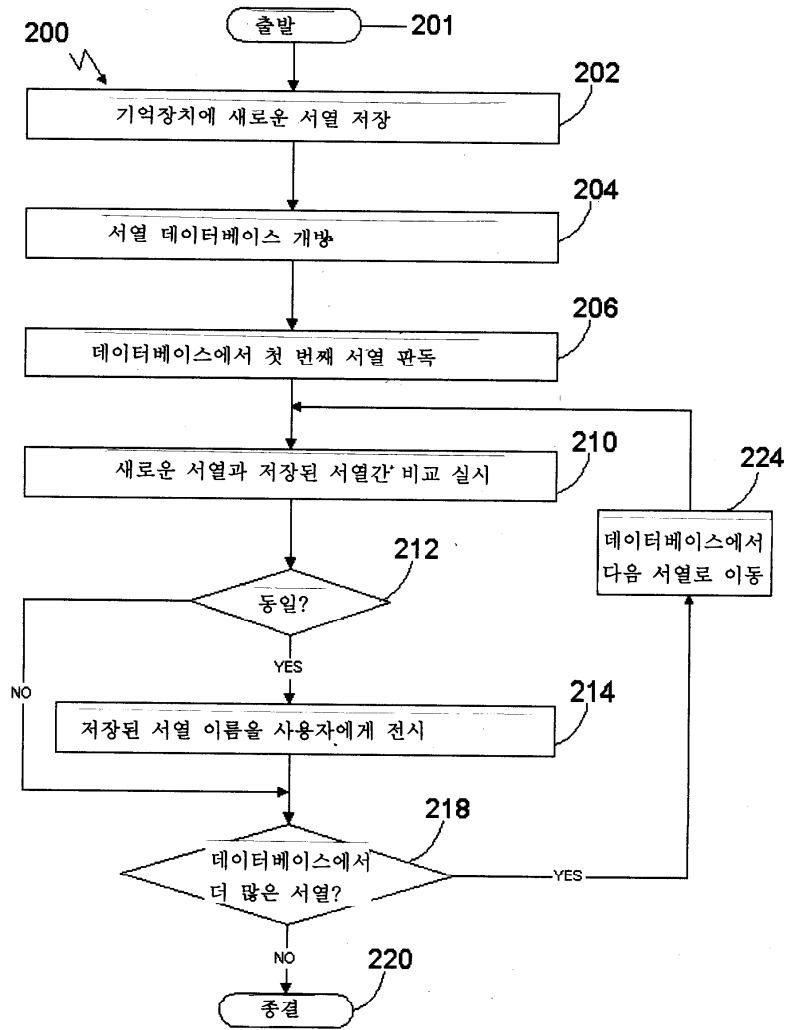
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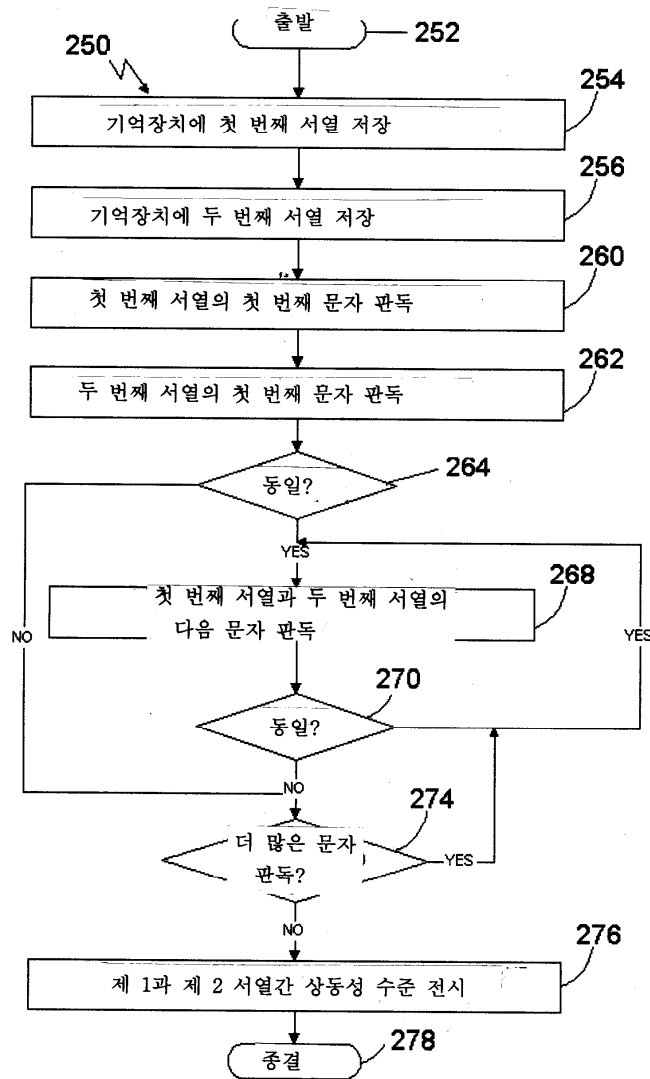
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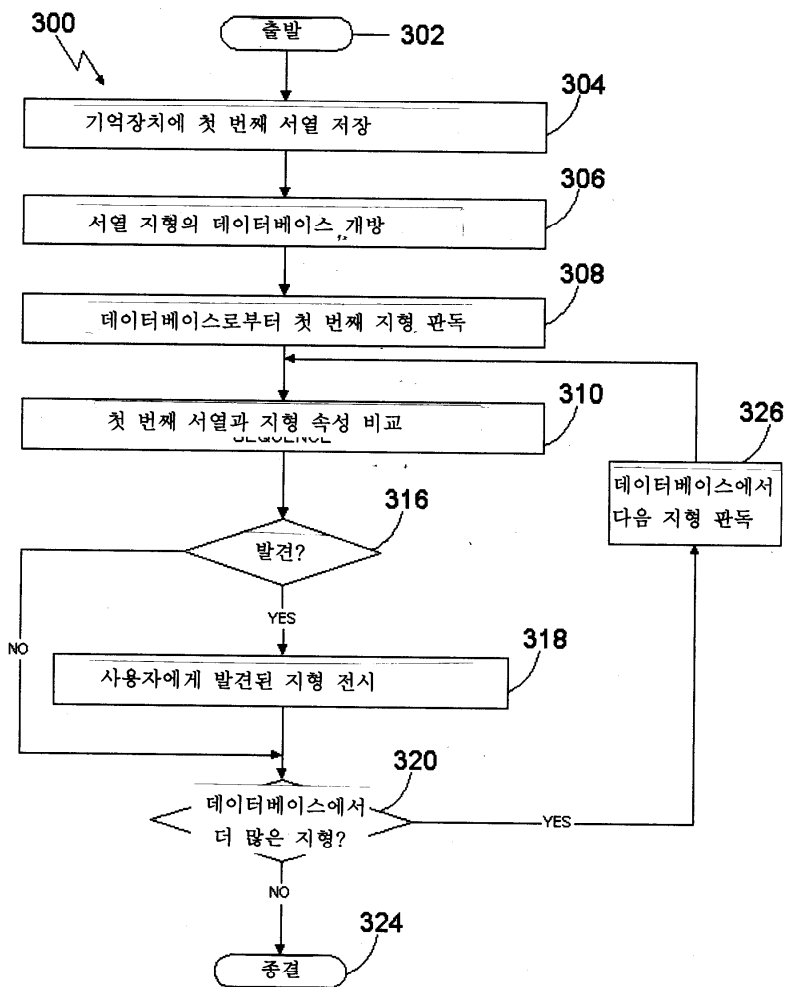


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Ile Ser Val Ile Ser Val Cys Met Asn Thr Pro Met Thr Phe Glu His

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Phe Leu Tyr Thr Ala Glu Met Ile Ala Lys Met His Ile Arg Gly Ile

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Glu Gln Ile Trp Ser Val Ser Ile Phe Leu Leu Phe Phe Leu Leu Leu			
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Ile Pro Asp Thr His Cys Ser Pro Glu Leu Glu Glu Gly Tyr Gln Cys			
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Pro Pro Gly Phe Lys Cys Met Asp Leu Glu Asp Leu Gly Leu Ser Arg			
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Gln Glu Leu Gly Tyr Ser Gly Phe Asn Glu Ile Gly Thr Ser Ile Phe			
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Ser Ser Leu His Lys Phe Glu Leu Leu Leu Val Ile Gly Thr Thr Leu	
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His Val Tyr Pro Asp Leu Tyr His Ser Gln Phe Thr Tyr Phe Gln Val  
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Asp Gln Lys Leu Arg Lys Ser Val Phe Ser Ile Arg Ala Arg Asn Leu				
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Leu Glu Lys Glu Thr Ala Val Thr Lys Ile Leu Arg Ala Cys Thr Arg				
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Thr Leu Thr Gln Asp His Ser Asn Thr Val Arg Tyr Arg Asn Ala Gln				
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Glu Met Lys Arg Lys Val Gln Glu Glu Glu Leu Arg Glu Asn His Pro				
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ttc acc ttc atc ttt gtt ctg gag gtt acc atg aag atc ata gca atg			3854
Phe Thr Phe Ile Phe Val Leu Glu Val Thr Met Lys Ile Ile Ala Met			
1250	1255	1260	
tcg cct gct ggc ttc tgg caa agc aga aga aac cga tac gat ctc ctg			3902
Ser Pro Ala Gly Phe Trp Gln Ser Arg Arg Asn Arg Tyr Asp Leu Leu			
1265	1270	1275	
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Val Thr Ser Leu Gly Val Val Trp Val Val Leu His Phe Ala Leu Leu			
1280	1285	1290	1295
aat gca tat act tac atg atg ggc gct tgt gtg att gta ttt agg ttt			3998
Asn Ala Tyr Thr Tyr Met Met Gly Ala Cys Val Ile Val Phe Arg Phe			
1300	1305	1310	
ttc tcc atc tgt gga aaa cat gta acg cta aag atg ctc ctc ttg aca			4046
Phe Ser Ile Cys Gly Lys His Val Thr Leu Lys Met Leu Leu Leu Thr			
1315	1320	1325	
gtg gtc gtc agc atg tac aag agc ttc ttt atc ata gta ggc atg ttt			4094
Val Val Val Ser Met Tyr Lys Ser Phe Phe Ile Ile Val Gly Met Phe			
1330	1335	1340	
ctc ttg ctg ctg tgt tac gct ttt gct gga gtt gtt tta ttt ggt act			4142
Leu Leu Leu Leu Cys Tyr Ala Phe Ala Gly Val Val Leu Phe Gly Thr			
1345	1350	1355	
gtg aaa tat ggg gag aat att aac agg cat gca aat ttt tct tcg gct			4190
Val Lys Tyr Gly Glu Asn Ile Asn Arg His Ala Asn Phe Ser Ser Ala			
1360	1365	1370	1375

gga aaa gct att acc gta ctg ttc cga att gtc aca ggt gaa gac tgg	4238
Gly Lys Ala Ile Thr Val Leu Phe Arg Ile Val Thr Gly Glu Asp Trp	
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aac aag att atg cat gac tgt atg gtt cag cct ccg ttt tgt act cca	4286
Asn Lys Ile Met His Asp Cys Met Val Gln Pro Pro Phe Cys Thr Pro	
1395 1400 1405	
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Asp Glu Phe Thr Tyr Trp Ala Thr Asp Cys Gly Asn Tyr Ala Gly Ala	
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ctt atg tat ttc tgt tca ttt tat gtc atc att gcc tac atc atg cta	4382
Leu Met Tyr Phe Cys Ser Phe Tyr Val Ile Ile Ala Tyr Ile Met Leu	
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aat ctg ctt gta gcc ata att gtg gag aat ttc tcc ttg ttt tat tcc	4430
Asn Leu Leu Val Ala Ile Ile Val Glu Asn Phe Ser Leu Phe Tyr Ser	
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act gag gag gac cag ctt tta agt tac aat gat ctt cgc cac ttt caa	4478
Thr Glu Glu Asp Gln Leu Leu Ser Tyr Asn Asp Leu Arg His Phe Gln	
1460 1465 1470	
atm ata tgg aac atg gtg gat gat aaa aga gag ggg gtg atc ccc acg	4526
Ile Ile Trp Asn Met Val Asp Asp Lys Arg Glu Gly Val Ile Pro Thr	
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Phe Arg Val Lys Phe Leu Leu Arg Leu Leu Arg Gly Arg Leu Glu Val	
1490 1495 1500	
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Asp Leu Asp Lys Asp Lys Leu Leu Phe Lys His Met Cys Tyr Glu Met	
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Glu Arg Leu His Asn Gly Gly Asp Val Thr Phe His Asp Val Leu Ser	
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Met Leu Ser Tyr Arg Ser Val Asp Ile Arg Lys Ser Leu Gln Leu Glu	
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gaa ctc ctg gcg agg gag cag ctg gag tac acc ata gag gag gag gtg	4766



Glu Leu Leu Ala Arg Glu Gln Leu Glu Tyr Thr Ile Glu Glu Glu Val  
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 gcc aag cag acc atc cgc atg tgg ctc aag aag tgc ctg aag cgc atc 4814  
 Ala Lys Gln Thr Ile Arg Met Trp Leu Lys Lys Cys Leu Lys Arg Ile  
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 Arg Ala Lys Gln Gln Gln Ser Cys Ser Ile Ile His Ser Leu Arg Glu  
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 Ser Gln Gln Gln Glu Leu Ser Arg Phe Leu Asn Pro Pro Ser Ile Glu  
 1600 1605 1610 1615  
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 Ser His Ser Val Ser Ser Val Asn Leu Arg Phe Gly Gly Arg Thr Thr  
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 Met Lys Ser Val Val Cys Lys Met Asn Pro Met Thr Asp Ala Ala Ser  
 1700 1705 1710  
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 Cys Gly Ser Glu Val Lys Lys Trp Trp Thr Arg Gln Leu Thr Val Glu  
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 Ser Asp Glu Ser Gly Asp Asp Leu Leu Asp Ile \*

1730

1735

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&lt;211&gt; 1738

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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 Ile Asn Lys Pro Trp Val His Ser Leu Leu Arg Ile Cys Ala Ile Ile  
 35 40 45  
 Ser Val Ile Ser Val Cys Met Asn Thr Pro Met Thr Phe Glu His Tyr  
 50 55 60  
 Pro Pro Leu Gln Tyr Val Thr Phe Thr Leu Asp Thr Leu Leu Met Phe  
 65 70 75 80  
 Leu Tyr Thr Ala Glu Met Ile Ala Lys Met His Ile Arg Gly Ile Val  
 85 90 95  
 Lys Gly Asp Ser Ser Tyr Val Lys Asp Arg Trp Cys Val Phe Asp Gly  
 100 105 110  
 Phe Met Val Phe Cys Leu Trp Val Ser Leu Val Leu Gln Val Phe Glu  
 115 120 125  
 Ile Ala Asp Ile Val Asp Gln Met Ser Pro Trp Gly Met Leu Arg Ile  
 130 135 140  
 Pro Arg Pro Leu Ile Met Ile Arg Ala Phe Arg Ile Tyr Phe Arg Phe  
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 Glu Leu Pro Arg Thr Arg Ile Thr Asn Ile Leu Lys Arg Ser Gly Glu  
 165 170 175  
 Gln Ile Trp Ser Val Ser Ile Phe Leu Leu Phe Phe Leu Leu Leu Tyr  
 180 185 190  
 Gly Ile Leu Gly Val Gln Met Phe Gly Thr Phe Thr Tyr His Cys Val  
 195 200 205  
 Val Asn Asp Thr Lys Pro Gly Asn Val Thr Trp Asn Ser Leu Ala Ile  
 210 215 220  
 Pro Asp Thr His Cys Ser Pro Glu Leu Glu Glu Gly Tyr Gln Cys Pro  
 225 230 235 240  
 Pro Gly Phe Lys Cys Met Asp Leu Glu Asp Leu Gly Leu Ser Arg Gln  
 245 250 255  
 Glu Leu Gly Tyr Ser Gly Phe Asn Glu Ile Gly Thr Ser Ile Phe Thr  
 260 265 270  
 Val Tyr Glu Ala Ala Ser Gln Glu Gly Trp Val Phe Leu Met Tyr Arg  
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Ala Ile Asp Ser Phe Pro Arg Trp Arg Ser Tyr Phe Tyr Phe Ile Thr  
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 Ile Ile Glu Thr Phe Ala Glu Ile Arg Val Gln Phe Gln Gln Met Trp  
 325 330 335  
 Gly Ser Arg Ser Ser Thr Thr Ser Thr Ala Thr Thr Gln Met Phe His  
 340 345 350  
 Glu Asp Ala Ala Gly Gly Trp Gln Leu Val Ala Val Asp Val Asn Lys  
 355 360 365  
 Pro Gln Gly Arg Ala Pro Ala Cys Leu Gln Lys Met Met Arg Ser Ser  
 370 375 380  
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 385 390 395 400  
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 405 410 415  
 Glu Phe Tyr Leu Ala Glu Val Ala Phe Thr Val Leu Phe Asp Leu Glu  
 420 425 430  
 Ala Leu Leu Lys Ile Trp Cys Leu Gly Phe Thr Gly Tyr Ile Ser Ser  
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 Ser Leu His Lys Phe Glu Leu Leu Leu Val Ile Gly Thr Thr Leu His  
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 Val Tyr Pro Asp Leu Tyr His Ser Gln Phe Thr Tyr Phe Gln Val Leu  
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 Arg Val Val Arg Leu Ile Lys Ile Ser Pro Ala Leu Glu Asp Phe Val  
 485 490 495  
 Tyr Lys Ile Phe Gly Pro Gly Lys Lys Leu Gly Ser Leu Val Val Phe  
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 Thr Ala Ser Leu Leu Ile Val Met Ser Ala Ile Ser Leu Gln Met Phe  
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 Cys Phe Val Glu Glu Leu Asp Arg Phe Thr Thr Phe Pro Arg Ala Phe  
 530 535 540  
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 545 550 555 560

Asp Gln Thr Leu Asn Ala Val Gly His Met Trp Ala Pro Val Val Ala  
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 595 600 605  
 Lys Lys Leu Lys Gln Leu Lys Gln Ser Glu Ala Asn Ala Asp Thr Lys  
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 Glu Lys Leu Pro Leu Arg Leu Arg Ile Phe Glu Lys Phe Pro Asn Arg  
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 Pro Gln Met Val Lys Ile Ser Lys Leu Pro Ser Asp Phe Thr Val Pro  
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 Lys Ile Arg Glu Ser Phe Met Lys Gln Phe Ile Asp Arg Gln Gln Gln  
 660 665 670  
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 675 680 685  
 Cys Asp His Ser Lys Arg Ser Ala Ile Glu Asp Asn Lys Tyr Ile Asp  
 690 695 700  
 Gln Lys Leu Arg Lys Ser Val Phe Ser Ile Arg Ala Arg Asn Leu Leu  
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 Glu Lys Glu Thr Ala Val Thr Lys Ile Leu Arg Ala Cys Thr Arg Gln  
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 Arg Met Leu Ser Gly Ser Phe Glu Gly Gln Pro Ala Lys Glu Arg Ser  
 740 745 750  
 Ile Leu Ser Val Gln His His Ile Arg Gln Glu Arg Arg Ser Leu Arg  
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 His Gly Ser Asn Ser Gln Arg Ile Ser Arg Gly Lys Ser Leu Glu Thr  
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 Leu Thr Gln Asp His Ser Asn Thr Val Arg Tyr Arg Asn Ala Gln Arg  
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 820 825 830

Phe Asp Lys Pro Leu Phe Ile Val Gly Arg Glu His Arg Phe Arg Asn  
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 850 855 860  
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 Met His Ala Pro Thr Leu Gln Ile Ala Glu Tyr Val Phe Val Ile Phe  
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 Pro Leu Arg Ile Phe Lys Leu Val Pro Gln Met Arg Lys Val Val Arg  
 995 1000 1005  
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Met Leu Ala Leu Phe Glu Val Leu Ser Leu Lys Gly Trp Val Glu Val  
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 His Val Phe Val Phe Leu Gly Cys Met Ile Gly Leu Thr Leu Phe Val  
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 Gly Val Val Ile Ala Asn Phe Asn Glu Asn Lys Gly Thr Ala Leu Leu  
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 Thr Val Asp Gln Arg Arg Trp Glu Asp Leu Lys Ser Arg Leu Lys Ile  
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 Ala Gln Pro Leu His Leu Pro Pro Arg Pro Asp Asn Asp Gly Phe Arg  
 1185                    1190                    1195                    1200  
 Ala Lys Met Tyr Asp Ile Thr Gln His Pro Phe Phe Lys Arg Thr Ile  
                          1205                    1210                    1215  
 Ala Leu Leu Val Leu Ala Gln Ser Val Leu Leu Ser Val Lys Trp Asp  
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 Val Glu Asp Pro Val Thr Val Pro Leu Ala Thr Met Ser Val Val Phe  
                          1235                    1240                    1245  
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                          1250                    1255                    1260  
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 Thr Ser Leu Gly Val Val Trp Val Val Leu His Phe Ala Leu Leu Asn  
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 Ser Ile Cys Gly Lys His Val Thr Leu Lys Met Leu Leu Leu Thr Val  
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 Lys Tyr Gly Glu Asn Ile Asn Arg His Ala Asn Phe Ser Ser Ala Gly  
                          1365                    1370                    1375

Lys Ala Ile Thr Val Leu Phe Arg Ile Val Thr Gly Glu Asp Trp Asn  
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ccatatatgc ttgtaaagag agggagtcta cagatatttg gagaaggac attctgggtg	360
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