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(51) 。 Int. Cl.7
C07K 16/18
G01N 33/53
C12Q 1/68

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(43)

10-2005-0004773
2005 01 12

(21) 10-2004-7011462 ()
(22) 2004 07 23
(62) 10-2001-7011361
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2004 07 23

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(86) PCT/US1999/028551
(86) 1999 12 02

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WO 2000/53750
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(30) 60/162,506 1999 10 29 (US)

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1		DNA44194-1317		PRO381
cDNA		(1)		
2	1	1	PRO381	(2)
3		DNA66520-1536		PRO1269
cDNA		(6)		
4	3	6	PRO1269	(7)
5		DNA68874-1622		PRO1410
cDNA		(8)		
6	5	8	PRO1410	(9)
7		DNA76396-1698		PRO1755
cDNA		(10)		
8	7	10	PRO1755	(11)
9		DNA71169-1709		PRO1780
cDNA		(12)		
10	9	12	PRO1780	(1
3)				
11		DNA77652-2505		PRO1788
cDNA		(17)		

12 18)	11	17		PRO1788	(
13 cDNA		DNA77631 - 2537 (22)	, ,	PRO3434	
14 23)	13	22		PRO3434	(
15 cDNA		DNA82307 - 2531 (24)	, ,	PRO1927	
16 25)	15	24		PRO1927	(
17 cDNA		DNA56049 - 2543 (26)	, ,	PRO3567	
18 27)	17	26		PRO3567	(
19 cDNA		DNA59218 (28)	, ,	PRO1295	
20 29)	19	28		PRO1295	(
21 cDNA		DNA60618 - 1557 (30)	, ,	PRO1293	
22 31)	21	30		PRO1293	(
23 cDNA		DNA65409 - 1566 (32)	, ,	PRO1303	
24 33)	23	32		PRO1303	(
25 cDNA		DNA84927 - 2585 (34)	, ,	PRO4344	
26 35)	25	34		PRO4344	(
27 cDNA		DNA92256 - 2596 (39)	, ,	PRO4354	
28 40)	27	39		PRO4354	(

29		DNA83505 - 2606			PRO4397
cDNA		(41)			
30	29	41			PRO4397 (
42)					
31		DNA92264 - 2616			PRO4407
cDNA		(46)			
32	31	46			PRO4407 (
47)					
33		DNA73744 - 1665			PRO1555
cDNA		(48)			
34	33	48			PRO1555 (
49)					
35		DNA61870			PRO1096 c
DNA		(50)			
36	35	50			PRO1096 (
51)					
37		DNA83014			PRO2038 cD
NA		(52)			
38	37	52			PRO2038 (
53)					
39		DNA88273			PRO2262
cDNA		(54)			
40	39	54			PRO2262 (
55)					

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[1993]).

(Boring et al., CA Cancer J. Clin., 43:7

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(,) 가 (Alitalo et al., Adv. Cancer Res., 47:235-281 [1986]).

(proto-oncogene) (EGFR) 185 k ErbB2 (her2 c-erbB-2 (Slamon et al., Science, 235: 177-182[1987]; Slamon et al., Science, 244:707-712[1989]).

(p185 HER2 ; HER2) ErbB2 (erbB2) 25% 30% (Schwab et al., Genes Chromosomes Cancer, 1:181-193[1990]; Alitalo et al.). , erbB2 (Slamon et al., [1987] [1989] ; Ravdin and Chamness, Gene, 159:19-27[1995]; Hynes and Stern, Biochim. Biophys. Acta. 1198:165-184[1994]), CMF() (Baselga et al., Oncology, 11(3 Suppl 1):43-48[1997]). , erbB2 , HER2- 가 (taxane) -ErB2(-HER2) (murine) (Herceptin)) 가 (Baselga et al., J. Clin. Oncol., 14:737-744 [1996]).

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ng region, CDR) (framework) (FR) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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가 가

가 -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262

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가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

DNA가

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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407,

-PRO1555, -PRO1096, -PRO2038 -PRO2262 가
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PR
O1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1
096, PRO2038 PRO2262

(a) (b)
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PR
O1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1
096, PRO2038 PRO2262

(a) -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO17
80, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PR
O4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262
(b) -PRO381, -PRO1269, -PR
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PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096,
-PRO2038 -PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO343
4, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555,
PRO1096, PRO2038 PRO2262

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-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1
780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PR
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PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PR
O4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1
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6, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1
780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO439
7, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 () ()

-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PR
O1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -
PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262 ,
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, , -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PR
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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 () -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 P

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 () , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (a)

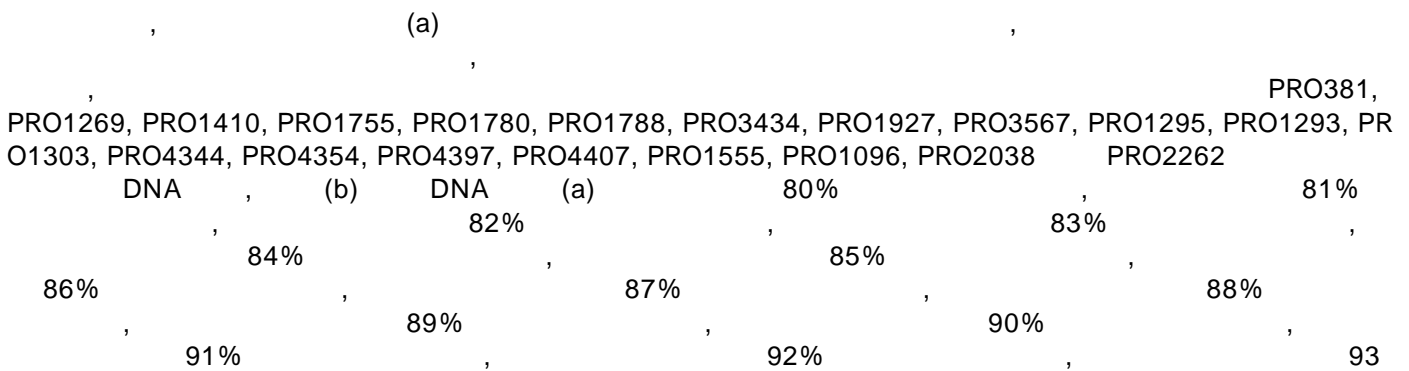
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (b)

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (b)

B. 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262



%, 98%, 96%, 94%, 97%, 95%, 99%

(a) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 cDNA DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(b) DNA (a) 80% 83% 81% 84% 82% 85% 86% 87% 89% 90% 88% 91% 92% 93% 94% 95% 96% 97% 98% 99%

가 (a) ATCC cDNA 80% 83% 81% (b) DNA (a) 85% 86% 84% 82% 87% 88% 89% 90% 91% 92% 93% 94% 95% 96% 97% 98% 99%

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262

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가 20 가 30 가 40 가 50 가 60 가 70 가 80 가 90 가 100 가 110 가 120

가 130 , 가 140 ,
 가 150 , 가 160 ,
 가 170 , 가 180 ,
 가 190 , 가 200 ,
 250 , 가 300 , 가 350 ,
 , 가 400 , 가 450 ,
 , 가 500 , 가 600 ,
 , 가 700 , 가 800 ,
 , 가 900 , 가 1000 ,
 , 10% 가 . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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80% , 81% , 82% ,
 , 83% , 84% ,
 , 85% , 86% , 87% ,
 % , 88% , 89% ,
 , 90% , 91% ,
 , 92% , 93% , 94% ,
 , 95% , 96% ,
 , 97% , 98% ,
 99% ,

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

가 , ATCC , cDNA ,
 , 80% , 81% , 82% ,
 , 83% , 84% ,
 , 85% , 86% ,
 , 87% , 88% , 89% ,
 , 90% , 91% ,
 , 92% , 93% ,
 , 94% , 95% , 96% ,

99% 97% 98%
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

가
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

80% 81% 82%
83% 84% 85%
86% 87% 88%
89% 90%
91% 92% 93%
94% 95% 96%
97% 98% 99%

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262

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(Murakami et al., The Molecular Basis of Cancer, Mendelsohn and Israel, eds., 'Cell cycle regulation, oncogenes, and antineoplastic drugs' (WB Saunders: Philadelphia, 1995), Chapter 1, 13)

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 , 'N', 'L' 'V'

[1a]

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M -8 /* value of a match with a stop */

int _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */ {-1, -2, -2, -2, 2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};
    
```

[1b]

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
    short          n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
};

struct diag {
    int            score;      /* score at last jmp */
    long           offset;     /* offset of prev block */
    short          jmp;        /* current jmp index */
    struct jmp     jp;         /* list of jmps */
};

struct path {
    int            spc;        /* number of leading spaces */
    short          n[JMPS]; /* size of jmp (gap) */
    int            x[JMPS]; /* loc of jmp (last elem before gap) */
};

char              *ofile;      /* output file name */
char              *name[2];    /* seq names: getseqs() */
char              *prog;       /* prog name for err msgs */
char              *seq[2];     /* seqs: getseqs() */
int               dmax;        /* best diag: nw() */
int               dmax0;       /* final diag */
int               dna;         /* set if dna: main() */
int               endgaps;     /* set if penalizing end gaps */
int               gapx, gapy;   /* total gaps in seqs */
int               len0, len1;   /* seq lens */
int               ngapx, ngapy; /* total size of gaps */
int               smax;        /* max score: nw() */
int               *xbm;        /* bitmap for matching */
long              offset;     /* current offset in jmp file */
struct            diag         *dx; /* holds diagonals */
struct            path         pp[2]; /* holds path for seqs */

char              *calloc(), *malloc(), *index(), *strcpy();
char              *getseq(), *g_malloc();

```

[1c]

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"

static  _dbval[26] = {
        1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static  _pbval[26] = {
        1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
        128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
        1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
        1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
int      ac;
char     *av[];
{
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";       /* output file */

    nw();                       /* fill in the matrix, get the possible jmps */
    readjmps();                 /* get the actual jmps */
    print();                     /* print stats, alignment */

    cleanup();                  /* unlink any tmp files */
}

```

[1d]

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
    char      *px, *py;      /* seqs and ptrs */
    int       *ndely, *dely; /* keep track of dely */
    int       ndelx, delx;   /* keep track of delx */
    int       *tmp;         /* for swapping row0, row1 */
    int       mis;          /* score for each type */
    int       ins0, ins1;    /* insertion penalties */
    register  id;           /* diagonal index */
    register  ij;           /* jmp index */
    register  *col0, *col1; /* score for curr, last row */
    register  xx, yy;       /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0; /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

[1e]

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
  mis = col0[yy-1];
  if (dna)
    mis += (xbrm[*px-'A']&xbrm[*py-'A'])? DMAT : DMIS;
  else
    mis += _day[*px-'A'][*py-'A'];

  /* update penalty for del in x seq;
   * favor new del over ongong del
   * ignore MAXGAP if weighting endgaps
   */
  if (endgaps || ndely[yy] < MAXGAP) {
    if (col0[yy] - ins0 >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else {
      dely[yy] -= ins1;
      ndely[yy]++;
    }
  } else {
    if (col0[yy] - (ins0+ins1) >= dely[yy]) {
      dely[yy] = col0[yy] - (ins0+ins1);
      ndely[yy] = 1;
    } else
      ndely[yy]++;
  }

  /* update penalty for del in y seq;
   * favor new del over ongong del
   */
  if (endgaps || ndelx < MAXGAP) {
    if (col1[yy-1] - ins0 >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else {
      delx -= ins1;
      ndelx++;
    }
  } else {
    if (col1[yy-1] - (ins0+ins1) >= delx) {
      delx = col1[yy-1] - (ins0+ins1);
      ndelx = 1;
    } else
      ndelx++;
  }

  /* pick the maximum score; we're favoring
   * mis over any del and delx over dely
   */
}

```

[1f]

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (ldna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
    dx[id].score = delx;
}
else {
    coll[yy] = dely[yy];
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (ldna || (ndely[yy] >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = -ndely[yy];
    dx[id].jp.x[ij] = xx;
    dx[id].score = dely[yy];
}
if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        coll[yy] -= ins0+ins1*(len1-yy);
    if (coll[yy] > smax) {
        smax = coll[yy];
        dmax = id;
    }
}
if (endgaps && xx < len0)
    coll[yy-1] -= ins0+ins1*(len0-xx);
if (coll[yy-1] > smax) {
    smax = coll[yy-1];
    dmax = id;
}
tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)coll);
}

```

[1g]

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC 3
#define P_LINE 256 /* maximum output line */
#define P_SPC 3 /* space between name or num and seq */

extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

print() print
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

[1h]

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)                                getmat
    int    lx, ly;      /* "core" (minus endgaps) */
    int    firstgap, lastgap;  /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
    char     outx[32];
    double   pct;
    register n0, n1;
    register char *p0, *p1;

    /* get total matches, score
     */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbrn[*p0-'A']&xbrn[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
     * if penalizing endgaps, base is the shorter seq
     * else, knock off overhangs and take shorter core
     */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
}

```


[1i]

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}
fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapy, (dna)? "base":"residue", (ngapy == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}
}
if (dna)
    fprintf(fx,
        "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINSO, DINS1);
else
    fprintf(fx,
        "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINSO, PINS1);
if (endgaps)
    fprintf(fx,
        "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
        lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
else
    fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;       /* lengths of stripped file names */
static      ij[2];      /* jmp index for a path */
static      nc[2];      /* number at start of current line */
static      ni[2];      /* current elem number -- for gapping */
static      siz[2];     /* ptr to current element */
static char *ps[2];     /* ptr to next output char slot */
static char *po[2];     /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = outf[i];
    }
}

```

...getmat

pr_align

[1j]

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i] + 1];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + 1];
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';
}

```

...pr_align

dumpblock

[1k]

...dumpblock

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
        putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)                                nums
{
    int    ix;        /* index in out[] holding seq line */
    char    nline[P_LINE];
    register    i, j;
    register char    *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax + P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i % 10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0) ? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j % 10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)                                putline
{
    int    ix;

```

[11]

...putline

```

int          i;
register char *px;

for (px = namex[ix], i = 0; *px && *px != '\0'; px++, i++)
    (void)putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void)putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void)putc(*px&0x7F, fx);
(void)putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
    int          i;
    register char *p0, *p1, cx, *px;

    if (!*out[0] || (*out[0] == ' ' && *(p0[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(p0[1]) == ' '))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbrm[*p0-'A']&xbrm[*p1-'A']) {
                cx = '*';
                nm++;
            }
            else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                cx = '.';
            else
                cx = ' ';
        }
        else
            cx = ' ';
        *px++ = cx;
    }
    *px++ = '\n';
    *px = '\0';
}

```

stars

[1m]

stripname

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
{
    char *pn; /* file name (may be path) */

    register char *px, *py;

    py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;

    if (py)
        (void)strcpy(pn, py);
    return(strlen(pn));
}

```

[1n]

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_malloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejms() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char *jname = "/tmp/homgXXXXXX"; /* tmp file for jmps */
FILE *fj;

int cleanup(); /* cleanup tmp file */
long lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i) cleanup
{
    int i;
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char *
getseq(file, len) getseq
{
    char *file; /* file name */
    int *len; /* seq len */

    char line[1024], *pseq;
    register char *px, *py;
    int natgc, tlen;
    FILE *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
}

```

[10]

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ':' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU",*(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

char *
g_alloc(msg, nx, sz)                                g_alloc
char *msg; /* program, calling routine */
int nx, sz; /* number and size of elements */
{
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()                                        readjmps
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (j = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;
        }
    }
}

```

[1p]

...readjumps

```

    if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
    }
    else
        break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) { /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;

        /* id = xx - yy + len1 - 1
        */
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy ++;
        ngapy -= siz;
    /* ignore MAXGAP when doing endgaps */
        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
        i1 ++;
    }
    else if (siz > 0) { /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx ++;
        ngapx += siz;
    /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
        i0 ++;
    }
}
else
    break;
}

/* reverse the order of jumps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}

```

[1q]

writejumps

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
    int    ix;
{
    char    *mktemp0;

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}

```

[2a]

PRO XXXXXXXXXXXXXXXX (아미노산 15개 길이)
 비교 단백질 XXXXXYYYYYYY (아미노산 12개 길이)

아미노산 서열 동일성(%) =

(ALIGN-2에 의해 두 폴리펩티드 서열 사이에서 동일하게 매치되는 것으로 결정된 아미노산 잔기의 수) ÷ (PRO 폴리펩티드의 아미노산 잔기의 총수)

5 ÷ 15 = 33.3%

[2b]

PRO XXXXXXXXXXX (아미노산 10개 길이)
 비교 단백질 XXXXXYYYYYYZZYZ (아미노산 15개 길이)

아미노산 서열 동일성(%) =

(ALIGN-2에 의해 두 폴리펩티드 서열 사이에서 동일하게 매치되는 것으로 결정된 아미노산 잔기의 수) ÷ (PRO 폴리펩티드의 아미노산 잔기의 총수)

5 ÷ 10 = 50%

[2c]

PRO-DNA NNNNNNNNNNNNN (뉴클레오티드 14개 길이)
 비교 DNA NNNNNLLLLLLLLL (뉴클레오티드 16개 길이)

핵산 서열 동일성(%) =

(ALIGN-2에 의해 두 핵산 서열 사이에서 동일하게 매치되는 것으로 결정된 뉴클레오티드의 수) ÷ (PRO-DNA 핵산 서열의 총 뉴클레오티드수)

6 ÷ 14 = 42.9%

[2d]

PRO-DNA NNNNNNNNNNN (뉴클레오티드 12개 길이)
 비교 DNA NNNLLLLV (뉴클레오티드 9개 길이)

핵산 서열 동일성(%) =

(ALIGN-2에 의해 두 핵산 서열 사이에서 동일하게 매치되는 것으로 결정된 뉴클레오티드의 수) ÷ (PRO-DNA 핵산 서열의 총 뉴클레오티드수)

4 ÷ 12 = 33.3%

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262 (%)' PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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ALIGN, ALIGN-2 Megalign (DNASTAR)

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A B , B , B) :

X/Y x100

, X A B ALIGN-2 A 가 B
, Y B A (%) A B A 가 B (%)
, B A , 2a 2b 'PRO'
(%)

T2(Altschul et al., Nucleic Acids Res., 25:3389-3402 (1997))
(http://www.ncbi.nlm.nih.gov)

가 = 10, = 15/5, e- = 0.01, = 25,
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NCBI-BLAST2가

A (%) (A B , B , B) :

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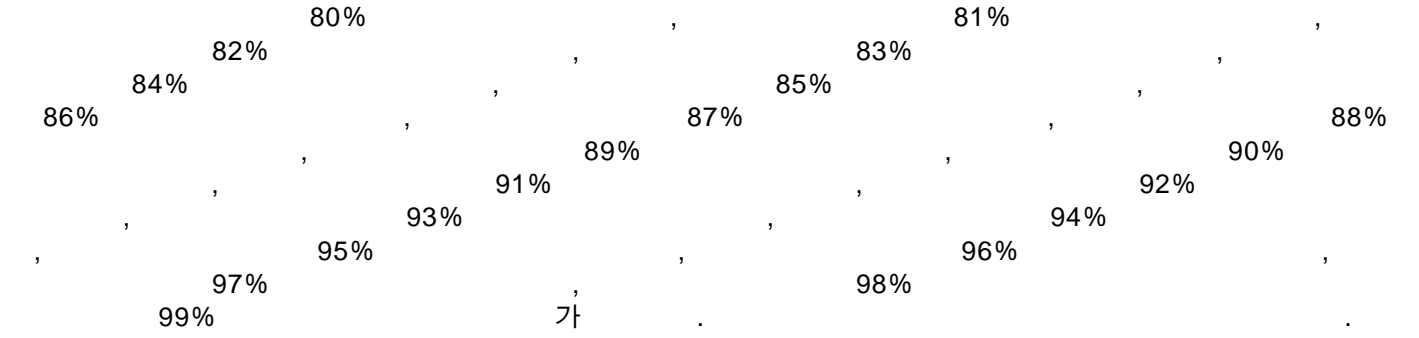
, X NCBI-BLAST2 NCBI-BLAST2 A 가
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y 266:460-80 (1996))

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BLAST, BLAST-2, ALIGN, ALIGN-2, Megalign (DNASTAR)

ALIGN-2, ALIGN-2, 20559, D.C., U510087, ALIGN-2, UNIX V4.0D, UNIX, ALIGN-2

D, D, D, D, D, C, (%) (C)

W/Z x 100

W, C, D, Z, D, ALIGN-2, C, 가, D, D, C, (%) C, D, 2c, 2d, 'PRO-DNA', (%)

hul et al., Nucleic Acids Res. 25:3389-3402 (1997) (http://www.ncbi.nlm.nih.gov)

(%) ALIGN-2, NCBI-BLAST2(Altschul), NCBI-BLAST2, NCBI-BLAST2, 가, = 15/5, - e- = 0.01, - = 25, = 10, = 25, = BLOSUM62

NCBI-BLAST2가, D, D, D, C, (%) (C), D, D, D, (%)

W/Z x 100

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WU-BLAST-2

, (b)
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B , B , B B , B , B A (%)
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X/Y x100

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 (Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers (1995))

(1) 가 가 , (2)
 50 0.015M /0.0015M /0.1% /0.1% /0.1% /50mM
 42 (pH 6.5) 750mM 0.1% , 75mM 50% (/)
 (3) 42 50% , 5x SSC (0.75M NaCl, 0.075M DNA (/
), 50mM (pH 6.8), 0.1% , 5x (Denhardt) , 0.2x SSC (/
 50µg/ml), 0.1% SDS, 10% , 42 0.1x SSC
), 55 50% , 55 EDTA가

(Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press 1989)
 SDS %) , 15mM) , 50mM (pH 7.6), 5x 20% , 5x SSC (150mM
 DNA 37 , 10% , 37 50
 1x SSC

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CDR

CDR FR
(Kabat et al., NIH Publ. N
o. 91-3242, Vol. , pages 647-669 (1991)).

가
'CDR'(가 24 34(L1), 50 56(L2) 89 97(L3), 가
31 35(H1), 50 65(H2) 95 102(H3); Kabat et al., Sequences of Proteins of Immu
nological Interests, 5th Ed. Public Health Services, National Institute of Health, Bethesda, MD. [1990])
()' 가 '(가 26 32(L1), 50 52(L2) 91 9
6(L3), 가 26 32(H1), 53 55(H2) 96 101(H3); Clothia and Lesk, J. Mo
l. Biol., 196:901-917[1987])
가 가 'FR'

가
Fab, Fab', F(ab')₂ Fv ; (diabody); 가 (Zapata et al., Protein Eng. 8(10):105
7-1062 (1995); ;

(papain) 2 가 'Fab' ,
가 F(ab')₂ 'Fc' , 2

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가 가 가 가
CDR 3 가 V_H-V_L 가 가 CDR
Fv) 가 (3 CDR

, Fab 1 (CH1) . Fab (hinge)
Fab' Fab'-SH CH1 가 가
Fab' F(ab')₂ Fab'

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A, IgD, IgE, IgG IgM 5 가 , (), IgG1, IgG2, IgG
3, IgG4, IgA IgA2 . 3
, , μ .

가 , , ,
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가
(Kohler et al., Nature, 256:495[1975])
DNA (4,816,576)
(Clackson et al., Nature, 352:624-628[1991] Marks et al., J. Mol. Biol., 222:
581-597(1991))

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() (4,816,567 ;

Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855[1984]).

(V_H , V_L) 가 (Fv, Fab, Fab', F(ab')₂)
 (CDR)
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 CDR FR
 (Fc)
 (Jones et al., Nature, 321: 522-525 (1986); Riechmann et al.,
 Nature, 332: 323-329 (1988); Presta, Curr. Op. Struct. Biol. 2:593-596 (1992)).
 PRIMATIZED()

Fv' 'sFv' V_H V_L
 , Fv sFv가 V_H V_L
 (sFv (Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Ro
 senburg Moore eds., Springer-Verlag, New York, pp. 269-315 (1994))).

(diabody)' 가 (V_L) 가 (V_H) ($V_H - V_L$) , 2 가 2
 404,097 , WO93/11611
 (Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993))

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 (1) (Lowry) 95 % , 가 99
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 SDS-PAGE

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 , I-131, I-123, I-125, Y-90, Re-188, Re-186, At-211, Cu-67, Bi-212
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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
'PRO381', 'PRO1269', 'PRO1410', 'PRO1755', 'PRO1780', 'PRO1788', 'PRO3434', 'PRO1927', 'PRO3567', 'PRO1295', 'PRO1293', 'PRO1303', 'PRO4344', 'PRO4354', 'PRO4397', 'PRO4407', 'PRO1555', 'PRO1096', 'PRO2038' PRO2262

PRO1096, PRO2038 PRO2262 cDNA ATCC

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
가

B. PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
DNA () PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
5,364,934

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262, PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262, PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262, PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 N- C-
 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (PCR)

DNA DNA
 PCR 5' 3' , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가
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3

3

[3]

Ala(A)	val, leu, ile	val
Arg(R)	lys, gln, asn	lys
Asn(N)	gln, his, lys, arg	gln
Asp(D)	glu	glu

Cys(C)	ser	ser
Gln(Q)	asn	asn
Glu(E)	asp	asp
Gly(G)	pro, ala	ala
His(H)	asn, gln, lys, arg	arg
Ile(I)	leu, val, met, ala, phe,	leu
Leu(L)	, ile, val, met, ala, phe	ile
Lys(K)	arg, gln, asn	arg
Met(M)	leu, phe, ile	leu
Phe(F)	leu, val, ile, ala, tyr	leu
Pro(P)	ala	ala
Ser(S)	thr	thr
Thr(T)	ser	ser
Trp(W)	tyr, phe	tyr
Tyr(Y)	trp, phe, thr, ser	phe
Val(V)	ile, leu, met, phe, ala,	leu

- (a) , (b) , (c)
- :
- (1) : , met, ala, val, leu, ile;
 - (2) : cys, ser, thr;
 - (3) : asp, glu;
 - (4) : asn, gln, his, lys, arg;
 - (5) : gly, pro;
 - (6) ; trp, tyr, phe.

() , PCR (Carter et al., Nucl. Acids Res.,13:4331 (1986); Zoller et al., Nucl. Acids Res.,10:6487 (1987)), (Wells et al., Gene,34:315 (1985)), (Wells et al., Philos. Trans. R. Soc. London SerA,317:415 (1986)) DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA , 가 , 가 (Cunningham and Wells, Science, 244: 1081-1085 (1989)). (Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)). (isoteric)

C. PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 N-

C- PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

1,1- ()-2- , 3,3'- () , N- 4- , -N- -1,8-) , -3- [(p-)]

(T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86(1983)), N- C- 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

() PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가 (O-

). PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA DNA

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

1987 9 11 WO87/05330 (Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981))

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(Hakimuddin, et al., Arch. Biochem. Biophys., 259:52(1987) Edge et al., Anal. Biochem., 118:131(1981))

(Thotakura et al., Meth. Enzymol., 138:350(1987)).

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

4,640,835 , 4,496,689 , 4,301,144 , 4,670,417 ,

4,791,192 4,179,337

(PEG),

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038

PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038

PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(poly - His) (poly - His - gly) , flu HA 12CA5 (Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)), c-myc 8F9, 3C7, 6E10, G4, B7 9E10

(Evan et al., Molecular and Cellular Biology, 5:3610-3636 (1985)),

D

(gD) (Paborsky et al., Protein Engineering, 3(6):547-553 (1990))

Flag- (Hopp et al., BioTechnology, 6:1204-1210 (1988)), KT3 (Martin et al., Science, 255:192-194 (1992)),

(Martin et al., Science, 255:192-194 (1992)),

6 (1991)) T7 10 (Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)) T7 10 (Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990))가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

2가

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IgG

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Ig PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

가 (

IgG1

, CH2

CH3, , CH1, CH2 CH3

, 1995 6

27 5,428,130

D. PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 (Stewart et al., Solid -Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)).

(Applied Biosystems Peptide Synthesizer)()
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

a. PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 DNA , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 mRNA 가 cDNA

O1780,	PRO1788,	PRO3434,	PRO1927,	PRO3567,	PRO1295,	PRO1293,	PR
O1303,	PRO4344,	PRO4354,	PRO4397,	PRO4407,	PRO1555,	PRO1096,	PR
O2038	PRO2262 DNA					cDNA	

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 20 80)
 cDNA (Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Haror Laboratory Press, 1989))

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PCR (Sambrook et al., ; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Haror Laboratory Press, 1995)).

cDNA 가 (false positive)
 , ³²P- DNA ATP (Sambrook et al.,)

GenBank

()

(Sambrook et al.,) , cDNA mRNA cDNA

b.

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

, pH (Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) Sambrook et al.,)

electroporation) CaCl₂, CaPO₄, - (

(Sambrook et al.,)

(*Agrobacterium tumefaciens*)

(Shaw et al., Gene , 23 :315(1983) 1989 6 29 WO89/05859)

(Graham and van d

er Eb, Virology, 52:456-457 (1978))

4,399,216

(Van Solinge

n et al., J. Bact., 130:949(1977) Hsiao et al., Proc. Natl. Acad. Sci.(USA), 76:3829(1979))

DNA

가

(Keown et al., Methods in Enzymology, 185:527-537 (1990)

Mansour et al., N

ature, 336:348-352 (1988))

DNA

가

(*E. coli*)

(Enterobacteriaceae)

K12

MM294 (ATCC 31,446),

X1776(ATCC 31,537),

W3110(ATCC 27,325)

K5 772(ATCC 53,635)

(*Eshcerichia*),

(*Enterobacter*),

(*Erwinia*),

(*Klebsiella*),

(*Prot*

eus), (*Salmonella*)

(*Salmonella typhimurium*),

(*Serratia*)

(*Serratia marcescans*)

(*Shigella*)

(*Enterobacteria*

ceae), (*Bacillus*)

(*B. subtilis*)

(*B. licheniformis* ;

, 1989 4 12

DD 266,710

(*B. licheniformis*) 41P),

(*Pseudomonas*)

(*P. aeruginosa*)

(*Streptomyces*)가

W3110

DNA

W3110

nA ptr3

W3110 9E4,

tonA

W3110 1A2,

to

pT rbs7 ilvG kan r

W3110 27C7(ATCC 55,244),

tonA ptr3 phoA E15(argF-lac)169 degP ompT kan r

6 W3110 40B4

W3110 37D6, -

tonA ptr3 phoA E15 (argF-lac)169 degP om

1990 8 7

가

4,946,783

PCR

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(*Saccharomyces cerevisiae*)가

(*Schizosaccharomyces pombe*) (Beach and Nurse, Nature, 290: 140 [1981];

1985 5 2

EP 139,383);

(*Kluyveromyces*)

(4,943,529 ; Flee

r et al., Bio/Technology, 9:968-975 (1991)), (*K. lactis*) (MW98-8C, CBS683, CBS4574 ; Louvencourt et al., J. Bacteriol., 737 [1983]), (*K. fragilis*) (ATCC 12,424), 가 (*K. bulgaricus*) (ATCC 16,045), (*K. wickerhamii*) (ATCC 24,178), (*K. waltii*) (A TCC 56,500), (*K. drosophilum*) (ATCC 36,906; Vanden Berg et al., Bio/Technology, 8:1 35(1990)), (*K. thermotolerans*) (*K. marxianus*); (*yarrowia*) (402,226); (*Pichia pastoris*) (183,070; Sreekrishna et al., J. Basic Mic robiol., 28:265-278 [1988]); (*Candida*); (*Trichoderma reesia*) (244,2 34); (*Neurospora crassa* ; Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); (*Schwanniomyces*), (*Schwanniomyces occidentali s*) (1990 10 31 394,538); (*Neurospora*), (*Penicillium*), (*Tolyocladium*) (1991 1 10 WO91/00357) (*Aspergillus*), (*A. nidulans*) (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci . USA, 81: 1470-1474 [1984]) (*A. niger*) (Kelly and Hynes, EMBO J., 4: 475-479 [1985])가 가 (*Hansenula*), (*Candida*), (*Kloeckera*) (*Pichia*), (*Saccharomyces*), (*Torulopsis*) (*Rhodotorula*) (C. Anthony, The Biochemistry of Methylotrophs, 269 (1982))

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PR O1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 P RO2262 S2 Sf9 가 가 (CHO) COS 가 SV40 CV1 (COS-7, ATCC CRL 1651), (293 2 93 , Graham et al., J. Gen Virol., 36:59(1997)), /-DHFR (CHO, Urlaub and Chasi n, Proc. Natl. Acad. Sci. USA, 77:4216(1980)), (TM4, Mather, Biol. Reprod., 23:243-251(1980)), (W138, ATCC CCL 75), (Hep G2, HB 8065), (MMT 060562, A TCC CCL51)

c. 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO 1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (, cDNA DNA) (DNA) 가 DNA ()

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO 1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 N-

PRO381, PRO1269, PRO1410, PRO1755, PR O1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4 397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA , lpp (*Saccharomyces*) - (*Kluyveromyces*) - (5,010,182 () (*C. albicans*) (1990 4 4 WO90/13646 362,179) 1990 11 15

가 1

pBR322

(SV40, , 2μ , VSV BPV)

(, D-) (a) , (b) , (c)

가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DHFR 가 DHFR DHFR CHO (Urlaub et al, Proc. Natl. Acad. Sci. USA, 77:4216(1980)) YRp7 trp1 (Stinchcomb et al., Nature, 282:39(1979); Kingsman et al., Gene, 7:141(1979); Tschemper et al., Gene, 10:157(1980)). trp1 (, ATCC 44076 PEP4-1 [Jones, Genetics, 85: 12 (1977)])

mRNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가 (Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)), (trp) (Goeddel, Nucleic acid Res., 8:4057 (1980); EP 36,776), tac (deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)) 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA 가 가 (S.D.)

em., 255:2073 (1980)) (Hess et al., J. Adv. Enzyme Reg., 7:149(1968); Holland, Biochemistry, 17:4900 (1978)), 3- (Hitzeman et al., J. Biol. Chemistry, 255:2073 (1980)) -3- , 3- 가 가 가 가 가 2, C, -3- 가 EP 73,657

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (1989 7 5 UK 2,211,504), (, 2), , B 40 (SV40))

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA 가 가 10 300 bp - DNA (, , -) SV40 (bp 100-270), 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780 , PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, P

RO4407, PRO1555, PRO1096, PRO2038 PRO2262 5' 3'
 , 5'
 (, , , ,)
 mRNA
 DNA cDNA 5' 3' PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 mRNA

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); 117,060 117,058)

d.

() mRNA (Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)), (DNA) (in situ) DNA (duplex), RNA , DNA-RNA DNA-가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA

e.

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (Triton-X 100) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 HPLC, (, DEAE) SDS-PAGE, (Sephadex) G-75 , IgG A PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982)) () , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, P

RO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

E. PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

DNA 가

가 () DNA

가 가 , 가 가 가 가

가 (MTX)

DNA . MTX (DHFR)가

MTX DFHR-RNA 가 (99.9% MTX)

(DHFR 가)

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A , DNA가 p53 가 p53 가 (G1) (S) DN

DNA DHFR

, *bcl-2*

가

ERB2 가

bcl-1 ras

NA 가 . ERB2 가

D

가 가

(CGH; comparative genomic hybridization) DNA

DNA (WO93

/18,186 ; Gray et al., Radiation Res., 137:275-289[1994]).

(DNA) . CGH DNA

DNA , (PCR) DNA , CGH , PCR DNA PCR(S. Gelmini et al., Clin. Chem., 43:752[1997]) DNA PCR (TaqMan) (ABI) DNA

A549(SRCC768), Calu-1(SRCC769), Calu-6(SRCC770), H157(SRCC771), H441(SRCC772), H460(SRCC773), SKMES-1(SRCC774), SW900(SRCC775), H522(SRCC832) H810(SRCC833) ARCC

SRCC724('AdenoCa')(LT 1), SRCC725('SqCCa')(LT1a), SRCC726()(LT2), SRCC727()(LT3), SRCC728()(LT4), SRCC729()(LT6), SRCC730(/)(LT7), SRCC731()(LT9), SRCC732()(LT10), SRCC733()(LT11), SRCC734()(LT12), SRCC735(/)(LT13), SRCC736()(LT15), SRCC737()(LT16), SRCC738()(LT17), SRCC739()(LT18), SRCC740()(LT19), SRCC741('LCCa')(LT21), SRCC811()(LT22), SRCC825()(LT8), SRCC886()(LT25), SRCC887()(LT26), SRCC888(-BAC)(LT27), SRCC889()(LT28), SRCC890()(LT29), SRCC891()(LT30), SRCC892()(LT31) SRCC894()(LT33) , SRCC1125 [HF-000631], SRCC1127 [HF-000641], SRCC1129 [HF-000643], SRCC1133 [HF-000840], SRCC1135 [HF-000842], SRCC1227 [HF-001291], SRCC1229 [HF-001293], SRCC1230 [HF-001294], SRCC1231 [HF-001295], SRCC1232 [HF-001296], SRCC1233 [HF-001297], SRCC1235 [HF-001299] SRCC1236 [HF-001300]

ATCC SW480(, SRCC776), SW620(, SRC C777), Colo320(, SRCC778), HT29(, SRCC779), HM7(UCSF (Dr. Robert Warren) ATCC SRCC780), CaWiDr(, SRCC781), HCT116(, SRCC782), SKCO1(, SRCC783), SW403(, SRCC784), LS174T(, SRCC785), Colo205(, SRCC828), HCT15(, SRCC829), HCC2998(, SRCC830) KM12(, SRCC831)가 CT2(SRCC742), CT3(SRCC743), CT8(SRCC744), CT10(SRCC745), CT12(SRCC746), CT14(SRCC747), CT15(SRCC748), CT16(SRCC749), CT17(SRCC750), CT1(SRCC751), CT4(SRCC752), CT5(SRCC753), CT6(SRCC754), CT7(SRCC755), CT9(SRCC756), CT11(SRCC757), CT18(SRCC758), CUT19(, SRCC906), CT20(, SRCC907), CT21(, SRCC908), CT22(, SRCC909), CT23(, SRCC910), CT24(, SRCC911), CT25(, SRCC912), CT26(, SRCC913), CT27(, SRCC914), CT28(, SRCC915), CT29(, SRCC916), CT30(, SRCC917), CT31(, SRCC918), CT32(, SRCC919), CT33(, SRCC920), CT35(, SRCC921) CT36 (, SRCC922) , SRCC1051 [HF-000499], SRCC1052 [HF-000539], SRCC1053 [HF-000575], SRC C1054 [HF-000698], SRCC1142 [HF-000762], SRCC1144 [HF-000789], SRCC1146 [HF-000795] SRC C1148 [HF-000811] 가 HBL100(SRCC759), MB435s(SRCC760), T47D(SRCC761), MB468(SRCC762), MB175(SRCC763), MB361(SRCC764), BT20(SRCC765), MCF7(SRCC766) SKBR3(SRCC767), SRC C1057[HF-000545] 가 , SRCC1094, SRCC1095, SRCC1096, S RCC1097, SRCC1098, SRCC1099, SRCC1100 SRCC1101 , SRCC893[LT32] - - -NS SRCC989[HF-000611] SRCC1014[HF-000613] SRCC1001[HF-000733], SRCC999[HF-000716] SRCC1002[HF-000831] SRCC1003[HF-000832]가

F. _____

가 , mRNA
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 mRNA (Thomas, Proc. Natl. Acad. Sci., USA, 77:5201-5205[1980]),
 (DNA),
 DNA , RNA DNA-RNA DNA-

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 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927,
 PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PR
 O2038 PRO2262 DNA
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, P
 RO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 DNA

G. _____

가 가
 가 가 (Stewart et al., Geno
 me Research, 7:422-433 (1997))

H. _____

-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788,
 -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354,
 -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262 가 ()
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295,
 PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 가
 (Zola, Monoclonal Antibodies: A Manual of Techniques, pp.. 147-158(CRS Press, Inc., 1
 987)).

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 2 가 3 () 4,376,110
 2 가 () 가
 ELISA 가

I. _____

(,)

가 .

DNA가 , NIH-3T3) *ras* , NIH-3T3 , B104-1 (*neu* , c)
 (ADCC) , 가

1 가 (transgenic animal,)
 (Small et al., Mol. Cell. Biol., 5:642-648 (1985)).

J. _____

(orhtopin) (, 1997 9 18 PCT)
 WO97/33551).
 가 (nude mouse) .
nu (, ASW, A/He, AKR, BALB/c, B10.LP, C17, C3H, C57BL, C57, CBA, DBA, DDD, I/st, NC, NFR, NFS, NFS/N, NZB, NZC, NZW, P, R SJL) (The Nude Mous e in Oncology Research, E. Boven and B. Winograd, eds., CRC Press, Inc. 1991)

, B104-1 (*neu*) ; Caco-2(ATCC HTB-37); NIH-3T3); *ras* NIH-3T3 , HT-29(ATCC HTB-38), (Karmali et al, Br. J. Cancer, 48:689-696[1983]).

(biopsy) , (Boven and Winogra d(1991))
 (Drebin et al., PNAS USA, 83:9129-9133 (1986))
 (*neu* 가) *neu* NIH-3T3

26-4728(1994) AntiCancer Inc.; Tooo et al., Cabcer Research, 55:681-684(1995) (Wang et al., Cancer Research, 54:47 (METAMOUSE) (

가 RNA 1

, Meth A, CMS4, CMS5, CMS21 WEHI-164 BALB/c (DeLeo et al., J. Exp. Med., 146:7 가 20[1997]) (Palladino et al., J. Immunol., 138:4023-4032 [1987]).

10x10⁶ 10x10⁷ /M ℓ
10 100 $\mu\ell$ 1 3

, 가 (3 LL) 가 (Zupi et al., Br. J. Cancer, 41:suppl. 4:309 [1980]) (SCCL)

가 2 3 . 2

nt. Workshop on Immune-Deficient Animals, Wu and Sheng eds., Basel, 1989, 301) (Rygaard and Spang-Thomsen, Proc. 6th I

가 가

()

가 (transgene) (microinjection)(Hoppe Wanger, 4,873,191); (Van der Putten et al., Proc. Natl. Acad. Sci. USA, 82:6148-615[1985]); (Thompson et al., Cell, 56:313-321[1989]); (Lo, Mol. Cell Bio l., 3:1803-1814[1983]); (Lavitrano et al., Cell, 57:717-73[1989]) 4,736,866

(concatamer) (' - - ') (head-to-head) (head-to-tail) (Lasko et al., Proc. Natl. Acad. Sci. USA, 89:6232-6236[1992])

CR mRNA P , PCR

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PR

O3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262
DNA (knock out)', PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262 cDNA
DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262 DNA
가
(kb) DNA(5' 3')가 ((Thomas and Capecchi, Cell, 51:503 (1987))). ((Li et al., Cell, 69:915(1992)). ((Bradley, in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. J. Robertson, ed.(IRL, Oxford, 1987), pp. 113-152)). 가
DNA
가 DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262

(SCC) SCC
60% 가
) , X (computed tomography, CT) 가 (가 CT . CT 가 ()

K.

가 , () - 가 가

가 , 가 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

가 (Chevary and Nathans, Proc. Natl. Acad. Sci. USA, 88:9578-9582(1991)) (Fields) (Fields and Song, Nature, 340:245-246(1989); Chien et al., Proc. Natl. Acad. Sci. U.S.A., 88:9578-9582(1991))

DNA (two-hybrid system) GAL4 DNA

4-L4 GAL1-lacZ GAL GA

(MATCHMAKER), (Clontech)

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

3 가 () 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가 , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

FACS (Coligan et al., Current Protocols in Immune., 1(2); Chapter 5(1991)) , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 RNA가 , RNA cDNA 가 , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927

7, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 COS PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 . 가 PAGE , X- (micro-sequencing) cDNA
 (degenerate)

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
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PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 RNA DNA mRNA mRNA RNA DNA

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 DNA RNA DNA RNA DNA RNA
 5' 가 10 40 bp RNA
 . DNA (

[Lee et al., Nucl. Acids Res., 6:3073(1979); Cooney et al., Science, 241:456(1988); Dervan et al., Science, 251:1360(1991)]) , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 . RNA
 mRNA , mRNA 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (

[Ojano, Neurochem., 56:560(1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression(CRC Press: Boca Raton, FL, 1988)]). RNA DNA
 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 DNA

-10 +10

가

DNA RNA 가 5 base , 10 base , 15 base , 20 base
 e , 25 base , 30 base , 35 base , 40 base , 45 base , 50 base ,
 55 base , 60 base , 65 base , 70 base , 75 base , 80 base , 85 ba
 se , 90 base , 95 base , 100 base .

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, P
 RO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO
 2038 PRO2262 P
 RO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1
 293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

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RNA

RNA

RNA

RNA

(Rossi, Current Biolo

gy, 4:469-471 (1994) 1997 9 PCT WO97/33551)

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 가 (Hoogsteen)

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 (PCT WO97/33551)

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RNA

DNA가

mRNA

mRNA

-10 +10

RNA

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RNA

RNA

(Rossi, Current Biolo

gy, 4:469-471 (1994) 1997 9 18 PCT WO97/33551)

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 (WO97/33551)

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M. _____

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1. _____

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(keyhole limpet) (Freund's complete adjuvant) MPL-TDM (A(monophosphoryl Lipid A),)가

2. _____

-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262 (Kohler and Milstein, Nature, 256:495 (1975)) (hybridoma)

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (peripheral blood lymphocyte: 'PBL') (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103).

(HGPRT HPRT) 가 HGPRT - ('HAT ') (Salk Institute Cell Distribution Center) (ATCC; American Type Culture Collection) 가 (Kozbor, J. Immunol., 133:3001 (1984)) Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (radioimmunoassay: RIA) - (enzyme-linked immunoabsorbent assay: ELISA) (Munson and Pollard, Anal. Biochem. 107:220 (1980)) (Scatchard)

(Goding, (Dulbecco's Modified Eagle's Medium) RPMI-1640 가

(A-)

4,816,567 DNA () DNA ()
 COS DNA (CHO) DNA ()
 (4,816,567 (Morrison)
 DNA 2가 가
 1가 1가 가 Fc
 가 Fab
 1가

3. _____

-PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434,
 -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397,
 -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO2262 가

(Fv, Fab, Fa (complementary det
 b', F(ab')₂)
 ermining region: CDR) 가,
) CDR ()
 Fv 가
 CDR CDR
 FR
 (Fc) (Jones et al, Nature 321: 522-525 (1986); Riechmann et al, Nature, 332:323-329 (1988); Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

가 (im
 port)' 가 (Winter) (J
 ones et al, Nature, 321: 522-525 (1986); Riechmann et al, Nature, 332:323-327 (1988); Verhoeyen et al, Science 239:1534-1536 (1988))
 CDR CDR
 가 CDR FR
 가

(phage display) (Hoogenboom and Winter, J. Mol. Biol., 227:381(1991); Marks et al, J. Mol. Biol., 222:581(1991)) 가
 (Cole) (Boerner) (Cole et al, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985); Boerner et al, J. Immunol., 147(1):86-95 (1991)). 가

(5,545,807 , 5,545,806 , 5,569,825
 , 5,625,126 , 5,633,425 , 5,661,016) (Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368, 856-859 (1994), Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995))

4. _____ (ADEPT)

(, , WO81/01145) (WO88/07378
ADEPT
4,975,278).

ADEPT
가

5- 5-
; D- G2 A) (B L
D- ; -
V
G 가 , (a
bzyme)'
Massey, Nature, 328:457-458 (1987)).

가 -PRO38
1, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PRO
3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -
PRO1555, -PRO1096, -PRO2038 -PRO2262

DNA (Neuberger et al., Nature, 312:604-608(1984)).

5. _____

가
PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1
788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO440
7, PRO1555, PRO1096, PRO2038 PRO2262

2 (Mi
Ilstein and Cuello, Nature, 305: 537-539 (1983)).

() 10 가 W
O93/08829 (1993 5 13) (Traunecker et al., EMBO J., 10: 3655-3659 (1991))

가 (-)
, CH2 CH3
1 (CH1)
DNA
(Suresh et al., Methods in Enzymology, 121: 210(1986))

WO96/27011

H3 , 1 1 C
() (cavity)' 2

가

(, F(ab')₂)

(Brennan et al., Science 229:81 (1985))

가

F(ab')₂

Fab'

(TNB) , Fab'-TNB
Fab'- Fab'-TNB

halaby et al., J. Exp. Med. 175:217-225 (1992))
Fab'

F(ab')₂ 가 (S

ErbB2

T

92)). , Fos Jun (Kostelny et al., J. Immunol. 148(5):1547-1553 (1992))
2 Fab'

Acad. Sci. USA 90:6444-6448 (1993)) (Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993))
가 (diabody)' 가 (V_L) (V_H)

V_L V_H , 2 , V_H V_L Fv(sFv)

:5368 (1994)) (Gruber et al., J. Immunol. 152

2가 가 (Tutt et al., J. Immunol. 147:60 (1991)).

가

R), Fc R (CD64), Fc R (CD32) Fc R (CD16) , CD2, CD3, CD28 B7), IgG Fc (arm) (Fc

TETA 가 EOTUBE, DPTA, DOTA 가 (TF)

6. _____

2 (EP 03089) 4,676,980), HIV 가 (WO91/00360 , WO92/200373 ,

4,676,980

-4-

7. _____

ADCC) (Fc (Caron et al., J. Exp Med., 176:1191-1195 (1992) Shopes, J. Immunol., 148:2918-

2922 (1992)) 가 (Wolff et al. Cancer Research, 53: 2560-2565 (1993)) Fc ADCC (Stevenson et al., Anti-Cancer Drug Desig n, 3:219-230 (1989)).

8. _____

(PAPI, PAP (PAP-S), 가 (sapaonaria officinalis) 가 (Pseudomonas aeruginosa), (Aleurites fordii), (Momordica charantia), (Phytolaca americana) CC1065가 212 Bi, 131 I, 131 In, 90 Y 186 Re가 (IT), N- -3-(2-) (SPDP), HCL), (p-), 2,6-), -14 (Vitetta et al., Science, 1- 238:1098 (1987)) (MX-DTPA) WO94/11026)

9. _____

(Epstein et al., Proc. Natl. Acad. Sci. USA, 82:3688 (1985); Hwang et al., Proc. Natl Acad. Sci. USA, 77:4030 (1980); 4,485,045 4,544,545) 5,013,556 PEG- (PEG-PE) (Martin et al., J. Biol. Chem., 257:286-288 (1982)) Fab' (Doxorubicin)) (Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989))

N. _____

가 가 가 가 가 DNA (Marasco et al., Pro

c. Natl. Acad. Sci. USA, 90:7889-7893 (1993)).

Remington's Pharmaceutical Sciences, 16th edition, Osol, A. ed. (1980)) (Re

가
(
3- ; m-); (10)
; EDTA
(, Zn-); () TWEEN(), PLURONICS() (PEG)
가

1 가 ,
(
(coacervation)
-()
(Remington's Pharmaceutical Sciences, 16th edition, O
sol, A. ed. (1980))

가
(
3,773,919), L-
가 LUPRON DEPOT()(-D-(-)-3-
100 가 37
S-S 가

O. _____

()
(
(
); (stromal)
()
가

가 ,
(Chemotherapy Service Ed., M.C.Perry, Williams & Wilkins, Baltimore, MD(1992))
(EP 616812

, ErbB2, EGFR, ErbB3, ErbB4 가 , (VEGF) 2 2
1
()

가
1µg/kg 15mg/kg(, 0.1 20mg/kg) 가 1
1µg/kg 100mg/kg
가

P. _____

(access port) ()가 (bag)
2
가

Q. _____

(,)
가
(')
가
5
(*in situ*)

< >

가 . ATCC(American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209)
 ((Budapest Treaty))
 30 ATCC
 ()
 35 USC § 122 (37 CFR § 1.14 , 886 O
 G 638) 가

(Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press N.Y., 1989; Ausubel et al., Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y., 1989; Innis et al., PCR Protocols: A Guide to Methods and Applications, Academic Press, Inc., Y.Y., 1990; Harlow et al., Antibodies: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, 1988; Gait, Oligonucleotide Synthesis, IRL Press, Oxford, 1984; R. I. Freshney, Animal Cell Culture, 1987; Coligan et al., Current Protocols in Immunology, 1991)
 DNA

1: cDNA

(Swiss-Prot) 950 (ECD)
) () EST . EST
 EQ(); Incyte Pharmaceuticals, Palo Alto, CA)가 . EST 6 , LIFES
 BLAST BLAST -2 (Altschul et al., Methods in Enzymology 266:
 460-480 (1996)) 70 (90)
 BLAST 'phrap' (Phil Green, University of Washington,
 Seattle Washington) DNA
 DNA phrap EST
 BLAST BLAST -2 phrap 가) EST
 , PCR
 cDNA PRO
 PCR 20 30
 55 bp 100 1000 bp PCR 1 1.5 kbp 가 가 40
 (Ausubel et al., Current Protocols in Molecular Biology) PCR DNA PCR
 cDNA cDNA (Invitrogen, San Diego, CA)
 . cDNA Not dT
 Sal , Not
 pRK5D ; (Holmes et al., Science , 253 : 1278-1280 (1991)) pRKB pRKD; pRK5B Sfi
 Not Xho

2: cDNA

(Genentech, Inc., South San Francisco, CA)

() () (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA)

EST EST

5'-

(ATG) DNA ATG

35

ATG가

ATG 가

EST

(가) DNA ATG

7

3: PRO381 cDNA

1

phrap

DNA

EST

DNA39651

DNA39651

, 1)

cDNA

PCR

, 2) PRO381

1 PCR () :

PCR (39651.f1)

5'-CTTTCCTTGCTTCAGCAACATGAGGC-3' (3)

PCR (39651.r1)

5'-GCCCAGAGCAGGAGGAATGATGAGC-3' (4)

가 DNA39651

(39651.p1)

5'-GTGGAACGCGGTCTTGACTCTGTTCTGTCACCTTCTTTGATTGGGGCTTTG-3' (5)

PCR

PCR

DNA

PCR

PRO381

. cDNA

RNA

(LIB227)

O381

DNA

DNA44194-1317 (1, 1)

PR

DNA44194-1317

1 (1)

DNA44194-1317

174 176

807

809

211

2 (2)

PR

O381

가

PRO381

1

20

176

180

N-

208

212

78

115

118

132

FKBP-

140

160

EF-

204,

184

204

aBP

DNA44194-1317 1998 4 28

204 S-100/IC

ATCC

209808

2

PRO381

ATCC 24,172

, pl 5.99

PRO381

가 FKBP

, 2 (2)

WU-BLAST2

(35.45 SwissProt 35) PRO381 AF040252_1, I49669, P_R935
 51, S71238, CELC05C8_1, CEU27353_1, MIP_TRYCR, CEZC455_3, FKB4_HUMAN I40718

4: PRO1269 cDNA

2 DNA66520-1536
 LIFESEQ() Incyte EST 101920
 EST () (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto,
 CA) EST (EST)
 BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996))
 70 (90) BLAST
 'phrap' (Phil Green, University of Washington, Seattle Washington) DNA
 DNA56509 DNA56509
 Incyte EST 103157 , Incyte EST 103157
 cDNA cDNA 3 (6) DNA6
 6520-1536
 DNA66520-1536 26 28 614
 616 (3).
 196 (4, 7). 4 PRO1269 21,731 , pl
 8.97 4 (7) PRO1269 가
 20 , 4 PRO1269 1
 112 PRO1269 116 N- 가
 DNA66520-1536 1998 9 15 ATCC ATCC 203226

4 (7) WU-BLAST2 (35.45
 SwissProt 35) PRO1269 P_W23722
 , PRO1269 MMTAG7_1, MTV026_16, NAAA_BPT3, S75616_1 N
 CP_PIG

5: PRO1410 cDNA

2 DNA68874-1622
 LIFESEQ() Incyte EST 98502
 EST () (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, C
 A) EST (EST)
 BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996))
 70 (90) BLAST
 'phrap' (Phil Green, University of Washington, Seattle Washington) DNA
 DNA56451 DNA56451
 Incyte EST 1257046 , Incyte EST 1257046
 , cDNA cDNA 5 (8) DN
 A68874-1622
 DNA68874-1622 152 154 866
 868 (5).
 238 (6, 9). 6 PRO1410 25,262 , pl
 6.44 6 (9) PRO1410 가
 20 , 6 PRO1410 1
 194 PRO1410 220 132
 136 N- 가 DNA68874-1622 1998 9 22
 ATCC ATCC 203277

6 (9) WU-BLAST2 (35.45
 SwissProt 35) PRO1410 I48652, P_R76466, HSMHC3W36A_2, EPB4_
 HUMAN, P_R14256, EPA8_MOUSE, P_R77285, P_W13569, AF000560_1 ASF1_HELAN

6: PRO1755 cDNA

2 DNA76396
 LIFESQ() Incyte EST 141872
 EST () (LIFESQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA) EST
 (EST) BLAST
 BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996))
 70 (90) BLAST
 'phrap' (Phil Green, University of Washington, Seattle Washington) DNA
 DNA55731
 DNA55731 Incyte EST 257323 , Incyte EST 257323
 cDNA cDNA
 76396-1698 , DNA76396 7 (10) DNA
 (, STR9372310)

DNA76396-1698 7 (10) DNA76396-1698
 58 60 886 888
 (7). 276 (8, 11). 8
 PRO1755 29,426 , pl 9.40 . 8 (11)
 PRO1755 가
 8 PRO1755 1 33 17
 8 198 , 210 214 cAMP- cGMP-
 , 117 123, 154 160
 214 220 N- 149 152
 DNA76396-1698 1998 11 17 ATCC ATCC
 203471

8 (11) WU-BLAST2 (35.45
 SwissProt 35) PRO1755 APG-BRANA, P_R37743, NAU88587_1, YHL
 1_EBV, P_W31855, CET10B10_4, AF039404_1, PRP1_HUMAN, AF038575_1 AF053091_1

7: PRO1780 cDNA

1 phrap DNA EST
 LIFESQ() DNA63837.init Incyte EST 3349314
 70 BLAST , DNA63837.init
 EST BLAST phrap 가
 DNA63837

DNA63837 , 1) cDNA PCR , 2) P
 RO1780

1 PCR () :

PCR (63837.f1)

5' - TGCCTTTGCTCACCTACCCAAGG - 3' (14)

PCR (63837.r1)

5'-TCAGGCTGGTCTCCAAAGAGAGGG-3' (15)

가

DNA63837

(63837.p1)

5'-CCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGG-3' (16)

PCR DNA PCR
 RNA PCR PRO1780 cDNA
 RO1780 DNA DNA71169-1709 (9, 12) P
 DNA71169-1709 9 (12) DNA71169-1709
 68 70 1637 1639
 523 10 (13)
 PRO1780 가
 10 PRO1780 1 19 4
 83 504 52 56 N-
 68 75 425 434 16
 22, 301 307, 370 376
 494 500 N- 493 515
 241 294 UDP- 가 DNA71169-
 1709 1998 11 17 ATCC ATCC 203467 10 PRO
 1780 59,581 , pl 8.68
 10 (13) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1780 UDA2_RABIT, CGT_HUMAN, UD11_HUMA
 N, P_R26153, UDB1_RAT, HSU59209_1, AB010872_1, UDB5_MOUSE, UDB8_HUMAN UD14_HUMAN

8: PRO1788 cDNA

Incyte 1 phrap DNA EST
 2968304 70 BLAST
 EST BLAST phrap 가
 , 1) cDNA DNA49648 DNA49648
 PCR , 2) PRO1788

1 PCR () :

PCR (49648.f1)

5'-CCCTGCCAGCCGAGAGCTTCACC-3' (19)

PCR (49648.r1)

5'-GGTTGGTGCCCGAAAGGTCCAGC-3' (20)

가

DNA49648

(49648.p1)

5'-CAACCCCAAGCTTAACTGGGCAGGAGCTGAGGTGTTTTTCAGGCC-3' (21)

PCR DNA PCR
 RNA PCR PRO1788 . cDNA
 RO1788 DNA DNA77652-2505 (11, 17) P
 DNA77652-2505 11 (17) DNA77652-2505
 64 66 1123 1125
 353 12 (18)
 PRO1788 가
 12 PRO1788 1 16
 215 232 287 304 74
 78 137 141 N- 45
 49 318 326
 13 19, 32 38, 88 94,
 214 220 223 229 N-
 284 306 DNA77652-2505 1998 1
 1 17 ATCC ATCC 203480 12 PRO1788
 37,847 , pl 6.80
 12 (18) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1788 AF030435_1, AF062006_1, DMTARTAN_1,
 GARP_HUMAN, S42799, P_R71294, HSU88879_1, DROWHEELER_1, A58532 AF068920_1

9: PRO3434 cDNA

2 DNA77631-2537
 LIFESEQ() EST
 (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA) EST ()
 (EST) BLAST BLAST2(Altschul et al.,
 Methods in Enzymology 266: 460-480 (1996)) 70 ()
 90) BLAST 'phrap' (Phil Green, Univ
 ersity of Washington, Seattle Washington) DNA
 DNA56099
 DNA56099 Incyte EST 3327089 , Incyte EST 3327089
 , cDNA cDNA 13 (22)
 DNA77631-2537
 DNA77631-2537 46 48 3133
 3135 (13).
 1029 (14, 23). 14 PRO3434 114,213
 , pl 6.42 . 14 (23) PRO3434 가
 1 16 , 14 PRO3434
 335, 616 154 158, 331
 895 cAMP- cGMP- 620, 785 789 891
 136 142, 224 230, 435 97,
 1, 439 445, 443 449, 665
 671 698 704 N- 329
 333 634 638 , 96 135
 가 DNA77631-2537 1999 2 9 ATCC

ATCC 203651

14 (23) WU-BLAST2 (35.4
 5 SwissProt 35) PRO3434 VATX_YEAST, P_R51171, POLS_IBDVP, I
 BDVORF_2, JC5043, IBDVPIV_1, VE7_HPV11, GEN14220, MUTS_THETH COAC_CHICK

10: PRO1927 cDNA

2 DNA82307-2531
 LIFESEQ() EST 1913
 () (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA) EST) EST
 (EST) BLAST BLAST2(Altschul
 et al., Methods in Enzymology 266: 460-480 (1996)) 70
 (90) BLAST 'phrap' (Phil Green
 , University of Washington, Seattle Washington) DNA
 'DNA20168' EST가
 DNA73896

DNA73896 Incyte EST 3326981H1 [RNA
] , Incyte EST 3326981H1 , cDNA
 . cDNA 15 (24) DNA82307-2531

DNA82307-2531 51 53 1695
 1697 (15).
 548 (16, 25). 16 PRO1927 63,198
 , pl 8.10 . 16 (25) PRO1927 가
 1 23 , 5 9, 87 91,
 103 107 465 469 N-
 6 12, 136 142, 370 376
 509 515 N- 가 DNA82307
 -2531 1998 12 15 ATCC ATCC 203537 .

16 (25) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1927 AB000628_1
 , PRO1927 가 HGS_A251, HGS_A197, CELC50H11_2, CPX
 M_BACSU,VF03_VACCC, VF03_VACCV, DYHA_CHLRE, C69084 A64315

11: PRO3567 cDNA

1 phrap DNA EST
 DNA52711 DNA52711 Merck EST AA0827
 50 , Merck EST AA082750 , cDNA
 17 (26) DNA56049-2543

DNA56049-2543 97 99 637
 639 18 (27) PRO3567 가 180
 25 , 18 PRO3567 1
 145 N- , 149 164 , 141
 112 , 16 25 31 135 141 N-
 115 , 27 1
 1 DNA56049-2543 1999 2 9 21 TonB-
 203662 . 18 PRO3567 ATCC ATCC
 , pl 8.

91

18 (27) WU-BLAST2 (35.4
 5 SwissProt 35) PRO3567 SPC2_CANFA, SPC2_CHICK, SPC2_CAEEL
 , AF057144_1, YD2B_SCHPO, S61639, SPC3_YEAST, AMU21992_1, EPU22004_1 CMU20539_1

12: PRO1295 cDNA

2 DNA59218-1559
 LIFESEQ() EST
 (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA) EST
 (EST) BLAST BLAST2(Altschul et al.,
 Methods in Enzymology 266: 460-480 (1996)) 70 (
 90) BLAST 'phrap' (Phil Green, Univ
 ersity of Washington, Seattle Washington) DNA

DNA56262 Incyte EST 3743334 EST
 , cDNA cDNA 19 (28)
 DNA59218-1559

DNA59218-1559 207 209 10
 47 1049 (19).
 280 (20, 29). 20 PRO1295 30,163
 , pl 6.87 . 20 (29) PRO1295 가
 1 18 , 20 PRO1295
 278 18 244 248 N-
 1998 9 29 ATCC ATCC 203287 가 DNA59218-1559

20 (29) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1295 AB011099_1, ILVE_MYCTU, ATTECR_2, A
 F010496_27, P_R15346, S37191, PER_DROMS, L2MU_ADECC P_W34238

13: PRO1293 cDNA

2 DNA60618-1557
 LIFESEQ() Incyte EST 115204
 EST () EST (LIFESEQ(), Incyte Pharmaceuticals, Inc.,
 Palo Alto, CA) EST (EST)
 BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996))
 70 (90) BLAST
 'phrap' (Phil Green, University of Washington, Seattle Washington) DNA
 DNA56522

DNA56522 Incyte EST 2966119 , Incyte EST 2966119
 , cDNA cDNA 21 (30)
 DNA60618-1557

DNA60618-1557 37 39 1060
 1062 (21).
 341 (22, 31). 22 PRO1293 38,070
 , pl 6.88 . 22 (31) PRO1293 가
 22 PRO1293

1 19 , 237 262 , 205
 209 N- , 151 154 ,
 115 141
 DNA60618-1557 1998 9 29 ATCC ATCC 203292

22 (31) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1293 HSVCD54_1, A33_HUMAN, AF009220_1,
 HSU82279_1, AF004230_1, P_R13272, AF004231_1, AF043644_1, S44125 HSIGGHC85_1

14: PRO1303 cDNA

1 phrap DNA EST
 DNA47347 DNA47347 DNA47347
 Incyte EST , Incyte 1430305 , cDNA
 23 (32) DNA65409-
 1566

DNA65409-1566 121 123 865
 867 248
 24 (33) PRO1303 가
 24 PRO1303 1
 17 , 24 28 163 167 N-
 58 64 ,
 47 64, 196 207 218 242
 47 65 194
 207 220 248 가
 DNA65409-1566 1998 9 15 ATCC ATCC 203232
 24 PRO1303 26,734 , pl 7.90

24 (33) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1303 AB009849_1, P_W08475, AF024605_1, A4
 2048_1, TRY3_RAT, MMAE00066414, TRY1_RAT, MMAE000663_4, MMAE000665_2 MMAE00066412

15: PRO4344 cDNA

1 phrap DNA EST
 DNA80203 DNA80203 , 1)
 cDNA PCR , 2) PRO4344

1 PCR () :

PCR

5'-CTTGCTCCTGGCCATCAAGTCAC-3' (36)

PCR

5'-GTTGAAGAAGTCCTCAGTGAAGTCCCAC-3' (37)

가

DNA80203

5'-CAGCTGAAGCTGGTGTTCCTCCTAGGGGTGGCAGGATCCG-3' (38)

PCR DNA PCR
 RNA PCR PRO4344 cDNA
 RO4344 DNA DNA84927-2585 (25, 34) P
 DNA84927-2585 25 (34) DNA84927-2585
 357 359 1491 1493
 378 26 (35)
 PRO4344 가
 26 PRO4344 1 39
 30 49 79 83, 104
 108 192 196 N- 194
 198 352 356 14
 20, 160 166 367 373 N-
 35 46 가
 DNA84927-2585 1999 3 23 ATCC ATCC 203865 26
 PRO4344 42,310 , pl 9.58
 26 (35) WU-BLAST2 (35.4
 5 SwissProt 35) PRO4344 P_W64558, P_W80212, AF029790_1, P_R5
 7433, AB003478_1, MMHC425O1814, DMU41449_1, DMSEG0007_10, DMC65G3_4 FNG_DROME

16: PRO4354 cDNA

2 DNA92256-2596
 LIFESEQ() 'DNA10195'
 EST (92909) () EST () (LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo A
 lto, CA) EST (EST)
 BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996))
 70 (90) BLAST
 'phrap' (Phil Green, University of Washington, Seattle Washington)
 DNA DNA56063

, DNA92264-2596
 27 (39)
 DNA92256-2596 108 110 852
 854 (27).
 248 (28, 40). 28 PRO4354 28,310
 , pl 4.63 28 (40) PRO4354 가
 21 28 PRO4354 1
 106 110 cAMP- cGMP-
 40, 80 84, 84
 88, 158 162, 202 206, 20
 7 211 213 217
 115 121 N- 70 가
 DNA92256-2596 1999 3 30 ATCC ATCC 203891

28 (40) WU-BLAST2 (35.
 45 SwissProt 35) PRO4354 HGS_RF300, CEVK04G11_2, CEC11H1_7,

HSU80744_1, CEF09E8_2, RNAJ2967_1, DDICOI_1, AB020648_1, P_W33887 A64319

17: PRO4397 cDNA

1 phrap DNA EST
 cDNA DNA79196 DNA79196 , 1)
 PCR , 2) PRO4397

1 PCR () :

PCR

5'-ACCTAACGCTCAAGGAGATCCACTTTC-3' (43)

PCR

5'-GGCTCCATTCTGGGTCTGAGTTAGG-3' (44)

가 DNA79196

5'-GCCTCAGCTTTCTGCCCGACGTGCGCTTCGTTTTTAAGG-3' (45)

PCR DNA PCR
 RNA PCR PRO4397 cDNA
 RO4397 DNA DNA83505-2606 (29, 41) P

DNA83505-2606 29 (41) DNA83505-2606
 254 256 1460 1462
 PRO4397 가 402 30 (42)
 30 PRO4397 1 27
 203 207 N- 124 128, 205
 209, 351 355 368 372
 116, 18 24, 31 37, 110
 163 169 157 163, 161 167,
 366 372 N- 107
 TCC 110 DNA83505-2606 1999 5 25 A
 43,751 ATCC , pl 9.42 30 PRO4397

30 (42) WU-BLAST2 (35.4
 5 SwissProt 35) PRO4397 P_W64558, P_W80212, HSGALT2_1, P_R5
 7433, AF100956_7, HS1033B10_2, AF029792_1, DMU41449_1, DMSEG0007_10 AF092051_1

18: PRO4407 cDNA

2 DNA92264-2616
 LIFESEQ() EST

(LIFESEQ(), Incyte Pharmaceuticals, Inc., Palo Alto, CA) EST () EST ()
 (EST) BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-480 (1996)) 70 ()
 90) BLAST 'phrap' (Phil Green, University of Washington, Seattle Washington) DNA
 , DNA92264-2616

31 (46) DNA92264-2616 109 111
 757 759
 (31). 216 (32, 47). 32 P
 RO4407 23,729 , pl 4.73 32 (47) PRO4407
 가 32
 PRO4407 1 25 , 41
 59 129 133 173 177
 , DNA92264-2616 1999 4 27 ATCC N- ATCC 가 203969
 32 (47) WU-BLAST2 (35.4
 5 SwissProt 35) PRO4407 SC1E6_12, D80003_1, HMGA_SOYBN, DRO
 TRO12_1, HSU91934_1, GEN14338, AF051945_1, A45644, P_W60213 P_W33807

19: PRO1555 cDNA

2 DNA73744-1665
 'DNA10316' LIFESEQ() EST 521
 () EST () (LIFESEQ(), Incyte
 Pharmaceuticals, Inc., Palo Alto, CA) EST (EST)
 BLAST BLAST2(Altschul et al., Methods in Enzymology 266: 460-4
 80 (1996)) 70 (90) BLAST
 ngton) DNA 'phrap' (Phil Green, University of Washington, Seattle Washi
 DNA56374 DNA56374
 , cDNA Incyte EST 2855769 , Incyte EST 2855769
 . cDNA . Incyte EST 2855769
 DNA73744-1665
 33 (48) DNA73744-1665 90 92
 828 830
 (33). 246 (34, 49). 34 PR
 O1555 26,261 , pl 5.65 34 (49) PRO1555
 가 34
 PRO1555 1 31 , 11
 32 195 217 , 111 115
 N- 2 6, 98 102 19
 1 195 , 146 152
 665 192 198 N- 가 DNA73744-1
 6 ATCC ATCC 203322

34 (49) WU-BLAST2 (35.4
 5 SwissProt 35) PRO1555 YKA4_CAEEL, AB014541_1, HVSX99518_
 2, S5U63019_1, GEN14286, MMU68267_1, XP2_XENLA, ICP4_HSV11, P_W40200 AE001360_1

20:

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

DNA . DNA
 DNA
 , 10
 () . 5' (, TaqMan™)
 PCR(, ABI (Prizm) 7700 (, Perkin Elmer, Applied Biosystems Division, Foster City, CA)) , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 DNA가
 4 가 4

(TaqMan)() ()Ct . 1 1 PCR 2
 , 2 4 , 3 8 가 . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 () 가
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 (, 3' -) . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 (,) :

PRO381 (DNA44194-1317)

44194.tm.f :

5'-CTTTGAATAGAAGACTTCTGGACAATTT-3' (56)

44194.tm.p:

5'-TTGCAACTGGGAATATACCACGACATGAGA-3' (57)

44194.tm.r:

5'-TAGGGTGCTAATTTGTGCTATAACCT-3' (58)

44194.tm.f2:

5'-GGCTCTGAGTCTCTGCTTGA-3' (59)

44194.tm.p2:

5'-TCCAACAACCATTTTCCTCTGGTCC-3' (60)

44194.tm.r2:

5'-AAGCAGTAGCCATTAACAAGTCA-3' (61)

PRO1269 (DNA66520-1536)

66520.tm.f1:

5'-AAAGGACACCGGGATGTG-3' (62)

66520.tm.p1:

5'-AGCGTACACTCTCTCCAGGCAACCAG-3' (63)

66520.tm.r1:

5'-CAATTCTGGATGAGGTGGTAGA-3' (64)

PRO1410 (DNA68874-1622)

68874.tm.f1:

5'-CAGGACTGAGCGCTTGTTTA-3' (65)

68874.tm.p1:

5'-CAAAGCGCCAAGTACCGGACC-3' (66)

68874.tm.r1:

5'-CCAGACCTCAGCCAGGAA-3' (67)

PRO1755 (DNA76396-1698)

76396.tm.f1:

5'-TCATGGTCTCGTCCCATTTC-3' (68)

76396.tm.p1:

5'-CACCATTTGTTTCTCTGTCTCCCCATC-3' (69)

76396.tm.r1:

5'-CCGGCATCCTTGGAGTAG-3' (70)

PRO1780 (DNA71169-1709)

71169.tm.f1:

5'-CTCTGGTGCCACAGTGA-3' (71)

71169.tm.p1:

5'-CCATGCCTGCTCAGCCAAGAA-3' (72)

71169.tm.r1:

5'-CAGGAAATCTGGAAACCTACAGT-3' (73)

PRO1788 (DNA77652-2505)

77652.tm.f1:

5' - TCCCCATTAGCACAGGAGTA - 3' (74)

77652.tm.p1:

5' - AGGCTCTTGCCCTGTCCTGCTGCT - 3' (75)

77652.tm.r1:

5' - GCCCAGAGTCCCCTTGT - 3' (76)

PRO3434 (DNA77631-2537)

77631.tm.f1:

5' - GTCCAGCAAGCCCTCATT - 3' (77)

77631.tm.p1:

5' - CTTCTGGGCCACAGCCCTGC - 3' (78)

77631.tm.r1:

5' - CAGTTCAGGTCGTTTCATTCA - 3' (79)

PRO1927 (DNA82307-2531)

82307.tm.f1:

5' - CCAGTCAGGCCGTTTTAGA - 3' (80)

82307.tm.p1:

5' - CGGGCGCCCAAGTAAAAGCTC - 3' (81)

82307.tm.r1:

5' - CATAAAGTAGTATATGCATTCCAGTGTT - 3' (82)

PRO3567 (DNA56049-2543)

56049.tm.f1:

5' - GGAAATGGTCTCAAGGGAAA - 3' (83)

56049.tm.p1:

5' - TCACTTTGACCCTGTCTTGGAACGTC - 3' (84)

56049.tm.r1:

5' - GGTAGAATTCCAGCATTTGGTA - 3' (85)

PRO1295 (DNA59218-1559)

59218.tm.f1:

5'-AGGACTTGCCCTCAGGAA-3' (86)

59218.tm.r1:

5'-CGCAGGACAGTTGTGAAAATA-3' (87)

59218.tm.p1:

5'-ATGACGCTCGTCCAAGGCCAC-3' (88)

PRO1293 (DNA60618-1557)

60618.tm.f1:

5'-CCCACCTGTACCACCATGT-3' (89)

60618.tm.p1:

5'-ACTCCAGGCACCATCTGTTCTCCC-3' (90)

60618.tm.r1:

5'-AAGGGCTGGCATTCAAGTU-3' (91)

PRO1303 (DNA65409-1566)

65409.tm.f1:

5'-CTGGCCCTCAGAGCACCAAT-3' (92)

*65409.tm.p1:

5'-TCCTCCATCACTTCCCCTAGCTCCA-3' (93)

65409.tm.r1:

5'-CTGGCAGGAGTTAAAGTTCCAAGA-3' (94)

PRO4344 (DNA84927-2585)

84927.tm.f1:

5'-GGGCAACAGCCTGAGAGT-3' (95)

84927.tm.p1:

5'-ACTCAGTGTTGATTCTCTATCGTGATGCG-3' (96)

84927.tm.r1:

5'-GAGCAGCAGGCATCAATTT-3' (97)

PRO4354 (DNA92256-2596)

92256.tm.f1:

5'-GGCCTGGAGTTGCTGATAA-3' (98)

92256.tm.p1:

5'-TTGAGCTTAAGTAGACCAAGTATCTATCCCACCTAAA-3' (99)

92256.tm.r1

5'-GGTGGGCTCTGGGTTACA-3' (100)

PRO4397 (DNA83505-2606)

83505.tm.f1:

5'-AGCCGGTTTCCCAGATTAT-3' (101)

83505.tm.p1:

5'-TGCCGTGTATGTGGTTCTTCCCTG-3' (102)

83505.tm.r1:

5'-GAGACAGGCACCTGGTGAT-3' (103)

PRO4407 (DNA92264-2616)

92264.tm.f1:

5'-TGTTTCTGCCTGGACATCA-3' (104)

92264.tm.r1:

5'-GCTTACCGTGGCCTGACT-3' (105)

92264.tm.p1:

5'-TCCTCAGGGTCCAAGTCCCCAT-3' (106)

PRO1555 (DNA73744-1665)

73744.tm.f1:

5'-CCTTGAAAAGGACCCAGTTT-3' (107)

73744.tm.p1:

5'-ATGAGTCGCACCTGCTGTTCCC-3' (108)

73744.tm.r1:

5'-TAGCAGCTGCCCTTGGTA-3' (109)

73744.tm.f2:

5'-AACAGCAGGTGCGACTCATCTA-3' (110)

73744.tm.p2:

5'-TGCTAGGCGACGACACCCAGACC-3' (111)

73744.tm.r2 :

5'-TGGACACGTGGCAGTGGA-3' (112)

PRO1096 (DNA61870)

61870.tm.f1:

5'-TGGACCATGAAGCCAGTTT-3' (113)

61870.tm.p1:

5'-CCTTTTTAGTTGGCTAACTGACCTGGAAAGAA-3' (114)

61870.tm.r1:

5'-TGAATAGTCACTTTGAGGTTATTGC-3' (115)

PRO2038 (DNA83014)

83014.tm.f1:

5'-CCTGGCTCCACCTGTGAT-3' (116)

83014.tm.p1:

5'-ACCTCCCCCTGCTTCCTGCTG-3' (117)

83014.tm.r1:

5'-CCTCAGACCCCATGAGTGA-3' (118)

PRO2262 (DNA88273)

88273.tm.f1:

5'-GAGGAATGGCCCAACAGT-3' (119)

88273.tm.p1:

5'-TGGCAGCCACCCTTCAGTGAG-3' (120)

88273.tm.r1:

5'-CAGCACATCACGTGTCCA-3' (121)

88273.tm.f2:

5'-GAGGAATGGCCCAACAGT-3' (122)

88273.tm.p2:

5'-TGTCCATGCCCTGGTCCAC-3' (123)

88273.tm.r2 :

5'-GAGGTACAGAGCAGCACATCA-3' (124)

5' , PCR- . PCR Taq DNA 5' 2
 . 3 . Taq DNA 2 PCR
 uencher) 가 , Taq DNA (q
 가 , Taq DNA
 2 (fluorophore) 가 1
 5' ABI 7700TM PCR
 (thermocycler), (CCD)
 96- CCD 96 가
 5' Ct, (threshold cycle) 가
 Ct , DNA DNA

4 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262 , T N 가

[4]

				T	N
AdenoCa(SRCC724)[LT1]	A			T1	N1
SqCCa(SRCC724)[LT1a]	B			T3	N0
AdenoCa(SRCC726)[LT2]	B			T2	N0
AdenoCa(SRCC727)[LT3]	A			T1	N2
AdenoCa(SRCC728)[LT4]	B			T2	N0
AdenoCa(SRCC729)[LT6]	B			T2	N0
Aden/SqCCa(SRCC730)[LT7]	A			T1	N0
AdenoCa(SRCC731)[LT9]	B			T2	N0
SqCCa(SRCC732)[LT10]	B			T2	N1
SqCCa(SRCC733)[LT11]	A			T1	N1
AdenoCa(SRCC734)[LT12]	V			T2	N0
AdenoSqCCa(SRCC735)[LT13]	B			T2	N0
SqCCa(SRCC736)[LT15]	B			T2	N0
SqCCa(SRCC737)[LT16]	B			T2	N0
SqCCa(SRCC738)[LT17]	B			T2	N1
SqCCa(SRCC739)[LT18]	B			T2	N0
SqCCa(SRCC740)[LT19]	B			T2	N0
LCCa(SRCC741)[LT21]	B			T3	N1
AdenoCa(SRCC811)[LT22]	1A			T1	N0
AdenoCa(SRCC742)[CT2]		M1	D	pT4	N0
AdenoCa(SRCC743)[CT3]			B	pT3	N0
AdenoCa(SRCC744)[CT8]			B	T3	N0
AdenoCa(SRCC745)[CT10]			A	pT2	N0

AdenoCa(SRCC746)[CT12]	MO, R1	B	T3	N0
AdenoCa(SRCC747)[CT14]	pMO, RO	B	pT3	pN0
AdenoCa(SRCC748)[CT15]	M1, R2	D	T4	N2
AdenoCa(SRCC749)[CT16]	pMO	B	pT3	pN0
AdenoCa(SRCC750)[CT17]		C1	pT3	pN1
AdenoCa(SRCC751)[CT1]	MO, R1	B	pT3	N0
AdenoCa(SRCC752)[CT4]		B	pT3	M0
AdenoCa(SRCC753)[CT5]	G2	C1	pT3	pN0
AdenoCa(SRCC754)[CT6]	pMO, RO	B	pT3	pN0
AdenoCa(SRCC755)[CT7]	G1	A	pT2	pN0
AdenoCa(SRCC756)[CT9]	G3	D	pT4	pN2
AdenoCa(SRCC757)[CT11]		B	T3	N0
AdenoCa(SRCC758)[CT18]	MO, RO	B	pT3	pN0

DNA :

DNA (Qiagen) DNA

(tip) 7.5×10^8 , 4 1000rpm 5
 , 1/2 PBS , 4 1000rpm 5
 2 #19155 ase A 가 ddH₂O 6.25ml (100mg/ml) 200µg/ml C1 20mg/ml G2 10ml RN
 10ml C1 (10ml, 4) ddH₂O(40ml, 4) 가 ,
 .4 (Beckman swing bucket) 2500rpm 15
 , 4 2500rpm 15 , C1 (4) 2ml ddH₂O 6ml
 30 (200µl, (10ml) 가 , 50 60 가
 60 , 4 3000xg 10). (, 가 30

, 50ml 250mg ()
 1 /). 가 ddH₂O 6.25ml 20mg/ml
 , 4 . DNase A 200µg/ml(100mg/ml) G2 (20ml)
 , G2 19ml (laminar-flow) TC , ddH₂O 2L 30
 2 가 , G2 (50ml) 가 .
 (, 1.0ml) 가 , (50 , 3
 , 4 3000xg 10). (, 가 30 60

H₂O 6.25ml
 DNase A 100mg/ml
 50ml
 20mg/ml
 10ml
 ddH₂O 30ml
 200µg/ml
 C1 (4) 2ml
 G2 (10ml)
 200µl
 ddH₂O 6ml(4)
 2500rpm
 10ml
 가 dd (10ml)
) 가 , 15
 가 , 30
 가 , 50
 가 , 60
 가 , 30
 가 , 60
 가 , 4
 3000xg 10

(1) DNA :

DNA QBT 10ml (maxi tip) 1) QF 50
 ml 2 30 , QC 15
 QF 15ml (50), 30ml (Corex) DNA
 (10.5ml) 가 , DNA가
 SS-34 15,000rpm 10
 , 70% 10ml(4) 가 .4 SS-34 1
 0,000rpm 10 37 10
 TE(pH 8.5) 1.0ml , 50 1 2 4
 (tuberculin) 26
 DNA 50 1 1.5ml 2
 DNA 50 1 2

(2) DNA :

DU640 0.1ml , 1:20 (5µl DNA + 95µl ddH₂O) A₂₆₀ D
 /A₂₈₀ TE(pH 8.5) DNA 가 200ng/ml . A₂₆₀ /A₂₈₀ 1.8 1.9 (700ng/µl)
 DNA가 50
 (Hoeffler) DyNA (Quant) 200 (20 600ng/ml) DNA (Hoechst)
 (#H33258, 10µl, 12) 1x TNE 100ml . 2ml
 ml 가 200 , 가 pGEM3Zf(+)(2µl, 360851026) 2
 가 pGEM2Zf(+) DNA 2µl 400 ± 10
 가 10ng/µl가 ddH₂O
 , 500 1000
 () B- GAPDH DNA Ct ± 1 Ct
 DNA 1.0ml -80
 4 1ml 8 9 64

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434,
 PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PR
 O1096, PRO2038 PRO2262 , Ct 5

[5aa]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
LT1	---	---	---	---	---	---	---	---	---	---
LT1-a	---	---	---	---	---	---	---	---	---	---
LT2	---	---	---	---	---	---	---	---	---	---
LT3	---	---	---	---	1.16	---	---	---	---	---
LT4	---	---	---	---	---	---	---	---	---	---
LT6	---	---	---	---	---	---	---	---	---	---
LT7	---	---	---	---	1.02	---	---	---	---	---
LT9	---	---	---	---	---	---	---	---	---	---
LT10	---	---	---	---	---	---	---	---	---	---
LT11	---	---	---	---	---	---	---	---	---	---
LT12	---	---	---	---	---	---	---	---	---	---
LT13	---	---	1.12 1.42	---	---	---	5.24 4.47	4.38 4.80	---	---
LT15	---	1.22	2.10 1.82	---	---	---	1.24	---	---	---

[5ab]

패 및 결장 원반성 중앙 및 세포주 모델에서의 ΔCt값

원반성 중앙 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
LTI6	--	1.14	1.44 1.45	1.36	--	--	3.65 3.19	2.73 2.74	--	--
LTI7	--	1.26	--	--	--	--	--	--	--	--
LTI8	--	--	--	1.18	--	--	--	--	--	--
LTI9	--	--	--	--	--	--	--	--	--	--
LTI21	--	--	--	--	--	--	--	--	--	--
GT2	--	--	2.36	2.35	--	--	--	--	--	--
GT3	--	--	1.09	--	--	1.35	--	--	--	--
GT8	--	--	--	1.64	--	1.26	--	--	--	--
GT10	--	--	1.41	2.05	--	1.37	--	--	--	--
GT12	--	--	--	1.15	--	1.24	--	--	--	--
GT14	--	--	1.46	1.40	--	2.58	--	--	--	--
GT15	--	--	--	--	--	--	1.19 1.40	1.10 1.30	--	--
GT16	--	--	--	--	--	--	--	--	--	--
GT17	--	--	--	--	--	--	--	--	--	--
GT1	--	--	--	--	--	1.09	--	--	--	--

[5ac]

계 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt 값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
CT4	---	---	---	---	---	1.22	---	---	---	---
CT5	---	---	2.14	---	---	---	---	---	---	---
CT6	---	---	---	---	---	---	---	---	---	---
CT7	---	---	---	---	---	---	---	---	---	---
CT9	---	---	---	---	---	1.52	---	---	---	---
CT11	---	---	1.29	---	---	---	---	---	---	---
CT18	---	---	---	---	---	---	---	---	---	---
HBL100	---	---	---	---	---	---	---	---	---	---
MB4355	---	---	---	---	---	---	---	---	---	---
T47D	---	---	---	---	---	---	---	---	---	---
MB468	---	---	---	---	---	---	---	---	---	---
MB175	---	---	---	---	---	---	---	---	---	---
MB361	---	---	---	---	---	---	---	---	---	---
B120	---	---	---	---	---	---	---	---	---	---
MCF7	---	---	---	---	---	---	---	---	---	---
SKBR3	---	---	---	---	---	---	---	---	---	---

[5ad]

폐 및 권장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
A549	---	---	---	---	---	---	1.09 1.51	---	---	---
Calu-1	---	---	---	---	---	---	---	---	---	---
Calu-6	---	---	---	---	---	---	1.60 1.22	---	---	---
H157	---	---	---	---	---	---	1.61	---	---	---
H441	---	---	---	---	---	---	1.07 1.15	---	---	---
H460	---	---	---	---	---	---	1.01	---	---	---
SKMES1	---	---	---	---	---	---	1.02	---	---	---
SW900	---	---	---	---	---	---	---	---	---	---
SW480	---	---	---	---	---	---	---	---	---	---
SW620	---	---	---	---	---	---	1.30	---	---	---
Colo320	---	---	---	---	---	---	1.78 1.76 1.74	1.51	2.31	---
H129	---	---	1.22	---	---	---	1.64	---	---	---
H47	---	---	---	---	---	---	---	---	---	---
WDR	---	---	---	---	---	---	---	---	---	---

[5ae]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO434	PRO1927	PRO3567	PRO1295
HCT116	---	---	---	---	---	---	2.15 2.22	1.41 1.47	---	---
SKCO1	---	---	---	---	---	---	---	---	---	---
SW403	---	---	---	---	---	---	1.75	---	1.07	---
LS174T	---	---	---	---	---	---	1.42	---	1.17	---
LT22	---	---	---	1.26	1.07	---	---	---	---	---
LT8	---	---	---	---	---	---	---	---	---	---
Colo205	---	---	---	---	---	---	---	---	---	---
HCT15	---	---	---	---	---	---	---	---	---	---
HCC998	---	---	---	---	---	---	1.15	---	---	---
KM12	---	---	---	---	---	---	---	---	---	---
H522	---	---	---	---	---	---	---	---	---	---
H810	---	---	---	---	---	---	1.20 1.54	---	---	---
LT26	---	---	---	---	---	---	---	---	---	---
LT27	---	---	---	---	---	---	---	---	---	---
LT28	---	---	---	---	---	---	---	---	---	---

[5af]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt 값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
LT29	---	---	---	---	---	---	---	---	---	---
LT30	---	---	---	---	---	---	---	---	---	---
LT31	---	---	---	---	---	---	---	---	---	---
LT33	---	---	---	---	---	---	---	---	---	---
CT25	---	---	---	---	---	---	---	---	---	---
CT28	---	---	---	---	---	---	---	---	---	---
CT35	---	---	---	---	---	---	---	---	---	---
HF-000716	---	---	---	---	---	---	---	---	---	---
HF-000733	---	---	---	---	---	---	---	---	---	---
HF-000831	---	---	---	---	---	---	---	---	---	---
HF-000832	---	---	---	---	---	---	---	---	---	---
HF-000613	---	---	---	---	---	---	---	---	---	---
HF-000499	---	---	---	---	---	---	---	---	---	---
HF-000539	---	---	---	---	---	---	---	---	---	1.49
HF-000575	---	---	---	---	---	---	---	---	---	---
HF-000698	---	---	---	---	---	---	---	---	---	1.09

[5ag]

폐 및 환경 원발성 종양 및 세포주 모델에서의 △CI값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
HF-000545	---	---	---	---	---	---	---	---	---	1.11
SRCC1094	---	---	---	---	---	---	---	---	---	---
SRCC1095	---	---	---	---	---	---	---	---	---	---
SRCC1096	---	---	---	---	---	---	---	---	---	---
SRCC1097	---	---	---	---	---	---	---	---	---	---
SRCC1098	---	---	---	---	---	---	---	---	---	---
SRCC1099	---	---	---	---	---	---	---	---	---	---
SRCC1100	---	---	---	---	---	---	---	---	---	---
SRCC1101	---	---	---	---	---	---	---	---	---	---
HF-000631	---	---	---	---	---	---	---	---	---	1.27
HF-000641	---	---	---	---	---	---	---	---	---	---
HF-000643	4.83	---	---	---	---	---	---	---	---	---
HF-000840	1.08	---	---	---	---	---	---	---	---	1.97
HF-000842	---	---	---	---	---	---	2.20	2.41	---	---
HF-000762	---	---	---	---	---	---	---	---	---	---
HF-000789	---	---	---	---	---	---	---	---	---	---

[5ah]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO381	PRO1269	PRO1410	PRO1755	PRO1780	PRO1788	PRO3434	PRO1927	PRO3567	PRO1295
HF-000795	---	---	---	---	---	---	---	---	---	---
HF-000811	2.09 3.15	---	---	---	---	---	---	---	---	---
HF-001294	1.14 1.08	---	---	---	---	---	1.17	2.31	---	---
HF-001293	---	---	---	---	---	---	---	---	---	---
HF-001300	---	---	---	---	---	---	---	---	---	---
HF-001297	---	---	---	---	---	---	---	---	---	---
HF-001295	---	---	---	---	---	---	---	---	---	---
HF-001299	---	---	---	---	---	---	1.11	2.40	---	---
HF-001296	3.18 3.53	---	---	---	---	---	4.64	5.14	---	---
HF-001291	1.17	---	---	---	---	---	---	---	---	---
HF-000842	---	---	---	---	---	---	---	---	---	---

[5ba]

폐 및 환경 일반성 종양 및 세포주 모델에서의 ΔCh₂

일반성 종양 또는 세포주	PRO1293	PRO1303	PRO344	PRO354	PRO397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
L11	---	---	---	---	---	---	---	---	---	---
L11-a	---	---	---	---	---	---	---	---	1.25	---
L12	---	---	---	---	---	---	---	---	---	---
L13	---	---	---	---	---	---	---	---	---	---
L14	---	---	---	---	---	---	---	---	---	---
L16	---	---	---	---	---	---	---	---	1.20	---
L17	---	---	---	---	---	---	---	---	1.66	---
L19	---	---	---	---	---	---	---	---	---	---
L110	---	---	---	---	---	---	---	---	---	---
L111	---	---	---	---	---	---	---	---	---	---
L112	---	---	---	---	---	---	---	---	1.27	---
L113	---	1.42	---	---	---	---	4.20 4.45	---	---	---
L115	---	1.17	---	---	---	---	1.36 1.15	---	---	---
L116	---	1.42	---	---	---	---	3.71 3.99	---	---	---
L117	---	---	---	---	---	---	---	---	---	---

[5bb]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
L118	---	---	---	---	---	---	---	---	---	---
L119	---	---	---	---	---	---	---	---	---	---
L121	---	---	---	---	---	---	---	---	---	---
CT2	---	---	---	---	---	---	---	---	---	---
CT3	---	---	---	---	---	---	---	---	---	---
CT8	---	---	---	---	---	---	---	---	---	---
CT10	---	---	---	---	---	---	---	---	---	---
CT12	---	---	---	---	---	---	---	---	---	---
CT14	---	---	---	---	---	---	---	---	---	---
CT15	---	---	---	---	---	---	1.34 1.62	---	---	---
CT16	---	1.13	---	---	---	---	1.04 1.05	---	---	---
CT17	---	---	---	---	---	---	1.16	---	---	---
CT1	---	---	---	---	---	---	---	---	---	---
CT4	---	---	---	---	---	---	---	---	---	---
CT5	---	---	---	---	---	---	---	---	---	---
CT6	---	---	---	---	---	---	---	---	---	---

[5bc]

패 및 결장 일반성 종양 및 세포주 모델에서의 ΔCt값

일반성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
CT7	---	---	---	---	---	---	---	---	---	---
CT9	---	---	---	---	---	---	---	---	---	---
CT11	---	---	---	---	---	---	---	---	---	---
CT18	---	---	---	---	---	---	---	---	---	---
HBL100	---	---	---	---	---	---	---	1.10	---	---
MB435s	---	---	---	---	---	---	---	---	---	---
T47D	---	---	---	---	---	---	---	1.37	---	---
MB468	---	---	---	---	---	---	---	---	---	---
MB175	---	---	---	---	---	---	---	---	---	---
MB361	---	---	---	---	---	---	---	---	---	---
B720	---	---	---	---	---	---	---	---	---	---
MCF7	---	---	---	---	---	---	---	---	---	---
SKBR3	---	---	---	---	---	---	---	---	---	---
A549	---	120	---	---	---	---	2.17 2.11	---	---	---
Calu-1	---	---	---	---	---	---	1.39	---	---	---
Calu-6	---	---	---	---	---	---	1.12	---	---	---
H157	---	---	---	---	---	---	---	---	---	---

[5bd]

패 및 결장 일발성 종양 및 세포주 모델에서의 ΔCt값

일발성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4334	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
H441	---	---	---	---	---	---	2.06	---	---	---
H460	---	---	---	---	---	---	1.88	---	---	---
SKMES1	---	---	---	---	---	---	1.90	---	---	---
SW990	---	---	---	---	---	---	---	---	---	---
SW480	---	---	---	---	---	---	---	1.41	---	---
SW620	---	---	---	---	---	---	2.24	---	---	---
Colo320	---	---	---	---	---	---	2.21 2.24	1.72	---	---
HT29	---	---	---	---	---	---	---	1.32	---	---
HM7	---	---	---	---	---	---	---	---	---	---
WIDr	---	---	---	---	---	---	---	1.57	---	---
HCT116	---	---	---	---	---	---	2.46 2.66	1.06	---	---
SKCO1	---	---	---	---	---	---	---	1.01	---	---
SW403	---	---	---	---	---	---	---	1.43	---	---
LS174T	---	---	---	---	---	---	---	---	---	---
L122	---	---	---	---	---	---	---	---	---	---

[5be]

폐 및 결장 일련성 종양 및 세포주 모델에서의 ΔCt값

일련성 종양 또는 세포주	PRO1293	PRO1303	PRO3344	PRO3354	PRO397	PRO407	PRO1555	PRO1096	PRO2038	PRO2262
LT8	---	---	---	---	---	---	---	---	1.74	---
Ca6203	---	---	---	---	---	---	---	---	---	---
HCT15	---	---	---	---	---	---	---	---	---	---
HCC398	---	---	---	---	---	---	---	---	---	---
KM12	---	---	---	---	---	---	---	---	---	---
H522	---	---	---	---	---	---	---	---	---	---
H810	---	---	---	---	---	---	---	---	---	---
LT25	---	---	---	---	---	---	---	---	---	---
LT26	---	---	---	---	---	---	---	---	1.01	---
LT27	---	---	---	---	---	---	---	---	---	---
LT28	---	---	---	---	---	---	---	---	1.32	---
LT29	---	---	---	---	---	---	---	---	---	---
LT30	---	---	---	---	---	---	---	---	---	---
LT31	---	---	---	---	---	---	---	---	---	---
LT32	---	---	---	---	---	---	---	---	---	---
LT33	---	---	---	---	---	---	---	---	---	---
CT19	---	---	---	---	---	---	---	---	---	---

[5bf]

폐 및 결장 원만성 중앙 및 세포주 모델에서의 ΔCt값

원만성 중앙 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
CT20	---	---	---	---	---	---	---	---	---	---
CT21	---	---	---	---	---	---	---	---	---	---
CT22	---	---	---	---	---	---	---	---	---	---
CT23	---	---	---	---	---	---	---	---	---	---
CT24	---	---	---	---	---	---	---	---	---	---
CT25	---	---	---	---	---	---	---	---	---	---
CT26	---	---	---	---	---	---	---	---	---	---
CT27	---	---	---	---	---	---	---	---	---	---
CT28	---	---	---	---	---	---	---	---	---	---
CT29	---	---	---	---	---	---	---	---	---	---
CT30	---	---	---	---	---	---	---	---	---	---
CT31	---	---	---	---	---	---	---	---	---	---
CT32	---	---	---	---	---	---	---	---	---	---
CT33	---	---	---	---	---	---	---	---	---	---
CT35	---	---	---	---	---	---	---	---	---	---
CT36	---	---	---	---	---	---	---	---	---	---
HF-000716	---	---	---	---	---	---	2.63 2.73	---	---	1.68

[5bg]

폐 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
HF-000733	---	---	---	---	---	---	2.58 2.71 1.39	---	---	2.04
HF-000831	---	---	---	---	---	---	---	---	---	---
HF-000832	---	---	---	1.10	---	1.31 1.18	---	---	---	1.13
HF-000611	---	---	---	---	---	---	4.99	---	---	---
HF-000613	---	---	---	---	---	---	---	---	---	---
HF-000499	---	---	---	---	---	---	---	---	---	---
HF-000539	2.33	---	1.32	1.39 1.09	---	1.79 1.61	3.13 2.55	---	---	2.03 1.86
HF-000575	---	---	1.21	1.14	---	1.48 1.25	1.32	---	---	1.16
HF-000698	---	---	---	1.14	---	1.14	---	---	---	1.40 1.22
HF-000345	---	---	1.62	2.12 1.72	---	1.52 1.63	1.59 1.68	---	---	1.17
SRCC1094	---	---	---	---	---	---	---	---	---	---
SRCC1095	---	---	---	---	---	---	---	---	---	---
SRCC1096	---	---	---	---	---	---	---	---	---	---
SRCC1097	---	---	---	---	---	---	---	---	---	---

[5bh]

패 및 결장 원발성 종양 및 세포주 모델에서의 ΔCt값

원발성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
SRCC1098	---	---	---	---	---	---	---	---	1.24	---
SRCC1099	---	---	---	---	---	---	---	---	---	---
SRCC1100	---	---	---	---	---	---	---	---	---	---
SRCC1101	---	---	---	---	---	---	---	---	---	---
HF-000631	---	---	---	---	---	---	1.37	---	---	---
HF-000641	---	---	---	---	---	---	---	---	---	---
HF-000643	---	---	---	---	---	---	---	---	---	---
HF-000840	1.71	---	1.03	---	2.09	1.50 1.42	3.63	---	---	1.49 1.49
HF-000842	---	---	---	---	---	1.24	1.99	---	---	---
HF-000762	---	---	---	1.39 1.15	---	---	---	---	---	---
HF-000789	---	---	---	---	---	---	---	---	---	---
HF-000795	1.13	---	1.12	---	---	1.02 1.04	---	---	---	---
HF-000811	---	---	---	---	---	---	---	---	---	---
HF-001291	---	---	---	---	---	---	---	---	---	---
HF-001293	---	---	---	---	---	---	---	---	---	---

[5bi]

일반성 종양 또는 세포주	PRO1293	PRO1303	PRO4344	PRO4354	PRO4397	PRO4407	PRO1555	PRO1096	PRO2038	PRO2262
HF-001294	---	---	---	---	---	---	---	---	---	---
HF-001295	---	---	---	---	---	---	---	---	---	---
HF-001296	---	---	---	2.11	---	2.21	---	---	---	2.18
HF-001297	---	---	---	---	---	---	---	---	---	---
HF-001299	---	---	---	---	---	---	---	---	---	---
HF-001300	---	---	---	---	---	---	---	---	---	---

폐 및 췌장 일반성 종양 및 세포주 모델에서의 ΔCt값

PRO3434:

(epicenter mapping)
 77631-2537) DNA77631 가 PRO3434(DNA
 , DNA77631 7
 가
 1% (cR) . 1 cR 20 (kilobase)
 . sWSS918 DNA77631-2537 7 가 가
 7 DNA77631 , 7 DNA77631

[6]

7		(cR)
G1	SHGC - 34913	17
G2	AFMa090xg1	25

G3	SHGC - 10715	16
G4	SHGC - 34866	5
G5	SHGC - 32510	48
DNA77631	-	-
G6	sWSS918	19
G7	AFMc027xb5	-

[7]

DNA77631에 대한 에피센터 마커의 증폭 (ΔCt)

종양	G1	G2	G3	G4	G5	DNA 77631	G6	G7
HF-000613	1.31	0.12	0.61	0.46	0.38	-0.28	0.48	0.58
HF-000545	1.55	0.55	0.09	0.16	0.27	0.69	0.26	0.25
HF-000539	1.53	-1.68	0.88	0.76	0.79	2.75	0.98	0.96
HF-000575	1.47	1.02	0.02	-0.17	0.15	0.48	0.20	0.33
HF-000698	0.73	-0.31	-0.08	-0.27	-0.07	-0.26	-0.21	-0.10
HF-000499	0.67	-0.05	0.04	0.12	0.23	-0.30	-0.14	0.21
HF-000733	1.08	1.19	0.41	0.39	0.46	3.00	0.51	0.68
HF-000716	0.65	0.56	-0.41	-0.02	-0.13	2.59	-0.23	0.01

:

PRO381(DNA44194 - 1317):

DNA44194 - 1317 Ct 5a 가 2 가
 1 Ct 5a (1)
 HF - 000643, HF - 000840, HF - 001291, HF - 001294 HF - 001296, (2) HF - 000811 , PRO
 381 DNA44194 - 1317 DNA44194 - 1317
 , DNA44194 - 1317 , DNA44
 194 - 1317 (PRO381) (,)가

PRO1269(DNA66520 - 1536):

DNA66520 - 1536 Ct 5a 가 2 가
 1 Ct 5a LT
 15, LT16 LT17 PRO1269 DNA66520 - 1536 . DNA66
 520 - 1536 , DNA66520 - 1536 (PRO1269) (,)가

PRO1410(DNA68874 - 1622):

DNA68874 - 1622 Ct 5a 가 2 가
 1 Ct 5a (1)
 LT13, LT15 LT16, (2) CT2, CT3, CT5, CT10, CT11 CT14, (3) HT29 ,
 PRO1410 DNA68874 - 1622가 . DNA68874 - 1622
 , DNA68874 - 1622

, DNA68874 - 1622 (PRO1410) (,)가

PRO1755(DNA76396 - 1698):

DNA76396 - 1698 Ct 5a 가 2 가
 1 Ct 5a (1)
 LT16, LT18 LT22, (2) CT2, CT8, CT10, CT12 CT14 , PRO1755
 DNA76396 - 1698 . DNA76396 - 1698
 , DNA76396 - 1698 , DNA76396 - 16
 98 (PRO1755) (,)가

PRO1780(DNA71169 - 1709):

DNA71169 - 1709 Ct 5a 가 2 가
 1 Ct 5a LT
 4, LT7 LT22 , PRO1780 DNA71169 - 1709가 . DNA711
 69 - 1709 , DNA71169 - 1709 (PRO1780)
 , DNA71169 - 1709 (,)가

PRO1788(DNA77652 - 2505):

DNA77652 - 2505 Ct 5a 가 2 가
 1 Ct 5a
 CT1, CT3, CT4, CT8, CT9, CT10, CT12 CT14 , PRO1788 DNA77652 - 2505가
 . DNA77652 - 2505 , DNA77652 - 2505
 , DNA77652 - 2505 (PRO17
 88) (,)가

PRO3434(DNA77631 - 2537):

DNA77631 - 2537 Ct 5a 가 2 가
 1 Ct 5a (1)
 LT13, LT15, LT16, HF - 000842, HF - 001294, HF - 001296 HF - 001299, (2) A549, Clau - 6, H15
 7, H441, H460, SKMES1 H810, (3) CT15, (4) SW620, Colo320, HT29,
 HCT116, SW430, SL174T HCC2998 , PRO3434 DNA77631 - 2537

DNA77631 - 2537 (7) , (1) HF - 000539, (2) HF
 - 000733 HF - 000716 , 가 가
 DNA77631 . DNA77631 - 2537 7

DNA77631 - 2537 , DNA77631 - 2537
 , DNA77631 - 2537 (PRO34
 34) (,)가

PRO1927(DNA82307 - 2531):

DNA82307 - 2531 Ct 5a 가 2 가
 1 Ct 5a (1)
 LT13, LT16, HF - 000842, HF - 001294, HF - 001296 HF - 001299, (2) CT15, (3)
 Colo320 HCT116 , PRO1927 DNA82307 - 2531
 . DNA82307 - 2531 , DNA82307 - 2531
 , DNA82307 - 2531 (PRO1927)
 (,)가

PRO3567(DNA56049-2543):

DNA56049-2543 Ct 5a 가 2 가
 1 Ct 5a Colo3
 20, SW403 LS174T , PRO3567 DNA56049-2543 . D
 NA56049-2543 , DNA56049-2543 , DNA56049-2543 (PRO3567) ()가

PRO1295(DNA59218-1559):

DNA59218-1559 Ct 5a 가 2 가
 1 Ct 5a (1) HF-0005
 HF-000631 HF-000840, (2) HF-000539 HF-000698, (3) HF-0005
 45 , PRO1295 DNA59218-1559가 . DNA59218-1559
 , DNA59218-1559 , DNA59218-1559 (PRO1295) (,)가

PRO1293(DNA60618-1557):

DNA60618-1557 Ct 5b 가 2 가
 1 Ct 5b (1) DNA60618-15
 HF-000840, (2) HF-000539 HF-000795 , PRO1293 DNA60618-15
 57 . DNA60618-1557 , DNA60618-1557
 DNA60618-1557 (PRO1293) (,)가

PRO1303(DNA65409-1566):

DNA65409-1566 Ct 5b 가 2 가
 1 Ct 5b (1) DNA6540
 LT13, LT15 LT16, (2) A549, (3) CT16 , PRO1303 DNA6540
 9-1566 . DNA65409-1566 , DNA6
 5409-1566 , DNA65409-1566
 (PRO1303) (,)가

PRO4344(DNA84927-2585):

DNA84927-2585 Ct 5b 가 2 가
 1 Ct 5b (1) HF-00054
 HF-000840, (2) HF-000539, HF-000575 HF-000795, (3) HF-00054
 5 , PRO4344 DNA84927-2585가 . DNA84927-2585
 , DNA84927-2585 , DNA84927-2585 (PRO4344) (,)가

PRO4354(DNA92256-2596):

DNA92256-2596 Ct 5b 가 2 가
 1 Ct 5b (1) DNA92256-2596
 HF-001296, (2) HF-000539, HF-000575, HF-000698 HF-000762, (3)
 HF-000545, (4) HF-000832 , PRO4354 DNA92256-2596
 . DNA92256-2596 , DNA92256-2596
 , DNA92256-2596 (PRO4354)
 (,)가

PRO4397(DNA83505-2606):

DNA83505-2606 Ct 5b 가 2 가
 1 Ct 5b HF
 -000840 PRO4397 DNA83505-2606 DNA83505-260
 6 , DNA83505-2606 (PRO4397) (,)가

PRO4407(DNA92264-2616):

DNA92264-2616 Ct 5b 가 2 가
 1 Ct 5b (1)
 HF-000840, HF-000842 HF-001296, (2) HF-000539, HF-000575, HF-000698 HF-0
 00795, (3) HF-000545, (4) HF-000832 , PRO4407 DNA92
 264-2616 DNA92264-2616 , DN
 A92264-2616 , DNA92264-2616
 (PRO4407) (,)가

PRO1555(DNA73744-1665):

DNA73744-1665 Ct 5b 가 2 가
 1 Ct 5b (1)
 LT13, LT15, LT16, HF-000631, HF-000840 HF-000842, (2) A549, Calu-1, Calu-6, H441, H
 460 SKMES1, (3) CT15, CT16, CT17, HF-000539 HF-000575,
 (4) SW620, Colo320 HCT116, (5) HF-000545, (6) HF-000
 611, (7) HF-000716, HF-000733 , PRO1555 DN
 A73744-1665가 DNA73744-1665 ,
 DNA73744-1665 , DNA73744-1665
 (PRO1555) (,)가

PRO1096(DNA61870):

DNA61870 Ct 5b 가 2 가
 1 Ct 5b (1) SW480, C
 olo320, HT29, WiDr, HCT116, SKCO1 SW403, (2) HBL100 T47D , PRO1096
 DNA61870 DNA61870 ,
 DNA61870 , DNA61870 (PR
 O1096) (,)가

PRO2038(DNA83014):

DNA83014 Ct 5b 가 2 가
 1 Ct 5b (1) LT1
 a, LT6, LT7, LT8, LT12, LT26 LT28, (2) SRCC1098 , PRO2038 DNA83
 014가 DNA83014 , DNA83014
 (,)가 (PRO2038)

PRO2262(DNA88273):

DNA88273 Ct 5b 가 2 가
 1 Ct 5b (1) HF-00
 0840 HF-001296, (2) HF-000539, HF-000575 HF-000698, (3) HF
 -000545, (4) HF-000716, HF-000733, (5) HF-000
 832 , PRO2262 DNA88273 DNA88273
 , DNA88273 , DNA88273
 (PRO2262) (,)가

21: PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO19

27. PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

cDNA 'PRO' DNA () DNA (, PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262)

DNA PRO381-, PRO1269-, PRO1410-, PRO1755-, PRO1780-, PRO1788-, PRO3434-, PRO1927-, PRO3567-, PRO1295-, PRO1293-, PRO1303-, PRO4344-, PRO4354-, PRO4397-, PRO4407-, PRO1555-, PRO1096-, PRO2038- PRO2262- 50% , 5xSSC, 0.1% SDS, 0.1% , 50 mM , pH 6.8, 2x (Denhardt's) 10% 42 20 . 0.1xSSC 0.1% SDS 42

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA DNA

22: (E. coli) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

(E. coli) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO DNA PCR 가 pBR322 (; Bolivar et al., Gene 2:95(1977))가 , PCR , trp , -His (6 ST , -His), PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 , argU

(Sambrook et al.) (E. coli) LB DNA , DNA 가 LB

가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO1788 PRO1555 (E. coli) -His 가 PRO1788 PRO1555 DNA

PCR, -His 가, 52(W3110fuhA(tonA
)longalErpoHts(htpRts) clpP(lacIq)) 50 mg
 /Ml (carbenicillin) LB O.D. 600 3 5 30
 CRAP (500 Ml 3.57 g (NH₄)₂SO₄, 0.71 g 2H₂
 O, 1.07 g KCl, 5.36 g (Difco) , 5.36 g (Sheffield hycase) SF, 110 mM MP
 OS, pH 7.3, 0.55% (w/v) 7 mM MgSO₄) 50 100 , 20
 30 30 SDS-PAGE

0.5 1L (*E. coli*) (6 10 g) 10 (w/v) 7 M , 20 mM Tris
 s, pH 8 0.1 M 0.02 M
 가 4 (Beckman) 40,000 rpm 30
 3 5 (6 M , 20 mM Tris, pH 7.4) 0.22 μm
 5 Ml . 50 mM (Calbiochem, Utrol) 가 (pH 7.
 4) . 250 mM 280 nm

20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M , 5 mM , 20 mM 1 mM EDTA ,
 100 μg/Ml가 4 12 36 가 가 50
 4% (pH 3)가 TFA 가 가 0.
 0.1% TFA 2 10%가 가 . 10 80% 0.22 μm
 . A₂₈₀ 가 (Poros) R1/H SDS
 가 가

PRO1788 PRO1555
 perfine, Pharmacia) 0.14 M 4% G25 (Su
 6.8 20 mM Hepes, pH

23: PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO19
27, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096,
PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO178
 8, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407,
 PRO1555, PRO1096, PRO2038 PRO2262

pRK5 (1989 3 15 EP 307,247) (Sambro
 ok et al.) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788,
 PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PR
 O1555, PRO1096, PRO2038 PRO2262 DNA pRK5 , PRO381, PRO1
 269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO130
 3, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA
 pRK5-PRO381, pRK5-PRO1269, pRK5-PRO1410, pRK5-PRO1755, pRK5-PRO178
 0, pRK5-PRO1788, pRK5-PRO3434, pRK5-PRO1927, pRK5-PRO3567, pRK5-PRO1295, pRK5-PRO1293, pR
 K5-PRO1303, pRK5-PRO4344, pRK5-PRO4354, pRK5-PRO4397, pRK5-PRO4407, pRK5-PRO1555, pRK5-P
 RO1096, pRK5-PRO2038 pRK5-PRO2262

293 (ATCC CCL 1573) (fetal ca
 If serum) () 가 DMEM 가 (c
 onfluent) . pRK5-PRO381, pRK5-PRO1269, pRK5-PRO1410, pRK5-PRO1755, pRK5-PRO1780, pR
 K5-PRO1788, pRK5-PRO3434, pRK5-PRO1927, pRK5-PRO3567, pRK5-PRO1295, pRK5-PRO1293, pRK5-P
 RO1303, pRK5-PRO4344, pRK5-PRO4354, pRK5-PRO4397, pRK5-PRO4407, pRK5-PRO1555, pRK5-PRO10
 96, pRK5-PRO2038 pRK5-PRO2262 DNA 10 µg VA RNA DNA(Thimmappaya et
 al., Cell, 31: 543(1982)) 1 µg , 1 mM Tris-HCl, 0.1 mM EDTA 0.227 M CaCl₂ 500 µl
 50 mM HEPES(pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄ 500 µl 가 25 10
 293 가 37 4 가
 PBS 20% 2 Ml 30 가 , 293
 가 5
 24 () 200 µCi/Ml ³⁵S- 200 µCi/Ml ³⁵S-
 . 12 , 15% SD
 S PRO381, PRO1269, PRO1410, PRO17
 55, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354,
 PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 가 ()
 , (Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575(1981))
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO129
 5, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO22
 62 DNA 293 . 293 가
 pRK5-PRO381, pRK5-PRO1269, pRK5-PRO1410, pRK5-PRO1755, pRK5-PRO1780, pRK5-PRO1788, pRK5
 -PRO3434, pRK5-PRO1927, pRK5-PRO3567, pRK5-PRO1295, pRK5-PRO1293, pRK5-PRO1303, pRK5-PR
 O4344, pRK5-PRO4354, pRK5-PRO4397, pRK5-PRO4407, pRK5-PRO1555, pRK5-PRO1096, pRK5-PRO203
 8 pRK5-PRO2262 DNA 700 µg 가 . PBS
 . DNA - 4 , 20% 90
 , 5 µg/Ml 0.1 µg/Ml
 4
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, P
 RO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038
 PRO2262 ()
 , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO356
 7, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038
 PRO2262 CHO . pRK5-PRO381, pRK5-PRO1269, pRK5-PRO1410, pRK5-PR
 O1755, pRK5-PRO1780, pRK5-PRO1788, pRK5-PRO3434, pRK5-PRO1927, pRK5-PRO3567, pRK5-PRO129
 5, pRK5-PRO1293, pRK5-PRO1303, pRK5-PRO4344, pRK5-PRO4354, pRK5-PRO4397, pRK5-PRO4407, pR
 K5-PRO1555, pRK5-PRO1096, pRK5-PRO2038 pRK5-PRO2262 , CaPO₄
 DEAE CHO ()
) ³⁵S- . PRO381, PRO1269, PR
 O1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4
 344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 , 6 가
 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO
 1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PR
 O2262
 , 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO19
 27, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096,
 PRO2038 PRO2262 CHO . PRO381, PRO1269, PRO1410, PRO1755, PRO17
 80, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397,
 PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 pRK5
 PCR -His 가
 -His 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, P
 RO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO
 4407, PRO1555, PRO1096, PRO2038 PRO2262 DHFR
 SV40 , CHO () SV40

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262

CHO () COS
 PRO381, PRO1410 PRO1303 CHO
 IgG1 IgG () () -His 가

PCR (Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, Johnn Wiley and So ns(1997))
 DNA 5' 3' CHO
 HO cDNA (Lucas et al., Nucl. Acids Res. 24:9 1774- 1779(1996))
 DHFR (DHFR) SV40 /

(Superfect, Qiagen), (Dosper) (Fuge ne, Boehringer Mannheim) DNA 12 µg 1000 CHO (Lucas et al.) 3 x 10⁷

DNA 10 Ml
 (0.2 µm 5% 1000 rpm 5 , 0.2 µm PS20) 10 Ml
 90 Ml 100 Ml 37 . 2 3 . 1 2 , PS20) 150 Ml 250 Ml
 3 x 10⁵ 37 . 2 3 250 Ml, 500 Ml 2000 Ml 1 Ml
 CHO , 5,122,469 (1992 6 16) pH
 . 3 L 1.2 x 10⁶ /Ml가 . 0 2
 1 33 500 g/L- 30 Ml 10% 0.6 Ml(, 35%
 , Dow Corning 365) 가 , pH 7.2가
 . 10 70% . 0.22 µm
 4

-His 가 , Ni-NTA (Qiagen)
 5 mM 가 . 0.3 M NaCl 5 mM 20 mM Hepes, pH 7
 .4 Ni-NTA 6 Ml 4 4 5 Ml/
 가 , 0.25 M
 4% 25 Ml G25 (Pharmacia) 10 mM Hepes, 0.14 M NaCl
 (pH 6.8) -80
 (Fc) 20 mM
 (pH 6.8) A (Pharmacia) 5 Ml
 100 mM (pH 3.5) . 275 µl 1 M Tris (pH 9)
 1 Ml (pH6.8) . SDS-PAGE -His 가

24: PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038, PRO2262

, ADH2/GAPDH PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 , ADH2/GAPDH , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 (, PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 DNA, () PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 D NA

AB110

10%

SDS-PAGE

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 . PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

25: PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

-His (IgG Fc)가 , pVL1393 (Novagen) , PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

) 5' 3' (, PCR . 5' ()

(GIBCO-BRL) () (BaculoGold™) DNA (Phamingen) (*Spodoptera frugiperda* , 'Sf9') (ATCC CRL 1711)

. 28 4 5 ,

(O'Reilley et al., Baculovirus Expression vectors

: A laboratory Manual, Oxford: Oxford University Press (1994))

-His 가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 , Ni²⁺ - (Rupert et al., Nature, 362: 175-179(1993)) - Sf9

TA; 10% Sf9 (25 Mℓ HEPES, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 0.1% NP-40; 0.4 M KCl) 20 2
 0.45 μm Ni²⁺-NTA (50 mM, 300 mM NaCl, 10% (Qiagen), pH 7.8) 50
 25 Mℓ 25 Mℓ 0.5 Mℓ
 (50 mM A₂₈₀; 300 mM NaCl, 10%, pH 6.0) 2 0 500 mM
 1 Mℓ A₂₈₀ SDS-PAGE Ni²⁺-NTA(Qiagen)
 His₁₀-가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

IgG 가 (Fc 가) PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 A

0.5 2 L (, 8 L) IgG1 I
 gG () () -His 가
 PCR 가 (IgG pb.PH.IgG, -His 가 (Gibco BRL) pb.PH.IgG, -His 가 (Pharmingen) DNA(Pharmingen) 105 ('Sf9') (ATCC CRL 1711) (Pharmingen) His Fc . pb.PH.IgG pb.PH.His.c pVL1393 (Phar mingen) His Fc . 10% FBS가 (Hink's) TNM-FH (multi plicity of infection; MOI) 10 28 5 10% FBS가 TNM-FH Sf9 가 1 가 28 3 -A CL-4B (Pharmacia) 25 Mℓ 1 Mℓ SDS-PAGE

1 Sf9 (500 Mℓ) MOI 0.1 , ESF-921 (Expression Systems LLC)가 28 3 SDS-PAGE

(0.5 3 L) , 0.22 μm -His 가 (Ni²⁺-NTA (Qiagen) , 0.22 μm 5 mM 가 . 0.3 M NaCl 5 mM 20 mM HEPES, pH 7.4 Ni-NTA 6 Mℓ 4 4 5 Mℓ/ 가 , 0.25 M 25 Mℓ G25 (Pharmacia) 10 mM Hep es, 0.14 M NaCl 4% (pH 6.8) -80

(Fc) 20 mM (pH 6.8) A (Pharmacia) 5 Mℓ 275 μℓ 1 M Tris (pH 9) 100 mM (pH 3.5) 가 -His 가 1 Mℓ (pH6.8) . SDS (PAG) N-

5(high 5) DNA Pfu(Stratagene) (5') -His (, IgG Fc)가 . pIE1-1(Novagen) (, IgG Fc)가 . pIE1-1 pIE1-2 i

e1

ie1- hr5

plE1-1 plE1-2 () 5'

3' PCR . 5' ()

(3') IgG Fc (pb.PH.IgG) 8 (pb.PH.His) , plE1-1

5 CO₂, 27 50%가

150 mm pIE 30µg Ex- (: Ex-C

ell 401 + 1/100 L-Glu, JHR Biosciences #14401-78P, :) 1 Mℓ

(CellFECTIN, Gibco BRL #10362-010) 100µℓ Ex- 1 Mℓ ()

2가 15 . Ex- 8 Mℓ DNA

2 Mℓ 가 , Ex- 1 5 가 .

1 . DNA Ex- 1

Ex- 30 Mℓ 가 28 3

가 Ni²⁺-NTA (QIAGEN) IgG 가

-A CL-4B (Pharmacia) 25 Mℓ 1 Mℓ

SDS-PAGE

(0.5 3 L) , 0.22 µm

-His 가 , Ni²⁺-NTA (Qiagen)

5 mM 가 . 0.3 M NaCl 5 mM

20 mM Hepes, pH 7.4 Ni-NTA 6 Mℓ 4 4 5 Mℓ/

가 , 0.25 M

es, 0.14 M NaCl 4% , 25 Mℓ G25 (Pharmacia) 10 mM Hep

(pH 6.8) (Fc) 20 mM

100 mM (pH 3.5) A (Pharmacia) 5 Mℓ ,

1 Mℓ . 275 µℓ 1 M Tris (pH 9)

N- . SDS -His 가

5 PRO381, PRO410 PRO4354

26: PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PR O2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 P RO2262

(Goding)

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, P RO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO 2038 PRO2262

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO178 8, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

PRO381, PRO1269, PRO1410 , PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, P RO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262 가

Balb/c PRO381, PRO1269, PRO1410, PRO1755, PRO1780
 , PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, P
 RO4407, PRO1555, PRO1096, PRO2038 PRO2262 1 100 µg
 MPL-TDM (Ribi Immunochemical Research, Hamilton, MT)
 가 가
 (retro-orbital bleeding) , ELISA -PRO3
 81, -PRO1269, -PRO1410, -PRO1755, -PRO1780, -PRO1788, -PRO3434, -PRO1927, -PR
 O3567, -PRO1295, -PRO1293, -PRO1303, -PRO4344, -PRO4354, -PRO4397, -PRO4407, -
 PRO1555, -PRO1096, -PRO2038 -PRO2262

가가 PRO381, PRO1269, PRO1410, PRO1755, PRO1780,
 PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PRO4397, PR
 O4407, PRO1555, PRO1096, PRO2038 PRO2262 . 3 4
 P3X63AgU.1 (35% HAT() ATCC CRL 1597 가
) 96

PRO381, PRO1269, PRO1410, PRO1755, PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO
 1293, PRO1303, PRO4344, PRO4354, PRO4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262
 ELISA . PRO381, PRO1269, PRO1410, PRO1755,
 PRO1780, PRO1788, PRO3434, PRO1927, PRO3567, PRO1295, PRO1293, PRO1303, PRO4344, PRO4354, PR
 O4397, PRO4407, PRO1555, PRO1096, PRO2038 PRO2262

Balb/c 가 -PRO381, -PRO1269, -PRO1410, -PRO1755, -PRO
 1780, -PRO1788, -PRO3434, -PRO1927, -PRO3567, -PRO1295, -PRO1293, -PRO1303, -P
 RO4344, -PRO4354, -PRO4397, -PRO4407, -PRO1555, -PRO1096, -PRO2038 -PRO226
 2

A G
 _____:
 20110-2209 10801
 (ATCC)

ATCC

DNA44194-1317	209808	1998	4	28
DNA66520-1536	203226	1998	9	15
DNA68874-1622	203277	1998	9	22
DNA76396-1698	203471	1998	11	17
DNA71169-1709	203467	1998	11	17
DNA77652-2505	203480	1998	11	17
DNA77631-2537	203651	1999	2	9
DNA82307-2531	203537	1998	12	15
DNA56049-2543	203662	1999	2	9

DNA59218-1559 203287 1998 9 29
 DNA60618-1557 203292 1998 9 29
 DNA65409-1566 203232 1998 9 15
 DNA84927-2585 203865 1999 3 23
 DNA92256-2596 203891 1999 3 30
 DNA83505-2606 132-PTA 1999 5 25
 DNA92264-2616 203969 1999 4 27
 DNA73744-1665 203322 1998 10 6

reaty)) (Budapest T
 30
 ATCC ATCC
 (37 CFR § 1.14 , 886 OG 638) 35 USC § 122
 가
 가 가

(57)

1. 42 PRO4397
2. 42
- 3.

1 , 42

3 4. 가 42

1 5. (CDR) (FR)

1 6. 가

1 7. , Fab, Fab', F(ab')₂ F_v, Fv

8. 42 PRO4397
42 50% , 5x SSC (0.75M NaCl, 0.075M), 50mM (p
H 6.8), 0.1% , 5x (Denhardt) , 42 DNA (50µg/ml), 0.1% SDS,
10% , 42 0.2x SSC (/), 55
50% , 55 EDTA가 0.1x SSC

9. 42 PRO4397
42

9 10. 42 PRO4397

10 11. 가

(a) 12. (b)
42 PRO4397

(a) 13. 42 PRO4397 (b) 가 42

13 14. 가 가

13 15.

- 16. 42 PRO4397 ,
- 16 17. 42 PRO4397 가 .
- 18. 42 PRO4397 , .
- 18 19. 42 PRO4397 , .
- 18 20. 42 PRO4397 , .
- 20 21. 가 .
- (a) 22. 42 PRO4397 ,
- (b) 가 ,
- 23. 42 PRO4397 , .
- 23 24. , .
- 25. 42 .
- 26. 41 .
- 27. 41 .
- ATCC 28. 132-PTA 41 DNA .
- 25 29. 28 .

29	30.				가	
29	31.					
31	32.					
31		, CHO				
31	33.					
31		, (<i>E. coli</i>)				
31	34.					
31	35.					
	36.					
		42		PRO4397		31
	37.					
		42				
ATCC	38.					
		132-PTA		41		DNA
	39.					
				Fc		37 38
37	40.					
		38				
40	41.					
		, Fab, Fab', F(ab') ₂		F _v , F _v		
(a)	42.					
		1 27		가		42
(b)		1 27		가		42
(c)		1 27		가		42
(a)	43.					
		1 27		가		42
(b)		1 27		가		42

1

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGCTCTTCTAAGAAGGGGGAGTCTGAACTTGTCTG
AAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTCGCTGCTTTTGTAGGG
ACTTCTTTCCCTTGCTTACGCAACATGAGGCTTTTCTTGTGGAACGCGGTCTTGACTCTGTTCGTCACCTTCTTTGA
TTGGGGCTTTGATCCCTGAACCAGAAGTGAATAATGAAGTCTCCAGAAGCCATTCTGCCATCGCAAGACCA
AAGGAGGGGATTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCATTTGGTTACCCCTGGGCATCCTGGAGGCTCTCAAAGTTGGGACCCAGGGCTTGA
AAGGAATGTGTAGGAGAGAAGAGAAGCTCATATTCTCTGCTCTGGGCTATGAAAAAGAAAGGAAAAGGTA
AAATTCCCCCAGAAAGTACACTGATATTTAATATTGATCTCCTGGAGATTGAAATGGACCAAGATCCCATGAAT
CATTTCAAAGAAATGGATCTTAATGATGACTGGAACTCTCTAAAGATGAGTTAAAGCATAATTTAAAGAAGGAT
TTGAAAAACATGGTGCCTGGTGAATGAAGTCATCATGATGCTTTGGTGGAGGATATTTTGGATAAAAGAGATG
AAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTAAGAGATACATCTACCCCTT
TTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCTCTTTAAAGAACATTTTATTTTATACAATGTTCTTTCT
TGCTTTGTTTTTATTTTATATATTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAAATTTTCACTTTC
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATTTGGCACTGGGAATATACCAGACATGA
GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTCCCTCTATTTTCTCCAAGTTAGAGSTCAACATTT
GAAAAGCCCTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATAATGAAATAGTTTATGTGTAATGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGGGCTGACTTGTAAATGGCTACTGCTTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAAACAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAATCCAGCACTTTGGGA
GGCTGAGGCGGGGATCACCTGAGGTTGGGAGTTGAGACCCAGCTGACCAACCGGAAACCTTATCTCTAC
TAAAATACAAAGTAGCCCGGCTGGTGTGCTGCTGTAATCCAGCTACCCAGGAAAGGCTGAGGCGGAGAAATC
ACTTTGAACCCGAGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAAGCTGGACACTCTGTCTCGAAAAAGAAAA
GAACACGGTTAATACCATATNAATATGATGCAATGAGACATGCTACCTAGGACTTAAGCTGATGAGCTTGGCT
CCTAGTGATTTGGCTTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAATGTATC
AATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGCTAGCGGAATATCTTCC
TGGTCTTTAATGGGTAGTCTATAGTATATTTACTACATAACATTTGATCATAAGATAAAGTAGTAAACAGT
CTACATTTTCCATTTCTGTCTCATCAAAACTGAAGTTAGCTGGGTGGTGGCTCATGCTGTAATCCAGCA
CTTTGGGGCCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACCAGCTGGCCAAATGTTGAAACCTTG
TCTCTACTAAAAATACAAAAATAGCCAGGCTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGA
CAGGAGATTTGCTTGAACCCGGGAGGCGGAGTTGCAAGTGGCCACTGCACCTCCAGCCTGGGT
ACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAGAGCAGACCTACAGCAGCTACTATTGAATAAATACCTATC
CTGGATTTT

2

- 신호 펩티드 : 아미노산 1-20
- N-클리코실화 부위 : 아미노산 176-180
- 소포체 표적화 서열 : 아미노산 208-212
- FKBP-형 펩티달-프롤린 시스-트랜스 이소머라제 부위 : 아미노산 78-115; 118-132
- EF-헨드 칼슘 결합 도메인 : 아미노산 191-204; 184-204; 140-160
- S-100/ICaBP형 칼슘 결합 도메인 : 아미노산 183-204

MRLFLWNAVLTFLVFTSLIGALIPPEVKEIVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSLFHSHTKHNNQPI
WFTLGLLEALKGWDQGLKGMCVGEKRLIIPALGYGKEGKGIPESTLIFNIDLLEIRNGPRSHESFQEMDLN
DDWKLKSDVEVKAYLKKEFEKHGAVVNESHHDALVEDIPDKEDEKDGFIISAREFTYKHDEL

3

TCCCGGACCCCTGCCCCCTGCCACTATGTCGCCCGCTCTATGTGCTTGCTGGGCTCTCCCCAGCCTCCTTCG
ACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCTGCTGCAGCCCCATAGTGCCTGGAAACGAGTGGAAAGCCCT
GGCATCAGAGTGCSCCAGCACCTGAGCCTGCCCTTACGCTATGTGGTGTATCGCACACGGCGGGCAGCAGCTG
CAACACCCCCCTCGTGCCAGCAGCAGCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGA
CGTGGGCTACAACCTCTGATTTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCCAGGGTGC
CTCAGGTCACCTATGGAACCCCATGTCATTTGGCATCAGCTTCAATGGCAACTACATGGATCGGGTGCACACC
CCAGGCCATCCGGGACGCCAGGCTACTGGCCTGCGGTGTGGCTCAGGAGCCCTGAGGTCACACTATGTGCT
CAAAGGACCCGGGATGTGCAGCGTACACTCTCTCCAGGCAACAGCTTACCACCTCATCCAGAATTTGGCCACA
CTACCGCTCCCCCTGAGGCCCTGTGATCCGCACCCCATTTCTCCCTCCCATGGCCAAAAACCCCACTGTCTCC
TTCTCCAATAAAGATGTAGCTC

4

신호 웨더드 : 아미노산 1-20
N-클리코실화 부위 : 아미노산 112-116

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRVVVVSHTAGSSCNTPASCQQ
QARNVQHYHMKTLGWCDVGVNFLIGEDGLVYEGRWNTGAHSGHLWNPMSIGISFMGNMMDRVPTPQAIRAAQG
LLACGVAQGALRSNYVLKGRDVRQLSPGNQLYHLIQNWPHYRSP

5

GTGCAAGGTTATAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCACAGCCTGAGATCT
TGGGGATCCCTCAGCCTAACACCCACAGAGCTCAGCTGGTGGATTCCCGCTGCATCAAGGCCTACCCACTGTCTCC
ATGCTGGGCTCCTCCCTGCCTTCTGTGGCTCTGGCCCGTACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCTC
CAAGACTTTGAAGAAGAGGAGGCAAGTGAAGCTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTCGACTAC
GACCACTGCCGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCCGGCCGGCCGCTGCCTGTGCCAGGA
CTCTCCAGCCCCCGCCAGCCGCCCCGACCCCGCCGCATGGGAGAAGTGCATTTGCCGCCGAGAGGGCCGCGCA
GTGGTCCACTGGTGTGCCCTTCTCCCGCTCCTCCACTACTGGCTGCTGCTTTGGGACGGCAGCGAGGCTGCG
CAGAAGGGGCCCCGCTGAAACGCTACCGTCCGAGAGCCGAACTGAAGGGGCTGAGCCAGGGGGCATTATGTCT
TTTTCCGTAGTGGCCGCTAACGAGCCGGGCAAGCCGCTGCCAGGCTGGAGGAGAGGGCCCTCGAGGGGGCC
GACATCCCTGCCTTCGGGCTTGCAGCCGCTTGCCTGCCGCAACCCCGCACTCTGGTCCACGCGCCGCTC
GGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCTGGTGTGGCACTTCTGCCTGCGCATCGCTGGGGC
TGCCCGCGCCGAGCCGCCCCGAGCCGCAAGGGGCGCTTGAAGGGGCTGGGGCATCTCGGGCACAGACAGC
CCCACCTGGGGCGCTCAGCTGGCCCCGGGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGC
TGGGAGCCAGCCAGGCTCCAGGGCCAGGGGAGTCAAGTCTCAGGACTGAGCGCTTGTAGTCCGGTA
CTTGGCGCTTTGTTCCTGGCTGAGTCTGGGAAAGGATGAAGGGGCCCCCAATTTTTTTTAAAGCGCCGAGA
TAATAAATATGTAACTTTGCGGTTAAAAA

6

신호 웨더드 : 아미노산 1-20
막횡단 도메인 : 아미노산 194-220
N-클리코실화 부위 : 아미노산 132-136

MLGSPCLLWLLAVTFLVPRAPQPLAPQDFEEBADEETETAWPPLPAVPCDYDHRHLQVPCHELQVRVPAACLCPG
LSSPAQPPDPFRMGEVRIAABEGRAVVHWCAPFSPVLHYWLLLDWGSEAAQKGPPLNATVRRBELKGLKPGGIYV
VCVVAANEAGASRVPAQGGEGLEGADIPAFGPCSRLAVFPNPRTLVHAAVGVGTALALLS CAALVWHFLDRRWG
CFRRAARAAGAL

7

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGAGTCCAGGATGTGG
CCTGCGCTGCTGCTGCCACTCTCCTCCTCTGCGCACTGCTGTGCTGCCCTCCACCGCCTGCATCAGGGC
TCTTCACTCTCCCTCGAATCCACAGCCCGCCGCTGTGCCAGGGGAGGCCCTCGGGCCACGCT
CATGTGTGCGTGTGGGAGCGAGCACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCTG
CCTGGCACTGCACCCAGCCACCCATCAGGCTTTGAGGAGGGCCGCTCATCCCAATACCCCTGGCTATC
GTGTGGGGTCCCAACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGGATTTCTGGACTATG
TTTGAGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACTCCATGCGAGGTGATGGAGATGGGCTTATC
CTTGGAGAGGCACCTGCCACCTTGGGCCATTCCTGTTCGGGGCCGTGGGGAAGGTGTGGACCCCAAGCTCTAT
GTCACAAATACCACTCCATCATTGTTCTCGTGCCACTGGCATCATCTTCAAGTTCGTGGGACCCGACG
CAGAAGCGACCGACACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGCCAGCAGCCACTGCAGACCTG
TCCCCGGCTGGAGTCACTGTGCTGGGGCCCTTCGGGGACTCACCTACCCCAACCCCTGACCATGAGGAGCCCCGA
GGGGACCCCGCCTGGGATGCCCAACCCCAAGGGGCTCCAGCCTTCCAGTTGAACCGGTGAGGGCAGGGGCAA
TGGGATGGGAGGGCAAAGAGGGAAAGCAACTTAGGTCTTCAGAGCTGGGGTGGGGTGCCTCTGGATGGGTAGT
GAGGAGGCGAGGCTGCCCTCCACAGCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTCTGGGAGGCACC
CTTCTTCTCCAGTCTCTCAGGATCTGTGCTCTATCTCTGCTGCCATAACTCCAACTCTGCCCTTTTGGTT
TTTTCTCATGCCACTTGTCTAAGACAACCTCTGCCCTCTAACCTTGATCCCCCTCTTGTCTGAACTTCCC
TTCTATTCTGGCTACCCCTTGGTTCTGACTGTGCCCTTTCCCTCTCTCCTCCTCAGGATTCCCTGGTGAATCTG
TGATGCCCCCAATGTTGGGGTGCAGCCAAGCAGGAGGCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGG
GGCAGCTGTGGGAGCTGGGGCCACAGGGGCTCCTGGCTCTGCCCTTGACACCCAGGCAACTCCCGAGC
CCCACGGGCAATCTATCTGCTCGCCCTCCTGCAGGTGGGGCCTCACATATCTGTGACTTCGGGTCCCTGTCCC
CACCTTGTGCACTCACATGAAAGCCTTGCACTCACTCCACTTCAAGCCATTTGCACACGCTCCTGCAC
CCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCTCATGTTCTCTCGTCTCACATTTGCACTCTCTCTCCC
ACATTTCTGTGCTCAGCTCACTCAGTGGTCCAGCTTCTCTGCACACTTTACTCTCATGTGCGTTTCCGGCCTGA
TGTGTGGTGGTGTGGGGGCTGCTCACTCTCCCTCATGAACACCCACCCACTCGTTTCCGAGCCCTCCGCT
GCTGTCTCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTTGGGCCCTCATCGGTGATGGTCTCGTCCCATCCA
CACCATTGTTTCTGTCTCCCATCTACTCCAAGGATGCCGGCATCACCTGAGGGCTCCCCCTTGGGAATG
GGGTAGTGGGCCCCAGACTTACCCCAAGGAGGAGGAGTCAAAAATCTGTTTCTGACAGATGGGTTTGGGAGT
GGCTGCTCACTACATGAGAAAGGACTCCCATTTGCCCTTCCCTTCTCCTCAGTCCCTTTGTCTGTGCTGT
CCTGGCTGTGTGTGTGCTTCTGACTTCAGAGCCCTGAGCCAGTCTCCCTTCCAGCCTCCCTTCCAGCCTCCCT
GGGCTCCCTAACTCCACTAGGCTGGGAGGAGGAGTCAAGGCAATCGGGAGCTCCGCTCC
AAGTCTACCTTCCCTCCCGACTCCCTCTGTCCCTCTTCTCCCTCTCTTCTTCCACTCTCTCTCTCT
TGCTTCCCTGCCCTTCCCTCCTCAGTCTCTCCCTCTCTCACTGGTTTTTCCACTTCCCTTCCCTT
TCCCTGGCTCCTAGGCTGTGATATATATTTTTGTATTATCTCTTCTCTCTGTGGTATCATCTGAATTA
CTGTGGATGTAAGTTTCAAAATTTCAAAATAAGCCCTTTCAGGATAA

8

신호 펩티드 :	아미노산 1-33
막횡단 도메인 :	아미노산 178-198
cAMP- 및 cGMP- 의존성 단백질 키나아제 인산화 부위 :	아미노산 210-214
N-미리스토일화 부위 :	아미노산 117-123; 154-160; 214-220
세포 부착 서열 :	아미노산 149-152

MESRMWPAALLSHLLPLWPLLLLPLPPPAQGGSSSPRTPPAPARPPCARGGPSAPRHVCVWERAPPPSRSPRVPR
 SRRQVLPGTAPPATPSGFEEGPPSSQYPWAIWGPVTSREDGGDPNSANPGFLDYGFAPHLGLATPHPNDSMRG
 DGDGLILGEAPATLRPPLFGGRGEGVDPQLYVTTITISIIIVLVATGIIIFKFCWDRSQKRRRPSGGQALRQEESSQ
 QPLTLDSLPAQVTVLGAFGDSPTPTPDHEEPRGGPRPGMPHPKGAFAFQLNR

9

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTCCCGTAGAAGTGAGCAAGGCTGG
 GCAGCGAGTGTCTTCTAGTGGGCTCCCTTCCCTGGGGTCTGCTCTCAGAGGCTGCCAAAATCCTGACAAT
 ATCTACAGTAGTGGAAGCCATATCTACTGATGGACCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGT
 CACCATGTCTAACACAAAAGAGGTCCTTTATGCCAGATTTTAAAAGGAGAAAATCATATCAAGTTATCAG
 TTGGCTTGACCTGAAGATCATCAAAGAGAAATTTAAAAGAGTTTGTATTTCTTGGAAAGAACTTTAGGTGG
 CAGAGGAAAATTTGAAAATTTAAATGTTCTAGAATACTTGGCGTTGACAGTGCAGTCAATTTTTAAATAGAAA
 GGATATCATGGATTCTTAAAGAAATGAGAACTTCGACATGGTGTAGTTGAACTTTTGACTACTGTCTTTCT
 GATTGCTGAGAAGCTTGGGAAGCCATTTGTGCCATTCTTCCACTTCATTCGGCTCTTTGAAATTTGGGCTACC
 AATCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGTCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAA
 TTTTCTGATGTTCTTATGTTCTGCGAGGCAACAGCACATGCAGTCTACATTTGACAACCCATCAAGGAACA
 TTTCACAGAAGGCTTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCAATAACTCTGACTT
 TGCCCTTGATTTGTCTGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGTGGAATAACCTATTAACC
 AGTACCACAAGACTTGGAGAATTCATGCAAGTTTGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCAT
 GGTGAACACCTGTGAGAATCCGAAAATCTTCAAGGAGATGAACAATGCTTTGCTCACCTACCCCAAGGGGTGAT
 ATGGAAGTGTGAGTCTCATTGGCCCAAAGATGTCCACTGGCTGCAATGTGAAAATTTGGACTGGCTCC
 TCAGAGTACCTCTGGCTCACCAAGCATCCGCTGTGTTGTCACCCACGGCGGCGAGAATAGCATAATGGAGGC
 CATCCAGATGGTGTGCCCATGGTGGGATCCCTCTCTTTGGAGACCAGCTGAAAACATGGTCCGAGTAGAAGC
 CAAAAGTTTGGTCTTCTATTAGTAAAGAAAGCTCAAGGCAGAGACATTTGGCTTAAAGATGAAAACAAATCAT
 GGAAGACAAAGATACAAGTCCGCGGAGTGGCTGCCAGTGTATCTGCGCTCCACCCGCTCAGCCCCACACA
 GCGGCTGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGCGCGACGACCTCAAGCCCTATGCTTTCAGCA
 GCCCTGGCATAGCAGTACCTGTTCGACGTTTTTGTGTTTCTGCTGGGGCTCACTTGGGACTCTATGGCTTTG
 TGGGAAGCTGTGGGATGGCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCA
 GCCTTGGCGGGTCTGTTTGGTGGGCGATGTCCACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATT
 TCTAGTCTTCTAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAATGGCCAAAATCATCTTCCACTGTGCTA
 ATTTTGTACAAAATCATCTTACTAGCTCCTGCTGCTAGCAGAAATCTTCCAGTCTCTTGTCTCTCTTTGT
 TTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTGAGTGACTTGGACCCTGACCCCTCAGATTTCCAGCCTT
 AAAATCCACTTCTCTCATGCGCCTCTCCGAATCACACCTGACTTCCAGCCTCCATGTCCAGACTGATGTC
 AGCCTCTCACTCCTGCCCTACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATATCTTTAGT
 TTCTGTTTTGTTCTCCACATATTTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTGAGGGCCGGAC
 ACAGGCTCACAGGTTCCACTTGGGTCCTGTCTGTTGTCGCCACAGTGGAGCTCTCTTGGCTGAGCAGGCAT
 GGAGACTGTAGGTTTTCCAGATTTCTGAAAATAAAAAGTTTACAGCGTTATCTCTCCCAACCTCACTAA

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신호 펩티드 :	아미노산 1-19
막횡단 도메인 :	아미노산 483-504
N-글리코실화 부위 :	아미노산 52-56
티로신 키나아제 인산화 부위 :	아미노산 68-75; 425-434
N-미리스토일화 부위 :	아미노산 16-22; 301-307; 370-376; 494-500
루이신 지퍼 헤턴 :	아미노산 493-515
UDP-글루코노실 부위 :	아미노산 241-294

MAGQRVLLLVGFLLPVLLSEAAKILITISTVGGSHYLLMDRVSQLQDQHGHNVTMLNHRKGPFPMPDFKKEESYQ
 VISWLAPEBDHQREFKKSDFDFLEETLGGRGKFNENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYV
 PFLIAEKLGKPFVAILSTSFGLSEFLGPIPLSYVVPVFRSLLDHMDFWGRVKNFLMFFSFCRRQHQMSDFDNTI
 KEHFTGSRPVLSHLLKAEWLFINSDFAFDFARPLLNTVYVGLMEKPIKPVQDLENFIAKFGDSGFVLVTL
 GGMVNTCCNPEIFKEMNNAFAHLPGQVIVKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPISIRLFTVTHGGQNSI
 MEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAVAASVILRSHLS
 PTQRVLVWIDHVLQTTGATHLKPYPVFPQPPWHEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWVLRGARKVKET

11

CGCGGCCGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCACCAATGCCGTGGCC
CTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCTTCCCGGGTGCCAAATGCGAGGTGGAG
ACCTTCGGCCTTTTTCGACAGCTTCAGCCTGACTCGGGTGGATTTGAGCGGCTGGGGCCCCACATCATGCCGGTG
CCCATCCCTCTGGACACAGCCCACTTGGACCTGCTCCCAACCGGCTGGAGATGATGAATGAGTCGGTGTGGCGGGG
CCGGGCTACACGACGTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACAGCATCTCACCCACTGCCTTCTCC
CGCTTCGCTACCTGGAGTGGCTTGACCTCAGCCACAATGGCTGACAGCCCTGCCAGCCGAGAGCTTACCAGC
TCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGGAGGCTCAGTGTCTGCCTTCACGACGACAGT
CAGGGCCGGGCACTACACGTGGACCTCTCCACAACCTCATTACCGCCTCGTCCCAACCCACAGGGCCGGC
CTGCTGCGCCACCATTTCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTG
CCCCGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATTGGTCCGGGTGCCCTTCGCGGGGCTGGGAGGC
CTTACACACCTGTCTCTGCGCAGCCTGACAGGCTCCCTGAGCTGGCGCCAGTGGCTTCGGTGGCTACCGGGC
CTGAGGTCCCTGGACCTGTGCGGCAACCCCAAGCTTAACTGGGCAGGAGCTGAGGTGTTTTGAGGCTGAGCTCC
CTGACGAGACTGGACCTTTCGGGCACCAACCTGGTGCCTTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTG
CAGAGCGTACGCTGGGCCAGGATGTGGGTGCCGGCCCTGGTGGGGAGGGCACCTACCCCGGAGGCTGGC
TCCAGCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCAACCTCTTGGTGA
ATGTFGTGGCCCGGGCCACATAACAGACTGCTGTCTGGGCTGCTCAGGTCCTCAGGTCCTCGAGTAACTATGTTCAATG
GCCAACACCAAGTGGGGAGCCCGCAGGCTATGTGGCAGCGTCACCACAGGAGTTGTGGGCTAGGAGAGGCTTTG
GACCTGGGAGCCACACTAGGAGCAAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGA
CTTCGACTGCAAAACCAGACTCGGGTCCCTCCTGCTTCCCTTCCCACTTATCCCAAGTGCTTCCCTCAGTGC
CTGGGCCGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGACGGGAGGTTTTCAGGTCCACTGG
GCTGAGTGTCCCTTGGGCCCATGGGCCAGTCACTCAGGGGCGAGTTTCTTTCTAACATAGCCCTTCTTTGGCC
ATGAGGCGATGAGGCCGCTTCATCTTTCTATTTCCCTAGAACCCTAATGGTGAAGGAATTCGAAGAATCA
AGTCCACCTTCTCATGTGACAGATGGGAACTGAGGCTTGAAGAAGAAAAGGCTAATCTAAGTCTCTGCGG
GCAGTGGCATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCAAATGCACTTCTTGTCTCCTTAATAAG
CCCCACCTCCCGCCTGGGCTCCCTTGTGCTCCCTGCTGCTTCCCTTCCCACTTAGCAGAGGATGAGCAGCAGGA
CAGGCAAGAGCCTCACAAAGTGGGACTCTGGGCTCTGACCAGCTGTGCGGCATGGGCTAAGTCACTCTGCCCTC
GGAGCCTCTGGAAGCTTAGGGCACATTTGGTTCAGCCTAGCCAGTTTCTCACCTGGGTTGGGGTCCCCAGCAT
CCAGACTGGAACCTACCCATTTCCCTGAGCATCCTTAGATGCTGCCCCAAGGAGTTGCTGCAAGTTCTGGAG
CCTCATCTGGTGGGATCTCCAAGGGGCTCCTGGATTGAGTCCCACTGGCCCTGAGCACGACAGCCCTCTTCA
CCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGCTTATGCTTACCCCGGGGAGCATCT
CAGCTCCGAACCTGGGCTGTTTCTTAGTCTTCAATTTATAAAAAGTTGTGCTTTTAAACGGAGTGTCACTT
TCAACCGGCTCCCTACCCCTGCTGGCCGGGATGGAGACATGTCATTTGTAAGCAGAAAAAGGTTGCATTT
GTTCACTTTTGAATAATTGCTCCCTGGGCTGTGTTGGGGTGTGGGGGAGCTGGGCATCAGTGGCCACATGGGCA
TCAGGGCTGGCCCAAGAGACCCACAGGGCAGTGGCTGCTGCTTCCCACTGCTTACCCCGGCTAGCCCATCTAT
CTAACCGGCTCTTGAATTAATAAACACTATAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAA
AAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTT

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- 신호 펩티드 : 아미노산 1-16
- 막횡단 도메인 : 아미노산 215-232 ; 287-304
- N-클리코실화 부위 : 아미노산 74-78 ; 137-141
- 글리코사미노글리칸 부착 부위 : 아미노산 45-49
- 티로신 키나아제 인산화 부위 : 아미노산 318-326
- N-미리스토일화 부위 : 아미노산 13-19 ; 32-38 ; 88-94 ; 214-220 ; 223-229
- 루이신 지퍼 해턴 : 아미노산 284-306

MPWPLLLLAVSGAQTTRPCFPQCCEVETFLFDSFSLTRVDCSGLGPHIMPVPIPLDTAHLDLSSNRLEMVNE
SVLAGPGYTTLAGLDLSHNLLTSISPAPFRSLRYLESLDLSHNGLTALPAESFTSSPLSDVNLNHLNQLREVSVA
FTTHSQGRALHVDLSHNLIHRLVPHPTAGLPAPTIQSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAF
AGLGGIHLSLASLQRLPELAPSGFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVLPEALLL
HLPALQSVSVGQDVRCLRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

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CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
ATCCTGCTGACGCTGGGCCCCCTCGAGCCGACGACAGCGAGTCCAGGCGCTGCTGGACATCTGGTTCCGGAG
GAGAAGCACTGCCACCCGCTTCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGTGAAGCTG
CGCATGATCCGTTCTGAGGTGCTCCGCTTGGTGGACGCGCCCTGCAGGACCTGGAGCCGACGACGCTGCTG
TTCGTGACGTCGTTTGGCATCCCCGTGTCAGCATGAGCAAACCTCCAGTTCTGGACCAGGCACTGGCCAC
GACCCCAAGACTCTGGAGCAGAACAATCAAGGACAAGAATTACATGGCCCACTGGTGGAGGTCAGCATGAGCC
GGCGCTCCGGAGGCCAGACTTCCACTCCTTGTCTCACAGCTCCTTGGCCCGCCGCGAGACGACAGCAGAGGCA
CCCAAACCAAAGAGCAGCCAGAGCAGCCATAGGCCAGGGCCGGATTGGGTGGGACCAGCTCCGGTGTCTG
GGCCCTGAGGACGACCTGGTGGCATGTTCTCCAGATTTTCCCGCTCAGCCGGACCTCGGTGGCAGAGCTCC
AGTCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCTCGTCCAGGCGAGCC
GAGGTGCGGGCATCACGGTGCCTGCTGCAGGCCCTCGCCACCTGCTCAGCTCCACACGGCGGTGCCCTG
GTGATGTCATGCACCGTAGCCACTTCTGGCCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCCTGTGTG
CCACAGGACACCGGCTTCTCTCGCTTCTCTGAAGGTGCTCTGACAGTGTGAGTGGCTGGACCAAGTCCCTGC
GTGGAGGCGGGCCCTGCGGGCACAGCTCAGGATGCTTGCAGCCAGGCCCTCAGCCGGCGCAGGCTCAGTGAT
GTGCGAGGGGGCTCTCGCCCTGGCCGAGGCCCTGGCCCTCCGCTCAGGACCTGGAGGTGGTCACTCCACCGTC
CGTCCGCTCATCGCCACCTGAGGTCTGGGAGCAGTGCAGCTGGAGCCGACCTGATCAGCAAGTCCCTGC
GGGTGATCGAGGTGAGGTCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTGCTGCTGCGGATGCTGCC
TCCCCGTTTCCAGCCTGAAGCCCGTGTGGTGGTGAAGTCCCTGCTGCTGCAGGAGGAGGAGCCCTGGCTGG
GGAAAGCGGGTGCAGCAGCGTGCAGCTGAGGCGCTGGCCCTGGCCCTCGTCCAGGCTCTTAGTGGTGG
CTGGAAATGCTGGACCCGAGGTGGTGCAGAGCTGCCCGACCTGCAGCTCAGGCTGCTTCTCCCGAGGAAG
GGCAAAGGTGAGGCCAGGTCGCTCGTCCGCTCCCTACCTCTGACCCCTCTTCAGCATCAGTCCAGCTGGCC
ACACTGCACAGTGCATCCGAGTCTGGGCAAGAGCCGGGAACAGAGGTGACCCCTTGCCTCTCTGGAC
TTCCTCTGGGCTGCATCCATGTTCTCGCATCTGGCAGGGGCGGGACCAGCGACCCCGCAGAAGCGGCGGGAG
GAGCTGGTGTGCGGGTCCAGGGCCCGAGCTCATCAGCTGGTGGAGTGAATCCGGCCGAGGCGGAGACCGCG
AGCCAGGACGGGACACAGCCGCTGCAGCTCATCCAGGCCGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG
GACGATGAGAGTGTGAGGAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGAGACAGCTGCTGGGA
AGGCGCTGCCAGACCTTCTCCTGCAGCTTACCTACAGCGCCGGAGCTGCGGGTGCCTGCTGAGGTCCCTA
CTGCACAGCGGAAGGGGCTGCCAGCAGCAGCTCTGCAAGCTGGACGATCATCCACCGTTCATCAGCTCCTT
GCGGACACAGCGACTCCCGGCGTGGAGAACCGAGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
GCGCACCCGCTGCTGCTGCTCAGGACCTGCCCATGATCGCGGCGCTTCTGCACGGCCGACCCCACTCAACTC
CAGGAGTTCGGGACGACAGCAACCACTGAGTGTCTTCTGACGCTGGGCTGCTGGAGCTGCTGAGGCTGCTG
GTGTTCCGACGAGCAGCAGGAGGCGCTGTTGGACTGCTTCTGCTCCTCATCCGCTGCTGCTGAATTACAGG
AAGTCTCCCGCATCTGGCTGCTTTCATCAACAAGTTTGTGACGTTTCCATAAGTACATACCTACAATGCC
CCAGCAGCCATCTCCTTCTGACAGAACCGCCAGCCGCTCCAGCAGCTGCTTCCGACCAACAGTGGAGTGG
ATGCTGAATCCCTCCTTGCAGGGCTCAGCTGCCAGCAGGACGACAGGACCCGAGGCTGGACGAAGAG
GGCGAGGAGGAGGCTCAGCCGCTCCTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
ATGGCCCTCATATGAACCGCTTTCGCGGCGCAACCGTGGAGGATCTGCTGGAGGTTCTGAGTGAATAGAC
GAGATGTCGCGGAGACCCGAGATCCTGAGCTTCTTCTGACCAACCTGCAGCGGCTGATGAGCTCGCCGAG
GAGTGTGCGGCAACCTCGCCTTGCAGCTGGCCCTGCGCTCCATGCAGAACAGCCCAAGCATGACAGCGCTT
CTGCGCCAGTTCATGTACTGCTGGGACCCAGGACTTTGAGGTGGTGCAGAGCGCCCTCCGGAACCTGCTGAG
TACGCTCTCCTGTCAGAGACCGCGGCTGTGCTGCTCCACCGGCGCTTCTGGTGGGATGATACGGCCAGATG
GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGCTGATGTAAGCCTGTGGCAGCCGA
CCCCCTCAAAGCCCGGCGCTCCCGTCCCGGGATCCTCGAGGCAAGCCAGGAAGCGTGGCGTGTGCTGG
TCTGTCCGAGGAGGTGAGGCGCCGAGCCCTGAGGCCAGGCGAGGAGCAATACTCCGAGCCCTGGGGTGG
CTCCGGGCGGCGCTGGCATCAGGGCCGCTCCAGCAAGCCCTCATTCACCTTCTGGGCGACAGCCCTGCCGCG
AGCGGCGGATCCCCCGGCGATGGCTGGGCTGGTTTTGAATGAACGACCTGAATGTCAA

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- 신호 펩티드 : 아미노산 1-16
- cAMP- 및 cGMP- 의존성 단백질 키나아제 인산화 부위 : 아미노산 154-158; 331-335; 616-620; 785-789; 891-895
- N-미리스토일화 부위 : 아미노산 91-97; 136-142; 224-230; 435-441; 439-445; 443-449; 665-671; 698-704
- 아미드화 부위 : 아미노산 329-333; 634-638
- 올리고아테닐레이트 합성효소 부위 : 아미노산 96-135

MHILVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEALLLPDWLKLRMIRSEVLRVLDAAAL
QDLEPQQLLVFVQSFVPIVSSMSKLLQFLDQAVAHDPQTLQNIQMDKNYMAHLVEVQHERGASGGQTFHSLLTAS
LPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLGPEDDLQAGMFLQIFPLSPDRWQSSSPRPVALALQALGQ
ELARVVQSGPEVPGITVTVLQALATLLSSPHGGALVMSMHRSHFLACPLLRQLCQYRCVVPQDTGFSFLFKVLL
QMLQWLDSPGVGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAEALAFRQDLEVVSSVTRAVIATLRSGEQCSV
EPDLISKVLQGLIEVRSPHLELLTAFFSATADAASPFACKPVVVSSLLQEEBFLAGGKPGADGGSEAVRL
GPSSGLLVWLEMLDPEVVSSCPDLQLRLLFSRRKGGQAQVPSFRPYLLTLPTHQSSWPTLHQCIIRVLGKSRE
QRFPDPSASLDFLWACIHVPRIWQGRDQRTQPKRREELVLRVQGPPELISLVELILAEATRSQDGTAAACSLIQR
LPLLLSCCCGDDSEVRKVTEHLSGCIQWGDVSVLGRRCRDLQLYLRPELVRVPEVLLHSEGAASSVCKLD
GLIHRFITLLADTSDSRALENRGADASMACRKLVAHPHLLLRHLRPMIAALLHGRTHLNFQEFROQNHLSCFLHV
LGLELLELQPHVFRSEHQALWDCLLSFIRLLNRYKSSRHAAAFINKFVQFIHKYITYNAPAAISFLOKHADPLH
DLSFDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEESAGSLPLVSVSLTPTLTAEMAPYMKRLSRGQTFV
DLLEVLSDIDEMSRRRPEILSFFSTNLQRLMSSARECCRNLAFLSALRSMQNSPSIAAFLPTFMYCLGSDQFEV
VQTLARNLPEYALLCQEHAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

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CCGGGCCATGCAGCCTCGGCCCGGGGGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGCAATGGCACCTTC
TGAGCGCTGCTGCTTCTGCTGTGGCCCTTCTCTCGCTGCTCTGGTACGCGGCACTCAGCGGCCAGAAAGGCG
ACGTTGTGGACGTTTACAGCGGGAGTTCCTGGCGCTGCGCGATCGGTTGCACGCGAGCTGAGCAGGAGAGCCTCA
AGCGCTCCAAGGAGCTCAACTGGTGTGGACGAGATCAAGAGGGCCGTGTGAGAAAGCGAGGCGCTCCGAGACG
GAGACGGCAATCGCACCTGGGGCCGCTAACAGAGGACCCCGATTGAAGCCGTGGAAACGGCTCACACCGGCACG
TGCTGCACCTGCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAAGGAGAGCAGTCTGCAGCCCGCGGTG
GCGTGGGCCAAGGGCCGACCGGAGTGTGCGTGGTATGGGCATCCCGAGCGTCCGCGCGAGGTTGCACTCGTACC
TGACTGCACCTCTGCACCTCGCTCATCTCCGAGCTGAGCCCGCAGGAGAAGGAGGACTCGGTCATCGTGGTCTGA
TCGCCGAGACTGACTCACAGTACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCACCGAGGATCCATT
CTGGGCTCTGGAGGTATCTCACCTCCCGCACTTCTACCCTGACTTCTCCCGCTCCGAGAGTCCCTTTGGGG
ACCCCAAGGAGAGGAGTCAAGTGGAGGACCAACAGAACCTCGATTACTGCTTCTCATGATGTACGCGCAGTCCA
AAGGCATCTACTACGTGACGCTGGAGGATGACATCGTGGCCAGCCCACTACCTGAGCACCATGAAGAACTTTG
CACTGCAGCAGCCTTACAGAGGACTGGATGATCCTGGAGTTCTCCAGCTGGGCTTATTGGTAAGATGTTCAAGT
CGCTGGACCTGAGCCTGATTGTAGAGTTCATCTCATGTTCTACCGGACAAGCCATCGACTGGCTCCTGGACC
ATATCTGTGGGTGAAAGTCTGCAACCCCGAGAAAGGATGCGAAGCACTGTGACCGCGAGAAAGCCAACTCGGGA
TCCGCTTCAAACCGTCCCTTCCAGCAGCTGGGCACTCACTCCTCGCTGGTGGCAAGATCCAGAACTGAAGG
ACAAAGACTTTGGAAAGCAGGCGCTCGGAAGGAGCATGTGAACCCGCAAGCAGAGGTGAGCAGAGCCTGAAGA
CATACGACTTCACTCCGAGAAAGCCTACCTGCGCGAGGACTTCTTCTGGGCTTCAACCTGCGCGGGGG
ACTTCATCCGCTTCCGCTTCTCAACCTTAAGACTGGAGCGGTTCTTCTCCGAGTGGGAACATCGAGCACC
CGGAGGACAAGCTTCAACAGCTCTGTGGAGGTGCTGCCCTTCGACAACCTCAGTCAGACAAGGAGCCCTGC
AGGAGGGCCGACCCGACCCCTCCGTAACCTCGGAGCCCGACGGTACCTCCAGATCGGCTCCTTACAAGG
GAGTGGCAGAGGAGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CTGTGTGGGTGATTCTGAGCGAGATCTTCTGAAAAGGCCGACTAAGCTGCGGCTTCTGAGGGTACCTGTGG
CCAGCCCTGAAGCCCACTTCTGGGGGTGTGCTCACTGCCGCTCCCGGAGGGCCAGATACGGCCCCCCCAAAG
GGTCTGCTGGCTGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG
CCCGCCCGGGGGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
TGCCCAAGTACAGCCGCTTTAGAAAGAGCTTTACTTGGGCGCCCGCTCTGCGCGAAGCACTGGAAATGCATA
TACTACTTTATGTGTGTTTTTATCTTGGATACATTTGATTTTTTACAGTAAGTCCACATATACTTCTATA
AGAGCGTACTTGTATAAAGGTTAATGAAGAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AAAAAAGG

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- 신호 펩티드 : 아미노산 1-23
- N-클리코실화 부위 : 아미노산 5-9; 87-91; 103-107; 465-469
- N-미리스토일화 부위 : 아미노산 6-12; 136-142; 370-376; 509-515

MRLRNGTFLTLLFLCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDLHAAEQESLKRKELNLVLDEIKRAV
SERQALRDGDNRTWRLTEDPRLKPWNGSHRHLVHLPTVFHHLPHLLAKESSLQPAVRVGGQRTGVSVVMGIPS
VRREVHSLYLDLHSLISELSPQEKEDSVIVVLIETDSQVTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDF
SRLRESFGDPKERVWRWTKQNLDYCFLLMYAQSKGIYVQLEDDIVAKPNYLSMKNFALQQPSEDMILEFSQL
GFIGKMPKSLDLSLIVEFILMFYRDKPIDWLLDHLWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGHSSSL
AGKIQLKDKDFGKQALRKEHVNPPEVSTSLKTYQHFTLEKAYLREDFWAFPTAAGDFIRFRFFQPLRLERFF
FRSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRSPDGYLQIGSFYKGVARGEVDPAFGPLEAL
RLSIQTDSFVWVILSEIFLKKAD

17

GCACCGCAGACGGCGCGGATCGCAGGGAGCCGGTCCGCCGCGGAACGGGAGCCTGGGTGTGCGTGTGGAGTCCG
GACTCGTGGGAGACGATCGCGATGAACACGGTGTGTGCGGGCGAACTCACTGTTTCGCTTCTCGCTGAGCGTG
ATGGCGCGCTCACTTCGGCTGCTTATCACCACCGCTTCAAAGACAGGAGCGTCCCGGTGCGGCTGCACGTC
TCGGGATCATGCTAAAAATGTAGAAGATTTCACTGGACCTAGAGAAAGAGTGTCTGGGATTTATCACATTT
GATATACTGCTGATCTAGAGAATATATTTGATTGGAATGTTAAGCAGTTGTTCTTTATTTATCAGCAGAATAT
TCAACAAAAAATAATGCTCTGAACCAAGTTGTCCTATGGGACAAGATTGTTTTGAGAGGTGATAATCCGAAGCTG
CTGCTGAAGATATGAAAAAATAATTTTTCTTTGACGATGGAATGCTCAAGGGAAACAGGAATGTCCT
TTGACCCGTCTTGGAAACGTCGTACCAAAATGCTGGAAATCTACCTCTTGTGACAGGATCAGGACACGATATCTGT
CCATTTCCAGATACATATGAAATAACGAAGGTTATTAATTTCTGAAATTTGAAACAAAA

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신호 펩티드 :	아미노산 1-25
막횡단 도메인 :	아미노산 149-164
N-글리코실화 부위 :	아미노산 141-145
N-미리스토일화 부위 :	아미노산 25-31; 135-141
원핵생물 세포막 지질 단백질 지질 부착 부위 :	아미노산 16-27
세포 부착 서열 :	아미노산 112-115
TonB- 의존성 수용체 단백질 시그너치 1 :	아미노산 1-21

MNTVLSRANSLFASFSLVMAALTFGCFFITFAFKDRSVPVRLHVSRIMLKNVEDFTGPRERSDLGFITFDITADLE
 NIFDWNVKQLFLYLSAEYSTKNNALNQVVLWDKI VLRGDNPKLLKDKMKTXYFFDDGNGLKGNNRVTLTLSWNV
 VFNAGILPLVVTGSGHVSVPFPDITYEITKSY

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GACCGGTCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTCTCACCG
 TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGTGGAATATACCGGGACATCTTCA
 CTCTCCTGCTCGCCCTGCACCGGAGCTTGGTGTGTCGCGAGAGAGTGGGGGAAGATGTTGTTTCTTCCGAACAGC
 TGCTGCTACTTGTCTGCTGGGCTGGCTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTTGGAAAGAGG
 GTCCCTCATATGCTTGTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCTGTGGTGGACAGC
 AGCTGCTCTACACCTGTGCCCCACATCGGAGAGCTCCGAAAACCTGCTCGCTTCTGTTGGTGTGACGGCAGTAGT
 GACGGAGTGGGGCTTCATGAGGAAATCACCCCACTACCACCAGCTGGGAGCCAGCCTTCCAGACCA
 GCCAGGGGCTGCAGGCACAGCTGCCCGAGCTTTTCCACAACCCAGCCCTCTCTGCGCCGACCGTAGAGT
 TCGTGGCAGAAAGAATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCAGCAG
 CAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGAGACCAGCCAGCTGTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGCCAGGCATTGGCCCTGGGGCGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCTGCTTCCAGAGGAGACC CGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGG
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGACCCAAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCGAGCCAGGCTCCTGAACCTGCTGCCCGGGGAGCGGAGGGCTGCTCCCGCCCTGAC
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTGACGAGGGAGTCTCCCAAGAGCATCTGGAAACAGCTCCTAGGC
 CAGCTGGCCAGAGCAGCTGCGGTGCCCGCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAAGTGTCTGTG
 GAGTGTAGCTTCCCTCCTGCTGAGATCAAATTCCTATCTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTCTTCTGTGGAAGGAAGACTTTCAGGGCCCGGTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACAAAGCCAAAGGAGTGGACTTGTGCTATTCTTGTCTA
 CGGGAGCTGGTGGAGAAAGGCTGTGATGGACGGATGGAGATAGAGGCTGCTTGGCCAGCTTCCACAGGCCCAG
 TGCCAGGGGACTTGTGTAAGAAATAGCAACACTGTCTAATCTGTCTTAGCCGAGCCCACTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGCAGCTGTGCTGGCCAGAGCTAGGGCTGAGAAAGTGGCC
 CTGCCCTTGGCATTGCAACAGAACCTGGACCCCGCTCACGAGGAGGCCAAAGTGCCAATGCAGACCCCTCAC
 TGGTGGGGTGTAGCTGGGTCTACAGTCAAGCTTCCCTGCTCTAAGGGTGTCTAGCTGGCCTGCCACCCAGCGA
 ATCTTAGAGGAAGGAGAGTTGGCTGATTTGGGATATGCGCAGAAAGTCCAGAGATGCCAGTCTGGAGTAGAA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTTGGCTGTCTCAACACAGAAATCAAGCCT
 CATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGGAAATCTATGACAGAGGCAATGACTCCTGCTTAAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCATAACAGGCCGGGTCTGGTGGCTCATGCTGTAATCCAGCACTTGGAGGCTGAGGTGGCGG
 ACTGCTGAGGTCAAGAAATCAAGACAGCCCTGGCCAAACATGGCAAAACCCATCTCTACTAAAAATAAAAAAT
 TATTAGCTGGGCATGGTGGTGTGTCCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAACC
 TGGAGGTGGAGGTGTCAGTGCAGCGAGGTGCGACCACTGCCTCAGTCTGGGTAACAGAGCGAGACTTCTAGA
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCTCCCTGTACTTCCAGCCCTGT
 GCAGGTAGTAACCTCTTGGACCTCTCCCTGACAGGGACCAAGCACAGGGCATTAGAGCTTTTGAATAAAC
 TGGTTTCTTTAAAAAAGGGGCGCCGCTTT
 TTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAATAATCTCCCCACAGATGGCTCCTGCAATCTGCCAGACTCT
 GGGCGTGTCTGTAGGAAAGGCCCTGTTTTCCCTGAGGCGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTGG
 CCGTCTTGGCCCTGGCGTGTGTCTAGCTGCTTCTTGGCGGCACAGAGCTGGGGGTCTGGGGCACCGGGA
 GCTAAGAGCAGGCTCTGGTGCAGGGGTGAGGCTGTCTCTTAAACGACACCTGAGGTGCTCCTGAGATGCTGG
 GTCCACCCTGAGTGGCACGGGAGCAGCTGTGGCCGGTGTCTCTTCTYTAGCCAGTCTGGGGAACTAAGCTCG
 GGCCCTCTTTGCAAGACCGAGGATGGGGTGGGTGTGGGGACTCATGGGAAATGGCTGAGGAGCTACGTGTG
 AAGAGGGCGCGTTTGTGGCTGCAGCGGCTGAGGCGCTCTCTCCTGAGCCTCAGTTTCCCTTCCGCTATA
 TGAAGAATGCGCTCTCGGTGTCTCAGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACGAGCTCATG
 TTATTTTCAACTGTCTCGACGTTGGCTGGGCACGTGGAATGGCCATGTCCCTGCTGCTGCGTGGACG
 TCGCGGTGGGAGTGCAGCCAGAGGGCGGGCCAGAGCTGCGCTGGGGGTGAGGGGAGGGCCCGGGAGGGG
 CTCACAGGAAGTTGGGCTCCCGCACCAAGCAGGCGGGCTCCCGCCCGCCCGCCCAACCCCTCAGGG
 GCCGGTAGACAAAGTGGAGTTCGGCTTGGCTGCGCAGCAGGTAGCCCTTGTGAGTGGCGCAGGCGCT
 CGTCCCGCAGCTGGAAGCAGCGCCCTCCACAGCACGAAACAGCCGTTGGCCT

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신호 웨퍼드 : 아미노산 1-18
 N-클리코실화 부위 : 아미노산 244-248
 미소체 C-말단 표적화 신호 : 아미노산 278-282

MCFLNKLLLLAVLWLFQIPTVPEDLFFLEBEGPSYAFEVDTVAPEHGLDNPVVDQQLLYTCCPYIGELRKLAS
 WVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPPSLRRTVEFVAERIGSNCKVHKIKATLV
 ADLVRQAESLLQEQLVTVQGEEGDPAQLLEILCSQLCPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSA
 ENIAVGLATEKACAWLSANITALIRREVKAASRTRAQGPPEPAARGERRGCSRA

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신호 웨퍼드 : 아미노산 1-19
 막형단 도메인 : 아미노산 237-262
 N-클리코실화 부위 : 아미노산 205-209
 세포 부착 서열 : 아미노산 151-154
 코프르포르피리노겐 III 옥시다제 단백질 : 아미노산 115-141

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23

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신호 펩티드 :	아미노산 1-17
N-글리코실화 부위 :	아미노산 24-28; 163-167
세린 프로테아제, 트립신 족, 히스티딘 활성 부위 :	아미노산 58-64
세린 프로테아제, 트립신 족, 히스티딘 단백질 도메인 :	아미노산 47-64; 196-207; 218-242
크링글 도메인 단백질 부위 :	아미노산 47-65; 194-207
에플 도메인 단백질 부위 :	아미노산 220-248

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25

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신호 펩티드 :	아미노산 1-39
II형 막횡단 도메인 :	아미노산 30-49
N-글리코실화 부위 :	아미노산 79-83; 104-108; 192-196
카제인 키나아제 II 인산화 부위 :	아미노산 194-198; 352-356
N-미리스토일화 부위 :	아미노산 14-20; 160-166; 367-373
원핵생물 세포막 지질단백질 지질 부착 부위 :	아미노산 35-46

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27

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- 신호 펩티드 : 아미노산 1-21
- cAMP- 및 cGMP- 의존성 단백질 키나아제 인산화 부위 : 아미노산 106-110
- 카제인 키나아제 II 인산화 부위 : 아미노산 36-40; 80-84; 84-88; 158-162; 202-206; 207-211; 213-217
- N-미리스토일화 부위 : 아미노산 115-121
- 아미드화 부위 : 아미노산 70-74

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29

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신호 펩티드 :	아미노산 1-31
막횡단 도메인 :	아미노산 11-32; 195-217
N-글리코실화 부위 :	아미노산 111-115
카제인 키나아제 II 인산화 부위 :	아미노산 2-6; 98-102; 191-195
N-미리스토일화 부위 :	아미노산 146-152; 192-198

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35

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신호 펩티드 :	아미노산 1-32
티로신 키나아제 인산화 부위 :	아미노산 233-241
아미드화 부위 :	아미노산 147-151

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37

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38

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- <110> Genentech, Inc.
- Botstein, David
- Goddard, Audrey
- Gurney, Austin, L.
- Roy, Margaret, Ann
- Watanabe, Colin, K
- Wood, William, I.

<120> COMPOSITONS AND METHODS FOR THE TREATMENT OF TUMOR

<130> P2831R1PCT

<140> PCT/US99/28551

<141> 1999-12-02

<150> PCT/US99/05028

<151> 1999-03-08

<150> PCT/US99/20111

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<151> 1999-12-01

<160> 124

<210> 1

<211> 2336

<212> DNA

<213> Homo Sapien

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 1

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tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttaggg 150

acttctttcc ttgcttcagc aacatgaggc ttttcttggt gaacgcggtc 200

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agtgaaaatt gaagtctcc agaagccatt catctgcat cgcaagacca 300

aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350

ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

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tgacagagca agactccatc tcaaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

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<211> 211

<212> PRT

<213> Homo Sapien

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Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu

20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly

35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly

50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile

65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln

80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile

95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro

110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg

125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn

140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys

155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His

170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys

185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu

200 205 210

Leu

211

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 3

ctttccttgc ttcagcaaca tgaggc 26

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 4

gcccagagca ggaggaatga tgagc 25

<210> 5

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 5

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<210> 6

<211> 697

<212> DNA

<213> Homo Sapien

<400> 6

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cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100

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<210> 7

<211> 196

<212> PRT

<213> Homo Sapien

<400> 7

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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
 20 25 30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
 35 40 45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
 50 55 60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
 65 70 75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
 80 85 90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
 95 100 105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
 110 115 120

Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
 125 130 135

Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
 140 145 150

Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
 155 160 165

Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
 170 175 180

Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
 185 190 195

Pro
 196

<210> 8

<211> 1170

<212> DNA

<213> Homo Sapien

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cagacgtcag ctggtggatt cccgctgcat caaggcctac cactgtctc 150

catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttg 200

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cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350

ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400

gaccgcccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450

agtgtccac tgggtgccc ctttctccc ggtcctccac tactggctgc 500

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ttaaaaaaaa aaaaaaaaaa 1170

<210> 9

<211> 238

<212> PRT

<213> Homo Sapien

<400> 9

Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
 1 5 10 15

Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
 20 25 30

Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
 35 40 45

Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
 50 55 60

Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
 65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
 80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
 95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
 110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
 125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
 140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
 155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
 170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
 185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
 200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
 215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
 230 235 238

<210> 10

<211> 2524

<212> DNA

<213> Homo Sapien

<400> 10

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<210> 11

<211> 276

<212> PRT

<213> Homo Sapien

<400> 11

Met Glu Ser Arg Met Trp Pro Ala Leu Leu Leu Ser His Leu Leu

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Pro Leu Trp Pro Leu Leu Leu Leu Pro Leu Pro Pro Pro Ala Gln

20 25 30

Gly Ser Ser Ser Ser Pro Arg Thr Pro Pro Ala Pro Ala Arg Pro
 35 40 45

Pro Cys Ala Arg Gly Gly Pro Ser Ala Pro Arg His Val Cys Val
 50 55 60

Trp Glu Arg Ala Pro Pro Pro Ser Arg Ser Pro Arg Val Pro Arg
 65 70 75

Ser Arg Arg Gln Val Leu Pro Gly Thr Ala Pro Pro Ala Thr Pro
 80 85 90

Ser Gly Phe Glu Glu Gly Pro Pro Ser Ser Gln Tyr Pro Trp Ala
 95 100 105

Ile Val Trp Gly Pro Thr Val Ser Arg Glu Asp Gly Gly Asp Pro
 110 115 120

Asn Ser Ala Asn Pro Gly Phe Leu Asp Tyr Gly Phe Ala Ala Pro
 125 130 135

His Gly Leu Ala Thr Pro His Pro Asn Ser Asp Ser Met Arg Gly
 140 145 150

Asp Gly Asp Gly Leu Ile Leu Gly Glu Ala Pro Ala Thr Leu Arg
 155 160 165

Pro Phe Leu Phe Gly Gly Arg Gly Glu Gly Val Asp Pro Gln Leu
 170 175 180

Tyr Val Thr Ile Thr Ile Ser Ile Ile Ile Val Leu Val Ala Thr
 185 190 195

Gly Ile Ile Phe Lys Phe Cys Trp Asp Arg Ser Gln Lys Arg Arg

	200	205	210
Arg Pro Ser Gly Gln Gln Gly Ala Leu Arg Gln Glu Glu Ser Gln			
	215	220	225
Gln Pro Leu Thr Asp Leu Ser Pro Ala Gly Val Thr Val Leu Gly			
	230	235	240
Ala Phe Gly Asp Ser Pro Thr Pro Thr Pro Asp His Glu Glu Pro			
	245	250	255
Arg Gly Gly Pro Arg Pro Gly Met Pro His Pro Lys Gly Ala Pro			
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Ala Phe Gln Leu Asn Arg			
	275	276	

<210> 12

<211> 2320

<212> DNA

<213> Homo Sapien

<400> 12

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<210> 13

<211> 523

<212> PRT

<213> Homo Sapien

<400> 13

Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro

1 5 10 15

Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr

20 25 30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile

35 40 45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg

50 55 60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln

65	70	75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys		
80	85	90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly		
95	100	105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln		
110	115	120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys		
125	130	135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys		
140	145	150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile		
155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro		
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met		
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe		
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile		
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu		
230	235	240

Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255

Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly
 260 265 270

Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn
 275 280 285

Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu
 290 295 300

Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu
 305 310 315

Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys
 320 325 330

Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn
 335 340 345

Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His
 350 355 360

Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile
 365 370 375

Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu
 380 385 390

Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys
 395 400 405

Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu

410 415 420

Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser

425 430 435

Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser

440 445 450

Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr

455 460 465

Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp

470 475 480

His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu

485 490 495

Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala

500 505 510

Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr

515 520 523

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 14

tgcctttgct cacctacccc aagg 24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 15

tcaggctggt ctcaaagag aggg 24

<210> 16

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

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<210> 17

<211> 2639

<212> DNA

<213> Homo Sapien

<400> 17

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tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagt 100

gggccagac aaccggcca tgctccccg ggtgccaatg cgaggtggag 150

accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200

cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250

tggacctgic ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300

gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350

caccagcatic tcaccactg ccttctcccg ccttcgctac ctggagtgcg 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450

agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500

ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550

acctctcca caacctcatt caccgcctg tgccccacc cagagggcc 600

ggcctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700

atgggaacc tctagctgtc attggtccg gtgccttcgc gggctggga 750

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gcccagtggc ttccgtgagc taccggcct gcaggtcctg gacctgtcgg 850

gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900

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aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 18

<211> 353

<212> PRT

<213> Homo Sapien

<400> 18

Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln

1 5 10 15

Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr

20 25 30

Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser

35 40 45

Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr

50 55 60

Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu

65 70 75

Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp

80 85 90

Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser

95 100 105

Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu

110 115 120

Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp

125 130 135

Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150
Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
				155					160					165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
				170					175					180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
				185					190					195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
				200					205					210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
				215					220					225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
				230					235					240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
				245					250					255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
				260					265					270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
				275					280					285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
				290					295					300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg

305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly

320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser

335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu

350 353

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 19

ccctgccagc cgagagcttc acc 23

<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 20

ggttggtgcc cgaaaggtcc agc 23

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 21

caacccaag ctaactggg caggagctga ggtgtttca ggcc 44

<210> 22

<211> 3437

<212> DNA

<213> Homo Sapien

<400> 22

caggaccagg tcttcctacg ctggagcagc ggggagacag ccaccatgca 50

catcctcgtg gtccatgcca tggatgacct gctgacgctg ggcccgcctc 100

gagccgacga cagcgagttc caggcgtgc tggacatctg gttccggag 150

gagaagccac tgcccaccgc cttcctggtg gacacatcgg aggaggcgct 200

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<210> 23

<211> 1029

<212> PRT

<213> Homo Sapien

<400> 23

Met His Ile Leu Val Val His Ala Met Val Ile Leu Leu Thr Leu

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20 25 30

Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val

35 40 45

Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu

50 55 60

Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu

65 70 75

Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe

80 85 90

Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp

95 100 105

Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met

110 115 120

Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg

125 130 135

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser

140 145 150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser

155 160 165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr

170 175 180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe

185 190 195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser

200	205	210
Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln		
215	220	225
Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile		
230	235	240
Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro		
245	250	255
His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu		
260	265	270
Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val		
275	280	285
Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu		
290	295	300
Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro		
305	310	315
Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly		
320	325	330
Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu		
335	340	345
Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val		
350	355	360
Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val		
365	370	375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val	380	385	390
Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala	395	400	405
Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val	410	415	420
Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly	425	430	435
Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu	440	445	450
Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp	455	460	465
Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu	470	475	480
Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe	485	490	495
Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro	500	505	510
Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu	515	520	525
Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys	530	535	540

Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro

545 550 555

Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu

560 565 570

Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg

575 580 585

Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg

590 595 600

Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val

605 610 615

Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly

620 625 630

Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu

635 640 645

Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu

650 655 660

Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp

665 670 675

Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp

680 685 690

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys

695 700 705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu

710	715	720
Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe		
725	730	735
Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val		
740	745	750
Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu		
755	760	765
His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu		
770	775	780
Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile		
785	790	795
Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala		
800	805	810
Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His		
815	820	825
Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu		
830	835	840
Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg		
845	850	855
Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu		
860	865	870
Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu		
875	880	885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
 890 895 900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
 905 910 915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
 920 925 930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
 935 940 945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
 950 955 960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
 965 970 975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys
 980 985 990

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
 995 1000 1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
 1010 1015 1020

Arg Ile Leu His Met Glu Ala Val Met
 1025 1029

<210> 24

<211> 2186

<212> DNA

<213> Homo Sapien

<400> 24

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cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150
acgttgtgga cgtttaccag cgggagtcc tggcgctcg cgatcggttg 200
cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250
gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgagagacg 300
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186

<210> 25

<211> 548

<212> PRT

<213> Homo Sapien

<400> 25

Met Arg Leu Arg Asn Gly Thr Phe Leu Thr Leu Leu Phe Cys

1 5 10 15

Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly

20 25 30

Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala	35	40	45
Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg	50	55	60
Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val	65	70	75
Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp	80	85	90
Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser	95	100	105
His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro	110	115	120
His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val	125	130	135
Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser	140	145	150
Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser	155	160	165
Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile	170	175	180
Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val	185	190	195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
 200 205 210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
 215 220 225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
 230 235 240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
 245 250 255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
 260 265 270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
 275 280 285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
 290 295 300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
 305 310 315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp
 320 325 330

Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
 335 340 345

Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
 350 355 360

Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu

365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln		
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr		
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu		
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe		
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe		
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn		
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys		
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg		
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val		
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu		
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser		
530	535	540

Glu Ile Phe Leu Lys Lys Ala Asp

545 548

<210> 26

<211> 663

<212> DNA

<213> Homo Sapien

<400> 26

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acacggtgct gtcgcggggc aactcactgt tcgccttctc gctgagcgtg 150

atggcggcgc tcaccttcgg ctgcttcac accaccgcct tcaaagacag 200

gagcgtcccg gtgcggctgc acgtctcgcg gatcatgcta aaaaatgtag 250

aagattcac tggacctaga gaaagaagt atctgggatt taccacattt 300

gatataactg ctgatctaga gaatatattt gattggaatg ttaagcagtt 350

gtttctttat ttatcagcag aatattcaac aaaaaataat gctctgaacc 400

aagtgtcct atgggacaag attgttttga gaggtgataa tccgaagctg 450

ctgctgaaag atatgaaaac aaaatatattt ttctttgacg atggaaatgg 500

tctcaaggga aacaggaatg tcactttgac cctgtcttgg aacgtcgtac 550

caaatgctgg aattctacct cttgtgacag gatcaggaca cgtatctgtc 600

ccatttccag atacatatga aataacgaag agttattaaa ttattctgaa 650

tttgaacaa aaa 663

<210> 27

<211> 180

<212> PRT

<213> Homo Sapien

<400> 27

Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser
 1 5 10 15

Leu Ser Val Met Ala Ala Leu Thr Phe Gly Cys Phe Ile Thr Thr
 20 25 30

Ala Phe Lys Asp Arg Ser Val Pro Val Arg Leu His Val Ser Arg
 35 40 45

Ile Met Leu Lys Asn Val Glu Asp Phe Thr Gly Pro Arg Glu Arg
 50 55 60

Ser Asp Leu Gly Phe Ile Thr Phe Asp Ile Thr Ala Asp Leu Glu
 65 70 75

Asn Ile Phe Asp Trp Asn Val Lys Gln Leu Phe Leu Tyr Leu Ser
 80 85 90

Ala Glu Tyr Ser Thr Lys Asn Asn Ala Leu Asn Gln Val Val Leu
 95 100 105

Trp Asp Lys Ile Val Leu Arg Gly Asp Asn Pro Lys Leu Leu Leu
 110 115 120

Lys Asp Met Lys Thr Lys Tyr Phe Phe Phe Asp Asp Gly Asn Gly

125 130 135

Leu Lys Gly Asn Arg Asn Val Thr Leu Thr Leu Ser Trp Asn Val

140 145 150

Val Pro Asn Ala Gly Ile Leu Pro Leu Val Thr Gly Ser Gly His

155 160 165

Val Ser Val Pro Phe Pro Asp Thr Tyr Glu Ile Thr Lys Ser Tyr

170 175 180

<210> 28

<211> 3580

<212> DNA

<213> Homo Sapien

<400> 28

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ctttgctgac catgttgttc ccttgctgga atattaccgg gacatcttca 150

ctctcctgct ggcctgcac cggagcttgg tgttgcgca ggagagtgag 200

gggaagatgt gtttctgaa caagctgctg ctacttgctg tcctgggctg 250

gcttttccag attcccacag tccctgagga ctgtttcttt ctggaagagg 300

gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350

gacaatgctc ctgtggtgga ccagcagctg ctctacacct gctgcccccta 400

catcggagag ctccggaac tgctcgcttc gtgggtgtca ggcagtagtg 450

gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500

ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550

ccaggccttt ttccacaacc agccgccctc ctgcgccgg accgtagagt 600

tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650

ctggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700

ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750

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gagttctgtc aaaggaagag ccctggggct gtgcgggcgc tgcttccaga 850

ggagaccccc gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900

ttgcaacaga gaaagcctgt gcttggtgtg cagccaacat cacagcactg 950

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catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000

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<210> 29

<211> 280

<212> PRT

<213> Homo Sapien

<400> 29

Met Cys Phe Leu Asn Lys Leu Leu Leu Leu Ala Val Leu Gly Trp

1

5

10

15

Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu
 20 25 30

Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
 35 40 45

His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
 50 55 60

Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
 65 70 75

Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
 80 85 90

Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
 95 100 105

Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
 110 115 120

Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
 125 130 135

Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
 140 145 150

Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu
 155 160 165

Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
 170 175 180

Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala

185 190 195

Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg

200 205 210

Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala

215 220 225

Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp

230 235 240

Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala

245 250 255

Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala

260 265 270

Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala

275 280

<210> 30

<211> 1990

<212> DNA

<213> Homo Sapien

<400> 30

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cgcgaccgag tggctgtggg cgcggatgcc ttgagcagc gtgacttctc 500

actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550

acctgcacca ccattactgt ggccctgcacg aacgcccgtt ctccacctg 600

acggtcggcg aacccacgc ggagccgccc ccccggggct ctccgggcaa 650

cggtccagc cacagcggcg ccccaggccc agacccaca ctggcgcgag 700

gccacaacgt catcaatgtc atcgtccccg agagccgagc ccaacttctc 750

cagcagctgg gctacgtgct ggccacgctg ctgctcttca tcctgtact 800

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cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900

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gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

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tctcctgtct gtgctcctcg gggcatctcc tgatgctccg gggctcacc 1150

cccttccagc ggctgggtccc gctttcctgg aatttggcct gggcgtatgc 1200

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ccacccctgc ggcctttgct cacgggtggc cctgccacc cctggcaca 1300

ccaaaatccc actgatgcc atcatgccct cagacccttc tgggctctgc 1350

ccgctggggg cctgaagaca ttctggagg aactcccat cagaacctgg 1400

cagccccaaa actgggtca gcctcagggc aggagtccca ctctccagg 1450

gctctgctcg tccggggctg ggagatgttc ctggaggagg aactcccat 1500

cagaacttg cagccttga gttgggtca gcctcggcag ggtccact 1550

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tgctgagga caggggagg agtgaagttg gtttggggtg gcctgtgttg 1900

ccactctcag caccccatat ttgcatctgc tggtaggacct gccaccatca 1950

caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1990

<210> 31

<211> 341

<212> PRT

<213> Homo Sapien

<400> 31

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
 1 5 10 15

Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
 20 25 30

Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
 35 40 45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
 50 55 60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
 65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg

110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro		
125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu		
140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp		
155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu		
170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala		
185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser		
200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val		
215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln		
230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu		
245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu		
260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn		
275	280	285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340 341

<210> 32

<211> 1091

<212> DNA

<213> Homo Sapien

<400> 32

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gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200

gtgtggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250

gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300

gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350

cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400

cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtcccgta accagcagcg ttcaaccct 500

gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550

gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600

tgcctcaacc tctccatcgt ctccatgcc acctgccatg gtgtgtatcc 650

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atgcctgcca ggggtattct gggggccccc tgggtgtgtgg gggagtcctt 750

caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850

tcatgaggaa caactgacct gtttcctcca cctccacccc caccccttaa 900

cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950

ccctagctcc actctgttg gcctgggaac ttcttgaac ttttaactcct 1000

gccagccctt ctaagacca cgagcgggt gagagaagtg tgcaatagtc 1050

tggataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 33

<211> 248

<212> PRT

<213> Homo Sapien

<400> 33

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser
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Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg
				20					25					30
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu
				35					40					45
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His
				65					70					75
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly
				80					85					90
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His
				95					100					105
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val
				110					115					120
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr
				125					130					135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His
				140					145					150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser
				155					160					165

Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile

170 175 180

Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala

185 190 195

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

200 205 210

Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp

215 220 225

Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp

230 235 240

Ile Arg Met Ile Met Arg Asn Asn

245 248

<210> 34

<211> 1643

<212> DNA

<213> Homo Sapien

<400> 34

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gaggcccaaa acccgcccc gccagaacct cgccccaaat tccacactcc 150

tccagaagcc ccgcccactc ccgagccccg agagctccgc gcacctgggc 200

gccatccgcc ctggctccgc tgcacgagct ccacgcccgt accccggcgt 250

cacgctcagc cgcggtgct cgcacacctg agactcatct cgcttcgacc 300

ccgccgccgc cgccgccgg catcctgagc acggagacag tctccagctg 350

ccgttcacgc ttctcccca gccttccgca gccaccagg gaaggggagg 400

taggagtggc cttttaccaa agggaccggc gatgctctgc aggctgtgct 450

ggctggctc gtacagcttg gctgtgctgt tgctcggctg cctgctctc 500

ctgaggaagg cggccaagcc cgcaggagac cccacggccc accagccttt 550

ctgggctccc ccaacacccc gtcacagccg gtgtccacc aaccacacag 600

tgtctagcgc ctctctgtcc ctgcctagcc gtcaccgtct ctcttgacc 650

tatcgtcact gccgaaattt ctctatcttg ctggagcctt caggctgttc 700

caaggatacc ttcttgctcc tggccatcaa gtcacagcct ggtcacgtgg 750

agcgacgtgc ggctatccgc agcacgtggg gcagggtggg gggatgggct 800

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aatgtacagg gccaccact acccaccta tgctggggg ggaggatatg 1200

tcatgtccag agccacagtg cggcgccctcc aggctatcat ggaagatgct 1250

gaactcttcc ccattgatga tgtctttgtg ggtatgtgcc tgaggaggct 1300

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caccgcctca gcccctcga gatgtggacc atgtgggcac tggtagacaga 1450

tgaggggctc aagtgtgcag ctggcccat accccagcgc tgaaggggtg 1500

gttgggcaac agcctgagag tggactcagt gttgattctc tatcgtgatg 1550

cgaattgat gcctgctgct ctacagaaaa tgccaacttg gtttttaac 1600

tcctctcacc ctgtagctc tgattaaaa cactgcaacc caa 1643

<210> 35

<211> 378

<212> PRT

<213> Homo Sapien

<400> 35

Met Leu Pro Pro Gln Pro Ser Ala Ala His Gln Gly Arg Gly Gly

1 5 10 15

Arg Ser Gly Leu Leu Pro Lys Gly Pro Ala Met Leu Cys Arg Leu

20 25 30

Cys Trp Leu Val Ser Tyr Ser Leu Ala Val Leu Leu Leu Gly Cys

35 40 45

Leu Leu Phe Leu Arg Lys Ala Ala Lys Pro Ala Gly Asp Pro Thr

50 55 60

Ala His Gln Pro Phe Trp Ala Pro Pro Thr Pro Arg His Ser Arg

65 70 75

Cys Pro Pro Asn His Thr Val Ser Ser Ala Ser Leu Ser Leu Pro

80 85 90

Ser Arg His Arg Leu Phe Leu Thr Tyr Arg His Cys Arg Asn Phe

95 100 105

Ser Ile Leu Leu Glu Pro Ser Gly Cys Ser Lys Asp Thr Phe Leu

110 115 120

Leu Leu Ala Ile Lys Ser Gln Pro Gly His Val Glu Arg Arg Ala

125 130 135

Ala Ile Arg Ser Thr Trp Gly Arg Val Gly Gly Trp Ala Arg Gly

140 145 150

Arg Gln Leu Lys Leu Val Phe Leu Leu Gly Val Ala Gly Ser Ala

155 160 165

Pro Pro Ala Gln Leu Leu Ala Tyr Glu Ser Arg Glu Phe Asp Asp

170 175 180

Ile Leu Gln Trp Asp Phe Thr Glu Asp Phe Phe Asn Leu Thr Leu

185 190 195

Lys Glu Leu His Leu Gln Arg Trp Val Val Ala Ala Cys Pro Gln

200	205	210
Ala His Phe Met Leu Lys Gly Asp Asp Asp Val Phe Val His Val		
215	220	225
Pro Asn Val Leu Glu Phe Leu Asp Gly Trp Asp Pro Ala Gln Asp		
230	235	240
Leu Leu Val Gly Asp Val Ile Arg Gln Ala Leu Pro Asn Arg Asn		
245	250	255
Thr Lys Val Lys Tyr Phe Ile Pro Pro Ser Met Tyr Arg Ala Thr		
260	265	270
His Tyr Pro Pro Tyr Ala Gly Gly Gly Gly Tyr Val Met Ser Arg		
275	280	285
Ala Thr Val Arg Arg Leu Gln Ala Ile Met Glu Asp Ala Glu Leu		
290	295	300
Phe Pro Ile Asp Asp Val Phe Val Gly Met Cys Leu Arg Arg Leu		
305	310	315
Gly Leu Ser Pro Met His His Ala Gly Phe Lys Thr Phe Gly Ile		
320	325	330
Arg Arg Pro Leu Asp Pro Leu Asp Pro Cys Leu Tyr Arg Gly Leu		
335	340	345
Leu Leu Val His Arg Leu Ser Pro Leu Glu Met Trp Thr Met Trp		
350	355	360
Ala Leu Val Thr Asp Glu Gly Leu Lys Cys Ala Ala Gly Pro Ile		
365	370	375

Pro Gln Arg

378

<210> 36

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 36

cttgctcctg gccatcaagt cac 23

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 37

gttgaagaag tcctcagtga agtcccac 28

<210> 38

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 38

cagctgaagc tgggttcct cctaggggtg gcaggatccg 40

<210> 39

<211> 1470

<212> DNA

<213> Homo Sapien

<400> 39

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ctttgtcatg ggacctgtgc ggttgggaat attgcttttc cttttttgg 150

ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200

gaacgcttgc ccagcaaatg cgaagtgtgt aagctgctga gcacagagct 250

acaggcggaa ctgagtcgca ccggtcgatc tcgagagggtg ctggagctgg 300

ggcaggtgct ggatacaggc aagaggaaga gacacgtgcc ttacagcgtt 350

tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400

ggactatagt gttcacgctg agcgaaggg ctactgaga tatgccaagg 450

gtcagagtca gaccatggca aactgaaag gcctagtgca gaaggggggtg 500

aagggtgcatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550

ggtcacatac ctcaagaagc agtgtgagac catgttggag gagtttgaag 600

acattgtggg agactggtac ttccaccatc aggagcagcc cctacaaaat 650
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<210> 40

<211> 248

<212> PRT

<213> Homo Sapien

<400> 40

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala
 1 5 10 15

Val His Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Asp Asp Asp
 20 25 30

Thr Glu Arg Leu Pro Ser Lys Cys Glu Val Cys Lys Leu Leu Ser
 35 40 45

Thr Glu Leu Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu
 50 55 60

Val Leu Glu Leu Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg
 65 70 75

His Val Pro Tyr Ser Val Ser Glu Thr Arg Leu Glu Glu Ala Leu
 80 85 90

Glu Asn Leu Cys Glu Arg Ile Leu Asp Tyr Ser Val His Ala Glu
 95 100 105

Arg Lys Gly Ser Leu Arg Tyr Ala Lys Gly Gln Ser Gln Thr Met
 110 115 120

Ala Thr Leu Lys Gly Leu Val Gln Lys Gly Val Lys Val Asp Leu

125	130	135
Gly Ile Pro Leu Glu Leu Trp Asp Glu Pro Ser Val Glu Val Thr		
140	145	150
Tyr Leu Lys Lys Gln Cys Glu Thr Met Leu Glu Glu Phe Glu Asp		
155	160	165
Ile Val Gly Asp Trp Tyr Phe His His Gln Glu Gln Pro Leu Gln		
170	175	180
Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala Glu Thr Ala		
185	190	195
Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp Gly Glu		
200	205	210
Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu Glu Glu		
215	220	225
Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His		
230	235	240
Pro Lys Leu Asp Arg Glu Asp Leu		
245	248	

<210> 41

<211> 2684

<212> DNA

<213> Homo Sapien

<220>

<221> unsure

<222> 2636-2637

<223> unknown base

<400> 41

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ggaggagaac aacgaaggg gctcaaccgt cggtcgctgg agccccccc 150

ggggcgtggc ctcccggccc ctacagctggg gagggcgggg ctgctgccc 200

cctgctgccg actgcgaccc ttacagggga gggagggcgc aggccgcgcg 250

gagatgagga ggaggctgcg cctacgcagg gacgcattgc tcacgctgct 300

ccttggcgcc tccctgggcc tcttactcta tgcgcagcgc gacggcgcgg 350

ccccgacggc gagcgcgccg cgagggcgag ggagggcggc accgaggccc 400

acccccggac cccgcgcggt ccagttaccg gacgcgggtg cagccccgcc 450

ggcctacgaa ggggacacac cggcgcggcc cacgcctacg ggaccctttg 500

acttcgcccc ctatttgcgc gccaaaggacc agcggcgggt tccactgctc 550

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tgctagacc aaatatttaa aaatgggata aaattntttt aaaaaaaaaa 2650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2684

<210> 42

<211> 402

<212> PRT

<213> Homo Sapien

<400> 42

Met Arg Arg Arg Leu Arg Leu Arg Arg Asp Ala Leu Leu Thr Leu
1 5 10 15

Leu Leu Gly Ala Ser Leu Gly Leu Leu Leu Tyr Ala Gln Arg Asp
20 25 30

Gly Ala Ala Pro Thr Ala Ser Ala Pro Arg Gly Arg Gly Arg Ala
35 40 45

Ala Pro Arg Pro Thr Pro Gly Pro Arg Ala Phe Gln Leu Pro Asp
50 55 60

Ala Gly Ala Ala Pro Pro Ala Tyr Glu Gly Asp Thr Pro Ala Pro
65 70 75

Pro Thr Pro Thr Gly Pro Phe Asp Phe Ala Arg Tyr Leu Arg Ala
80 85 90

Lys Asp Gln Arg Arg Phe Pro Leu Leu Ile Asn Gln Pro His Lys

95	100	105
Cys Arg Gly Asp Gly Ala Pro Gly Gly Arg Pro Asp Leu Leu Ile		
110	115	120
Ala Val Lys Ser Val Ala Glu Asp Phe Glu Arg Arg Gln Ala Val		
125	130	135
Arg Gln Thr Trp Gly Ala Glu Gly Arg Val Gln Gly Ala Leu Val		
140	145	150
Arg Arg Val Phe Leu Leu Gly Val Pro Arg Gly Ala Gly Ser Gly		
155	160	165
Gly Ala Asp Glu Val Gly Glu Gly Ala Arg Thr His Trp Arg Ala		
170	175	180
Leu Leu Arg Ala Glu Ser Leu Ala Tyr Ala Asp Ile Leu Leu Trp		
185	190	195
Ala Phe Asp Asp Thr Phe Phe Asn Leu Thr Leu Lys Glu Ile His		
200	205	210
Phe Leu Ala Trp Ala Ser Ala Phe Cys Pro Asp Val Arg Phe Val		
215	220	225
Phe Lys Gly Asp Ala Asp Val Phe Val Asn Val Gly Asn Leu Leu		
230	235	240
Glu Phe Leu Ala Pro Arg Asp Pro Ala Gln Asp Leu Leu Ala Gly		
245	250	255
Asp Val Ile Val His Ala Arg Pro Ile Arg Thr Arg Ala Ser Lys		
260	265	270

Tyr Tyr Ile Pro Glu Ala Val Tyr Gly Leu Pro Ala Tyr Pro Ala
 275 280 285

Tyr Ala Gly Gly Gly Gly Phe Val Leu Ser Gly Ala Thr Leu His
 290 295 300

Arg Leu Ala Gly Ala Cys Ala Gln Val Glu Leu Phe Pro Ile Asp
 305 310 315

Asp Val Phe Leu Gly Met Cys Leu Gln Arg Leu Arg Leu Thr Pro
 320 325 330

Glu Pro His Pro Ala Phe Arg Thr Phe Gly Ile Pro Gln Pro Ser
 335 340 345

Ala Ala Pro His Leu Ser Thr Phe Asp Pro Cys Phe Tyr Arg Glu
 350 355 360

Leu Val Val Val His Gly Leu Ser Ala Ala Asp Ile Trp Leu Met
 365 370 375

Trp Arg Leu Leu His Gly Pro His Gly Pro Ala Cys Ala His Pro
 380 385 390

Gln Pro Val Ala Ala Gly Pro Phe Gln Trp Asp Ser
 395 400 402

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 43

acctaacgct caaggagatc cactttc 27

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 44

ggctccattc tgggtctgag ttagg 25

<210> 45

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 45

gcctcagctt tctgccccga cgtgcgcttc gttttaagg 40

<210> 46

<211> 1226

<212> DNA

<213> Homo Sapien

<400> 46

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gaggggcat ggtgccaatg cacttactgg ggagactgga gaagccgctt 150
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ctggcaacat ttggtgacct accccatatac caatatttcc agcgtagat 1000

tgaggatgag gtagggaggt gatccagaga aggcggagaa ggaagaagta 1050

acctctgagt ggcggctatt gcttctgttc caggtgctgt tcgagctgtt 1100

agaaccctta ggcttgacag ctttctgagt tattattgaa aatgaggat 1150

tccaagagtc agaggagttt gataatgtgc acgagggcac actgctagta 1200

aataacatta aaataactgg aatgaa 1226

<210> 47

<211> 216

<212> PRT

<213> Homo Sapien

<400> 47

Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu

1 5 10 15

Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly

20 25 30

Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu

35 40 45

Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu

50 55 60

Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro

65 70 75

Gly Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro

80 85 90

Val Tyr Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro

95 100 105

Gln Glu Leu Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro

110 115 120

Pro Ala Pro Glu Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg

125 130 135

Arg Ala Lys Leu Glu Gln Arg Arg Met Ala Ser Glu Gly Ser Met

140 145 150

Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro Ile Asn Leu Arg Leu

155 160 165

Arg Gly Pro Arg Ala Val Ser Thr Ala Pro Asp Leu Gln Ser Leu

170 175 180

Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro Pro Ala Tyr

185 190 195

Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe Tyr Glu

200 205 210

Asp Asn Trp Ala Pro Pro

215 216

<210> 48

<211> 1310

<212> DNA

<213> Homo Sapien

<400> 48

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agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100

tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150

ttctggtgct ggccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gaccactgc cccagccgtc agggaccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccca ggggagaga 300

ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350

gggttcacag caacaccgcc agccccggac tccccgagg agcccctcgt 400

gctacggctg aaattcctca atgattcaga gcaggtggcc aggcctggc 450

cccagacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500

cagcaggtgc gactcatcta ccaaggcag ctgctaggcg acgacacca 550

gaccctgggc agccttacc tccctccaa ctgcgttctc cactgccagc 600

tgtccagag agtcggtccc ccaaatcccc cctgcccgcc ggggtccgag 650

cccgcccct cgggctgga aatcggcagc ctgctgctgc ccctgctgct 700

cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750

ttcccctgac cgccactctg ggcctggccg gcttcaccct gtcctcagt 800

ctcctggcct ttgcatgta ccgcccgtag tgctcccg ggcgcttggc 850

agcgtcggc gcccctccg accttgctcc ccgcccgcg gcgggagctg 900

ctgcctgcc aggccgcct ctccggcctg cctcttccg ctgccctgga 950

gcccagcct gcgccgaga ggactcccg gactggcgga ggccccgcc 1000

tgcgaccgc ggggctcgg gccacctccc ggggctgctg aacctcagcc 1050

cgactggga gtgggctcct cggggtcgg catctgctgt cgtgcctcg 1100

gccccggca gagccggcc gccccgggg cccgtcttag tgttctgcc 1150

gaggaccag ccgcctcaa tccctgacag ctccctgggc tgagttggg 1200

acgccaggtc ggtgggaggc tggtaaggg gagcggggag gggcagagga 1250

gttccccga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaa 1300

aaaaaaaaa 1310

<210> 49

<211> 246

<212> PRT

<213> Homo Sapien

<400> 49

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe

1 5 10 15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser

20 25 30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly

35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp

50 55 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg

65 70 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr

80 85 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu

95 100 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp

110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly

125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly

140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys

155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro

	170	175	180
Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile			
	185	190	195
Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu			
	200	205	210
Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala			
	215	220	225
Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala			
	230	235	240
Phe Ala Met Tyr Arg Pro			
	245	246	

<210> 50

<211> 1042

<212> DNA

<213> Homo Sapien

<400> 50

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tggaggtcca ggggggacct agcctgggac agacctgcgt gctgatcgtg 150

atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta 200

ctttaccaac gagctgaagc agatgcagga caagtactcc aaaagtggca 250

ttgcttgttt cttaaaagaa gatgacagtt attgggacct caatgacgaa 300

gagagtatga acagcccctg ctggcaagtc aagtggcaac tccgtcagct 350
cgtagaaaag atgattttga gaacctctga ggaaccatt tctacagttc 400
aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtcctcag 450
agagtagcag ctacataac tgggaccaga ggaagaagca acacattgtc 500
ttctccaaac tccaagaatg aaaaggctct gggccgcaa ataaactcct 550
gggaatcatc aaggagtggg cattcattcc tgagcaactt gcacttgagg 600
aatggtgaac tggcatcca tgaaaaggg ttttactaca tctattcca 650
aacatacttt cgatttcagg aggaaataaa agaaaacaca aagaacgaca 700
aacaatggt ccaatatatt tacaataca caagttatcc tgaccctata 750
ttgttgatga aaagtgctag aaatagttgt tggctaaag atgcagaata 800
tggactctat tccatctatc aagggggaat atttgagctt aaggaaaatg 850
acagaatfff tgtttctgta acaaatgagc acttgataga catggacat 900
gaagccagtt ttttcggggc ctttttagtt ggctaactga cctggaaaga 950
aaaagcaata acctcaaagt gactattcag ttttcaggat gatacactat 1000
gaagatgttt caaaaaatct gaccaaaca aacaacaga aa 1042

<210> 51

<211> 281

<212> PRT

<213> Homo Sapien

<400> 51

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr
 1 5 10 15

Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys
 20 25 30

Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met
 35 40 45

Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu
 50 55 60

Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser
 65 70 75

Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys
 80 85 90

Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
 95 100 105

Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
 110 115 120

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 125 130 135

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
 140 145 150

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser

155 160 165

Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly

170 175 180

Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu

185 190 195

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile

200 205 210

Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser

215 220 225

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr

230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg

245 250 255

Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His

260 265 270

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly

275 280 281

<210> 52

<211> 540

<212> DNA

<213> Homo Sapien

<400> 52

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gctcgtggca gcctggagca tgggctgtgg tgaggccctc aagtgtaca 100

cctgcaagga gcccatgacc agtgcttctt gcaggacat taccgctgc 150

aagccagagg acacagcctg catgaccacg ctggtgacgg tggaggcaga 200

gtacccttc aaccagagcc ccgtggtgac ccgctcctgc tccagctcct 250

gtgtggccac cgaccccgac agcatcgggg ccgcccacct gatcttctgc 300

tgcttccgag acctctgcaa ctcggaactc tgaaccagg gcggcaggc 350

ggaagtgct cctcaggcac ctctctctg acggggcctg gctccacctg 400

tgatcacctc cccctgcttc ctgctgctgt ggcacagctc actcatgggg 450

tctgagggga gagaagcaca ccaggggccc cctctgcctt ccatacccca 500

cgcttataaa acataactaa gccaaaaaaaa aaaaaaaaaa 540

<210> 53

<211> 103

<212> PRT

<213> Homo Sapien

<400> 53

Met Ala Ser Arg Trp Ala Val Gln Leu Leu Leu Val Ala Ala Trp

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20 25 30

Pro Met Thr Ser Ala Ser Cys Arg Thr Ile Thr Arg Cys Lys Pro

35 40 45

Glu Asp Thr Ala Cys Met Thr Thr Leu Val Thr Val Glu Ala Glu

50 55 60

Tyr Pro Phe Asn Gln Ser Pro Val Val Thr Arg Ser Cys Ser Ser

65 70 75

Ser Cys Val Ala Thr Asp Pro Asp Ser Ile Gly Ala Ala His Leu

80 85 90

Ile Phe Cys Cys Phe Arg Asp Leu Cys Asn Ser Glu Leu

95 100 103

<210> 54

<211> 1183

<212> DNA

<213> Homo Sapien

<400> 54

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gccccgggct ctgctggccg cactctgggc gctggaagcc gccgggaccg 150

ccgcgcttcg catcgagcc ttcaacattc agagcttcgg tgacagcaaa 200

gtgtcggacc ccgcttgcgg cagcatcatc gcgaagatcc tggtggcta 250

tgacctcgcg ctggtgcagg aggtgcgaga cccagacctc agcgcctgt 300

ccgcgctcat ggagcagatc aacagcgtgt ccgagcacga gtacagcttt 350

gtgagcagcc agcccctggg ccgggaccag tacaaggaga tgtacctgtt 400
cgtgtacagg aaagacgagg tgtcggctgt ggacacctac ctgtaccag 450
accccagga cgtcttcagc cgcgagccct tcgtgggtcaa gttctcggcc 500
cccggcaccg gtgagcgggc cccgcccctc ccctcccgcc gagctctgac 550
gccccaccc cttcccgcag cagcacagaa cctgggtgctg atcccgtgc 600
acgcggcgcc gcatcaagcc gtggcggaga tcgacgcgct ctacgacgtg 650
tacctggacg tgatcgacaa gtggggcacc gacgacatgc gttcctggg 700
cgacttcaac gccgactgca gctatgtgcg ggcgaggac tggccgcca 750
tccgtctgag gagcagtgag gtcttcaagt ggctcatccc tgacagcgcc 800
gacaccacgg tgggcaactc agactgcgcc tacgaccgca ttgtggcctg 850
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gaccactttc cagtggaggt gaccctcaag ttccaccgat gactcgaggc 1000
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agtggcccct tcagggtggc agccaccctt cagtgaggcc ccaaggcaga 1100
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<210> 55

<211> 299

<212> PRT

<213> Homo Sapien

<400> 55

Met Gly Gly Pro Arg Ala Leu Leu Ala Ala Leu Trp Ala Leu Glu
 1 5 10 15

Ala Ala Gly Thr Ala Ala Leu Arg Ile Gly Ala Phe Asn Ile Gln
 20 25 30

Ser Phe Gly Asp Ser Lys Val Ser Asp Pro Ala Cys Gly Ser Ile
 35 40 45

Ile Ala Lys Ile Leu Ala Gly Tyr Asp Leu Ala Leu Val Gln Glu
 50 55 60

Val Arg Asp Pro Asp Leu Ser Ala Val Ser Ala Leu Met Glu Gln
 65 70 75

Ile Asn Ser Val Ser Glu His Glu Tyr Ser Phe Val Ser Ser Gln
 80 85 90

Pro Leu Gly Arg Asp Gln Tyr Lys Glu Met Tyr Leu Phe Val Tyr
 95 100 105

Arg Lys Asp Ala Val Ser Val Val Asp Thr Tyr Leu Tyr Pro Asp
 110 115 120

Pro Glu Asp Val Phe Ser Arg Glu Pro Phe Val Val Lys Phe Ser
 125 130 135

Ala Pro Gly Thr Gly Glu Arg Ala Pro Pro Leu Pro Ser Arg Arg
140 145 150

Ala Leu Thr Pro Pro Pro Leu Pro Ala Ala Ala Gln Asn Leu Val
155 160 165

Leu Ile Pro Leu His Ala Ala Pro His Gln Ala Val Ala Glu Ile
170 175 180

Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Ile Asp Lys Trp Gly
185 190 195

Thr Asp Asp Met Leu Phe Leu Gly Asp Phe Asn Ala Asp Cys Ser
200 205 210

Tyr Val Arg Ala Gln Asp Trp Ala Ala Ile Arg Leu Arg Ser Ser
215 220 225

Glu Val Phe Lys Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Val
230 235 240

Gly Asn Ser Asp Cys Ala Tyr Asp Arg Ile Val Ala Cys Gly Ala
245 250 255

Arg Leu Arg Arg Ser Leu Lys Pro Gln Ser Ala Thr Val His Asp
260 265 270

Phe Gln Glu Glu Phe Gly Leu Asp Gln Thr Gln Ala Leu Ala Ile
275 280 285

Ser Asp His Phe Pro Val Glu Val Thr Leu Lys Phe His Arg
290 295 299

<210> 56

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 56

cttgaatag aagacttctg gacaattt 28

<210> 57

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 57

ttgcaactgg gaatatacca cgacatgaga 30

<210> 58

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 58

tagggtgcta atttggcta taacct 26

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 59

ggctctgagt ctctgcttga 20

<210> 60

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 60

tccaacaacc attttctct ggtcc 25

<210> 61

<211> 23

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 61

aagcagtagc cattaacaag tca 23

<210> 62

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 62

aaaggacacc gggatgtg 18

<210> 63

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 63

agcgtacact ctctccaggc aaccag 26

<210> 64

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 64

caattctgga tgaggtggta ga 22

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 65

caggactgag cgcttgttta 20

<210> 66

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 66

caaagcgcca agtaccggac c 21

<210> 67

<211> 18

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 67

ccagacctca gccaggaa 18

<210> 68

<211> 19

<212> DNA

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<400> 68

tcatggtctc gtccattc 19

<210> 69

<211> 27

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<223> Synthetic Oligonucleotide Probe

<400> 69

caccatttgt ttctctgtct ccccatc 27

<210> 70

<211> 18

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 70

ccggcatcct tggagtag 18

<210> 71

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

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<400> 71

ctctggtgcc cacagtga 18

<210> 72

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 72

ccatgcctgc tcagccaaga a 21

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 73

caggaaatct ggaaacctac agt 23

<210> 74

<211> 20

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 74

tccccattag cacaggagta 20

<210> 75

<211> 23

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

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aggctcttgc ctgtcctgct gct 23

<210> 76

<211> 18

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<210> 77

<211> 18

<212> DNA

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gtccagcaag ccctcatt 18

<210> 78

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 78

cttctgggcc acagccctgc 20

<210> 79

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 79

cagttcaggt cgtttcattc a 21

<210> 80

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 80

ccagtcaggc cgttttaga 19

<210> 81

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<210> 82

<211> 28

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 82

cataaagtag tatatgcatt ccagtggt 28

<210> 83

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 83

ggaaatggtc tcaagggaaa 20

<210> 84

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 84

tcactttgac cctgtcttgg aacgtc 26

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 85

ggtagaattc cagcatttgg ta 22

<210> 86

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<223> Synthetic Oligonucleotide Probe

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aggacttgcc ctcaggaa 18

<210> 87

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 87

cgcaggacag ttgtgaaat a 21

<210> 88

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 88

atgacgctcg tccaaggcca c 21

<210> 89

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 89

cccacctgta ccacatgt 19

<210> 90

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 90

actccaggca ccatctgttc tccc 24

<210> 91

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 91

aagggtggc attcaagtu 19

<210> 92

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 92

ctggccctca gagcaccaat 20

<210> 93

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 93

tcctccatca cttcccctag ctcca 25

<210> 94

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 94

ctggcaggag ttaaagttcc aaga 24

<210> 95

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 95

gggcaacagc ctgagagt 18

<210> 96

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 96

actcagtgtt gattctctat cgtgatgcg 29

<210> 97

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 97

gagcagcagg catcaattt 19

<210> 98

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 98

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<210> 99

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<210> 100

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 100

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<210> 101

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 101

agccggtttc ccagattat 19

<210> 102

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 102

tgccgtgat gtggttcttc cctg 24

<210> 103

<211> 19

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 103

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<210> 104

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 104

tgtttctgcc tggacatca 19

<210> 105

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 105

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<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 107

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 107

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<210> 108

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 108

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<210> 109

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 110

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 110

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<210> 111

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 111

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<210> 112

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 112

tggacacgtg gcagtgga 18

<210> 113

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 113

tgaccatga agccagttt 19

<210> 114

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 114

cctttttagt tggctaactg acctggaaag aa 32

<210> 115

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 115

tgaatagtca ctttgaggtt attgc 25

<210> 116

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 116

cctggctcca cctgtgat 18

<210> 117

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 117

acctcccct gcttctgct g 21

<210> 118

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 118

cctcagacc catgagtga 19

<210> 119

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 119

gaggaatggc ccaacagt 18

<210> 120

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 120

tggcagccac ccttcagtga g 21

<210> 121

<211> 18

<212> DNA

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