Fig. 1

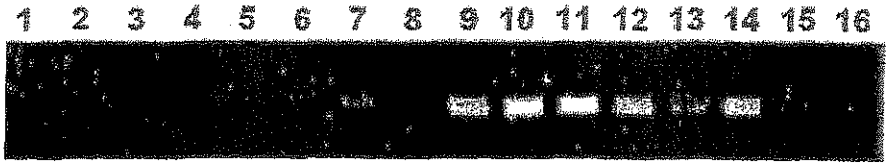


Fig. 2

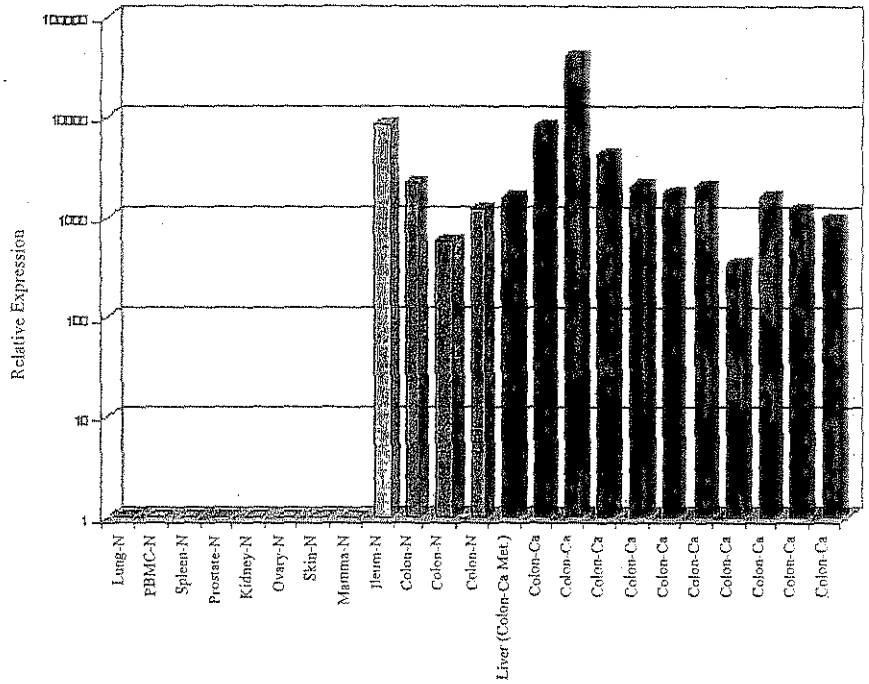

Relative Expression
100000
10000
1000
100
10
1
Lung-N
PBMC-N
Spleen-N
Prostate-N
Kidney-N
Ovary-N
Skin-N
Mamma-N
Jleum-N
Colon-N
Colon-N
Colon-N
Liver (Colon-Ca Met.)
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca
Colon-Ca

Fig. 3

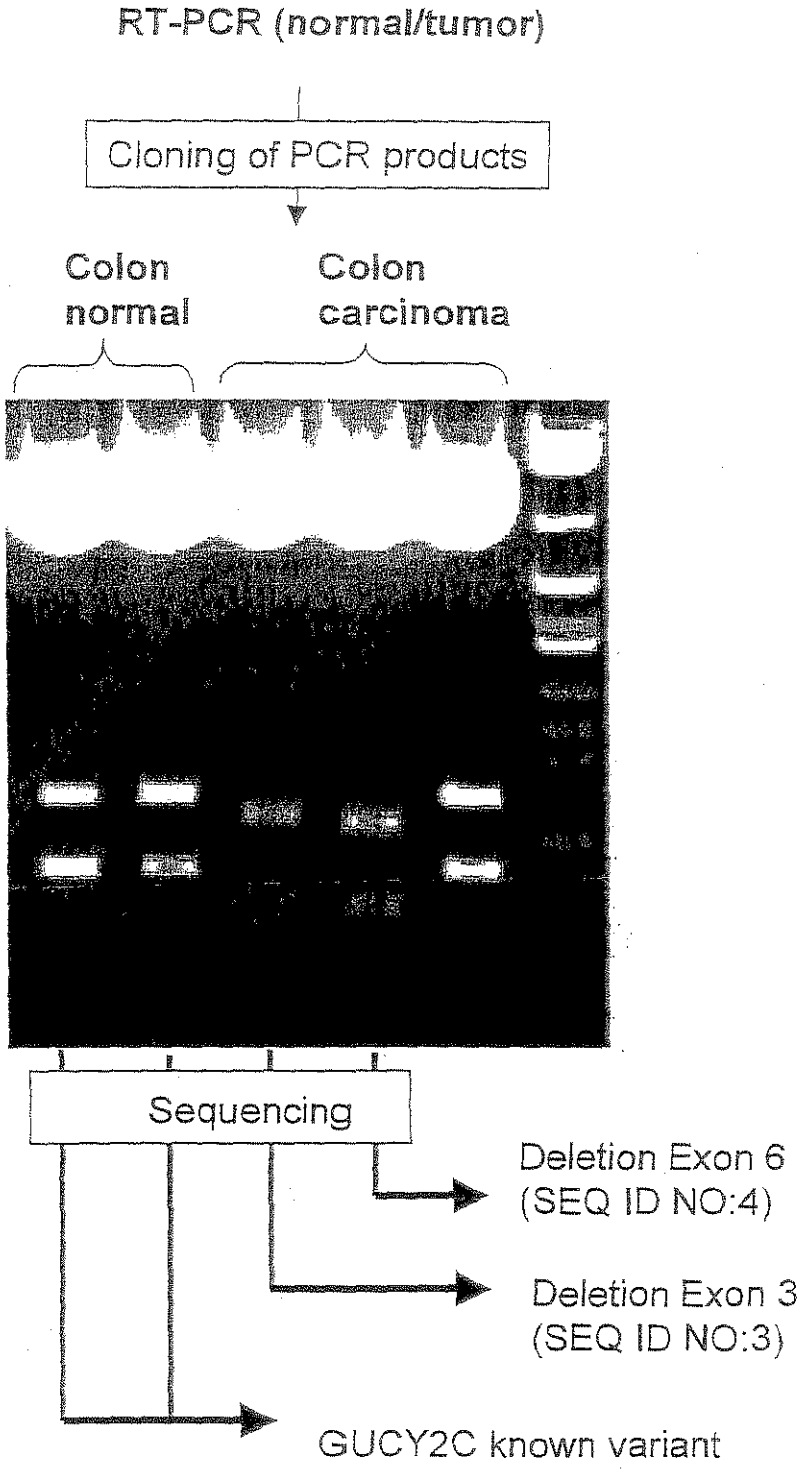

RT-PCR (normal/tumor)
Cloning of PCR products
Colon normal
Colon carcinoma
Sequencing
Deletion Exon 6 (SEQ ID NO:4)
Deletion Exon 3 (SEQ ID NO:3)
GUCY2C known variant

Fig. 4

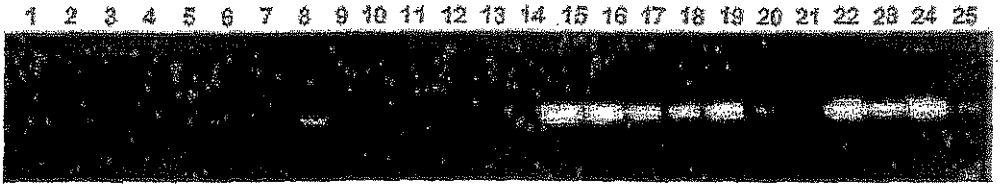


Fig. 5

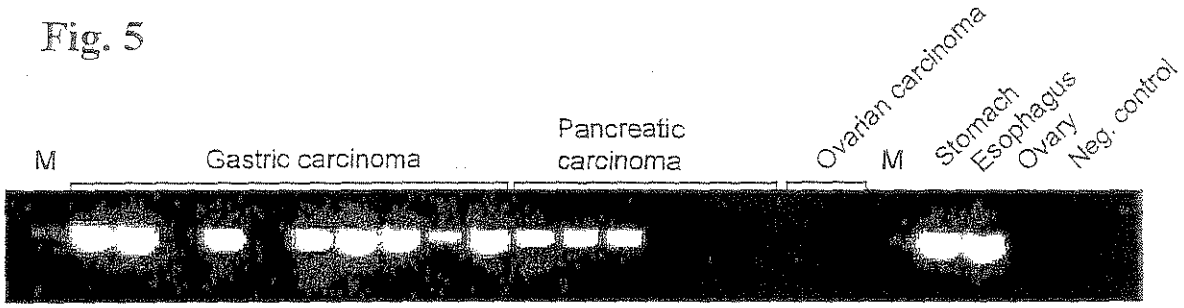

M
Gastric carcinoma
Pancreatic carcinoma
Ovarian carcinoma
M
Stomach
Esophagus
Ovary
Neg. control

Fig. 6

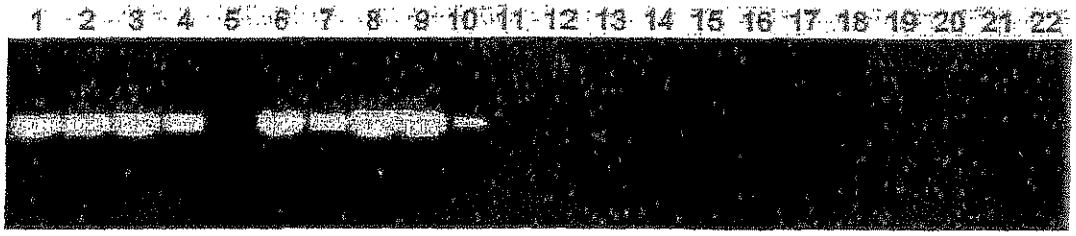


Fig 7

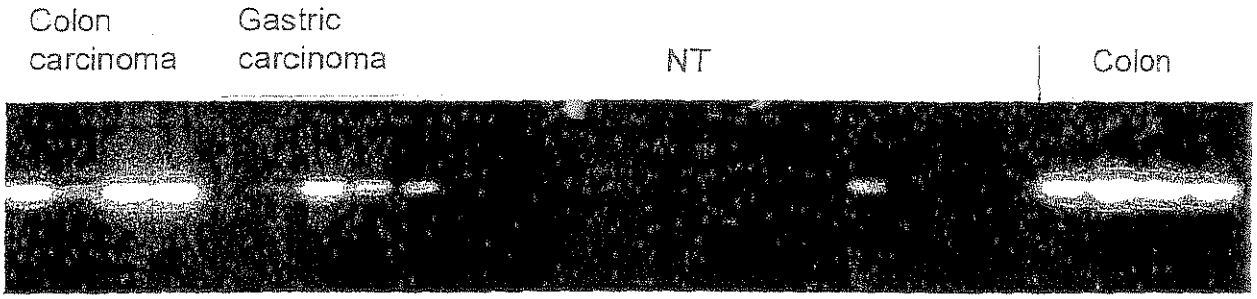


Fig. 8

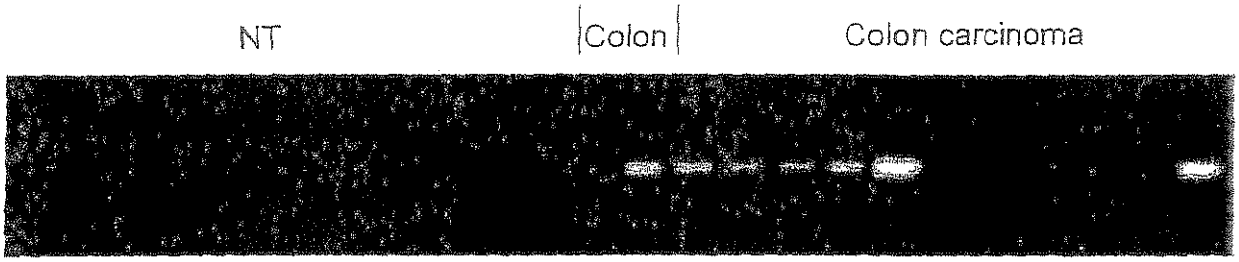


Fig. 9

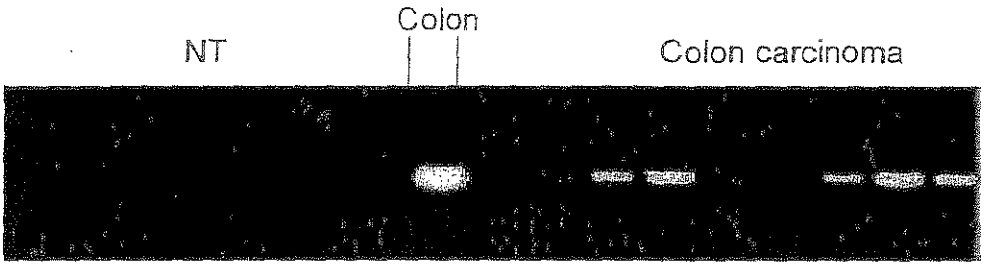


Fig. 10

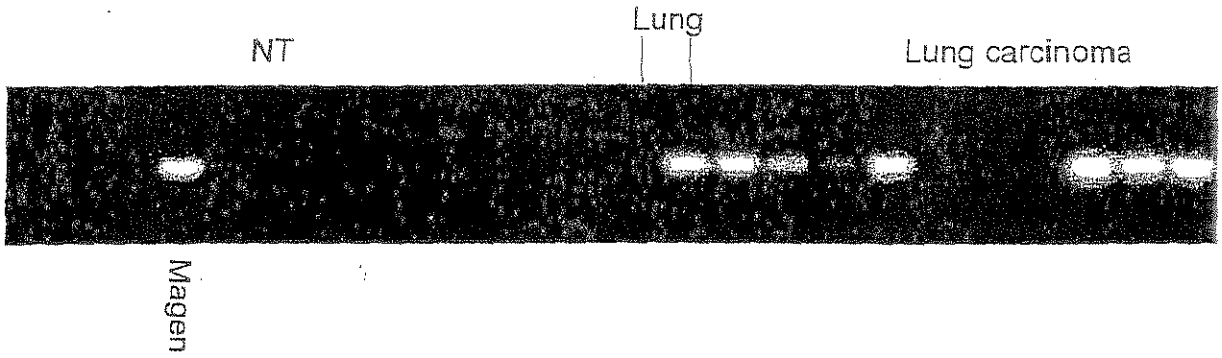


Fig. 11

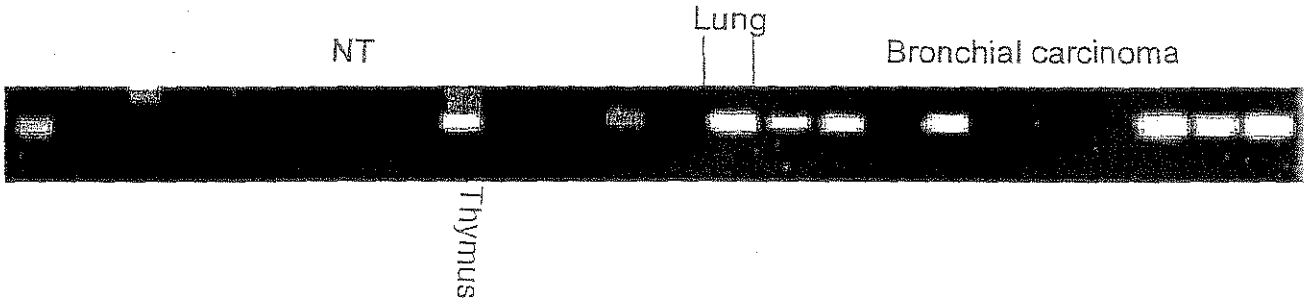


Fig. 12

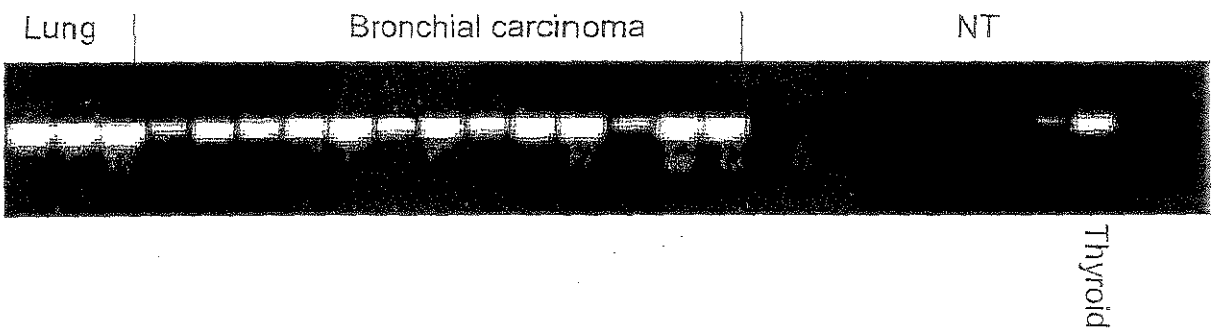


Fig. 13

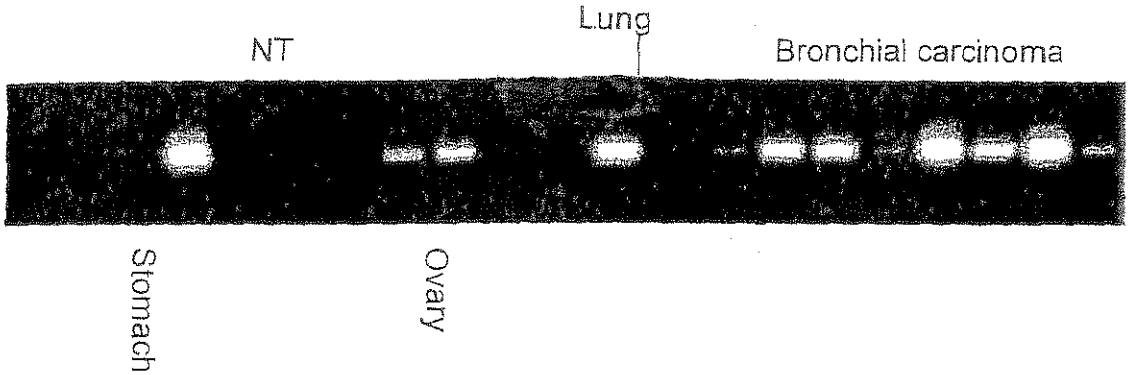


Fig. 14

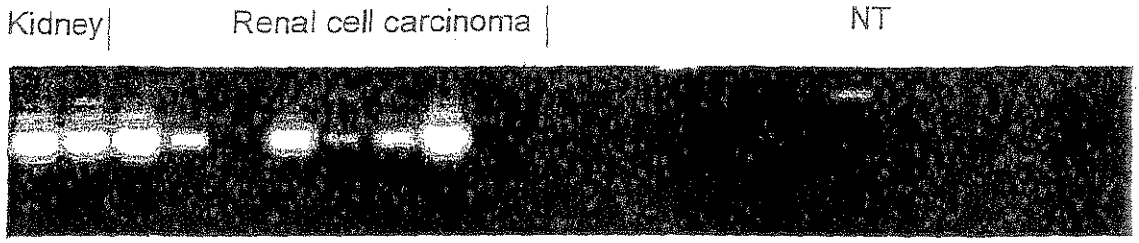


Fig. 15

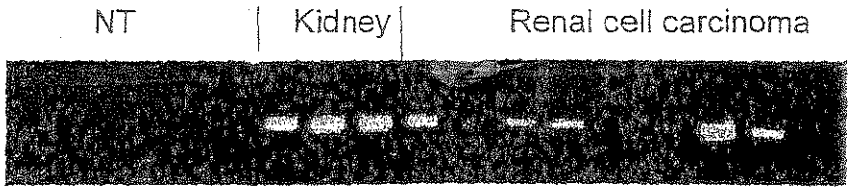
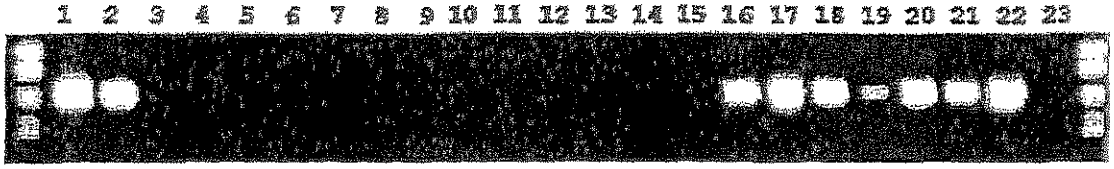
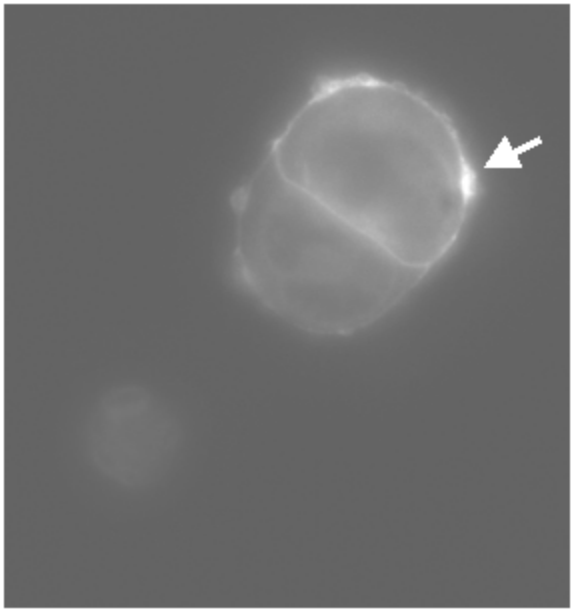


Fig. 16





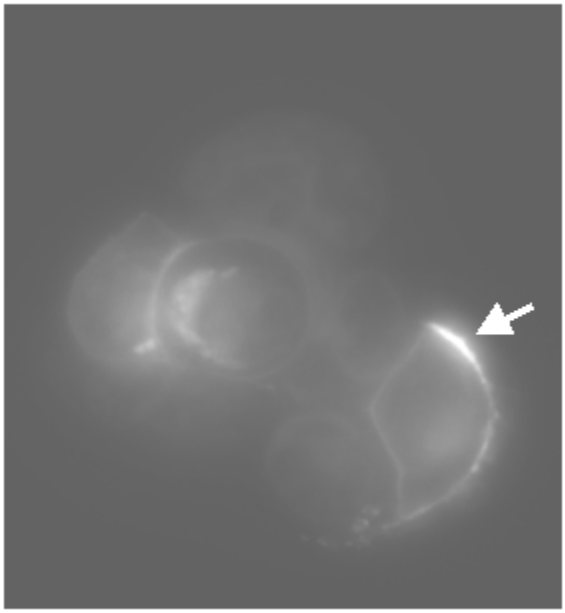
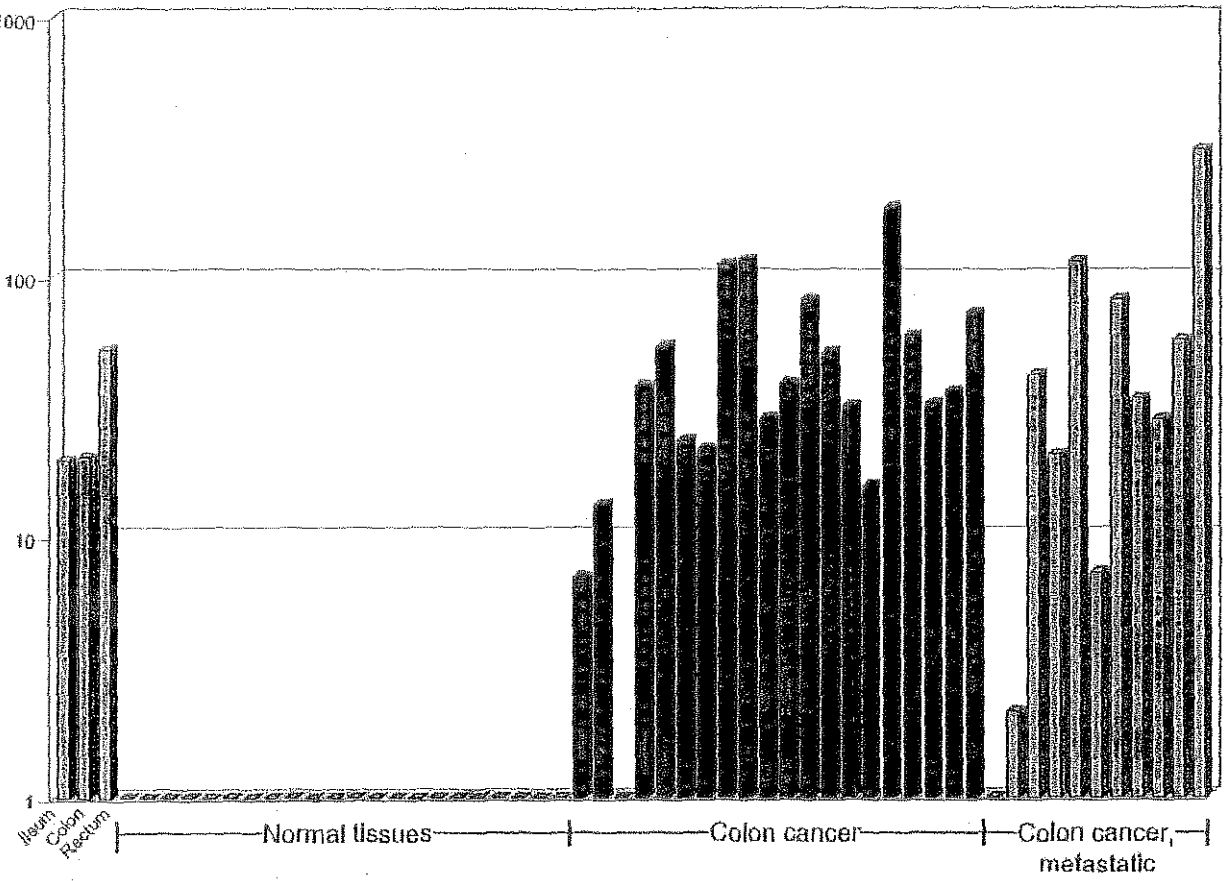


Fig. 17

Fig. 18

A

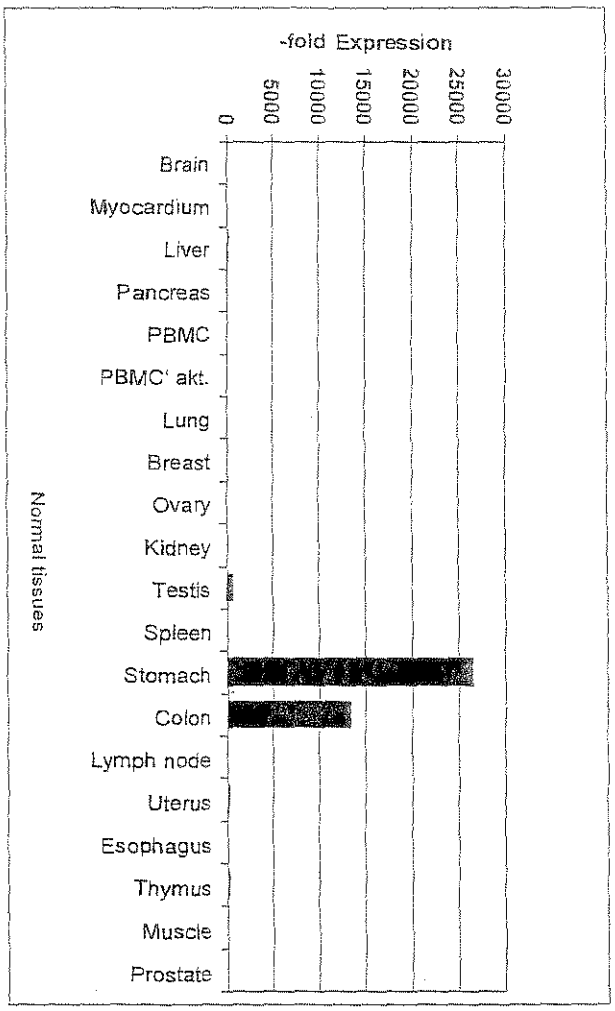


B

Cancer type	Expression	%
colorektal, primary	19/20	95
colorektal, metast.	14/15	93

Fig. 16

A


-fold Expression
0
5000
10000
15000
20000
25000
30000
Brain
Myocardium
Liver
Pancreas
PBMC
PBMC' akt.
Lung
Breast
Ovary
Kidney
Testis
Spleen
Stomach
Colon
Lymph node
Uterus
Esophagus
Thymus
Muscle
Prostate
Normal tissues

B

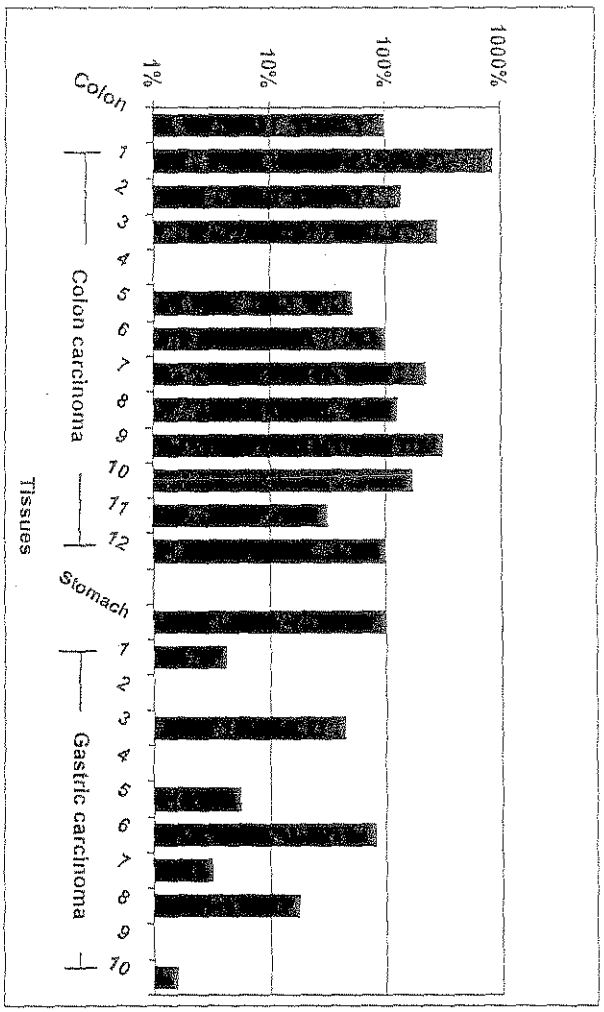
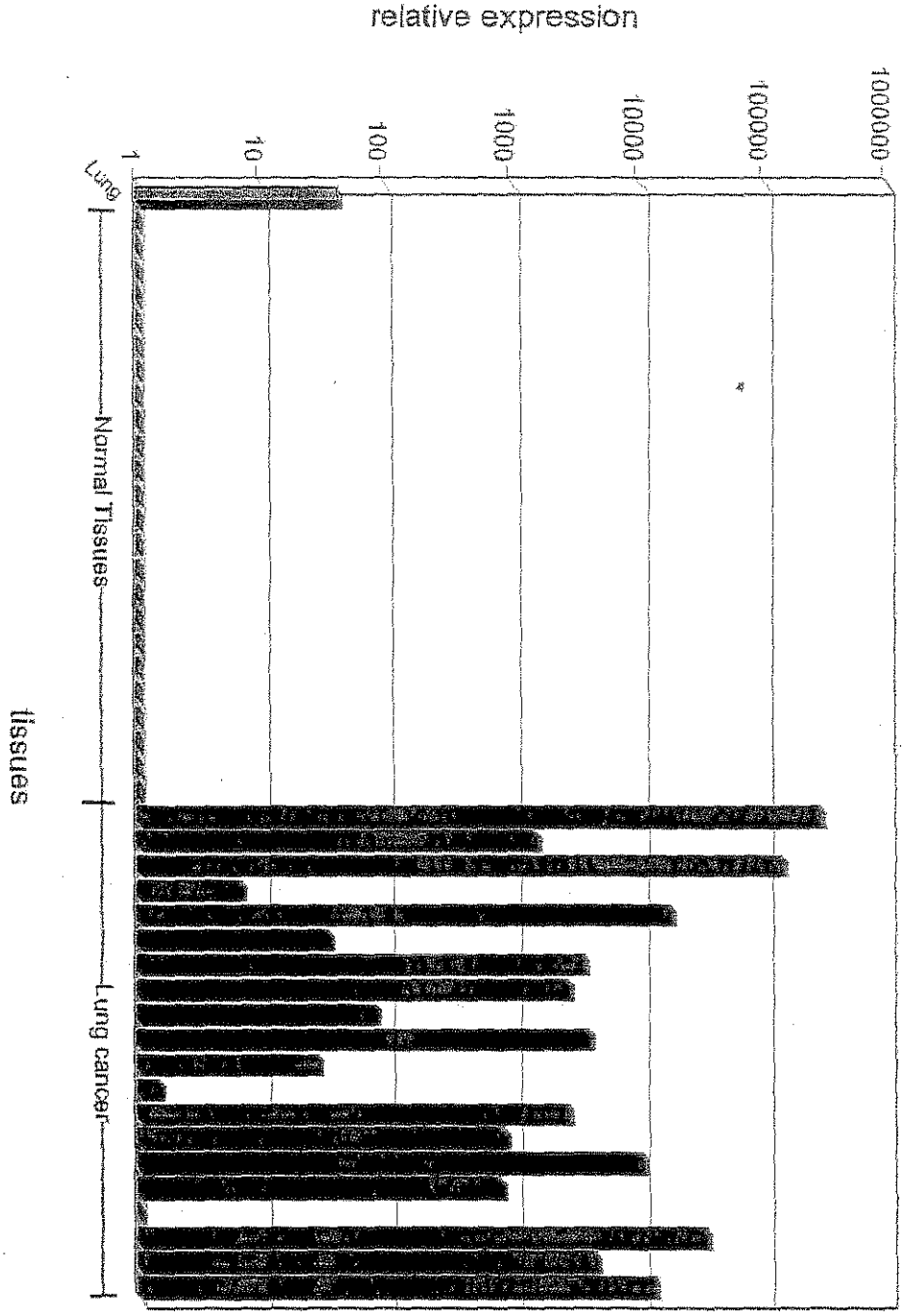
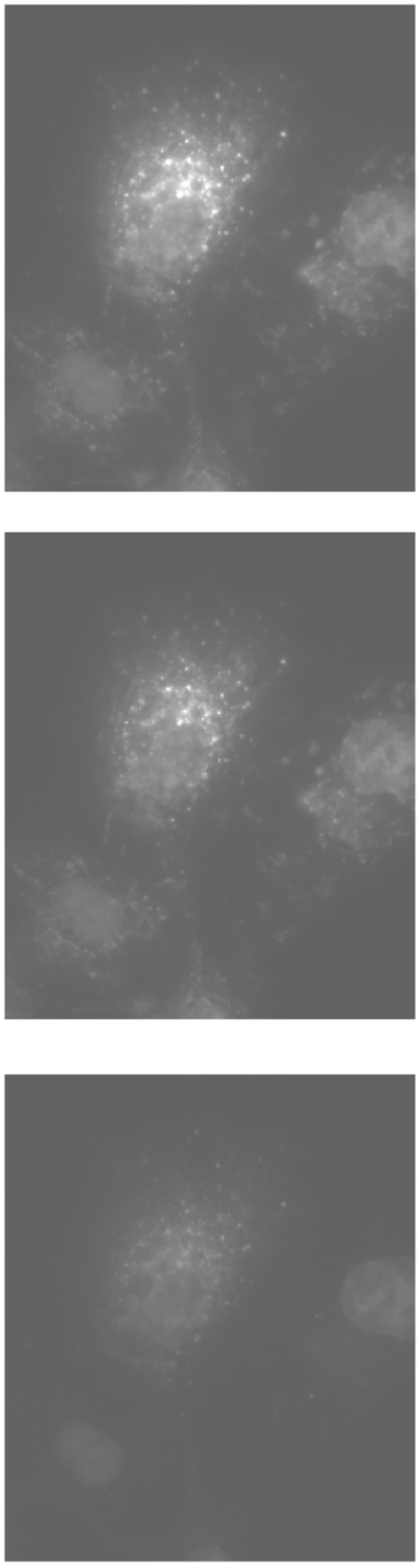

1%
10%
100%
1000%
Colon
1
2
3
4
5
6
7
8
9
10
11
12
Colon carcinoma
Stomach
1
2
3
4
5
6
7
8
9
10
Gastric carcinoma
Tissues

Fig. 20


relative expression
1
10
100
1000
10000
100000
1000000
Lung
Normal Tissues
Lung cancer
tissues



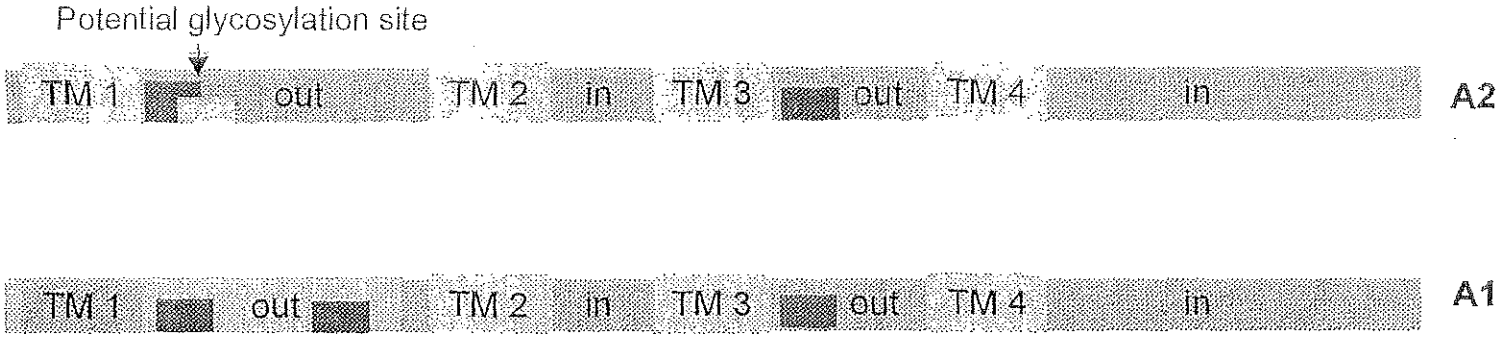
C.

B.

A.

Fig. 21

Fig. 22



Predicted glycosylation sites (amino acid positions)

Gastric variant

SeqName	Position	Potential	Jury	NGlyc	Agreement	Result
Sequence	37	0.7219	(9/9)			++
Sequence	38	0.6502	(8/9)			+
Sequence	45	0.6026	(8/9)			+
Sequence	116	0.5713	(7/9)			+
Sequence	141	0.6348	(7/9)			+
Sequence	146	0.5187	(6/9)			+
Sequence	153	0.4696	(5/9)			-
Sequence	205	0.6011	(8/9)			+
Sequence	234	0.3960	(8/9)			-
Sequence	237	0.4602	(6/9)			-

Lung variant

SeqName	Position	Potential	Jury	NGlyc	Agreement	Result
Sequence	38	0.7102	(9/9)			++
Sequence	116	0.5713	(7/9)			+
Sequence	141	0.6347	(7/9)			+
Sequence	146	0.5186	(6/9)			+
Sequence	153	0.4696	(5/9)			-
Sequence	205	0.6009	(8/9)			+
Sequence	234	0.3956	(8/9)			-
Sequence	237	0.4603	(6/9)			-

Fig. 23

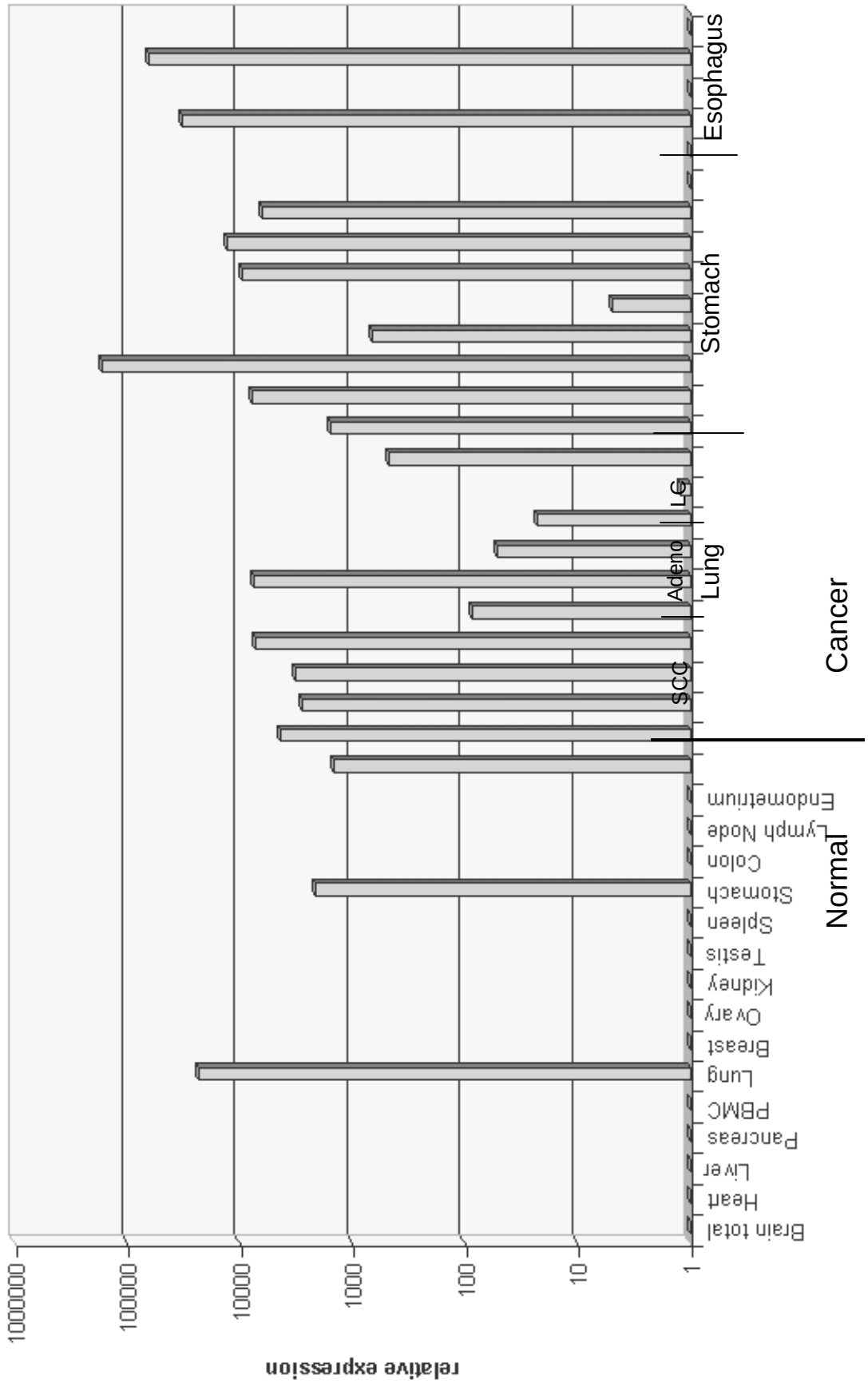

relative expression
1000000
100000
10000
1000
100
10
1
Brain total
Heart
Liver
Pancreas
PBMC
Lung
Breast
Ovary
Kidney
Testis
Spleen
Stomach
Colon
Lymph Node
Endometrium
Normal
SCC
Adeno
LG
Lung
Stomach
Esophagus
Cancer

Fig. 24

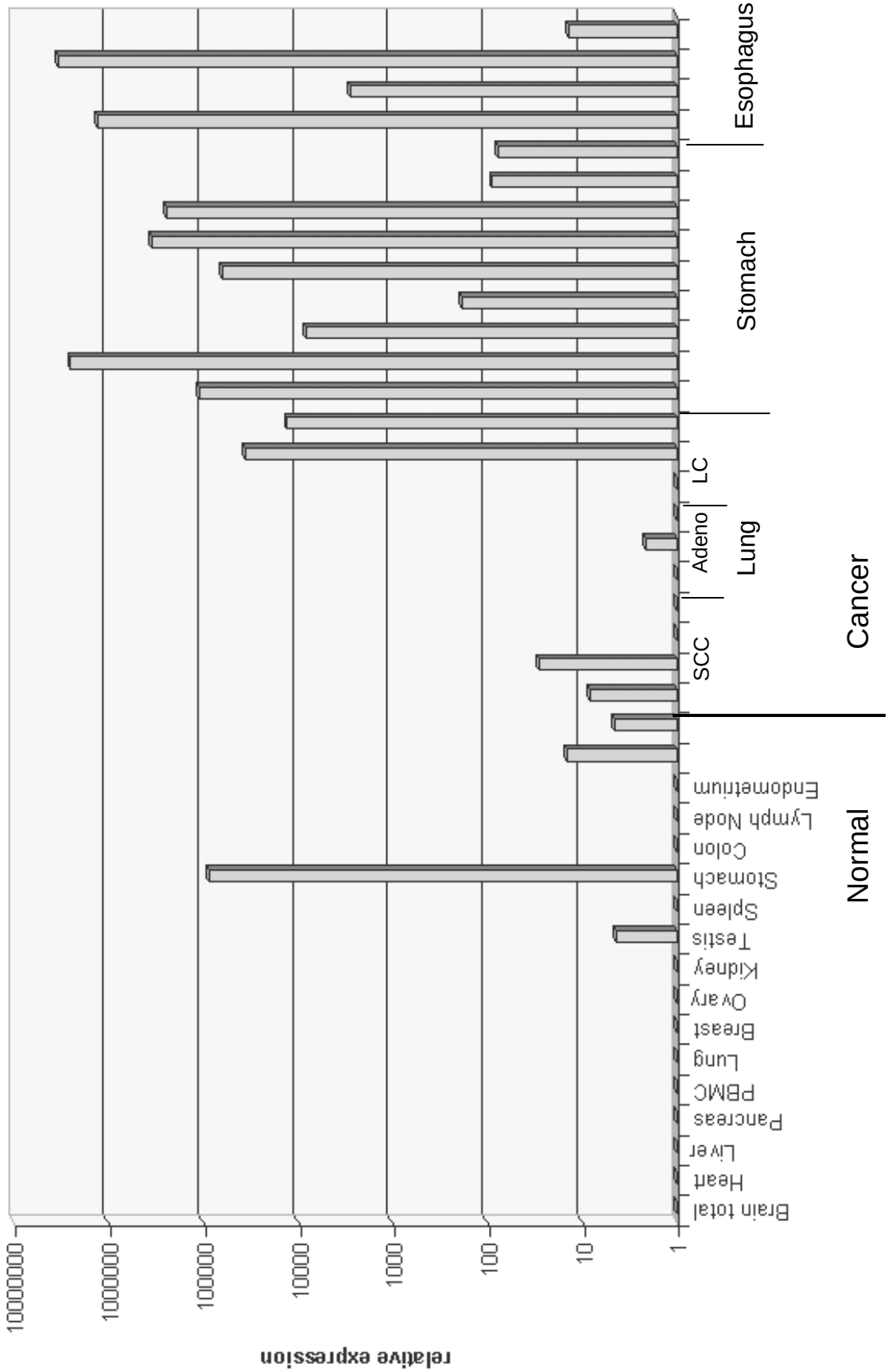
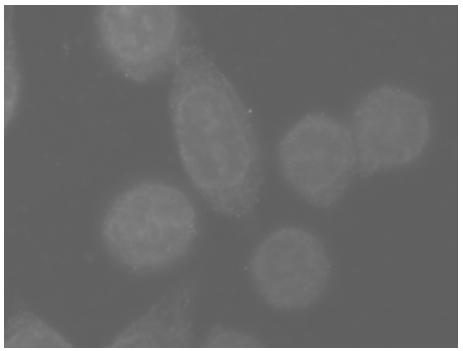
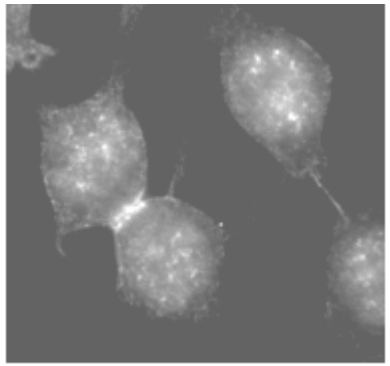

relative expression
10000000
1000000
100000
10000
1000
100
10
1
Brain total
Heart
Liver
Pancreas
PBMC
Lung
Breast
Ovary
Kidney
Testis
Spleen
Stomach
Colon
Lymph Node
Endometrium
Normal
SCC
Adeno
LC
Lung
Stomach
Esophagus
Cancer

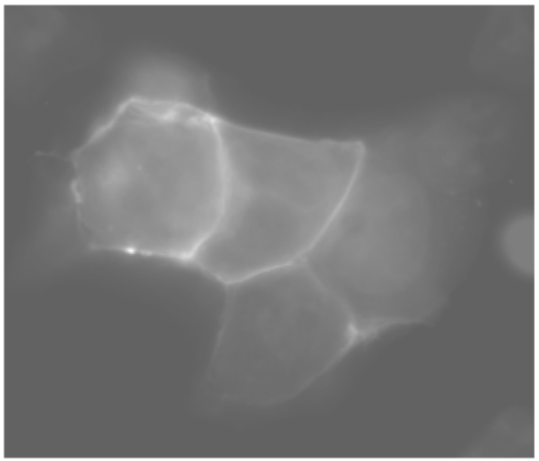
Fig. 25



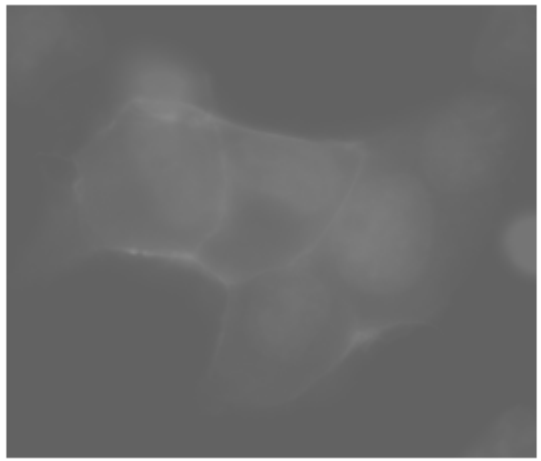
A.



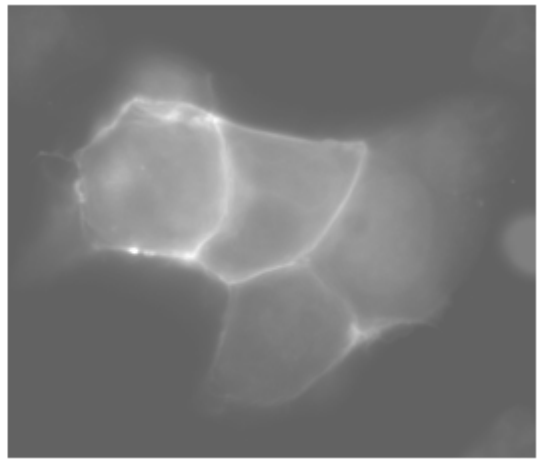
B.



A.



B.



C.

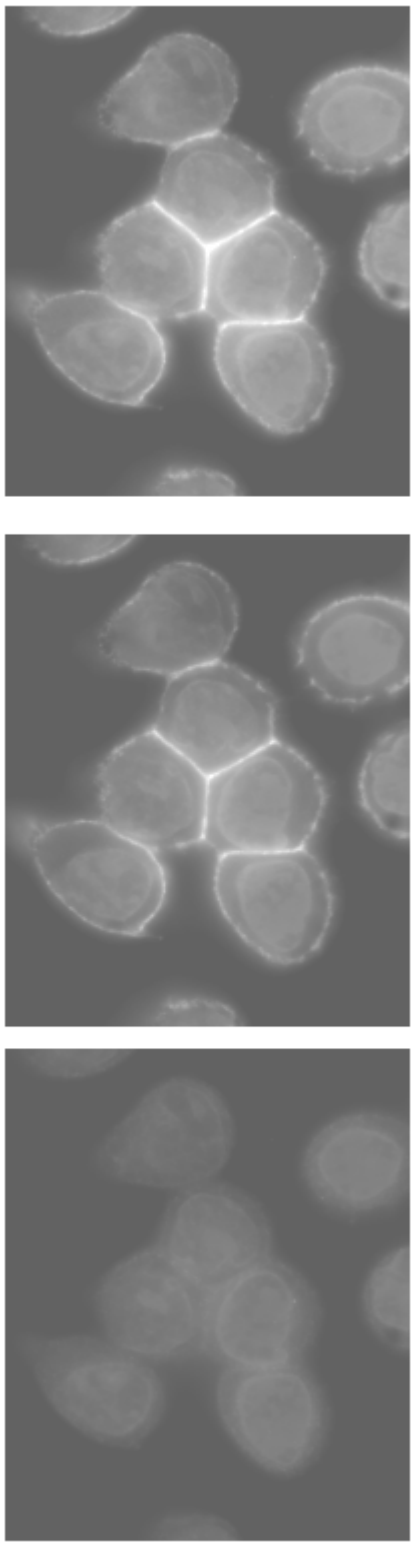


Fig. 26

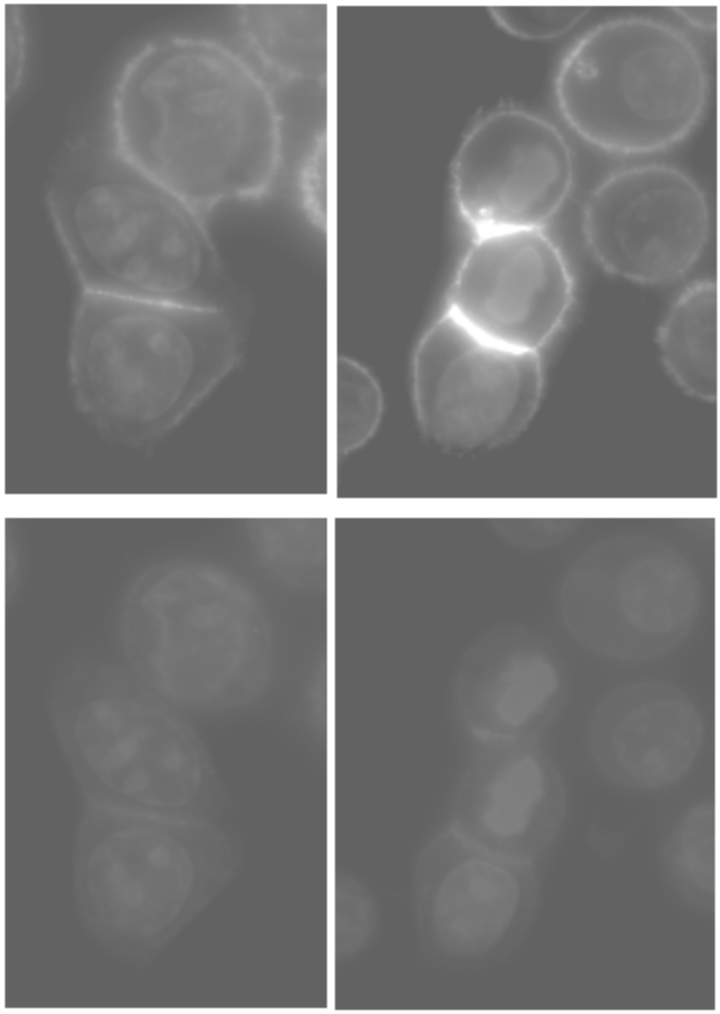


Fig. 27

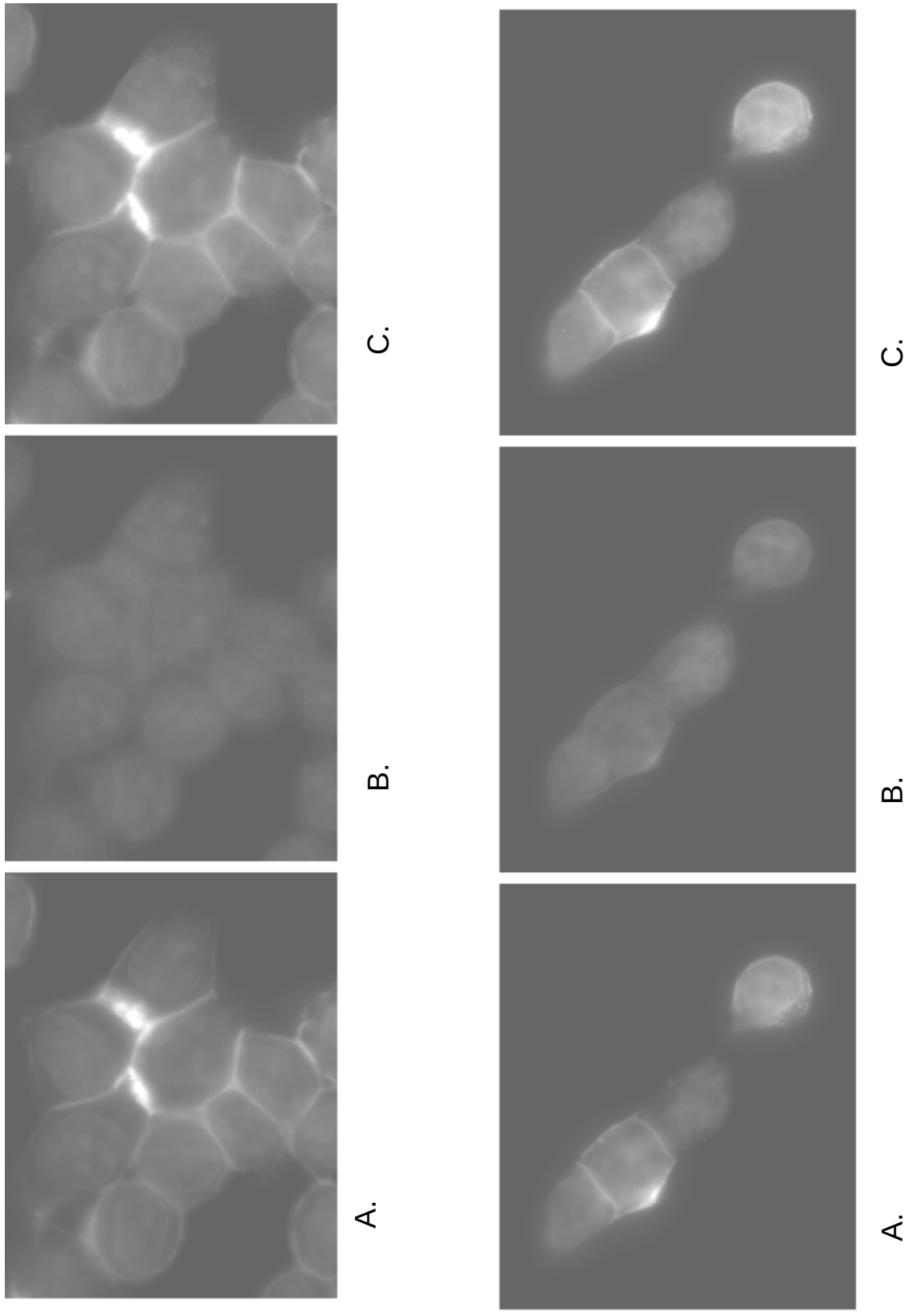


Fig. 28

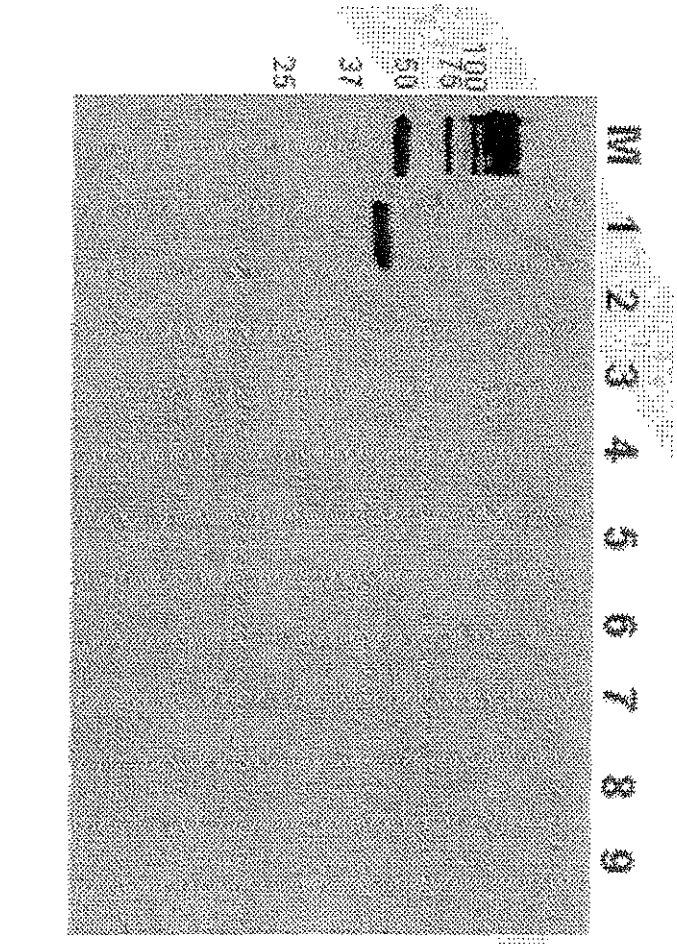


Fig. 29

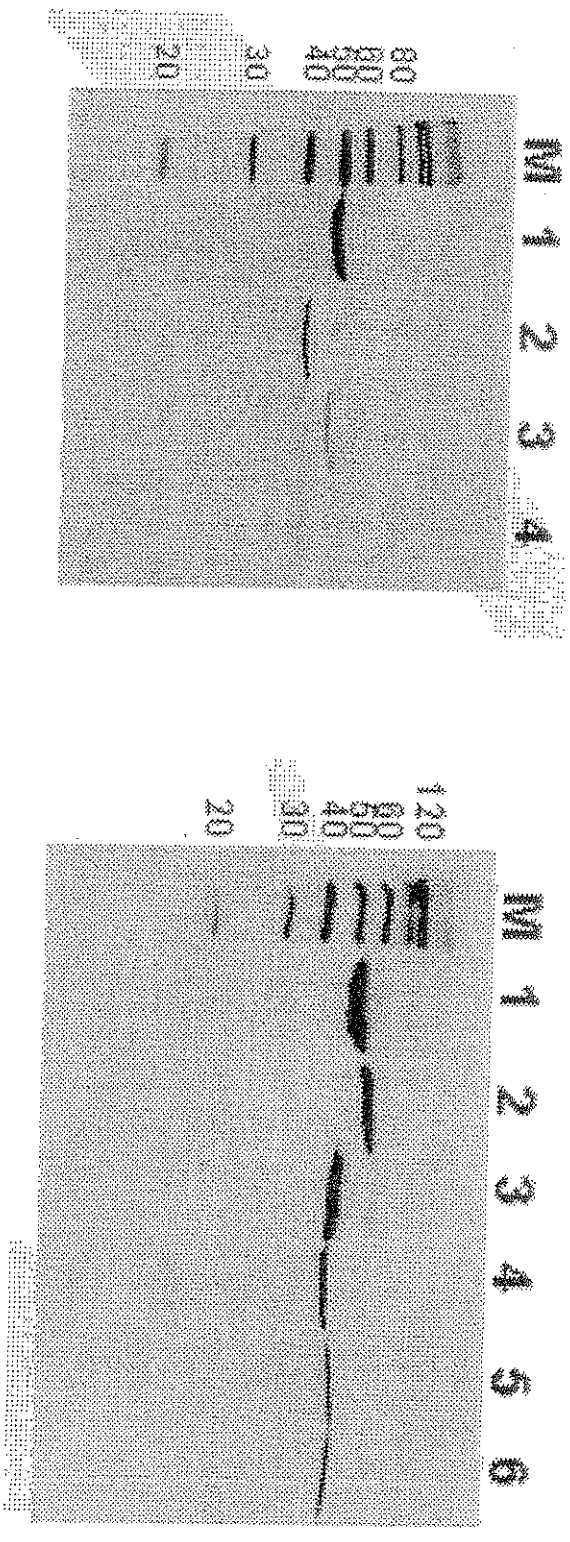


Fig. 30

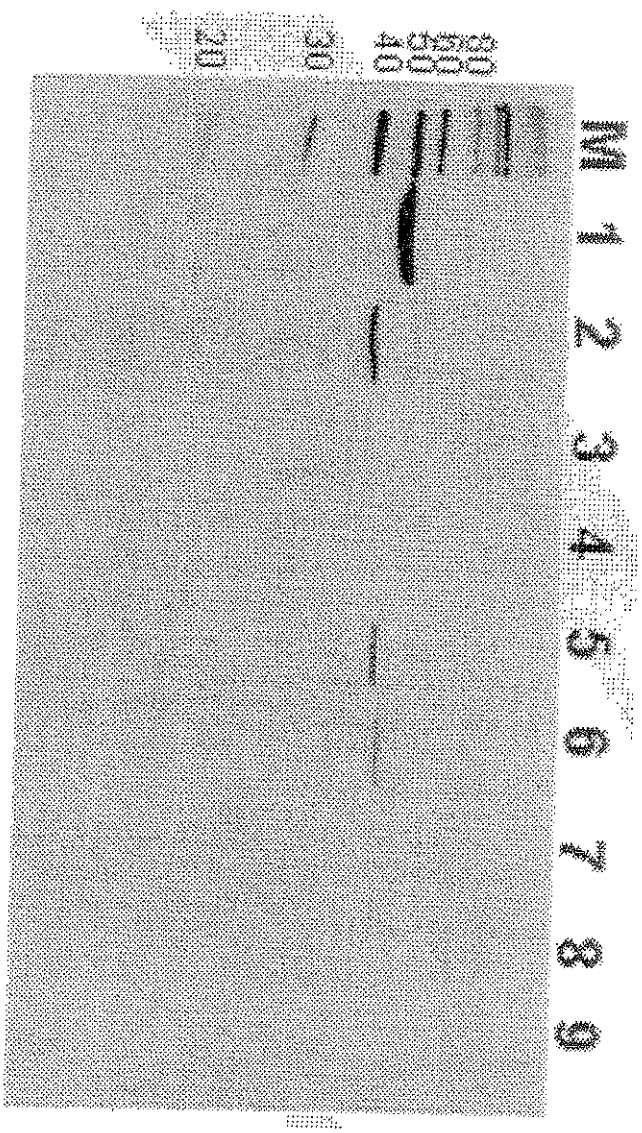
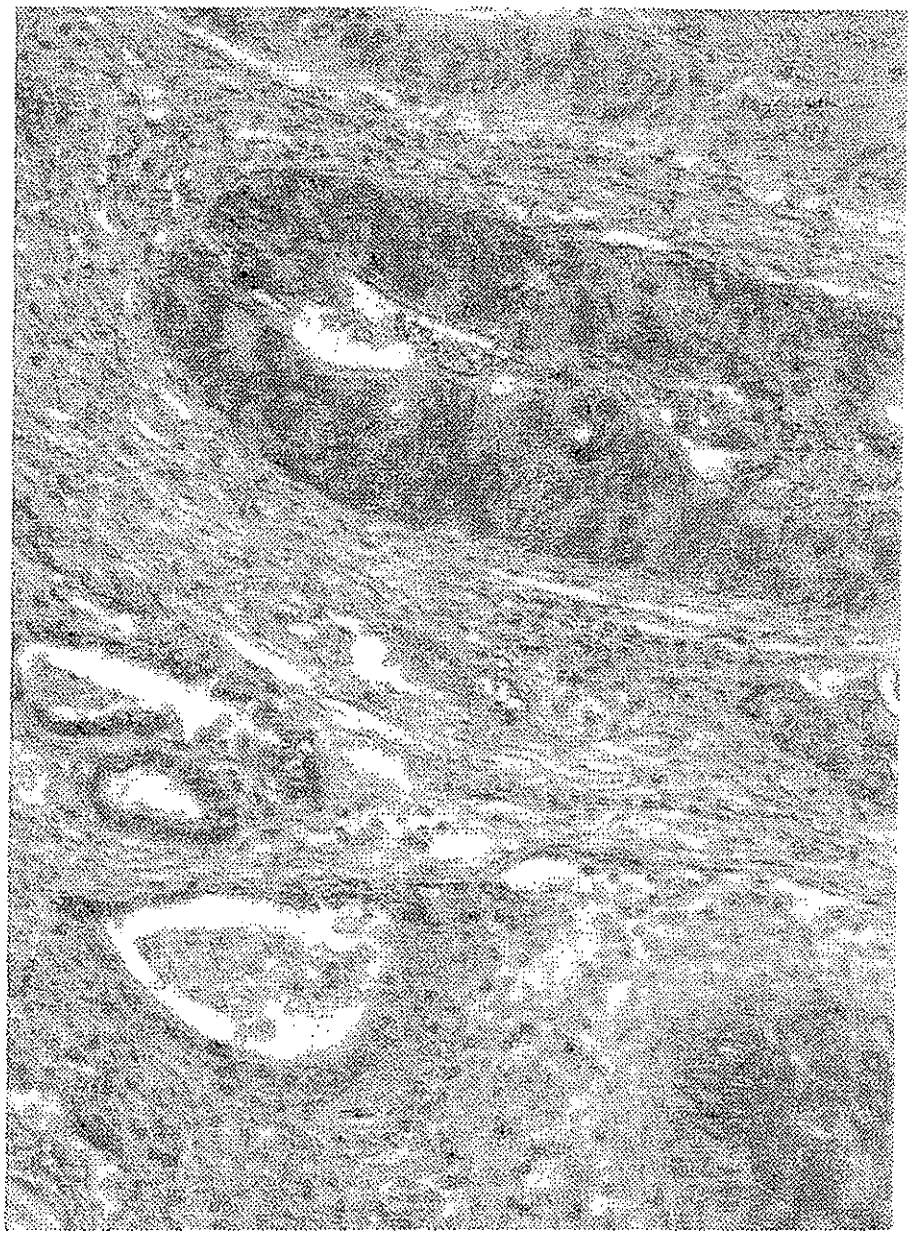
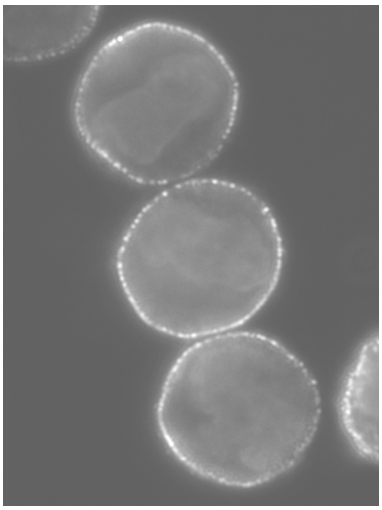


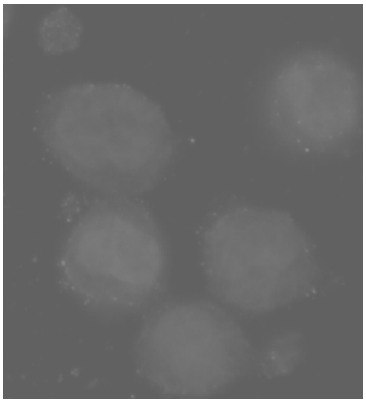
Fig. 31

Fig. 32





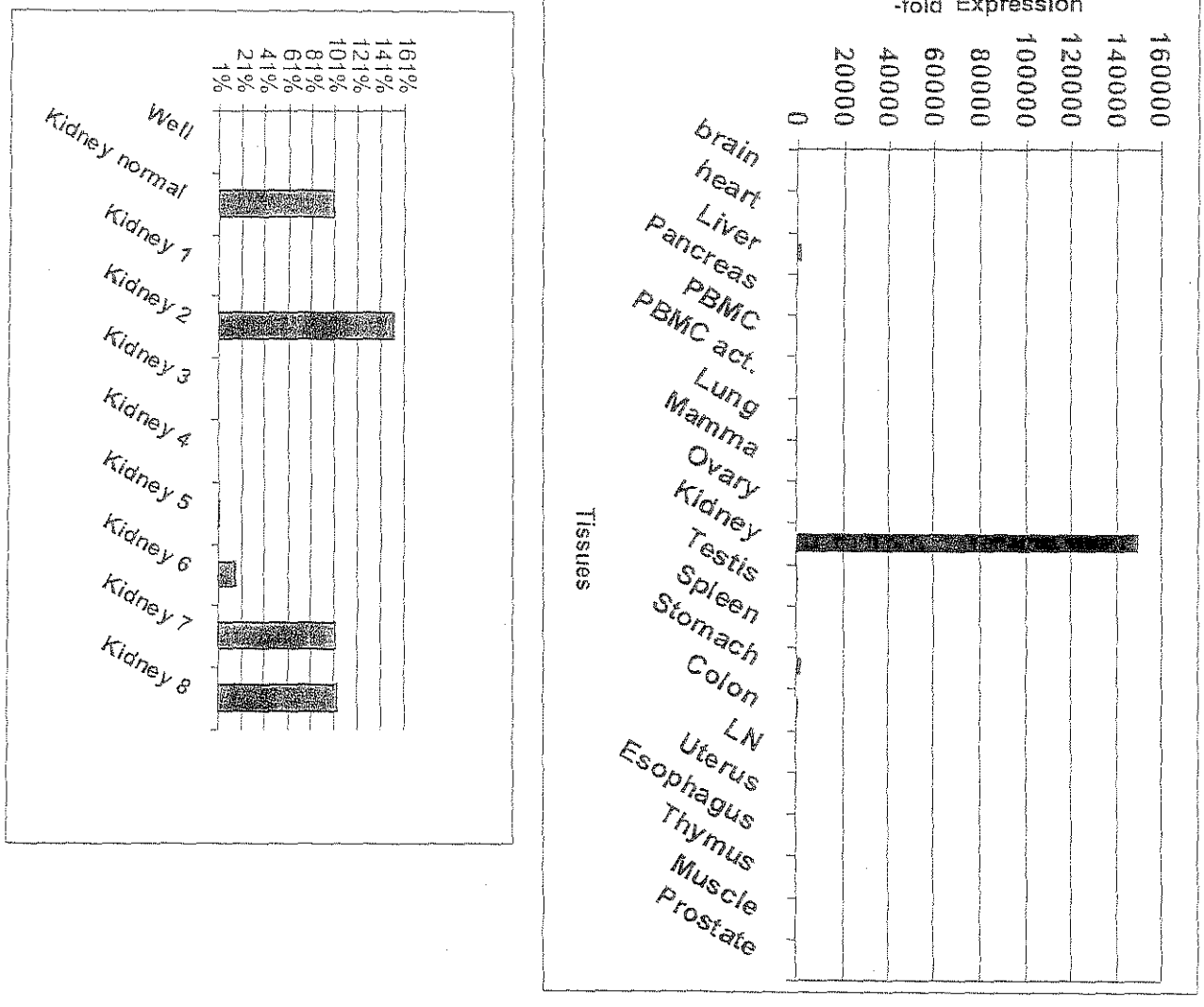
B.



A.

Fig. 33

Fig. 34


A
-fold Expression
0
20000
40000
60000
80000
100000
120000
140000
160000
brain
heart
Liver
Pancreas
PBMC
PBMC act.
Lung
Mamma
Ovary
Kidney
Testis
Spleen
Stomach
Colon
LN
Uterus
Esophagus
Thymus
Muscle
Prostate
Tissues
B
Well
Kidney normal
Kidney 1
Kidney 2
Kidney 3
Kidney 4
Kidney 5
Kidney 6
Kidney 7
Kidney 8
1%
21%
41%
61%
81%
101%
121%
141%
161%

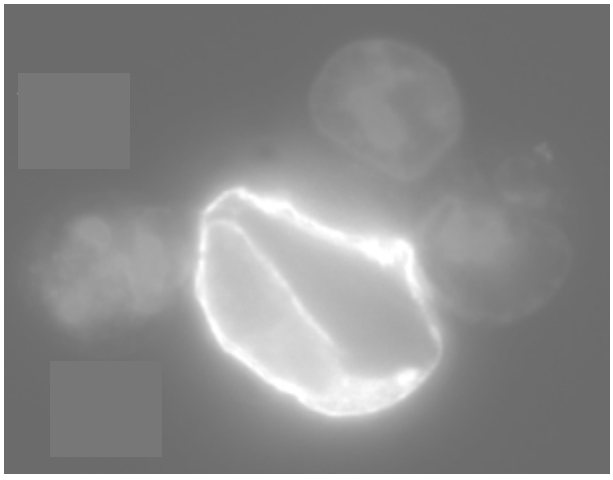
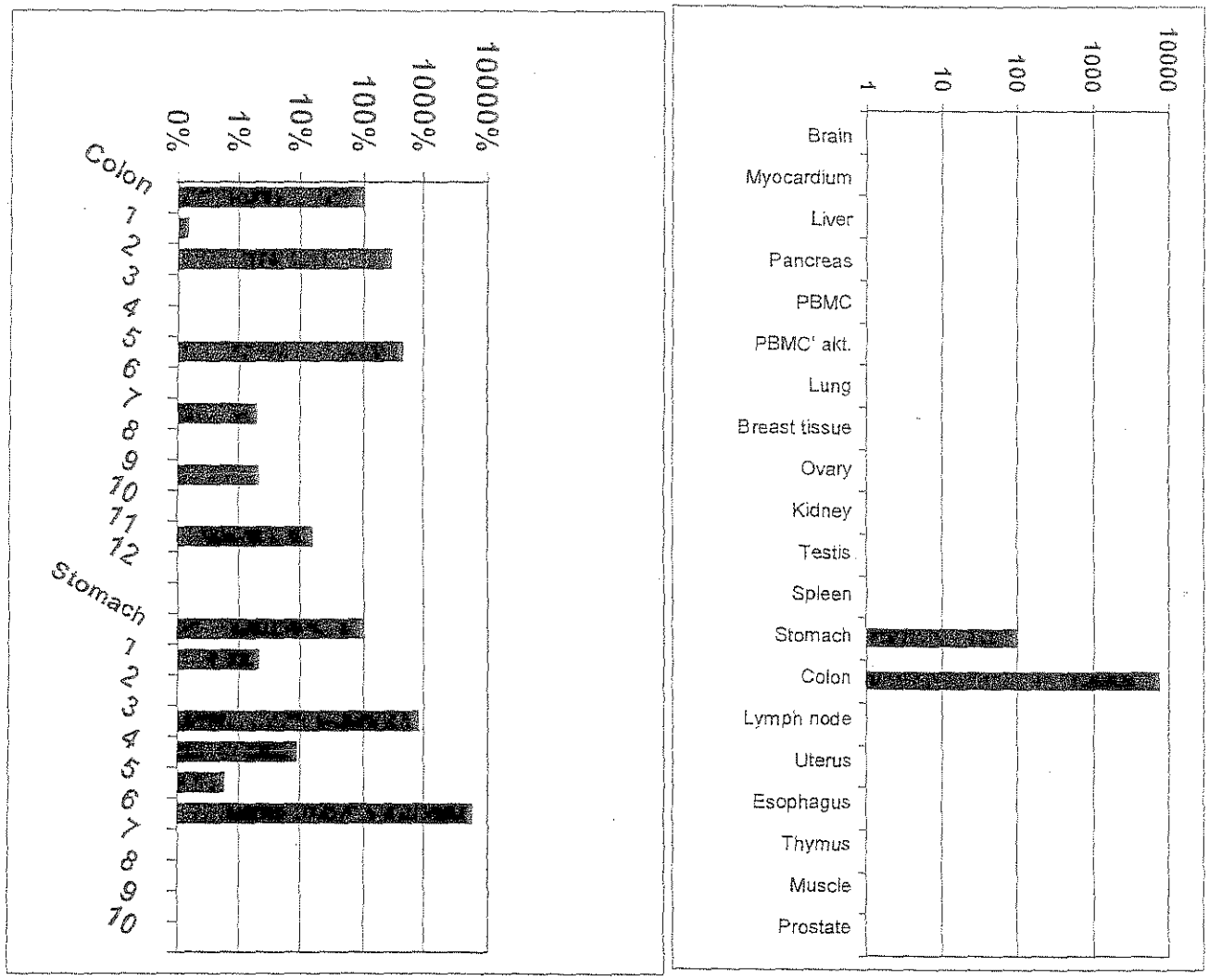


Fig. 35

Fig. 36


A
1
10
100
1000
10000
Brain
Myocardium
Liver
Pancreas
PBMC
PBMC' akt.
Lung
Breast tissue
Ovary
Kidney
Testis
Spleen
Stomach
Colon
Lymph node
Uterus
Esophagus
Thymus
Muscle
Prostate
B
0%
1%
10%
100%
1000%
10000%
Colon
1
2
3
4
5
6
7
8
9
10
11
12
Stomach
1
2
3
4
5
6
7
8
9
10

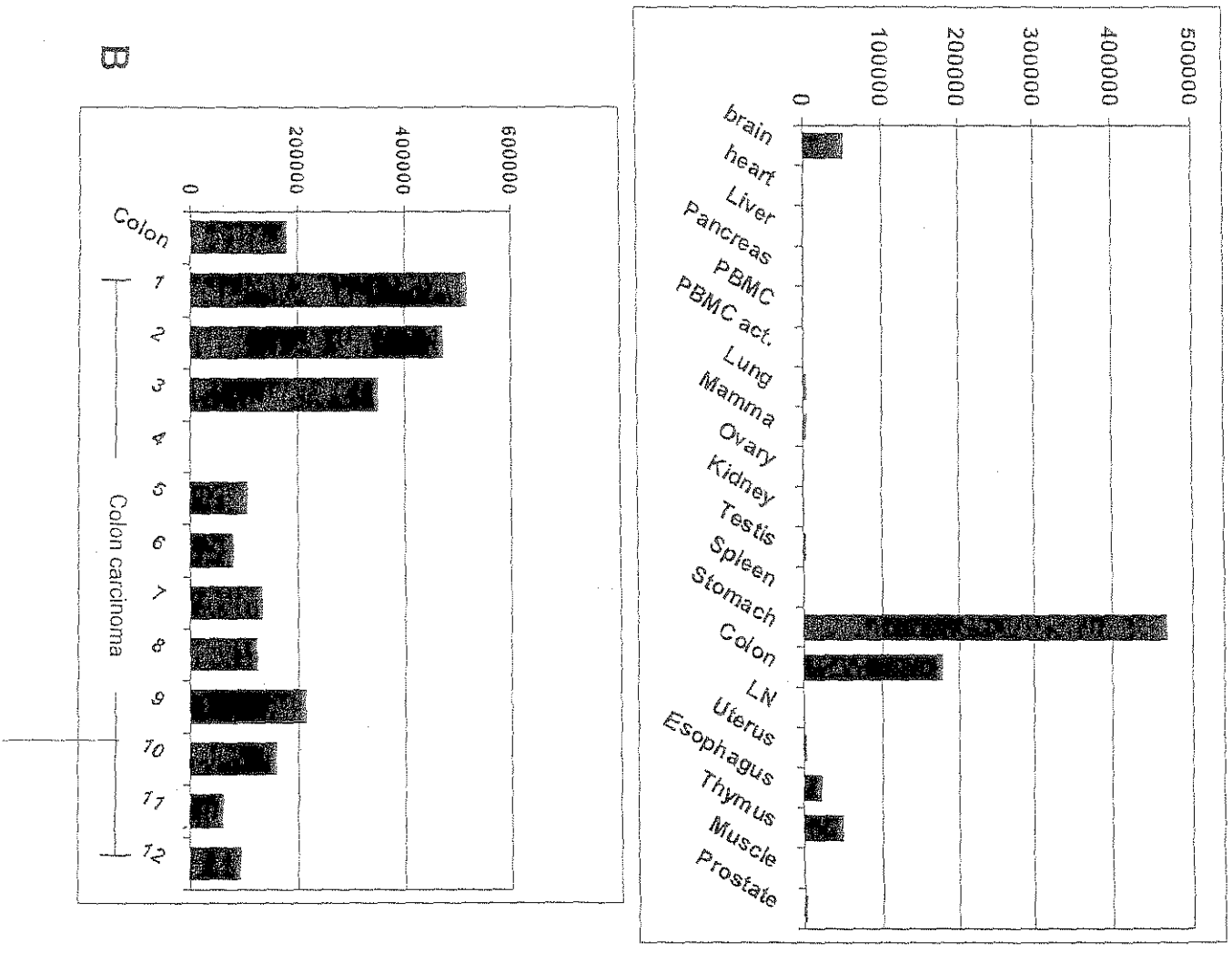

A
0
100000
200000
300000
400000
500000
brain
heart
Liver
Pancreas
PBMC
PBMC act.
Lung
Mamma
Ovary
Kidney
Testis
Spleen
Stomach
Colon
LN
Uterus
Esophagus
Thymus
Muscle
Prostate
B
0
200000
400000
600000
Colon
1
2
3
4
5
6
7
8
9
10
11
12
Colon carcinoma

Fig. 37

Fig. 38

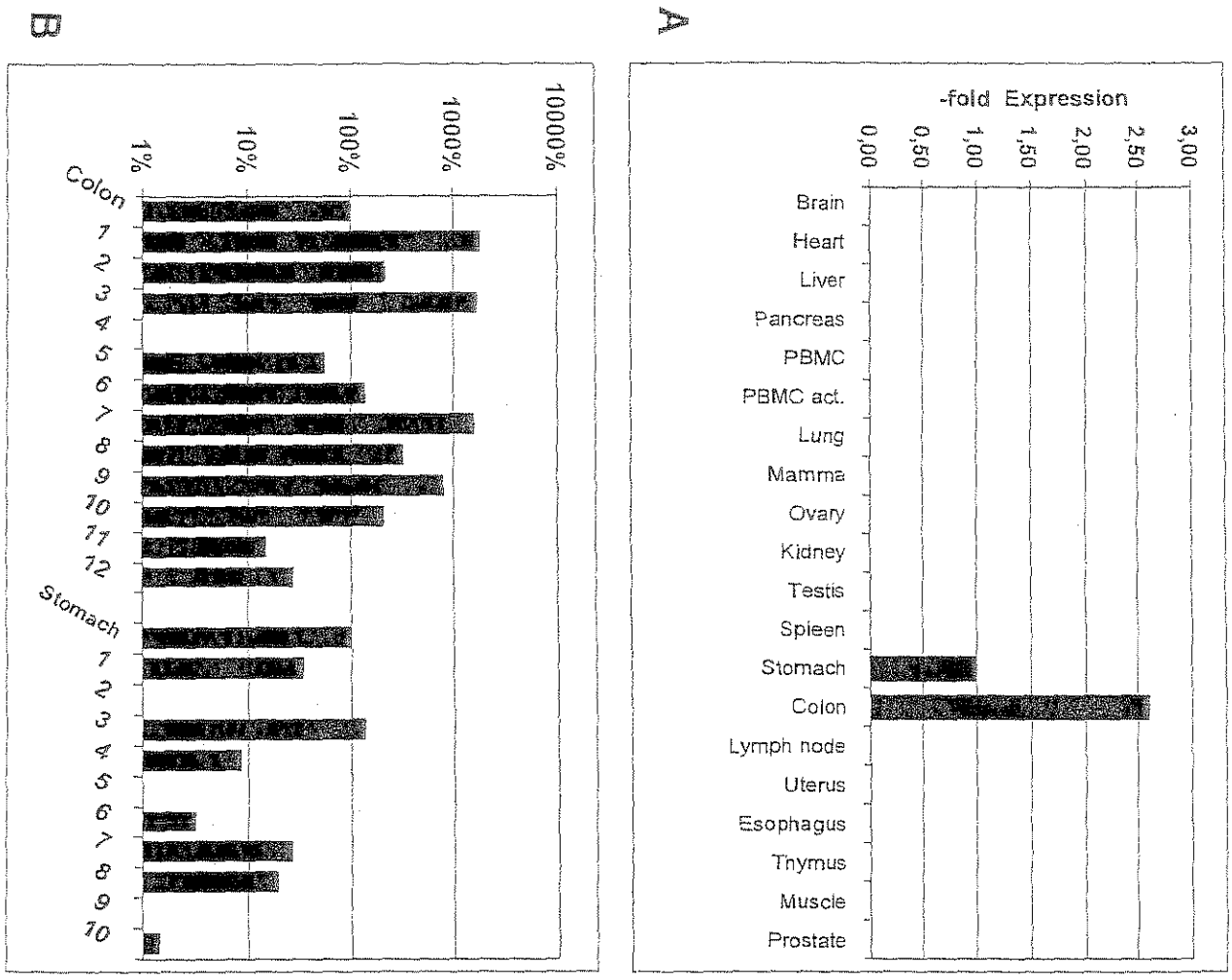
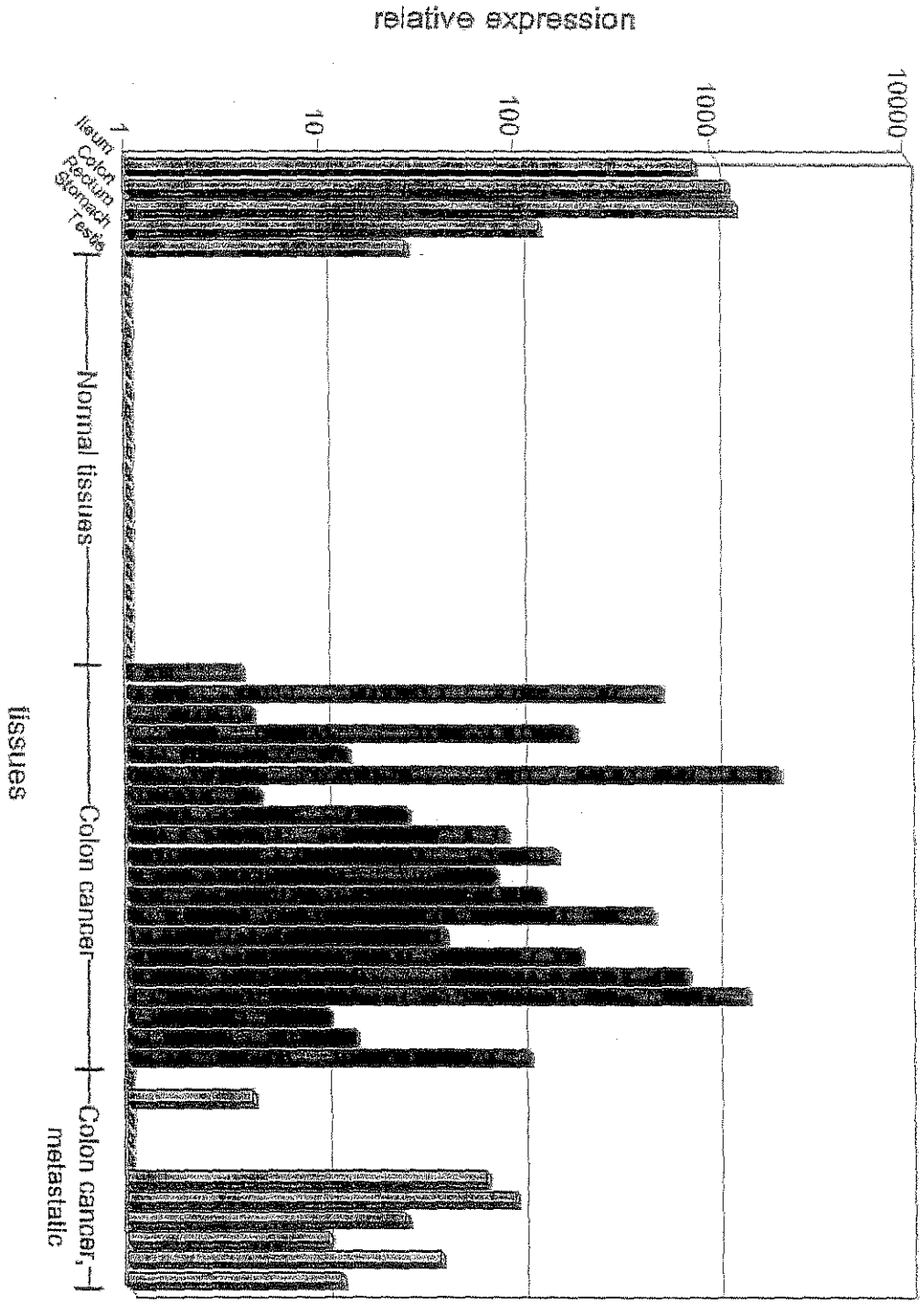

A
-fold Expression
0,00
0,50
1,00
1,50
2,00
2,50
3,00
Brain
Heart
Liver
Pancreas
PBMC
PBMC act.
Lung
Mamma
Ovary
Kidney
Testis
Spleen
Stomach
Colon
Lymph node
Uterus
Esophagus
Thymus
Muscle
Prostate
B
1%
10%
100%
1000%
10000%
Colon
1
2
3
4
5
6
7
8
9
10
11
12
Stomach
1
2
3
4
5
6
7
8
9
10

Fig. 39


relative expression
1
10
100
1000
10000
Ileum
Colon
Rectum
Stomach
Testis
Normal tissues
Colon cancer
Colon cancer, metastatic
tissues

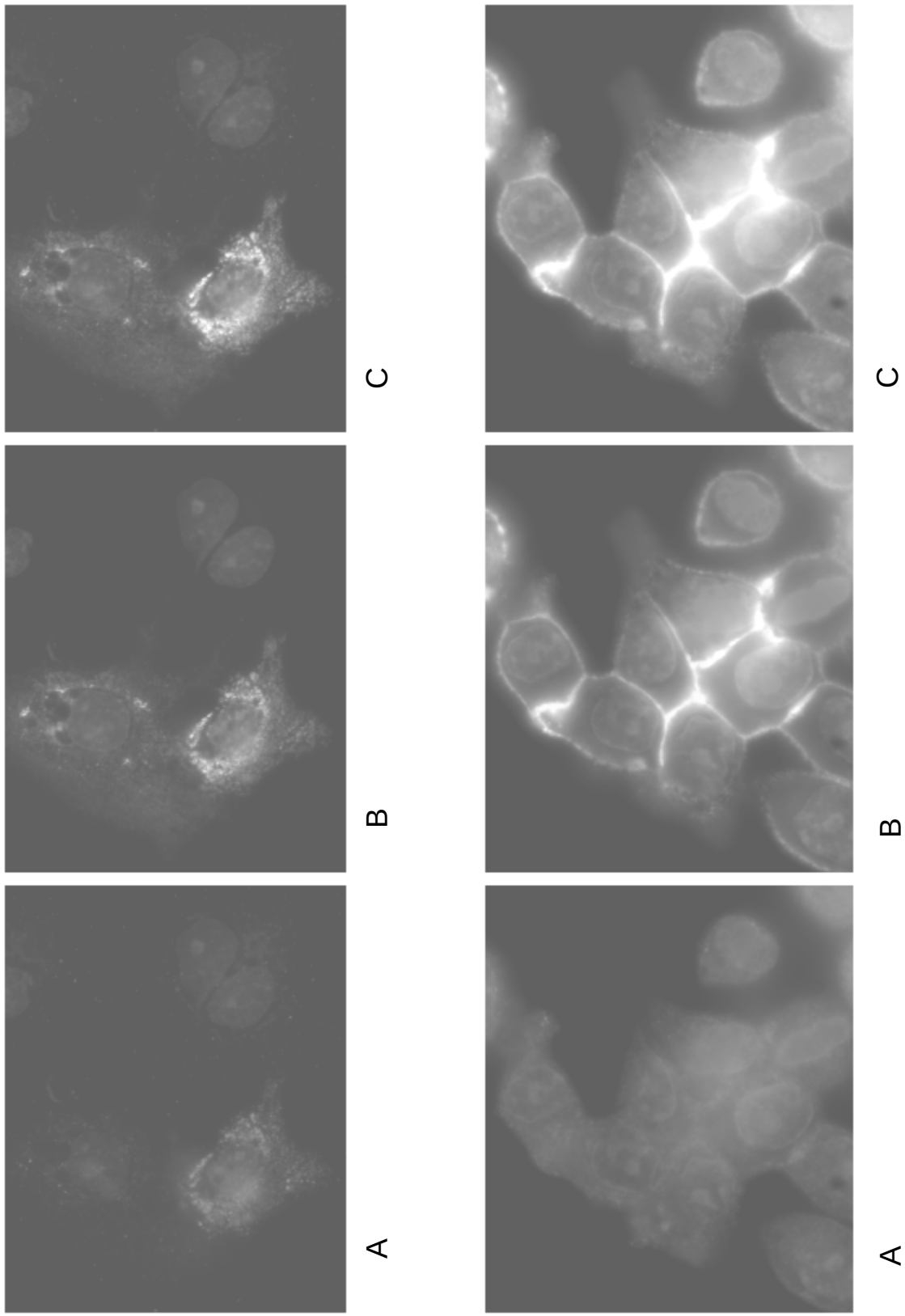


Fig. 40

Fig. 41

ID	Sequence
#1	caggccagagtcccagctgtcctggactctgctgtggggaagggctgatgcaggtgtgga gtcaaatgtgggtgcctcctgcagccgggtgccaggaggggtggaggggccaccctgggc tttgtccgggagcctggtcttcccgtccttgggctgacaggtgctgctgcctctgagccc tccctgctaagagctgtgtgctgggtaaggctggtggccctttgggctccctgtccagga tttgtgctctggagggtagggcttgctgggctggggactggaggggaacgtggagctcct tctgcctcctttcctgccccatgacagcaggcagatcccaggagagaagagctcaggaga tgggaagaggatctgtccaggggttagacctcaagggtgacttggagttctttacggcac ccatgctttctttgaggagttttgtgtttgtgggtgtggggtcggggctcacctcctccc acatccctgcccagaggtgggcagagtgggggcagtgccttgctcccctgctcgctctc tgctgacctccggctccctgtgctgccccaggaccatgaatggcacctacaacacctgtg gctccagcgacctcacctggcccccagcgatcaagctgggcttctacgcctacttgggcg tcctgctggtgctaggcctgctgctcaacagcctggcgctctgggtgttctgctgccgca tgcagcagtggacggagacccgcatctacatgaccaacctggcggtggccgacctctgcc tgctgtgcaccttgcccttcgtgctgcactccctgcgagacacctcagacacgccgctgt gccagctctcccagggcatctacctgaccaacaggtacatgagcatcagcctggtcacgg ccatcgccgtggaccgctatgtggccgtgcggcacccgctgcgtgcccgcgggctgcggt cccccaggcaggctgcggccgtgtgcgcggtcctctgggtgctggtcatcggctccctgg tggctcgctggctcctggggattcaggagggcggcttctgcttcaggagcacccggcaca atttcaactccatggcgttcccgctgctgggatttctacctgccctggccgtggtggtct tctgctccctgaaggtggtgactgccctggcccagaggccacccaccgacgtggggcagg cagaggccacccgcaaggctgcccgcatggtctgggccaacctcctggtgttcgtggtct gcttcctgcccctgcacgtggggctgacagtgcgcctcgcagtgggctggaacgcctgtg ccctcctggagacgatccgtcgcgccctgtacataaccagcaagctctcagatgccaact gctgcctggacgccatctgctactactacatggccaaggagttccaggaggcgtctgcac tggccgtggctcccagtgctaaggcccacaaaagccaggactctctgtgcgtgaccctcg cctaagaggcgtgctgtgggcgctgtgggccaggtctcgggggctccgggaggtgctgcc tgccaggggaagctggaaccagtagcaaggagcccgggatcagccctgaactcactgtgt attctcttggagccttgggtgggcagggacggcccaggtacctgctctcttgggaagaga gagggacagggacaagggcaagaggactgaggccagagcaaggccaatgtcagagacccc cgggatggggcctcacacttgccacccccagaaccagctcacctggccagagtgggttcc tgctggccagggtgcagccttgatgacacctgccgctgcccctcggggctggaataaaac tccccacccagagtc
#2	ATGAAGACGTTGCTGTTGGACTTGGCTTTGTGGTCACTGCTCTTCCAGCCCGGGTGGCTGTCCTTTAGTT CCCAGGTGAGTCAGAACTGCCACAATGGCAGCTATGAAATCAGCGTCCTGATGATGGGCAACTCAGCCTT TGCAGAGCCCCTGAAAAACTTGGAAGATGCGGTGAATGAGGGGCTGGAAATAGTGAGAGGACGTCTGCAA AATGCTGGCCTAAATGTGACTGTGAACGCTACTTTCATGTATTCGGATGGTCTGATTCATAACTCAGGCG ACTGCCGGAGTAGCACCTGTGAAGGCCTCGACCTACTCAGGAAAATTTCAAATGCACAACGGATGGGCTG TGTCCTCATAGGGCCCTCATGTACATACTCCACCTTCCAGATGTACCTTGACACAGAATTGAGCTACCCC ATGATCTCAGCTGGAAGTTTTGGATTGTCATGTGACTATAAAGAAACCTTAACCAGGCTGATGTCTCCAG CTAGAAAGTTGATGTACTTCTTGGTTAACTTTTGGAAAACCAACGATCTGCCCTTCAAAACTTATTCCTG GAGCACTTCGTATGTTTACAAGAATGGTACAGAAACTGAGGACTGTTTCTGGTACCTTAATGCTCTGGAG GCTAGCGTTTCCTATTTCTCCCACGAACTCGGCTTTAAGGTGGTGTTAAGACAAGATAAGGAGTTTCAGG ATATCTTAATGGACCACAACAGGAAAAGCAATGTGATTATTATGTGTGGTGGTCCAGAGTTCCTCTACAA GCTGAAGGGTGACCGAGCAGTGGCTGAAGACATTGTCATTATTCTAGTGGATCTTTTCAATGACCAGTAC TTGGAGGACAATGTCACAGCCCCTGACTATATGAAAAATGTCCTTGTTCTGACGCTGTCTCCTGGGAATT CCCTTCTAAATAGCTCTTTCTCCAGGAATCTATCACCAACAAAACGAGACTTTGCTCTTGCCTATTTGAA TGGAATCCTGCTCTTTGGACATATGCTGAAGATATTTCTTGAAAATGGAGAAAATATTACCACCCCCAAA TTTGCTCATGCTTTCAGGAATCTCACTTTTGAAGGGTATGACGGTCCAGTGACCTTGGATGACTGGGGGG ATGTTGACAGTACCATGGTGCTTCTGTATACCTCTGTGGACACCAAGAAATACAAGGTTCTTTTGACCTA TGATACCCACGTAAATAAGACCTATCCTGTGGATATGAGCCCCACATTCACTTGGAAGAACTCTAAACTT CCTAATGATATTACAGGCCGGGGCCCTCAGATCCTGATGATTGCAGTCTTCACCCTCACTGGAGCTGTGG TGCTGCTCCTGCTCGTCGCTCTCCTGATGCTCAGAAAATATAGAAAAGATTATGAACTTCGTCAGAAAAA ATGGTCCCACATTCCTCCTGAAAATATCTTTCCTCTGGAGACCAATGAGACCAATCATGTTAGCCTCAAG ATCGATGATGACAAAAGACGAGATACAATCCAGAGACTACGACAGTGCAAATACGACAAAAAGCGAGTGA TTCTCAAAGATCTCAAGCACAATGATGGTAATTTCACTGAAAAACAGAAGATAGAATTGAACAAGTTGCT TCAGATTGACTATTACAACCTGACCAAGTTCTACGGCACAGTGAAACTTGATACCATGATCTTCGGGGTG ATAGAATACTGTGAGAGAGGATCCCTCCGGGAAGTTTTAAATGACACAATTTCCTACCCTGATGGCACAT TCATGGATTGGGAGTTTAAGATCTCTGTCTTGTATGACATTGCTAAGGGAATGTCATATCTGCACTCCAG TAAGACAGAAGTCCATGGTCGTCTGAAATCTACCAACTGCGTAGTGGACAGTAGAATGGTGGTGAAGATC

Fig. 41 (continued)

	ACTGATTTTGGCTGCAATTCCATTTTACCTCCAAAAAAGGACCTGTGGACAGCTCCAGAGCACCTCCGCC AAGCCAACATCTCTCAGAAAGGAGATGTGTACAGCTATGGGATCATCGCACAGGAGATCATTCTGCGGAA AGAAACCTTCTACACTTTGAGCTGTCGGGACCGGAATGAGAAGATTTTCAGAGTGGAAAATTCCAATGGA ATGAAACCCTTCCGCCCAGATTTATTCTTGGAAACAGCAGAGGAAAAAGAGCTAGAAGTGTACCTACTTG TAAAAAACTGTTGGGAGGAAGATCCAGAAAAGAGACCAGATTTCAAAAAAATTGAGACTACACTTGCCAA GATATTTGGACTTTTTCATGACCAAAAAAATGAAAGCTATATGGATACCTTGATCCGACGTCTACAGCTA TATTCTCGAAACCTGGAACATCTGGTAGAGGAAAGGACACAGCTGTACAAGGCAGAGAGGGACAGGGCTG ACAGACTTAACTTTATGTTGCTTCCAAGGCTAGTGGTAAAGTCTCTGAAGGAGAAAGGCTTTGTGGAGCC GGAACTATATGAGGAAGTTACAATCTACTTCAGTGACATTGTAGGTTTCACTACTATCTGCAAATACAGC ACCCCCATGGAAGTGGTGGACATGCTTAATGACATCTATAAGAGTTTTGACCACATTGTTGATCATCATG ATGTCTACAAGGTGGAAACCATCGGTGATGCGTACATGGTGGCTAGTGGTTTGCCTAAGAGAAATGGCAA TCGGCATGCAATAGACATTGCCAAGATGGCCTTGGAAATCCTCAGCTTCATGGGGACCTTTGAGCTGGAG CATCTTCCTGGCCTCCCAATATGGATTCGCATTGGAGTTCACTCTGGTCCCTGTGCTGCTGGAGTTGTGG GAATCAAGATGCCTCGTTATTGTCTATTTGGAGATACGGTCAACACAGCCTCTAGGATGGAATCCACTGG CCTCCCTTTGAGAATTCACGTGAGTGGCTCCACCATAGCCATCCTGAAGAGAACTGAGTGCCAGTTCCTT TATGAAGTGAGAGGAGAAACATACTTAAAGGGAAGAGGAAATGAGACTACCTACTGGCTGACTGGGATGA AGGACCAGAAATTCAACCTGCCAACCCCTCCTACTGTGGAGAATCAACAGCGTTTGCAAGCAGAATTTTC AGACATGATTGCCAACTCTTTACAGAAAAGACAGGCAGCAGGGATAAGAAGCCAAAAACCCAGACGGGTA GCCAGCTATAAAAAAGGCACTCTGGAATACTTGCAGCTGAATACCACAGACAAGGAGAGCACCTATTTTT AA
#3	ATGAAGACGTTGCTGTTGGACTTGGCTTTGTGGTCACTGCTCTTCCAGCCCGGGTGGCTGTCCTTTAGTT CCCAGGTGAGTCAGAACTGCCACAATGGCAGCTATGAAATCAGCGTCCTGATGATGGGCAACTCAGCCTT TGCAGAGCCCCTGAAAAACTTGGAAGATGCGGTGAATGAGGGGCTGGAAATAGTGAGAGGACGTCTGCAA AATGCTGGCCTAAATGTGACTGTGAACGCTACTTTCATGTATTCGGATGGTCTGATTCATAACTCAGGCG ACTGCCGGAGTAGCACCTGTGAAGGCCTCGACCTACTCAGGAAAATTTCACCTTGA
#4	ATGAAGACGTTGCTGTTGGACTTGGCTTTGTGGTCACTGCTCTTCCAGCCCGGGTGGCTGTCCTTTAGTT CCCAGGTGAGTCAGAACTGCCACAATGGCAGCTATGAAATCAGCGTCCTGATGATGGGCAACTCAGCCTT TGCAGAGCCCCTGAAAAACTTGGAAGATGCGGTGAATGAGGGGCTGGAAATAGTGAGAGGACGTCTGCAA AATGCTGGCCTAAATGTGACTGTGAACGCTACTTTCATGTATTCGGATGGTCTGATTCATAACTCAGGCG ACTGCCGGAGTAGCACCTGTGAAGGCCTCGACCTACTCAGGAAAATTTCAAATGCACAACGGATGGGCTG TGTCCTCATAGGGCCCTCATGTACATACTCCACCTTCCAGATGTACCTTGACACAGAATTGAGCTACCCC ATGATCTCAGCTGGAAGTTTTGGATTGTCATGTGACTATAAAGAAACCTTAACCAGGCTGATGTCTCCAG CTAGAAAGTTGATGTACTTCTTGGTTAACTTTTGGAAAACCAACGATCTGCCCTTCAAAACTTATTCCTG GAGCACTTCGTATGTTTACAAGAATGGTACAGAAACTGAGGACTGTTTCTGGTACCTTAATGCTCTGGAG GCTAGCGTTTCCTATTTCTCCCACGAACTCGGCTTTAAGGTGGTGTTAAGACAAGATAAGGAGTTTCAGG ATATCTTAATGGACCACAACAGGAAAAGCAATGTGACCAGTACTTGGAGGACAATGTCACAGCCCCTGAC TATATGA
#5	ATGAAGACGTTGCTGTTGGACTTGGCTTTGTGGTCACTGCTCTTCCAGCCCGGGTGGCTGTCCTTTAGTT CCCAGGTGAGTCAGAACTGCCACAATGGCAGCTATGAAATCAGCGTCCTGATGATGGGCAACTCAGCCTT TGCAGAGCCCCTGAAAAACTTGGAAGATGCGGTGAATGAGGGGCTGGAAATAGTGAGAGGACGTCTGCAA AATGCTGGCCTAAATGTGACTGTGAACGCTACTTTCATGTATTCGGATGGTCTGATTCATAACTCAGGCG ACTGCCGGAGTAGCACCTGTGAAGGCCTCGACCTACTCAGGAAAATTTCAAATGCACAACGGATGGGCTG TGTCCTCATAGGGCCCTCATGTACATACTCCACCTTCCAGATGTACCTTGACACAGAATTGAGCTACCCC ATGATCTCAGCTGGAAGTTTTGGATTGTCATGTGACTATAAAGAAACCTTAACCAGGCTGATGTCTCCAG CTAGAAAGTTGATGTACTTCTTGGTTAACTTTTGGAAAACCAACGATCTGCCCTTCAAAACTTATTCCTG GAGCACTTCGTATGTTTACAAGAATGGTACAGAAACTGAGGACTGTTTCTGGTACCTTAATGCTCTGGAG GCTAGCGTTTCCTATTTCTCCCACGAACTCGGCTTTAAGGTGGTGTTAAGACAAGATAAGGAGTTTCAGG ATATCTTAATGGACCACAACAGGAAAAGCAATGTGATTATTATGTGTGGTGGTCCAGAGTTCCTCTACAA GCTGAAGGGTGACCGAGCAGTGGCTGAAGACATTGTCATTATTCTAGTGGATCTTTTCAATGACCAGTAC TTGGAGGACAATGTCACAGCCCCTGACTATATGAAAAATGTCCTTGTTCTGACGCTGTCTCCTGGGAATT CCCTTCTAAATAGCTCTTTCTCCAGGAATCTATCACCAACAAAACGAGACTTTGCTCTTGCCTATTTGAA TGGAATCCTGCTCTTTGGACATATGCTGAAGATATTTCTTGAAAATGGAGAAAATATTACCACCCCCAAA TTTGCTCATGCTTTCAGGAATCTCACTTTTGAAGGGTATGACGGTCCAGTGACCTTGGATGACTGGGGGG ATGTTGACAGTACCATGGTGCTTCTGTATACCTCTGTGGACACCAAGAAATACAAGGTTCTTTTGACCTA TGATACCCACGTAAATAAGACCTATCCTGTGGATATGAGCCCCACATTCACTTGGAAGAACTCTAAACTT CCTAATGATATTACAGGCCGGGGCCCTCAGATCCTGATGATTGCAGTCTTCACCCTCACTGGAGCTGTGG TGCTGCTCCTGCTCGTCGCTCTCCTGATGCTCAGAAAATATAGAAAAGATTATGAACTTCGTCAGAAAAA ATGGTCCCACATTCCTCCTGAAAATATCTTTCCTCTGGAGACCAATGAGACCAATCATGTTAGCCTCAAG ATCGATGATGACAAAAGACGAGATACAATCCAGAGACTACGACAGTGCAAATACGACAAAAAGCGAGTGA

Fig. 41 (continued)

	TTCTCAAAGATCTCAAGCACAATGATGGTAATTTCACTGAAAAACAGAAGATAGAATTGAACAAGATTGA CTATTACAACCTGACCAAGTTCTACGGCACAGTGAAACTTGATACCATGATCTTCGGGGTGATAGAATAC TGTGAGAGAGGATCCCTCCGGGAAGTTTTAAATGACACAATTTCCTACCCTGATGGCACATTCATGGATT GGGAGTTTAAGATCTCTGTCTTGTATGACATTGCTAAGGGAATGTCATATCTGCACTCCAGTAAGACAGA AGTCCATGGTCGTCTGAAATCTACCAACTGCGTAGTGGACAGTAGAATGGTGGTGAAGATCACTGATTTT GGCTGCAATTCCATTTTACCTCCAAAAAAGGACCTGTGGACAGCTCCAGAGCACCTCCGCCAAGCCAACA TCTCTCAGAAAGGAGATGTGTACAGCTATGGGATCATCGCACAGGAGATCATTCTGCGGAAAGAAACCTT CTACACTTTGAGCTGTCGGGACCGGAATGAGAAGATTTTCAGAGTGGAAAATTCCAATGGAATGAAACCC TTCCGCCCAGATTTATTCTTGGAAACAGCAGAGGAAAAAGAGCTAGAAGTGTACCTACTTGTAAAAAACT GTTGGGAGGAAGATCCAGAAAAGAGACCAGATTTCAAAAAAATTGAGACTACACTTGCCAAGATATTTGG ACTTTTTCATGACCAAAAAAATGAAAGCTATATGGATACCTTGATCCGACGTCTACAGCTATATTCTCGA AACCTGGAACATCTGGTAGAGGAAAGGACACAGCTGTACAAGGCAGAGAGGGACAGGGCTGACAGACTTA ACTTTATGTTGCTTCCAAGGCTAGTGGTAAAGTCTCTGAAGGAGAAAGGCTTTGTGGAGCCGGAACTATA TGAGGAAGTTACAATCTACTTCAGTGACATTGTAGGTTTCACTACTATCTGCAAATACAGCACCCCCATG GAAGTGGTGGACATGCTTAATGACATCTATAAGAGTTTTGACCACATTGTTGATCATCATGATGTCTACA AGGTGGAAACCATCGGTGATGCGTACATGGTGGCTAGTGGTTTGCCTAAGAGAAATGGCAATCGGCATGC AATAGACATTGCCAAGATGGCCTTGGAAATCCTCAGCTTCATGGGGACCTTTGAGCTGGAGCATCTTCCT GGCCTCCCAATATGGATTCGCATTGGAGTTCACTCTGGTCCCTGTGCTGCTGGAGTTGTGGGAATCAAGA TGCCTCGTTATTGTCTATTTGGAGATACGGTCAACACAGCCTCTAGGATGGAATCCACTGGCCTCCCTTT GAGAATTCACGTGAGTGGCTCCACCATAGCCATCCTGAAGAGAACTGAGTGCCAGTTCCTTTATGAAGTG AGAGGAGAAACATACTTAAAGGGAAGAGGAAATGAGACTACCTACTGGCTGACTGGGATGAAGGACCAGA AATTCAACCTGCCAACCCCTCCTACTGTGGAGAATCAACAGCGTTTGCAAGCAGAATTTTCAGACATGAT TGCCAACTCTTTACAGAAAAGACAGGCAGCAGGGATAAGAAGCCAAAAACCCAGACGGGTAGCCAGCTAT AAAAAAGGCACTCTGGAATACTTGCAGCTGAATACCACAGACAAGGAGAGCACCTATTTTTAA
#6	ggggacactttgtatggcaagtggaaccactggcttggtg gattttgctagatttttctgatttttaaactcctgaaaaatatcccagataactgtcatgaagctggtaacta tcttcct gctggtgaccatcagcctttgtagttactctgctactgcc ttcctcatcaacaaagtgccccttcctgttgacaagttggcacctttacctctggacaacattcttccctttta tggatcc attaaagcttcttctgaaaactctgggcatttctgttgag caccttgtggaggggctaaggaagtgtgtaaatgagctgggaccagaggcttctgaagctgtgaagaaactgc tggaggc gctatcacacttggtgtgacatcaagataaagagcggagg tggatggggatggaagatgatgctcctatcctccctgcctgaaacctgttctaccaattatagatcaaatgcc ctaaaatgtagtgacccgtgaaaaggacaaataaagcaatgaatactaaaaaaaaaaaaaaaaaaaa aaaaaaaaaa
#7	ATGGCCGTGACTGCCTGTCAGGGCTTGGGGTTCGTGGTTTCACTGATTGGGATTGCGGGCATCATTGCTG CCACCTGCATGGACCAGTGGAGCACCCAAGACTTGTACAACAACCCCGTAACAGCTGTTTTCAACTACCA GGGGCTGTGGCGCTCCTGTGTCCGAGAGAGCTCTGGCTTCACCGAGTGCCGGGGCTACTTCACCCTGCTG GGGCTGCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCC TCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACAT GACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGTTTGCC AACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGGGATGGTGCAGA CTGTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTGGGCTGGGTCGCTGGAGGCCTCACACTAAT TGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCT TATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCA ACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAA GCACGACTATGTGTAA
#8	tgcgccaccatggccgtgactgcctgtcagggcttggggttcgtggtttcactgattggg attgcgggcatcattgctgccacctgcatggaccagtggagcacccaagacttgtacaac aaccccgtaacagctgttttcaactaccaggggctgtggcgctcctgtgtccgagagagc
#9	MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMT NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRH PLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF

Fig. 41 (continued)

	YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVR LAVGWNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQEASALAVAPRAKAHKS QDSLCVTLA
#10	MTAGRSQERRAQEMGRGSVQGLDLKGDLEFFTAPMLSLRSFVFVGVGSGLTSSHIPAQRWAEWGQCLAPPARS LLTSGSLCCPRTMNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGL LLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGI YLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLWVLVIGSLVARWLLG IQEGGFCFRSTRHNFNSMAFPLLGFYLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKA ARMVWANLLVFVVCFLPLHVGLTVRLAVGWNACALLETIRRALYITSKLSDANCCLDAIC YYYMAKEFQEASALAVAPSAKAHKSQDSLCVTLA
#11	MKTLLLDLALWSLLFQPGWLSFSSQVSQNCHNGSYEISVLMMGNSAFAEPLKNLEDAVNEGLEIVRGRLQ NAGLNVTVNATFMYSDGLIHNSGDCRSSTCEGLDLLRKISNAQRMGCVLIGPSCTYSTFQMYLDTELSYP MISAGSFGLSCDYKETLTRLMSPARKLMYFLVNFWKTNDLPFKTYSWSTSYVYKNGTETEDCFWYLNALE ASVSYFSHELGFKVVLRQDKEFQDILMDHNRKSNVIIMCGGPEFLYKLKGDRAVAEDIVIILVDLFNDQY LEDNVTAPDYMKNVLVLTLSPGNSLLNSSFSRNLSPTKRDFALAYLNGILLFGHMLKIFLENGENITTPK FAHAFRNLTFEGYDGPVTLDDWGDVDSTMVLLYTSVDTKKYKVLLTYDTHVNKTYPVDMSPTFTWKNSKL PNDITGRGPQILMIAVFTLTGAVVLLLLVALLMLRKYRKDYELRQKKWSHIPPENIFPLETNETNHVSLK IDDDKRRDTIQRLRQCKYDKKRVILKDLKHNDGNFTEKQKIELNKLLQIDYYNLTKFYGTVKLDTMIFGV IEYCERGSLREVLNDTISYPDGTFMDWEFKISVLYDIAKGMSYLHSSKTEVHGRLKSTNCVVDSRMVVKI TDFGCNSILPPKKDLWTAPEHLRQANISQKGDVYSYGIIAQEIILRKETFYTLSCRDRNEKIFRVENSNG MKPFRPDLFLETAEEKELEVYLLVKNCWEEDPEKRPDFKKIETTLAKIFGLFHDQKNESYMDTLIRRLQL YSRNLEHLVEERTQLYKAERDRADRLNFMLLPRLVVKSLKEKGFVEPELYEEVTIYFSDIVGFTTICKYS TPMEVVDMLNDIYKSFDHIVDHHDVYKVETIGDAYMVASGLPKRNGNRHAIDIAKMALEILSFMGTFELE HLPGLPIWIRIGVHSGPCAAGVVGIKMPRYCLFGDTVNTASRMESTGLPLRIHVSGSTIAILKRTECQFL YEVRGETYLKGRGNETTYWLTGMKDQKFNLPTPPTVENQQRLQAEFSDMIANSLQKRQAAGIRSQKPRRV ASYKKGTLEYLQLNTTDKESTYF*
#12	MKTLLLDLALWSLLFQPGWLSFSSQVSQNCHNGSYEISVLMMGNSAFAEPLKNLEDAVNEGLEIVRGRLQ NAGLNVTVNATFMYSDGLIHNSGDCRSSTCEGLDLLRKISP*
#13	MKTLLLDLALWSLLFQPGWLSFSSQVSQNCHNGSYEISVLMMGNSAFAEPLKNLEDAVNEGLEIVRGRLQ NAGLNVTVNATFMYSDGLIHNSGDCRSSTCEGLDLLRKISNAQRMGCVLIGPSCTYSTFQMYLDTELSYP MISAGSFGLSCDYKETLTRLMSPARKLMYFLVNFWKTNDLPFKTYSWSTSYVYKNGTETEDCFWYLNALE ASVSYFSHELGFKVVLRQDKEFQDILMDHNRKSNVTSTWRTMSQPLTI*
#14	MKTLLLDLALWSLLFQPGWLSFSSQVSQNCHNGSYEISVLMMGNSAFAEPLKNLEDAVNEGLEIVRGRLQ NAGLNVTVNATFMYSDGLIHNSGDCRSSTCEGLDLLRKISNAQRMGCVLIGPSCTYSTFQMYLDTELSYP MISAGSFGLSCDYKETLTRLMSPARKLMYFLVNFWKTNDLPFKTYSWSTSYVYKNGTETEDCFWYLNALE ASVSYFSHELGFKVVLRQDKEFQDILMDHNRKSNVIIMCGGPEFLYKLKGDRAVAEDIVIILVDLFNDQY LEDNVTAPDYMKNVLVLTLSPGNSLLNSSFSRNLSPTKRDFALAYLNGILLFGHMLKIFLENGENITTPK FAHAFRNLTFEGYDGPVTLDDWGDVDSTMVLLYTSVDTKKYKVLLTYDTHVNKTYPVDMSPTFTWKNSKL PNDITGRGPQILMIAVFTLTGAVVLLLLVALLMLRKYRKDYELRQKKWSHIPPENIFPLETNETNHVSLK IDDDKRRDTIQRLRQCKYDKKRVILKDLKHNDGNFTEKQKIELNKIDYYNLTKFYGTVKLDTMIFGVIEY CERGSLREVLNDTISYPDGTFMDWEFKISVLYDIAKGMSYLHSSKTEVHGRLKSTNCVVDSRMVVKITDF GCNSILPPKKDLWTAPEHLRQANISQKGDVYSYGIIAQEIILRKETFYTLSCRDRNEKIFRVENSNGMKP FRPDLFLETAEEKELEVYLLVKNCWEEDPEKRPDFKKIETTLAKIFGLFHDQKNESYMDTLIRRLQLYSR NLEHLVEERTQLYKAERDRADRLNFMLLPRLVVKSLKEKGFVEPELYEEVTIYFSDIVGFTTICKYSTPM EVVDMLNDIYKSFDHIVDHHDVYKVETIGDAYMVASGLPKRNGNRHAIDIAKMALEILSFMGTFELEHLP GLPIWIRIGVHSGPCAAGVVGIKMPRYCLFGDTVNTASRMESTGLPLRIHVSGSTIAILKRTECQFLYEV RGETYLKGRGNETTYWLTGMKDQKFNLPTPPTVENQQRLQAEFSDMIANSLQKRQAAGIRSQKPRRVASY KKGTLEYLQLNTTDKESTYF*
#15	MKLVTIFLLVTISLCSYSATAKLINKCPLPVDKLAPLPLDNILPFMDPLK LLLKTLGISVEHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
#16	MAVTACQGLGFVVSLIGIAGIIAATCMDQWSTQDLYNNPVTAVFNYQGLWRSCVRESSGFTECRGYFTLL

Fig. 41 (continued)

	GLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGLCAIAGVSVFA NMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIACRGLAPEETNYKAVS YHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDYV*
#17	DQWSTQDLYN
#18	NNPVTAVFNYQ
#19	MAVTACQGLGFVVSLIGIAGIIAATCMDQWSTQDLYNNPVTAVFNYQ
#20	AGGTACATGAGCATCAGCCTG
#21	GCAGCAGTTGGCATCTGAGAG
#22	GCAATAGACATTGCCAAGATG
#23	AACGCTGTTGATTCTCCACAG
#24	GGATCCTCCTTTAGTTCCCAGGTGAGTCAGAAC
#25	TGCTCTGGAGGCTAGCGTTTC
#26	ACCAATCATGTTAGCCTCAAG
#27	AGCTATGGGATCATCGCACAG
#28	CCTTTGAGCTGGAGCATCTTC
#29	CTTTCTAGCTGGAGACATCAG
#30	CACCATGGTACTGTCAACATC
#31	ATGTCATACAAGACAGAGATC
#32	TCTGCCTTGTACAGCTGTGTC
#33	TCTGTGGTATTCAGCTGCAAG
#34	TACTCAGGAAAATTTCACCTTG
#35	GACCACAACAGGAAAAGCAATGTGACC

Fig. 41 (continued)

#36	GATAGAATTGAACAAGATTGAC
#37	CAGCCTTTGTAGTTACTCTGC
#38	TGTCACACCAAGTGTGATAGC
#39	GGTTCGTGGTTTCACTGATTGGGATTGC
#40	CGGCTTTGTAGTTGGTTTCTTCTGGTG
#41	ctattgaagccacctgctcaggacaatgaaattcttcagttacattctggtttatcgccg atttctcttcgtggttttcactgtgttggttttactacctctgcccatcgtcctccacac caaggaagcagaatgtgcctacacactctttgtggtcgccacattttggctcacagaagc attgcctctgtcggtaacagctttgctacctagtttaatgttacccatgtttgggatcat gccttctaagaaggtggcatctgcttatttcaaggattttcacttactgctaattggagt tatctgtttagcaacatccatagaaaaatggaatttgcacaagagaattgctctgaaaat ggtgatgatggttggtgtaaatcctgcatggctgacgctggggttcatgagcagcactgc ctttttgtctatgtggctcagcaacacctcgacggctgccatggtgatgcccattgcgga ggctgtagtgcagcagatcatcaatgcagaagcagaggtcgaggccactcagatgactta cttcaacggatcaaccaaccacggactagaaattgatgaaagtgttaatggacatgaaat aaatgagaggaaagagaaaacaaaaccagttccaggatacaataatgatacagggaaaat ttcaagcaaggtggagttggaaaagaactcaggcatgagaaccaaatatcgaacaaagaa gggccacgtgacacgtaaacttacgtgtttgtgcattgcctactcttctaccattggtgg actgacaacaatcactggtacctccaccaacttgatctttgcagagtatttcaatacacg ctatcctgactgtcgttgcctcaactttggatcatggtttacgttttccttcccagctgc ccttatcattctactcttatcctggatctggcttcagtggctttttcctaggattcaattt taaggagatgttcaaatgtggcaaaaccaaaacagtccaacaaaaagcttgtgctgaggt gattaagcaagaataccaaaagcttgggccaataaggtatcaagaaattgtgaccttggt cctcttcattataatggctctgctatggtttagtcgagaccccggatttgttcctggttg gtctgcactttttttcagagtaccctggttttgctacagattcaactgttgctttacttat agggctgctattctttcttatcccagctaagacactgactaaaactacacctacaggaga aattgttgcttttgattactctccactgattacttggaaagaattccagtcattcatgcc ctgggatatagccattcttgttggtggagggtttgccctggcagatggttgtgaggagtc tggattatctaagtggataggaaataaattatctcctctgggttcattaccagcatggct aataattctgatatcttctttgatggtgacatctttaactgaggtagccagcaatccagc taccattacactctttctcccaatattatctccattggccgaagccattcatgtgaaccc tctttatattctgataccttctactctgtgtacttcatttgcattcctcctaccagtagc aaatccacccaatgctattgtcttttcatatggtcatctgaaagtcattgacatggttaa agctggacttggtgtcaacattgttggtgttgctgtggttatgcttggcatatgtacttg gattgtacccatgtttgacctctacacttacccttcgtgggctcctgctatgagtaatga gaccatgccataataagcacaaaatttctgactatcttgcggtaatttctggaagacatt aatgattgactgtaaaatgtggctctaaataactaatgacacacatttaaatcagttatg gtgtagctgctgcaattcccgtgaatacccgaaacctgctggtataactcagagtccata tttgttattgcagtgcaactaaagagcatctatgtgccttcatcaagaagcccatgtttt gagattttgctcatgaaccatctgcaacttgcttcatcataagaataatttataacttga ccttcaaagagattagagcatttgtttcatcttacagttggagttcaatgtaacatttta aatgcaatttattatttcagaaatttcccatgaaactaaaaatagaaaataagatataca agttaattcggtacttggataaatcatttctgcattgttgttccagagaatttgctgaga aatcaaagccatggtcatctggtgatgaagagaaaaggttaatctaaatgatatgtgcat ttcctcatttaaaaaatccaattggattattcttaatatatacatgtaatatgaaaattg agattgaagcactaattccaaaattatggctgaatatactaaataacagaaaagttacag ataagaatttatttctactgaactctatagttagtgtaatataattcatatttttatgat attggcacactgagaaattcattttgtagagctatggataaggcttgctatgatttgcac tattagtacagtatagttagaaaggaaagctgaacactataaaactattaacatattttc gtatatgagtaacaactttgcttaagtgtttatcttagttcagaaatacataatgtcata tgttaaaaataaagagatgtagaaatctaaatgaattatcactgtgtatacagacagaaa aatcacataactctggtgtgttaacattgcaatgaaaaaatgaaaaaaagaaggaaaaaa gaataagaatgaaaactgctgacgtattacaaaacagaaaaataaatgatttaaaatcaa

Fig. 41 (continued)

	atcaaaaagaaaaaaactaaacatttaaacaaaaatgggataagaatagtcttctagaag tgaggatgcgtaaaagaatgagtttccaattaccctgatgtgacaattacacattgtaga caggtagcaaaatatcacatacacccccaaaatatgtacaaatattatatatcaataaat aaatttttaaagagtaagtgctattggcattccaaaattcagctaaaggaaaaatgatca aaaacaaagtaaggtgcacagttagcaaaagatgcagatgttatatcacagcaattctca tgctaaaaatacaacaaaagacaaagcaaaaaataaacctttgcttttttttttttttt tttttttttgagacggagtctcgctctgtcgcccaggctggagtgcagtggcgggatct cggctcactgcaagctccgcctcccaggttcacgccattctcctgcctcagccaaacctt tgctatttttaatcttcgttggcactttccagctgttactgaccttgtcatttttgttc aaataagattatttacaaacttattcttgaaactaaatatagtaaagagggtttttaaaa taatatttaacatacgaattattaattggccatgttcattatttatctatgtttattaat gggccaatgcaaaaaatcatttttttcaaagaaaaatttgtccatgtaaagcttaaattat aatattgctgctttgtataactcttctatgtttattctattcatttgttcctttccctac catattttacacatgtatttataatctgtagtatttattacatttctgcttttttctagt cattcaatttatcactgctgaattgcatcagatcatggatgcatttttattatgaaaaaa taaaatgacttttcaaattaaaaaaaaaaaaaaa
#42	caggacaatgaaattcttcagttacattctggtttatcgccgatttctcttcgtggttttcactgtgttggtt ttactacctctgcccatcgtcctccacaccaaggaagcagaatgtgcctacacactctttgtggtcgccacat tttggctcacagaagcattgcctctgtcggtaacagctttgctacctagtttaatgttacccatgtttgggat catgccttctaagaaggtggcatctgcttatttcaaggattttcacttactgctaattggagttatctgttta gcaacatccatagaaaaatggaatttgcacaagagaattgctctgaaaatggtgatgatggttggtgtaaatc ctgcatggctgacgctggggttcatgagcagcactgccttttgtctatgtggctcagcaacacctcgacggc tgccatggtgatgcccattgcggaggctgtagtgcagcagatcatcaatgcagaagcagaggtcgaggccact cagatgacttacttcaacggatcaaccaaccacggactagaaattgatgaaagtgttaatggacatgaaataa atgagaggaaagagaaaacaaaaccagttccaggatacaataatgatacagggaaaatttcaagcaaggtgga gttggaaaagactgtttaactactgaaatgaagctattctcctgactaaacataactgaaaaaccattcatta aatg
#43	gccactcagatgacttacttcaacggatcaaccaaccacggactagaaattgatgaaagtgttaatggacatg aaataaatgagaggaaagagaaaacaaaaccagttccaggatacaataatgatacagggaaaatttcaagcaa ggtggagttggaaaagcactggaaacttgcagttcaagatggctccccatctcctctgtccattctgtatcg cagctagctgctcaaggaaaggagaaagtggaaggcatatgtacttagaaattattctattactttcctggat ttaagagtattcagattttctatttcaacatcaaacaattgcatttttaaaaagaaatttatgtgttccatgt caaatttagtagtgtgtggttgtttataatatttttcttatatctacttaatttctatagtatttatagttata tgtctttatttctaacatttttcttgtgcttttaaagattatttaaagattatttttaaataatctttatttc atttaaataaaatattttatttaagtct
#44	cacggactagaaattgatgaaagtgttaatggacatgaaataaatgagaggaaagagaaaacaaaaccagttc caggatacaataatgatacagggaaaatttcaagcaaggtggagttggaaaagaactcaggcatgagaaccaa atatcgaacaaagaagggccacgtgacacgtaaacttacgtgtttgtgcattgcctactcttctaccattggt ggactgacaacaatcactggtacctccaccaacttgatctttgcagagtatttcaatacattccatccacaca gaagaggagatcgtacaaggcatgtacaccaggaggcagaaatttgaggcatatcttggaactctgtctacca catcctgaacatcacacagtttccactcttgttgccttcaatcctgagaatgcatccaggagccattctgttt tatgtcaattactaattagatcatgtcacgttactaacttactacgttccaattagtccttattgcatttgta ataaaatccgcatactttcggactggctacaaggttatacatgat
#45	MKFFSYILVYRRFLFVVFTVLVLLPLPIVLHTKEAECAYTLFVV ATFWLTEALPLSVTALLPSLMLPMFGIMPSKKVASAYFKDFHLLLIGVICLATSIEKW NLHKRIALKMVMMVGVNPAWLTLGFMSSTAFLSMWLSNTSTAAMVMPIAEAVVQQIIN AEAEVEATQMTYFNGSTNHGLEIDESVNGHEINERKEKTKPVPGYNNDTGKISSKVEL EKNSGMRTKYRTKKGHVTRKLTCLCIAYSSTIGGLTTITGTSTNLIFAEYFNTRYPDC RCLNFGSWFTFSFPAALIILLLSWIWLQWLFLGFNFKEMFKCGKTKTVQQKACAEVIK QEYQKLGPIRYQEIVTLVLFIIMALLWFSRDPGFVPGWSALFSEYPGFATDSTVALLI GLLFFLIPAKTLTKTTPTGEIVAFDYSPLITWKEFQSFMPWDIAILVGGGFALADGCE ESGLSKWIGNKLSPLGSLPAWLIILISSLMVTSLTEVASNPATITLFLPILSPLAEAI HVNPLYILIPSTLCTSFAFLLPVANPPNAIVFSYGHLKVIDMVKAGLGVNIVGVAVVM LGICTWIVPMFDLYTYPSWAPAMSNETMP"

Fig. 41 (continued)

#46	RTMKFFSYILVYRRFLFVVFTVLVLLPLPIVLHTKEAECAYTLFVVATFWLTEALPLSVTALLPSLMLPMFGI MPSKKVASAYFKDFHLLLIGVICLATSIEKWNLHKRIALKMVMMVGVNPAWLTLGFMSSTAFLSMWLSNTSTA AMVMPIAEAVVQQIINAEAEVEATQMTYFNGSTNHGLEIDESVNGHEINERKEKTKPVPGYNNDTGKISSKVE LEKTV*
#47	ATQMTYFNGSTNHGLEIDESVNGHEINERKEKTKPVPGYNNDTGKISSKVELEKHWKLAVQDGSPSPSVHSVS QLAAQGKEKVEGICT*
#48	HGLEIDESVNGHEINERKEKTKPVPGYNNDTGKISSKVELEKNSGMRTKYRTKKGHVTRKLTCLCIAYSSTIG GLTTITGTSTNLIFAEYFNTFHPHRRGDRTRHVHQEAEI*
#49	CCAGCTTTAACCATGTCAATG
#50	CAGATGGTTGTGAGGAGTCTG
#51	TGCTAATGCTTTTGGTACAAATGGATGTGGAATATAATTGAATATTTTCTTGTTTAAGGGGAGCATGAAGAGG TGTTGAGGTTATGTCAAGCATCTGGCACAGCTGAAGGCAGATGGAAATATTTACAAGTACGCAATTTGAGACT AAGATATTGTTATCATTCTCCTATTGAAGACAAGAGCAATAGTAAAACACATCAGGTCAGGGGGTTAAAGACC TGTGATAAACCACTTCCGATAAGTTGGAAACGTGTGTCTATATTTTCATATCTGTATATATATAATGGTAAAG AAAGACACCTTCGTAACCCGCATTTTCCAAAGAGAGGAATCACAGGGAGATGTACAGCAATGGGGCCATTTAA GAGTTCTGTGTTCATCTTGATTCTTCACCTTCTAGAAGGGGCCCTGAGTAATTCACTCATTCAGCTGAACAAC AATGGCTATGAAGGCATTGTCGTTGCAATCGACCCCAATGTGCCAGAAGATGAAACACTCATTCAACAAATAA AGGACATGGTGACCCAGGCATCTCTGTATCTGTTTGAAGCTACAGGAAAGCGATTTTATTTCAAAAATGTTGC CATTTTGATTCCTGAAACATGGAAGACAAAGGCTGACTATGTGAGACCAAAACTTGAGACCTACAAAAATGCT GATGTTCTGGTTGCTGAGTCTACTCCTCCAGGTAATGATGAACCCTACACTGAGCAGATGGGCAACTGTGGAG AGAAGGGTGAAAGGATCCACCTCACTCCTGATTTCATTGCAGGAAAAAAGTTAGCTGAATATGGACCACAAGG TAAGGCATTTGTCCATGAGTGGGCTCATCTACGATGGGGAGTATTTGACGAGTACAATAATGATGAGAAATTC TACTTATCCAATGGAAGAATACAAGCAGTAAGATGTTCAGCAGGTATTACTGGTACAAATGTAGTAAAGAAGT GTCAGGGAGGCAGCTGTTACACCAAAAGATGCACATTCAATAAAGTTACAGGACTCTATGAAAAAGGATGTGA GTTTGTTCTCCAATCCCGCCAGACGGAGAAGGCTTCTATAATGTTTGCACAACATGTTGATTCTATAGTTGAA TTCTGTACAGAACAAAACCACAACAAAGAAGCTCCAAACAAGCAAAATCAAAAATGCAATCTCCGAAGCACAT GGGAAGTGATCCGTGATTCTGAGGACTTTAAGAAAACCACTCCTATGACAACACAGCCACCAAATCCCACCTT CTCATTGCTGCAGATTGGACAAAGAATTGTGTGTTTAGTCCTTGACAAATCTGGAAGCATGGCGACTGGTAAC CGCCTCAATCGACTGAATCAAGCAGGCCAGCTTTTCCTGCTGCAGACAGTTGAGCTGGGGTCCTGGGTTGGGA TGGTGACATTTGACAGTGCTGCCCATGTACAAAGTGAACTCATACAGATAAACAGTGGCAGTGACAGGGACAC ACTCGCCAAAAGATTACCTGCAGCAGCTTCAGGAGGGACGTCCATCTGCAGCGGGCTTCGATCGGCATTTACT GTGATTAGGAAGAAATATCCAACTGATGGATCTGAAATTGTGCTGCTGACGGATGGGGAAGACAACACTATAA GTGGGTGCTTTAACGAGGTCAAACAAAGTGGTGCCATCATCCACACAGTCGCTTTGGGGCCCTCTGCAGCTCA AGAACTAGAGGAGCTGTCCAAAATGACAGGAGGTTTACAGACATATGCTTCAGATCAAGTTCAGAACAATGGC CTCATTGATGCTTTTGGGGCCCTTTCATCAGGAAATGGAGCTGTCTCTCAGCGCTCCATCCAGCTTGAGAGTA AGGGATTAACCCTCCAGAACAGCCAGTGGATGAATGGCACAGTGATCGTGGACAGCACCGTGGGAAAGGACAC TTTGTTTCTTATCACCTGGACAACGCAGCCTCCCCAAATCCTTCTCTGGGATCCCAGTGGACAGAAGCAAGGT GGCTTTGTAGTGGACAAAAACACCAAAATGGCCTACCTCCAAATCCCAGGCATTGCTAAGGTTGGCACTTGGA AATACAGTCTGCAAGCAAGCTCACAAACCTTGACCCTGACTGTCACGTCCCGTGCGTCCAATGCTACCCTGCC TCCAATTACAGTGACTTCCAAAACGAACAAGGACACCAGCAAATTCCCCAGCCCTCTGGTAGTTTATGCAAAT ATTCGCCAAGGAGCCTCCCCAATTCTCAGGGCCAGTGTCACAGCCCTGATTGAATCAGTGAATGGAAAAACAG TTACCTTGGAACTACTGGATAATGGAGCAGGTGCTGATGCTACTAAGGATGACGGTGTCTACTCAAGGTATTT CACAACTTATGACACGAATGGTAGATACAGTGTAAAAGTGCGGGCTCTGGGAGGAGTTAACGCAGCCAGACGG AGAGTGATACCCCAGCAGAGTGGAGCACTGTACATACCTGGCTGGATTGAGAATGATGAAATACAATGGAATC CACCAAGACCTGAAATTAATAAGGATGATGTTCAACACAAGCAAGTGTGTTTCAGCAGAACATCCTCGGGAGG CTCATTTGTGGCTTCTGATGTCCCAAATGCTCCCATACCTGATCTCTTCCCACCTGGCCAAATCACCGACCTG AAGGCGGAAATTCACGGGGGCAGTCTCATTAATCTGACTTGGACAGCTCCTGGGGATGATTATGACCATGGAA CAGCTCACAAGTATATCATTCGAATAAGTACAAGTATTCTTGATCTCAGAGACAAGTTCAATGAATCTCTTCA AGTGAATACTACTGCTCTCATCCCAAAGGAAGCCAACTCTGAGGAAGTCTTTTTGTTTAAACCAGAAAACATT ACTTTTGAAAATGGCACAGATCTTTTCATTGCTATTCAGGCTGTTGATAAGGTCGATCTGAAATCAGAAATAT CCAACATTGCACGAGTATCTTTGTTTATTCCTCCACAGACTCCGCCAGAGACACCTAGTCCTGATGAAACGTC TGCTCCTTGTCCTAATATTCATATCAACAGCACCATTCCTGGCATTCACATTTTAAAAATTATGTGGAAGTGG ATAGGAGAACTGCAGCTGTCAATAGCCTAGGGCTGAATTTTTGTCAGATAAATAAAATAAATCATTCATCCTT TTTTTGATTATAAAATTTTCTAAAATGTATTTTAGACTTCCTGTAGGGGGCGATATACTAAATGTATATAGTA

Fig. 41 (continued)

	CATTTATACTAAATGTATTCCTGTAGGGGGCGATATACTAAATGTATTTTAGACTTCCTGTAGGGGGCGATAA AATAAAATGCTAAACAACTGGGTAAA
#52	AATTAAATTATGAGAATTAAAAAGACAACATTGAGCAGAGATGAAAAAGGAAGGGAGGAAAAGGTGGAAAAGA AAAGAAGACAAGAAGCGAGTAGTGGTCTCTAACTTGCTCTTTGAAGGATGGTCTCACAAAGAGAACCCCAACA GACATCATCGTGGGAATCAAATCAAGACCAGCAAGTACACCGTGTTGTCCTTCGTCCCCAAAAACATTTTTGA GCAGCTACACCGGTTTGCCAATCTCTATTTTGTGGGCATTGCGGTTCTGAATTTTATCCCTGTGGTCAATGCT TTCCAGCCTGAGGTGAGCATGATACCAATCTGTGTTATCCTGGCAGTCACTGCCATCAAGGACGCTTGGGAAG ACCTCCGGAGGTACAAATCGGATAAAGTCATCAATAACCGAGAGTGCCTCATCTACAGCAGAAAAGAGCAGAC CTATGTGCAGAAGTGCTGGAAGGATGTGCGTGTGGGAGACTTCATCCAAATGAAATGCAATGAGATTGTCCCA GCAGACATACTCCTCCTTTTTTCCTCTGACCCCAATGGGATATGCCATCTGGAAACTGCCAGCTTGGATGGAG AGACAAACCTCAAGCAAAGACGTGTCGTGAAGGGCTTCTCACAGCAGGAGGTACAGTTCGAACCAGAGCTTTT CCACAATACCATCGTGTGTGAGAAACCCAACAACCACCTCAACAAATTTAAGGGTTATATGGAGCATCCTGAC CAGACCAGGACTGGCTTTGGCTGTGAGAGTCTTCTGCTTCGAGGCTGCACCATCAGAAACACCGAGATGGCTG TTGGCATTGTCATCTATGCAGGCCATGAGACGAAAGCCATGCTGAACAACAGTGGCCCCCGGTACAAACGCAG CAAGATTGAGCGGCGCATGAATATAGACATCTTCTTCTGCATTGGGATCCTCATCCTCATGTGCCTTATTGGA GCTGTAGGTCACAGCATCTGGAATGGGACCTTTGAAGAACACCCTCCCTTCGATGTGCCAGATGCCAATGGCA GCTTCCTTCCCAGTGCCCTTGGGGGCTTCTACATGTTCCTCACAATGATCATCCTGCTCCAGGTGCTGATCCC CATCTCTTTGTATGTCTCCATTGAGCTGGTGAAGCTCGGGCAAGTGTTCTTCTTGAGCAATGACCTTGACCTG TATGATGAAGAGACCGATTTATCCATTCAATGTCGAGCCCTCAACATCGCAGAGGACTTGGGCCAGATCCAGT ACATCTTCTCCGATAAGACGGGGACCCTGACAGAGAACAAGATGGTGTTCCGACGTTGCACCATCATGGGCAG CGAGTATTCTCACCAAGAAAATGGTATAGAAGCTCCCAAGGGCTCCATCCCTCTTTCTAAAAGGAAATACCCT GCTCTCCTAAGAAACGAGGAGATAAAAGACATTCTCCTGGCTCTCTTAGAGGCTGTGTGGCATTTCCACAAGT TGCTTCCTGTATCCCTGTGGTCTTCCTTGTCACAGATCAGGGCTGTTCCAATTACTTGTAAACTTTCATTTGT TTACAAAGGTTAGAAGTTATCCCATATGTGGTTCCCCTTCAGCTGATCTTTGTCTGGTGCCAGACAAAGCACT TTATGAGACGAGTTTTTTATCTGTCAGCAATGGATTGGAGACATTTCCCAATTGTGTGCCAGTCACACAACCA AGGCTTAGGAATTTCTCAGGCCACCTTACCTGACATGTCAGGGCAGGTCTGTGTCTAGGTGCATGGTCAGATT TAATACATCCAGAAGATGTCTTCTATTCTAACAGATCTCTTAGCTTGTCACTGAGGCAAAGTTTTGATTTAGG AGATAGGGCTATAAAATGCCTGGACTGTTACCTTGCATGGACTGAATATGACTCATAAAACTGATCTGATTCC TTCAGCCATCATCTGCCCAACTTGGTTCCCCTCCCCACCCCCCCACAACACACACACACACTTTCTAAGAAAA GAAAAGAAATTCTTTTTTTTCAATACTTTAAGTTCTGGGATACATGTGCAGAATGTGCAGGTTTGTTACATAG GTATACATGTGTCATGGTGGTTTGCAGCACCCACCAACCCATCATCTACCTTAGGTATTTCTCCTAATGCTAT CCCTCCCCTAGCCCCCAACCCCCCGATGGGCTCCAGTGTGTGATGTTCCCCTCCATGTCCATGTGTTCTCATT GTTCAATTCCCACTTATGAGTGAGAACATGCAGTATTTGGTTTTCTGTTCTTGTGTTAGTTTGCTGATGGTTT CCTGTTCATCCGTGTCCCTGCAAAGGACATGAACTCATCCTTTTTTATGGCTGCATAATATTCCATGGTGTAT ATGTGCCACATTTTCTTTATCCAGTCTATCGCTGATGGGCACTGGGGTTGGTTCCAAGTCTTTGCTATTGTGA ACAGTGCTGCAATAAACTTACATGTGCATGTGTCTTTAGTAGAATGATTTATAATCCTTTGGGTATATACCCA GTAATGGGATTGCTGGTCAAATGGTATTTCTGGTTCTAGATCCTTGAGGAATCTTTGTCTTCCACAATGGTTG AACTAATTTGTACTCCCACCAACAGTGTAAAAGTATTCCTGTTTCTCTACATCCTCTTCAGCATCTGTTGTGT CCTGACATTTTAATGATCACTATTCTCACTGGCGTGAGATGTTATCTCATTGTGGTTTTGATTTGCATTTCTC TAATGACCAGTAATGATGAGCTTTTTTTCATATGTTTGTTGGCTGCATAAATGTCTTCTTTTGAGAAGTGTCT GTTCATATCCTTCACCCATTTTTTGAAGAAAACAAACTCTTAAGAGAGCAGTATTCATTCTTTTGAGTGTGAG GGATGGAGAAAGAGAAAGATGGAGAGAGTATTATAAGCAGCTGTATCCCCTTTGCCATGGTGATAGCAGACCA TTCACATGGGAGCTTCTGGTCTCTTTGTAATAATAATAAGAGCCACATTACCAGTACTTAGAGTATGCTAGTT ATTTTAACACATTGTATCATTAAATCTTCAAAACATCCCTATGAGTTAGAAACCTAAAAAAAAAAAAAAAAAA A
#53	CTCATTTTGATGTCTAGAATCAGGGGATCCAGGATCATCACCAAGGTCATTTTCCCAGGTATGGAGGGGTCTT TCTGCTTCTTTCTTGTCATGCACAGCTGCTGAGGAAGGGGCTGGGAGTAAAGACAGTGAAATGGGGAGGAGGA GTCCATTCAAACCGAGAAACAAAGTGTTTGGTTTTTCTTACCCCTGGTGTAGAAGCTACCAACCTTTTCCAAG AAAGAGGGCCTGGCCCCCTTCTCGGGTCTGGCTGGGTGCCTGCTGTGCCTCTCTGGCCTCCCCTCCGAAGGGC ACCATTCCCTCGGGTGAGTACTACCGGCCTGCACCGTCTTCCAGTGGGGACAGCCTGAGAAGAGAGTCTGGGG CCTTACTTCAGTACCTTCCTTCACTGGCCTCACCCTGTGCAAATCATGCCACACGCTGCAGCCTCCTTTTCCC TATCTATAAAATAAAAATGACCCTGCTCTATCTCACTGGGCTGGCAAGAACACACTGTTGTTGCCTTGCAGAC AGATGTGCTGAGGCTGTAGAAAGTGCTTTTTATTTGGTTGGGAGCTTGTGCATAAATGCGAGAGGGGCTGCAC ATCTGACGGACTAGAGGTGACTCATGGCTGAACCGGAACAGGACATCGGGGAGAAGCCAGCAGCCATGCTGAA CTCTCCACAGGGCCCTGTGAAAAGCTCTTCACCTCCTCTGCCCTCTGGATCTAGTGAAGCCTATTCATCCTTC AGATGTCAGCTCAAATAATCAACCTTCATGGAGGCCTCCCTTGACCCCTAACATGCTTTCAAAGTACTGTGTA TTTCACATTCATCATGCCCCGACAACTGTGATTTCCCATTTATTAATATCTGTCTCTTCTGCTGGCCTGCAAA CTCCAGGAGCACAGAGACATCTTTGGGATTTTTGAACATGATTTCCCCAGGGCTTAGCCCAGTGCCTGGTGCA AAGCAGGCTTTCAACATGTTCAGTGGATATTGTAAGAAAGAAAGAAATACACAAAAGGCCTGGCATATGCAAA GCACTCTAAATATTCACTCCTTTCCCTTCCCTCTGGGTGAGAAAATTTCTCCTTATAAAGACACCCTCCTAAC TGTATCTCTGCTAGAGAACTGAAGACATAAAGCACTCTGTGCCAAAAATATTTAAGTAAAAACTTGAGCTAAG CACAGAGATTATAAATATTTCTTCCCCAGATTACGCACCATTTAAAAATACTGTCTCAGCTCCTTTTCATGAT

Fig. 41 (continued)

	TTGGGTGGTGATTAAAGAAAATTACTCTTCAAGACTGAAAGTCATTACTGCCCTTTTCCTGACTTGCCTTTTC CCTTGAGAAGGGGAGGATAAGCTGCAGGGCAGGAAGTGGAAGTGGGGCATCCTTGTCCTTTGTCTGGCAGACA GCCAACTGGTCAGGTACTGCTCCTTCTCAACTCTTTCCTGATTCCCAGGTGAATATAAACAAGAAGGCACAAA TCCACACTTGCCAACAACGGACCCAAGTGATAACAAGAAACCCAGTGACACCTGTCTAGGTGAAGACTCAGCC CCTATGTGACCAGGTTGCAAAGCCAAACTGACCATCTGCTTTCCATTTGGACTTTTAGTTCATACTGTATCTT CTCAGGACAGTTAAGTTGGAATACAATGCCACTGTCCTGAAAGATGGTAGAATTATCCTATTTCTGGAGGAGT GGGGGTGGTGGGTAGGAATCTCAAGAGCGATTTGCTCCTCTGCACAATAGCTTCTTTAAGGACACCAGGGCCC CCAGGGCTATACATTTCCCTGAAGCTTTCCAGATAAGCAACAAGGTATGAGCACCTGCTATGTATTGCCCAAG GGTGATGTGTTTAAATATCCATTGCATATTTTAAATCCTTGGCTGGCTTAAAGCTGCAAGCTTTCTGTCTTCA GTGGATATAATGGGGGCATACATCCCAGAGCTTGCCCAACACTCCAAGAAAAGAACCCTCAGCTAATGCAAAG TGTGTATGTGCCCATGAAAGCTCCATGTCTACTTAACATTCAGTTTTTAGGATTATTTATGCTGTAATAATAG ATATGAAAATCTCTGACAGGTATTTTGTTTCCTTTACAAACTGTATTTGAATTTATGGGTGATTTAGAGCTTG TGTTTAAAGTCAGAATTCAGAACCCCAAAGAAAATGACTTCATTGAAATTGAACTGAAGAGACAAGAACTGAG TTACCAAAACCTACTAAACGTGAGTTGCTGTGAACTGGGGATTAAACCAGAACGAGTGGAGAAGATCAGAAAG CTACCAAACACACTGCTCAGAAAGGACAAAGACATTCGAAGACTGCGGGACTTTCAGGAAGTGGAACTCATTT TAATGAAAAATGGAAGCTCCAGATTGACAGAATATGTGCCATCTCTGACAGAAAGGCCCTGCTATGATAGCAA AGCTGCAAAAATGACTTATTAAATACTCCCAGGAATGGCCGCGCATGGTGGCTCACCCCCTGTAATCCCAGCA CTTTGGGAAGCCAAGGTGGGCGGATCACCTGAGGTCAGGAGTTCTAGACCAGCCTGGCCAACATATAGTGAAA CCCAGTCTCTACTAAAAAAAATACAAAAATTAGCTAGGTGTGGTGGCGCACACCTGTAGTAGTCCCAGCTACA TGGGAAGCTGAGGCAGGAGAATCACCTGAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATTGCGCCACTGC ACTCCAGCCTGGCGACAGAGCAAGACTCTGTCTCTCAAAATAAATAAATAAATAAATAAATAAATAAATAAAT AATC
#54	GCCCGGGAGAGGAGAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCT GACACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAA GCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGA AGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGG CATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAAC ATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGG CTGGATTCAACACGCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCG CATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGC ATCCAACTGCTGCATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCAT CCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCT CCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATC AAGGGTGACACCATTCAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCA ATAACTCTGCAGCTTCCCTGACAATGCCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCAGGACGT GGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAG AGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGA TCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGAT CGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAA GCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGA TGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCACTCCATCCT GCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGGCCTTGGGATTCGAGGCA GCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTGGAAACCCAGCTCTCCTGTCT CCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATA GACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAT
#55	GGAGTGGGGGAGAGAGAGGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAAGAGCAAAGAT GTTTCAAACTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGGCCCAGTTTGGAGGCCTGCCC GTGCCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTGCCCTTGAGTCCCACAGGTCTTGCAGGAA GCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCTGGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCT GGACATCCTGAAGCCTGGAGGAGGTACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTCAGTG ATTCCTGGCCTGAACAACATCATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACTTGGCCTTGTGCAGA GCCCTGATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTGGTCGG TGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTGAGAGATAAGCAGGAG AGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTGCAAATTTCTCTGCTTGATGGACTTG GCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACAGGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCA GGGCAACGTGTGCCCTCTGGTCAATGAGGTTCTCAGAGGCTTGGACATCACCCTGGTGCATGACATTGTTAAC ATGCTGATCCACGGACTACAGTTTGTCATCAAGGTCTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTG CTTCCCAGTGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCTGC CCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCTCTTCTTCTGCAA AAAAAAAAAAAAAAAAAAAAAAAAAA

Fig. 41 (continued)

#56	GAGCAGAGCCCTTTCACACACCTCAGGAACACCTTTCGGCTGCCCGCTCCCCAGACACACCTGCAGCCCTGCC
	CAGCCGGCTTTGCTCACCCACTGCTTGTAAATGCCCCAGATATGAGCCAGCCCAGGCCCCGCTACGTGGTAGA
	CAGAGCCGCATACTCCCTTACCCTCTTCGACGATGAGTTTGAGAAGAAGGACCGGACATACCCAGTGGGAGAG
	AAACTTCGCAATGCCTTCAGATGTTCCTCAGCCAAGATCAAAGCTGTGGTGTTTGGGCTGCTGCCTGTGCTCT
	CCTGGCTCCCCAAGTACAAGATTAAAGACTACATCATTCCTGACCTGCTCGGTGGACTCAGCGGGGGATCCAT
	CCAGGTCCCACAAGGCATGGCATTTGCTCTGCTGGCCAACCTTCCTGCAGTCAATGGCCTCTACTCCTCCTTC
	TTCCCCCTCCTGACCTACTTCTTCCTGGGGGGTGTTCACCAGATGGTGCCAGGTACCTTTGCCGTTATCAGCA
	TCCTGGTGGGTAACATCTGTCTGCAGCTGGCCCCAGAGTCGAAATTCCAGGTCTTCAACAATGCCACCAATGA
	GAGCTATGTGGACACAGCAGCCATGGAGGCTGAGAGGCTGCACGTGTCAGCTACGCTAGCCTGCCTCACCGCC
	ATCATCCAGATGGGTCTGGGCTTCATGCAGTTTGGCTTTGTGGCCATCTACCTCTCCGAGTCCTTCATCCGGG
	GCTTCATGACGGCCGCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTACATCTTCGGACTGACCATCCCCTC
	CTACACAGGCCCAGGGTCCATCGTCTTTACCTTCATTGACATTTGCAAAAACCTCCCCCACACCAACATCGCC
	TCGCTCATCTTCGCTCTCATCAGCGGTGCCTTCCTGGTGCTGGTGAAGGAGCTCAATGCTCGCTACATGCACA
	AGATTCGCTTCCCCATCCCTACAGAGATGATTGTGGTGGTGGTGGCAACAGCTATCTCCGGGGGCTGTAAGAT
	GCCCAAAAAGTATCACATGCAGATCGTGGGAGAAATCCAACGCGGGTTCCCCACCCCGGTGTCGCCTGTGGTC
	TCACAGTGGAAGGACATGATAGGCACAGCCTTCTCCCTAGCCATCGTGAGCTACGTCATCAACCTGGCTATGG
	GCCGGACCCTGGCCAACAAGCACGGCTACGACGTGGATTCGAACCAGGAGATGATCGCTCTCGGCTGCAGCAA
	CTTCTTTGGCTCCTTCTTTAAAATTCATGTCATTTGCTGTGCGCTTTCTGTCACTCTGGCTGTGGATGGAGCT
	GGAGGAAAATCCCAGGTGGCCAGCCTGTGTGTGTCTCTGGTGGTGATGATCACCATGCTGGTCCTGGGGATCT
	ATCTGTATCCTCTCCCTAAGTCTGTGCTAGGAGCCCTGATCGCTGTCAATCTCAAGAACTCCCTCAAGCAACT
	CACCGACCCCTACTACCTGTGGAGGAAGAGCAAGCTGGACTGTTGCATCTGGGTAGTGAGCTTCCTCTCCTCC
	TTCTTCCTCAGCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTGGTCTTCCAGACTC
	AGTTTCGAAATGGCTATGCACTGGCCCAGGTCATGGACACTGACATTTATGTGAATCCCAAGACCTATAATAG
	GGCCCAGGATATCCAGGGGATTAAAATCATCACGTACTGCTCCCCTCTCTACTTTGCCAACTCAGAGATCTTC
	AGGCAAAAGGTCATCGCCAAGACAGGCATGGACCCCCAGAAAGTATTACTAGCCAAGCAAAAATACCTCAAGA
	AGCAGGAGAAGCGGAGAATGAGGCCCACACAACAGAGGAGGTCTCTATTCATGAAAACCAAGACTGTCTCCCT
	GCAGGAGCTGCAGCAGGACTTTGAGAATGCGCCCCCCACCGACCCCAACAACAACCAGACCCCGGCTAACGGC
	ACCAGCGTGTCCTATATCACCTTCAGCCCTGACAGCTCCTCACCTGCCCAGAGTGAGCCACCAGCCTCCGCTG
	AGGCCCCCGGCGAGCCCAGTGACATGCTGGCCAGCGTCCCACCCTTCGTCACCTTCCACACCCTCATCCTGGA
	CATGAGTGGAGTCAGCTTCGTGGACTTGATGGGCATCAAGGCCCTGGCCAAGCTGAGCTCCACCTATGGGAAG
	ATCGGCGTGAAGGTCTTCTTGGTGAACATCCATGCCCAGGTGTACAATGACATTAGCCATGGAGGCGTCTTTG
	AGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGTCCTCTTTGCCCAGGCAAATGC
	TAGAGACGTGACCCCAGGACACAACTTCCAAGGGGCTCCAGGGGATGCTGAGCTCTCCTTGTACGACTCAGAG
	GAGGACATTCGCAGCTACTGGGACTTAGAGCAGGAGATGTTCGGGAGCATGTTTCACGCAGAGACCCTGACCG
	CCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTGGCACTTGGGACTTCCATAAAGGATGAG
	CCTGGGGTCACAGGGGGTGTCGGGCGGAGGAAAGTGCATCCCCCAGAGCTTGGGTTCCTCTCTCCTCTCCCCC
	TCTCTCCTCCCTTCCTTCCCTCCCCGCATCTCCAGAGAGAGCCTCTCAGCAGCAGGGGGGTGCTACCCTTACG
	GGAGTGAGAGTCTGGTGAGCCCACTCTTCACCCGTCAGGCCCTGGCCGCAATGGACAAGCCTCCTGCTCACTC
	CACCCCACCCACATCTGCCCTGTCCTTGGCAGCTGAAGGACACCTTGACTTCCAGCTTTTACGAGTGAGCCAA
	AAACAGAAGGACAAGTACAACTGTGCTGGCCTGCTGTACAAGCTTCAAAAAGTGTCCCAGAGCCCGCACGGCT
	CGGTGTCAGATGGTGTCAGGCTGTCACGGACATAGGGATAAACTTGGTTAGGACTCTGGCTTGCCTTCCCCAG
	CTGCCTCAACTCTGTCTCTGGCAGCTCTGCACCCAGGGACCATGTGCTCTCCACACCCAGGAGTCTAGGCCTT
	GGTAACTATGCGCCCCCCCCTCCATCATCCCCAAGGCTGCCCAAACCACCACTGCTGTCAGCAAGCACATCAGA
	CTCTAGCCTGGACAGTGGCCAGGACCGTCGAGACCACCAGAGCTACCTCCCCGGGGACAGCCCACTAAGGTTC
	TGCCTCAGCCTCCTGAAACATCACTGCCCTCAGAGGCTGCTCCCTTCCCCTGGAGGCTGGCTAGAAACCCCAA
	AGAGGGGGATGGGTAGCTGGCAGAATCATCTGGCATCCTAGTAATAGATACCAGTTATTCTGCACAAAACTTT
	TGGGAATTCCTCTTTGCACCCAGAGACTCAGAGGGGAAGAGGGTGCTAGTACCAACACAGGGAAAACGGATGG
	GACCTGGGCCCAGACAGTCCCCCTTGACCCCAGGGCCCATCAGGGAAATGCCTCCCTTTGGTAAATCTGCCTT
	ATCCTTCTTTACCTGGCAAAGAGCCAATCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGAGACACAATGG
	GGTCCTTCTGTAGGCAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCCCTAACTGCATGCAGATGTGGAAA
	GGGGCTGATCCAGATTGGGTCTTCCTGCACAGGAAGACTCTTTAACACCCTTAGGACCTCAGGCCATCTTCTC
	CTATGAAGATGAAAATAGGGGTTAAGTTTTCCATATGTACAAGGAGGTATTGAGAGGAACCCTACTGTTGACT
	TGAAAATAAATAGGTTCCATGTGTAAGTGTTTTGTAAAATTTCAGTGGAAATGCACAGAAAATCTTCTGGCCT
	CTCATCACTGCTTTTCTCAAGCTTCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGCCCAGCCTAG
	GAAAACATCCCCATTTCTAACTTCAGCCAGACCTGCGTTGTGTGTCTGTGTGTTGAGTGAGCTGGTCAGCTAA
	CAAGTCTTCTTAGAGTTAAAGGAGGGGGTGCTGGCCAAGAGCCAACACATTCTTGGCCCAGGAGCATTGCTTT
	TCTGTGAATTCATTATGCCATCTGGCTGCCAATGGAACTCAAAACTTGGAAGGCGAAGGACAATGTTATCTGG
	GATTCACCGTGCCCAGCACCCGAAGTGCCAAATTCCAGGAGGACAAGAGCCTTAGCCAATGACAACTCACTCT
	CCCCTACTCCACCTCCTTCCAAGTCCAGCTCAGGCCCAGGAGGTGGGAGAAGGTCACAGAGCCTCAGGAATTT
	CCAAGTCAGAGTCCCCTTTGAACCAAGTATCTAGATCCCCTGAGGACTTGATGAAGTGATCCTTAACCCCCAA
	GTAATCATTAACCCCCAGACCAGCCTCAGAACTGAAGGAGATTGTTGACCCAGTGACCTGGAGTTGAGGCTCA

Fig. 41 (continued)

	GGGAGAGATCTGCCACATGTCTGAGGGTTGCAGAGCCCGCTGTGGAGGTAAGATTGGAAACACATGAGGCAGA GGGAAGACATTGAAGAAAACATCTCTGCTGGAATATTTGGAAAAGAACACTCTTCTGGACCTGGTTGAAGCAG GAAAGATGGAGGCAAAGTAGTGAAATAATCCAGAATTTCAATGCTTTTGAATGTTCTTAGTGATACTGACCTG TGATAATATAATTCCCAGGGAGGACTGGGAACCTTATCTCTTGAGATATTTGCATAATTTATTTAATTTAAGC CTCATTCTCCTTTTGTTCATTTTGGTAATAAACTGGATTTGAATTGTGAACAAAAAAAAAAAAAAAAAA
#57	AATGCTCTAAGACCTCTCAGCACGGGCGGAAGAAACTCCCGGAGAGCTCACCCAAAAAACAAGGAGATCCCAT CTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTCATCTTTGGAGAGGCCAAA TGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTA TAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTA ATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATC TATTTCCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTT GAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATA TTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCAAAGTCATT TTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTT TCCTGAGCTCTCCACTGGAGTCCTCTTTCTGTCGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATT TTTTTTAATTTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAA TAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTG TAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACTGATCCTAATTCTTTCCCTTTGAGGTCTCTATGG CTCTGATTGTACATGATAGTAAGTGTAAGCCATGTAAAAAGTAAATAATGTCTGGGCACAGTGGCTCACGCCT GTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAA CATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATACACCTGTAGTC CCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATC ACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACA GCAAGTCCTAGGAAGTAGGTTAAAACTAATTCTTTAAAAAAAAAAAAAAAGTTGAGCCTGAATTAAATGTAATG TTTCCAAGTGACAGGTATCCACATTTGCATGGTTACAAGCCACTGCCAGTTGGCAGTAGCACTTTCCTGGCAC TGTGGTCGGTTTTGTTTTGTTTTGCTTTGTTTAGAGACGGGGTCTCACTTTCCAGGCTGGCCTCAAACTCCTG CACTCAAGCAATTCTTCTACCCTGGCCTCCCAAGTAGCTGGAATTACAGGTGTGCGCCATCACAACTAGCTGG TGGTCAGTTTTGTTACTCTGAGAGCTGTTCACTTCTCTGAATTCACCTAGAGTGGTTGGACCATCAGATGTTT GGGCAAAACTGAAAGCTCTTTGCAACCACACACCTTCCCTGAGCTTACATCACTGCCCTTTTGAGCAGAAAGT CTAAATTCCTTCCAAGACAGTAGAATTCCATCCCAGTACCAAAGCCAGATAGGCCCCCTAGGAAACTGAGGTA AGAGCAGTCTCTAAAAACTACCCACAGCAGCATTGGTGCAGGGGAACTTGGCCATTAGGTTATTATTTGAGAG GAAAGTCCTCACATCAATAGTACATATGAAAGTGACCTCCAAGGGGATTGGTGAATACTCATAAGGATCTTCA GGCTGAACAGACTATGTCTGGGGAAAGAACGGATTATGCCCCATTAAATAACAAGTTGTGTTCAAGAGTCAGA GCAGTGAGCTCAGAGGCCCTTCTCACTGAGACAGCAACATTTAAACCAAACCAGAGGAAGTATTTGTGGAACT CACTGCCTCAGTTTGGGTAAAGGATGAGCAGACAAGTCAACTAAAGAAAAAAGAAAAGCAAGGAGGAGGGTTG AGCAATCTAGAGCATGGAGTTTGTTAAGTGCTCTCTGGATTTGAGTTGAAGAGCATCCATTTGAGTTGAAGGC CACAGGGCACAATGAGCTCTCCCTTCTACCACCAGAAAGTCCCTGGTCAGGTCTCAGGTAGTGCGGTGTGGCT CAGCTGGGTTTTTAATTAGCGCATTCTCTATCCAACATTTAATTGTTTGAAAGCCTCCATATAGTTAGATTGT GCTTTGTAATTTTGTTGTTGTTGCTCTATCTTATTGTATATGCATTGAGTATTAACCTGAATGTTTTGTTACT TAAATATTAAAAACACTGTTATCCTACAAAAAAACCCTCAAAGGCTGAAAATAAAGAAGGAAGATGGAGACAC CCTCTGGGGGTCCTCTC
#58	CTTTGCAGTGGATGCCCTTGGCAGGGTGAGCCCACAAGGAGCAATGGAGCAGGGCAGCGGCCGCTTGGAGGAC TTCCCTGTCAATGTGTTCTCCGTCACTCCTTACACACCCAGCACCGCTGACATCCAGGTGTCCGATGATGACA AGGCGGGGGCCACCTTGCTCTTCTCAGGCATCTTTCTGGGACTGGTGGGGATCACATTCACTGTCATGGGCTG GATCAAATACCAAGGTGTCTCCCACTTTGAATGGACCCAGCTCCTTGGGCCCGTCCTGCTGTCAGTTGGGGTG ACATTCATCCTGATTGCTGTGTGCAAGTTCAAAATGCTCTCCTGCCAGTTGTGCAAAGAAAGTGAGGAAAGGG TCCCGGACTCGGAACAGACACCAGGAGGACCATCATTTGTTTTCACTGGCATCAACCAACCCATCACCTTCCA TGGGGCCACTGTGGTGCAGTACATCCCTCCTCCTTATGGTTCTCCAGAGCCTATGGGGATAAATACCAGCTAC CTGCAGTCTGTGGTGAGCCCCTGCGGCCTCATAACCTCTGGAGGGGCAGCAGCCGCCATGTCAAGTCCTCCTC AATACTACACCATCTACCCTCAAGATAACTCTGCATTTGTGGTTGATGAGGGCTGCCTTTCTTTCACGGACGG TGGAAATCACAGGCCCAATCCTGATGTTGACCAGCTAGAAGAGACACAGCTGGAAGAGGAGGCCTGTGCCTGC TTCTCTCCTCCCCCTTATGAAGAAATATACTCTCTCCCTCGCTAGAGGCTATTCTGATATAATAACACAATGC TCAGCTCAGGGAGCAAGTGTTTCCGTCATTGTTACCTGACAACCGTGGTGTTCTATGTTGTAACCTTCAGAAG TTACAGCAGCGCCCAGGCAGCCTGACAGAGATCATTCAAGGGGGGAAAGGGGAAGTGGGAGGTGCAATTTCTC AGATTGGTAAAAATTAGGCTGGGCTGGGGAAATTCTCCTCCGGAACAGTTTCAAATTCCCTCGGGTAAGAAAT CTCCTGTATAAGGTTCAGGAGCAGGAATTTCACTTTTTCATCCACCACCCTCCCCCTTCTCTGTAGGAAGGCA TTGGTGGCTCAATTTTAACCCCAGCAGCCAATGGAAAAATCACGACTTCTGAGACTTTGGGAGTTTCCACAGA GGTGAGAGTCGGGTGGGAAGGAAGCAGGGAAGAGAAAGCAGGCCCAGCTGGAGATTTCCTGGTGGCTGTCCTT

Fig. 41 (continued)

	GGCCCCAAAGCAGACTCACTAATCCCAAACAACTCAGCTGCCATCTGGCCTCTCTGAGGACTCTGGGTACCTT AAAGACTATA
#59	CAGGAAAGTTCGTGCTGCTAGGCAGAGGAACTGCAGCTTGTTGGCAGGTGAAGGGAGCCTGTTTAGCTGTGTC CAGCAACAACTTACGTGGTCCTGCTTGTGTTCCAGGTGAAGCGTCTGGCCGCCGAGCAGAGGAATCAAGACCT GCTCATTCTTTCCTCGGGGGATCCATCCAGCAATGACATCATCTCATGCTGCCACAAGGACCCCAAGTCTGGG CTGCTGGGGACCAGCCACGCTCCCCACTGCTCATTCCTTCATCCTAGAGACATTCTGACTCTCCTCCGACTGC GCTGTGCACAGGCGTGACAAGCTCTTTTACATCTCAGTCTGCACAACTTCAGGCACTTAGCAGATTGATATGC ATCCAACAAATATTGATTGAATATCTGCTAAATACCCAGTAATGTTTCATGAGTGATTGGGTGAATAAAGGAA TGCTGGTTCCTTCTGGCCATATTAACTCCTGCACAATACTAAGAAAAATAAATTGCACTAGCTGTGGAATAAT GTGAATCCCAATGTCATCTATTGAAATATTACCTGACTATTAAGAGGTATTTATTTTTGTATCTTTTCTAGCA AAGTAAATAAAATTCTTAATACAGCATATCCCCTTATTCACGGGGGGTATGTTCCAAGACCCCCGGTGGATGC CTGAAACTATGGATAATACCAGATCC
#60	MGPFKSSVFILILHLLEGALSNSLIQLNNNGYEGIVVAIDPNVPEDETLIQQIKDMVTQASLYLFEATGKRFY FKNVAILIPETWKTKADYVRPKLETYKNADVLVAESTPPGNDEPYTEQMGNCGEKGERIHLTPDFIAGKKLAE YGPQGKAFVHEWAHLRWGVFDEYNNDEKFYLSNGRIQAVRCSAGITGTNVVKKCQGGSCYTKRCTFNKVTGLY EKGCEFVLQSRQTEKASIMFAQHVDSIVEFCTEQNHNKEAPNKQNQKCNLRSTWEVIRDSEDFKKTTPMTTQP PNPTFSLLQIGQRIVCLVLDKSGSMATGNRLNRLNQAGQLFLLQTVELGSWVGMVTFDSAAHVQSELIQINSG SDRDTLAKRLPAAASGGTSICSGLRSAFTVIRKKYPTDGSEIVLLTDGEDNTISGCFNEVKQSGAIIHTVALG PSAAQELEELSKMTGGLQTYASDQVQNNGLIDAFGALSSGNGAVSQRSIQLESKGLTLQNSQWMNGTVIVDST VGKDTLFLITWTTQPPQILLWDPSGQKQGGFVVDKNTKMAYLQIPGIAKVGTWKYSLQASSQTLTLTVTSRAS NATLPPITVTSKTNKDTSKFPSPLVVYANIRQGASPILRASVTALIESVNGKTVTLELLDNGAGADATKDDGV YSRYFTTYDTNGRYSVKVRALGGVN AARRRVIPQQSGALYIPGWIENDEIQWNPPRPEINKDDVQHKQVCFSRTSSGGSFVASDVPNAPIPDLFPPGQ ITDLKAEIHGGSLINLTWTAPGDDYDHGTAHKYIIRISTSILDLRDKFNESLQVNTTALIPKEANSEEVFLFK PENITFENGTDLFIAIQAVDKVDLKSEISNIARVSLFIPPQTPPETPSPDETSAPCPNIHINSTIPGIHILKI MWKWIGELQLSIA
#61	MKKEGRKRWKRKEDKKRVVVSNLLFEGWSHKENPNRHHRGNQIKTSKYTVLSFVPKNIFEQLHRFANLYFVGI AVLNFIPVVNAFQPEVSMIPICVILAVTAIKDAWEDLRRYKSDKVINNRECLIYSRKEQTYVQKCWKDVRVGD FIQMKCNEIVPADILLLFSSDPNGICHLETASLDGETNLKQRRVVKGFSQQEVQFEPELFHNTIVCEKPNNHL NKFKGYMEHPDQTRTGFGCESLLLRGCTIRNTEMAVGIVIYAGHETKAMLNNSGPRYKRSKIERRMNIDIFFC IGILILMCLIGAVGHSIWNGTFEEHPPFDVPDANGSFLPSALGGFYMFLTMIILLQVLIPISLYVSIELVKLG QVFFLSNDLDLYDEETDLSIQCRALNIAEDLGQIQYIFSDKTGTLTENKMVFRRCTIMGSEYSHQENGIEAPK GSIPLSKRKYPALLRNEEIKDILLALLEAVWHFHKLLPVSLWSSLSQIRAVPITCKLSFVYKG
#62	MGRRSPFKPRNKVFGFSYPWCRSYQPFPRKRAWPPSRVWLGACCASLASPPKGTIPSGEYYRPAPSSSGDSLR RESGALLQYLPSLASPCANHATRCSLLFPIYKIKMTLLYLTGLARTHCCCLADRCAEAVESAFYLVGSLCINA RGAAHLTD
#63	MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREKPAGGIPVL GSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTTEAQATIRMDTS ASGPTRLVLSDCATSHGSLRIQLLHKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLV KVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVTKWFNNSAASLTMPTLDNIPFSLIVSQDVVKAA VAAVLSPEEFMVLLDSVLPESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEV FPSSEALRPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQ NGKLRSGVPVSLVKALGFEAAESSLTKDALVLTPASLWKPSSPVSQ
#64	MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPL LDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSPDGHRLYVTIPLGIKLQVNTPLV GASLLRLAVKLDITAEILAVRDKQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPELV QGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
#65	MSQPRPRYVVDRAAYSLTLFDDEFEKKDRTYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIP DLLGGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVGNICLQLAPES KFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVAIYLSESFIRGFMTAAGLQILISV

Fig. 41 (continued)

	LKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASLIFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVV VATAISGGCKMPKKYHMQIVGEIQRGFPTPVSPVVSQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDS NQEMIALGCSNFFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGALI AVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQTQFRNGYALAQVMDT DIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIFRQKVIAKTGMDPQKVLLAKQKYLKKQEKRRMRPTQQRR SLFMKTKTVSLQELQQDFENAPPTDPNNNQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPGEPSDMLASVP PFVTFHTLILDMSGVSFVDLMGIKA LAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQANARDVTPGHNFQGAPG DAELSLYDSEEDIRSYWDLEQEMFGSMFHAETLTAL
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Fig. 41 (continued)

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#96	GIQEGGFCFRSTRHNFNSMRFP
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#99	TCGCTTTTTGTCGTATTTGC
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Fig. 41 (continued)

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Fig. 41 (continued)

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<211> 550
<212> DNA

<213> Homo sapiens

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gaagtgtgta aatgagctgg gaccagaggc ttctgaagct gtgaagaaac tgctggaggc 360
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aaaaaaaaaa 550

<210> 7
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<212> DNA
<213> Homo sapiens

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<211> 180

<212> DNA

<213> Homo sapiens

<400> 8

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<210> 9

<211> 309

<212> PRT

<213> Homo sapiens

<400> 9

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1 5 10 15

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro
165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
180 185 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
195 200 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
210 215 220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
245 250 255

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
260 265 270

Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
275 280 285

Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu
290 295 300

Cys Val Thr Leu Ala
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<210> 10

<211> 394

<212> PRT

<213> Homo sapiens

<400> 10

Met Thr Ala Gly Arg Ser Gln Glu Arg Arg Ala Gln Glu Met Gly Arg
1 5 10 15

Gly Ser Val Gln Gly Leu Asp Leu Lys Gly Asp Leu Glu Phe Phe Thr
20 25 30

Ala Pro Met Leu Ser Leu Arg Ser Phe Val Phe Val Gly Val Gly Ser
35 40 45

Gly Leu Thr Ser Ser His Ile Pro Ala Gln Arg Trp Ala Glu Trp Gly
50 55 60

Gln Cys Leu Ala Pro Pro Ala Arg Ser Leu Leu Thr Ser Gly Ser Leu
65 70 75 80

Cys Cys Pro Arg Thr Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser
85 90 95

Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu
100 105 110

Gly Val Leu Leu Val Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp
115 120 125

Val Phe Cys Cys Arg Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met
130 135 140

Thr Asn Leu Ala Val Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe
145 150 155 160

Val Leu His Ser Leu Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu
165 170 175

Ser Gln Gly Ile Tyr Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val
180 185 190

Thr Ala Ile Ala Val Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg
195 200 205

Ala Arg Gly Leu Arg Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val
210 215 220

Leu Trp Val Leu Val Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly
225 230 235 240

Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn
245 250 255

Ser Met Ala Phe Pro Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val
260 265 270

Val Phe Cys Ser Leu Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro
275 280 285

Thr Asp Val Gly Gln Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val
290 295 300

Trp Ala Asn Leu Leu Val Phe Val Val Cys Phe Leu Pro Leu His Val
305 310 315 320

Gly Leu Thr Val Arg Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu
325 330 335

Glu Thr Ile Arg Arg Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala
340 345 350

Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe
355 360 365

Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys
370 375 380

Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
385 390

<210> 11

<211> 1073

<212> PRT

<213> Homo sapiens

<400> 11

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1 5 10 15

Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20 25 30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35 40 45

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50 55 60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85 90 95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
100 105 110

Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
115 120 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
130 135 140

Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
145 150 155 160

Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
165 170 175

Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val

180 185 190

Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
195 200 205

Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
210 215 220

Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
225 230 235 240

Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr
245 250 255

Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu
260 265 270

Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro
275 280 285

Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser
290 295 300

Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp
305 310 315 320

Phe Ala Leu Ala Tyr Leu Asn Gly Ile Leu Leu Phe Gly His Met Leu
325 330 335

Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala
340 345 350

His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr
355 360 365

Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr
370 375 380

Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His
385 390 395 400

Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys
405 410 415

Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu
420 425 430

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu
435 440 445

Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg
450 455 460

Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu
465 470 475 480

Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg
485 490 495

Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
500 505 510

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys
515 520 525

Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Ile Asp Tyr Tyr Asn Leu
530 535 540

Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val
545 550 555 560

Ile Glu Tyr Cys Glu Arg Gly Ser Leu Arg Glu Val Leu Asn Asp Thr
565 570 575

Ile Ser Tyr Pro Asp Gly Thr Phe Met Asp Trp Glu Phe Lys Ile Ser
580 585 590

Val Leu Tyr Asp Ile Ala Lys Gly Met Ser Tyr Leu His Ser Ser Lys
595 600 605

Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser
610 615 620

Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro
625 630 635 640

Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn
645 650 655

Ile Ser Gln Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu
660 665 670

Ile Ile Leu Arg Lys Glu Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg
675 680 685

Asn Glu Lys Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe
690 695 700

Arg Pro Asp Leu Phe Leu Glu Thr Ala Glu Glu Lys Glu Leu Glu Val
705 710 715 720

Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro
725 730 735

Asp Phe Lys Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe
740 745 750

His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu
755 760 765

Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln
770 775 780

Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu
785 790 795 800

Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu
805 810 815

Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly
820 825 830

Phe Thr Thr Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met
835 840 845

Leu Asn Asp Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp
850 855 860

Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly
865 870 875 880

Leu Pro Lys Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met
885 890 895

Ala Leu Glu Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu
900 905 910

Pro Gly Leu Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys
915 920 925

Ala Ala Gly Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly
930 935 940

Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
945 950 955 960

Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
965 970 975

Cys Gln Phe Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg
980 985 990

Gly Asn Glu Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe
995 1000 1005

Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln
1010 1015 1020

Ala Glu Phe Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln
1025 1030 1035

Ala Ala Gly Ile Arg Ser Gln Lys Pro Arg Arg Val Ala Ser Tyr
1040 1045 1050

Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
1055 1060 1065

Glu Ser Thr Tyr Phe
1070

<210> 12

<211> 111

<212> PRT

<213> Homo sapiens

<400> 12

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1 5 10 15

Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20 25 30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35 40 45

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50 55 60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85 90 95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Pro
100 105 110

<210> 13

<211> 258

<212> PRT

<213> Homo sapiens

<400> 13

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Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
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Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
            20                  25                  30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
        35                  40                  45

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
    50                  55                  60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65                  70                  75                  80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
                85                  90                  95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
            100                 105                 110

Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
        115                 120                 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
    130                 135                 140

Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
145                 150                 155                 160

Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
                165                 170                 175

Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
            180                 185                 190

Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
        195                 200                 205

Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
    210                 215                 220

Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
225                 230                 235                 240

Arg Lys Ser Asn Val Thr Ser Thr Trp Arg Thr Met Ser Gln Pro Leu
                245                 250                 255

Thr Ile
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<210> 14

<211> 1070

<212> PRT

<213> Homo sapiens

<400> 14

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Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1               5                  10                  15

Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
            20                  25                  30

Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
        35                  40                  45

Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
    50                  55                  60

Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65                  70                  75                  80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
                85                  90                  95

Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
            100                 105                 110

Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
        115                 120                 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
    130                 135                 140

Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
145                 150                 155                 160

Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
                165                 170                 175

Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
            180                 185                 190

Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
        195                 200                 205

Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
    210                 215                 220
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Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
225 230 235 240

Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr
245 250 255

Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu
260 265 270

Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro
275 280 285

Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser
290 295 300

Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp
305 310 315 320

Phe Ala Leu Ala Tyr Leu Asn Gly Ile Leu Leu Phe Gly His Met Leu
325 330 335

Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala
340 345 350

His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr
355 360 365

Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr
370 375 380

Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His
385 390 395 400

Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys
405 410 415

Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu
420 425 430

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu
435 440 445

Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg
450 455 460

Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu
465 470 475 480

Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg
485 490 495

Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
500 505 510

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys
515 520 525

Gln Lys Ile Glu Leu Asn Lys Ile Asp Tyr Tyr Asn Leu Thr Lys Phe
530 535 540

Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr
545 550 555 560

Cys Glu Arg Gly Ser Leu Arg Glu Val Leu Asn Asp Thr Ile Ser Tyr
565 570 575

Pro Asp Gly Thr Phe Met Asp Trp Glu Phe Lys Ile Ser Val Leu Tyr
580 585 590

Asp Ile Ala Lys Gly Met Ser Tyr Leu His Ser Ser Lys Thr Glu Val
595 600 605

His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser Arg Met Val
610 615 620

Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro Pro Lys Lys
625 630 635 640

Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn Ile Ser Gln
645 650 655

Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu Ile Ile Leu
660 665 670

Arg Lys Glu Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg Asn Glu Lys
675 680 685

Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe Arg Pro Asp
690 695 700

Leu Phe Leu Glu Thr Ala Glu Glu Lys Glu Leu Glu Val Tyr Leu Leu
705 710 715 720

Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro Asp Phe Lys
725 730 735

Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe His Asp Gln
740 745 750

Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu Gln Leu Tyr
755 760 765

Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln Leu Tyr Lys

770 775 780

Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu Leu Pro Arg
785 790 795 800

Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu Pro Glu Leu
805 810 815

Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly Phe Thr Thr
820 825 830

Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met Leu Asn Asp
835 840 845

Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp Val Tyr Lys
850 855 860

Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly Leu Pro Lys
865 870 875 880

Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met Ala Leu Glu
885 890 895

Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu Pro Gly Leu
900 905 910

Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys Ala Ala Gly
915 920 925

Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly Asp Thr Val
930 935 940

Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu Arg Ile His
945 950 955 960

Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu Cys Gln Phe
965 970 975

Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg Gly Asn Glu
980 985 990

Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe Asn Leu Pro
995 1000 1005

Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln Ala Glu Phe
1010 1015 1020

Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln Ala Ala Gly
1025 1030 1035

Ile Arg Ser Gln Lys Pro Arg Arg Val Ala Ser Tyr Lys Lys Gly
1040 1045 1050

Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys Glu Ser Thr
1055 1060 1065

Tyr Phe
1070

<210> 15

<211> 93

<212> PRT

<213> Homo sapiens

<400> 15

Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
1 5 10 15

Tyr Ser Ala Thr Ala Lys Leu Ile Asn Lys Cys Pro Leu Pro Val Asp
20 25 30

Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe Met Asp Pro
35 40 45

Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
50 55 60

Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly Pro Glu Ala Ser Glu
65 70 75 80

Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
85 90

<210> 16

<211> 261

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
1 5 10 15

Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr
20 25 30

Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln Gly
35 40 45

Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60

Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80

Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95

Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110

Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115 120 125

Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130 135 140

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160

Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175

Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190

Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205

Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220

Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255

Lys His Asp Tyr Val
260

<210> 17

<211> 10

<212> PRT

<213> Homo sapiens

<400> 17

Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn
1 5 10

<210> 18

<211> 11

<212> PRT

<213> Homo sapiens

<400> 18

Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln
1 5 10

<210> 19

<211> 47

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
1 5 10 15

Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr
20 25 30

Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln
35 40 45

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 20
aggtacatga gcatcagcct g 21

<210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 21
gcagcagttg gcatctgaga g 21

<210> 22

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 22
gcaatagaca ttgccaagat g 21

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 23
aacgctgttg attctccaca g 21

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 24
ggatcctcct ttagttccca ggtgagtcag aac 33

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 25
tgctctggag gctagcgttt c 21

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 26
accaatcatg ttagcctcaa g 21

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 27
agctatggga tcatcgcaca g 21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 28
cctttgagct ggagcatctt c 21

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 29
ctttctagct ggagacatca g 21

<210> 30

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 30
caccatggta ctgtcaacat c 21

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 31
atgtcataca agacagagat c 21

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 32
tctgccttgt acagctgtgt c 21

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 33
tctgtggtat tcagctgcaa g 21

<210> 34

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 34
tactcaggaa aatttcacct tg 22

<210> 35

<211> 27

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 35
gaccacaaca ggaaaagcaa tgtgacc 27

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 36
gatagaattg aacaagattg ac 22

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 37
cagcctttgt agttactctg c 21

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 38
tgtcacacca agtgtgatag c 21

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 39
ggttcgtggt ttcactgatt gggattgc 28

<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Oligonucleotide

<400> 40
cggctttgta gttggtttct tctggtg 27

<210> 41

<211> 3814

<212> DNA

<213> Homo sapiens

<400> 41
ctattgaagc cacctgctca ggacaatgaa attcttcagt tacattctgg tttatcgccg 60
atttctcttc gtggttttca ctgtgttggt tttactacct ctgcccatcg tcctccacac 120
caaggaagca gaatgtgcct acacactctt tgtggtcgcc acattttggc tcacagaagc 180
attgcctctg tcggtaacag ctttgctacc tagtttaatg ttacccatgt ttgggatcat 240
gccttctaag aaggtggcat ctgcttattt caaggatttt cacttactgc taattggagt 300
tatctgttta gcaacatcca tagaaaaatg gaatttgcac aagagaattg ctctgaaaat 360
ggtgatgatg gttggtgtaa atcctgcatg gctgacgctg gggttcatga gcagcactgc 420
ctttttgtct atgtggctca gcaacacctc gacggctgcc atggtgatgc ccattgcgga 480
ggctgtagtg cagcagatca tcaatgcaga agcagaggtc gaggccactc agatgactta 540
cttcaacgga tcaaccaacc acggactaga aattgatgaa agtgttaatg gacatgaaat 600
aaatgagagg aaagagaaaa caaaaccagt tccaggatac aataatgata cagggaaaat 660
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gggccacgtg acacgtaaac ttacgtgttt gtgcattgcc tactcttcta ccattggtgg 780
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gagattttgc tcatgaacca tctgcaactt gcttcatcat aagaataatt tataacttga 2100
ccttcaaaga gattagagca tttgtttcat cttacagttg gagttcaatg taacatttta 2160
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tgttaaaaat aaagagatgt agaaatctaa atgaattatc actgtgtata cagacagaaa 2760
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caggtagcaa aatatcacat acacccccaa aatatgtaca aatattatat atcaataaat 3060
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cggctcactg caagctccgc ctcccaggtt cacgccattc tcctgcctca gccaaacctt 3360
tgctattttt aatcttcgtt ggcactttcc agctgttact gaccttgtca ttttttgttc 3420
aaataagatt atttacaaac ttattcttga aactaaatat agtaaagagg gtttttaaaa 3480
taatatttaa catacgaatt attaattggc catgttcatt atttatctat gtttattaat 3540
gggccaatgc aaaaaatcat tttttcaaag aaaaatttgt ccatgtaaag cttaaattat 3600

aatattgctg ctttgtataa ctcttctatg tttattctat tcatttgttc ctttccctac 3660
catattttac acatgtattt ataatctgta gtatttatta catttctgct tttttctagt 3720
cattcaattt atcactgctg aattgcatca gatcatggat gcatttttat tatgaaaaaa 3780
taaaatgact tttcaaatta aaaaaaaaaa aaaa 3814

<210> 42
<211> 734
<212> DNA
<213> Homo sapiens

<400> 42
caggacaatg aaattcttca gttacattct ggtttatcgc cgatttctct tcgtggtttt 60
cactgtgttg gttttactac ctctgcccat cgtcctccac accaaggaag cagaatgtgc 120
ctacacactc tttgtggtcg ccacattttg gctcacagaa gcattgcctc tgtcggtaac 180
agctttgcta cctagtttaa tgttacccat gtttgggatc atgccttcta agaaggtggc 240
atctgcttat ttcaaggatt ttcacttact gctaattgga gttatctgtt tagcaacatc 300
catagaaaaa tggaatttgc acaagagaat tgctctgaaa atggtgatga tggttggtgt 360
aaatcctgca tggctgacgc tggggttcat gagcagcact gccttttttgt ctatgtggct 420
cagcaacacc tcgacggctg ccatggtgat gcccattgcg gaggctgtag tgcagcagat 480
catcaatgca gaagcagagg tcgaggccac tcagatgact tacttcaacg gatcaaccaa 540
ccacggacta gaaattgatg aaagtgttaa tggacatgaa ataaatgaga ggaaagagaa 600
aacaaaacca gttccaggat acaataatga tacagggaaa atttcaagca aggtggagtt 660
ggaaaagact gtttaactac tgaaatgaag ctattctcct gactaaacat aactgaaaaa 720
ccattcatta aatg 734

<210> 43
<211> 539
<212> DNA
<213> Homo sapiens

<400> 43
gccactcaga tgacttactt caacggatca accaaccacg gactagaaat tgatgaaagt 60
gttaatggac atgaaataaa tgagaggaaa gagaaaacaa aaccagttcc aggatacaat 120
aatgatacag ggaaaatttc aagcaaggtg gagttggaaa agcactggaa acttgcagtt 180
caagatggct ccccatctcc ctctgtccat tctgtatcgc agctagctgc tcaaggaaag 240
gagaaagtgg aaggcatatg tacttagaaa ttattctatt actttcctgg atttaagagt 300

attcagattt tctatttcaa catcaaacaa ttgcattttt aaaaagaaat ttatgtgttc 360

catgtcaaat ttagtagtgt gtggttgttt ataatatttt cttatatcta cttaatttct 420

atagtattta tagttatatg tctttatttc taacattttt cttgtgcttt taaagattat 480

ttaaagatta tttttaaata atctttattt catttaaata aaatatttta tttaagtct 539

<210> 44

<211> 556

<212> DNA

<213> Homo sapiens

<400> 44

cacggactag aaattgatga aagtgttaat ggacatgaaa taaatgagag gaaagagaaa 60

acaaaaccag ttccaggata caataatgat acagggaaaa tttcaagcaa ggtggagttg 120

gaaaagaact caggcatgag aaccaaatat cgaacaaaga agggccacgt gacacgtaaa 180

cttacgtgtt tgtgcattgc ctactcttct accattggtg gactgacaac aatcactggt 240

acctccacca acttgatctt tgcagagtat ttcaatacat tccatccaca cagaagagga 300

gatcgtacaa ggcatgtaca ccaggaggca gaaatttgag gcatatcttg gaactctgtc 360

taccacatcc tgaacatcac acagtttcca ctcttgttgc cttcaatcct gagaatgcat 420

ccaggagcca ttctgtttta tgtcaattac taattagatc atgtcacgtt actaacttac 480

tacgttccaa ttagtcctta ttgcatttgt aataaaatcc gcatactttc ggactggcta 540

caaggttata catgat 556

<210> 45

<211> 595

<212> PRT

<213> Homo sapiens

<400> 45

Met Lys Phe Phe Ser Tyr Ile Leu Val Tyr Arg Arg Phe Leu Phe Val
1 5 10 15

Val Phe Thr Val Leu Val Leu Leu Pro Leu Pro Ile Val Leu His Thr
20 25 30

Lys Glu Ala Glu Cys Ala Tyr Thr Leu Phe Val Val Ala Thr Phe Trp
35 40 45

Leu Thr Glu Ala Leu Pro Leu Ser Val Thr Ala Leu Leu Pro Ser Leu
50 55 60

Met Leu Pro Met Phe Gly Ile Met Pro Ser Lys Lys Val Ala Ser Ala
65 70 75 80

Tyr Phe Lys Asp Phe His Leu Leu Leu Ile Gly Val Ile Cys Leu Ala
85 90 95

Thr Ser Ile Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Lys Met
100 105 110

Val Met Met Val Gly Val Asn Pro Ala Trp Leu Thr Leu Gly Phe Met
115 120 125

Ser Ser Thr Ala Phe Leu Ser Met Trp Leu Ser Asn Thr Ser Thr Ala
130 135 140

Ala Met Val Met Pro Ile Ala Glu Ala Val Val Gln Gln Ile Ile Asn
145 150 155 160

Ala Glu Ala Glu Val Glu Ala Thr Gln Met Thr Tyr Phe Asn Gly Ser
165 170 175

Thr Asn His Gly Leu Glu Ile Asp Glu Ser Val Asn Gly His Glu Ile
180 185 190

Asn Glu Arg Lys Glu Lys Thr Lys Pro Val Pro Gly Tyr Asn Asn Asp
195 200 205

Thr Gly Lys Ile Ser Ser Lys Val Glu Leu Glu Lys Asn Ser Gly Met
210 215 220

Arg Thr Lys Tyr Arg Thr Lys Lys Gly His Val Thr Arg Lys Leu Thr
225 230 235 240

Cys Leu Cys Ile Ala Tyr Ser Ser Thr Ile Gly Gly Leu Thr Thr Ile
245 250 255

Thr Gly Thr Ser Thr Asn Leu Ile Phe Ala Glu Tyr Phe Asn Thr Arg
260 265 270

Tyr Pro Asp Cys Arg Cys Leu Asn Phe Gly Ser Trp Phe Thr Phe Ser
275 280 285

Phe Pro Ala Ala Leu Ile Ile Leu Leu Leu Ser Trp Ile Trp Leu Gln
290 295 300

Trp Leu Phe Leu Gly Phe Asn Phe Lys Glu Met Phe Lys Cys Gly Lys
305 310 315 320

Thr Lys Thr Val Gln Gln Lys Ala Cys Ala Glu Val Ile Lys Gln Glu
325 330 335

Tyr Gln Lys Leu Gly Pro Ile Arg Tyr Gln Glu Ile Val Thr Leu Val

340 345 350

Leu Phe Ile Ile Met Ala Leu Leu Trp Phe Ser Arg Asp Pro Gly Phe
355 360 365

Val Pro Gly Trp Ser Ala Leu Phe Ser Glu Tyr Pro Gly Phe Ala Thr
370 375 380

Asp Ser Thr Val Ala Leu Leu Ile Gly Leu Leu Phe Phe Leu Ile Pro
385 390 395 400

Ala Lys Thr Leu Thr Lys Thr Thr Pro Thr Gly Glu Ile Val Ala Phe
405 410 415

Asp Tyr Ser Pro Leu Ile Thr Trp Lys Glu Phe Gln Ser Phe Met Pro
420 425 430

Trp Asp Ile Ala Ile Leu Val Gly Gly Gly Phe Ala Leu Ala Asp Gly
435 440 445

Cys Glu Glu Ser Gly Leu Ser Lys Trp Ile Gly Asn Lys Leu Ser Pro
450 455 460

Leu Gly Ser Leu Pro Ala Trp Leu Ile Ile Leu Ile Ser Ser Leu Met
465 470 475 480

Val Thr Ser Leu Thr Glu Val Ala Ser Asn Pro Ala Thr Ile Thr Leu
485 490 495

Phe Leu Pro Ile Leu Ser Pro Leu Ala Glu Ala Ile His Val Asn Pro
500 505 510

Leu Tyr Ile Leu Ile Pro Ser Thr Leu Cys Thr Ser Phe Ala Phe Leu
515 520 525

Leu Pro Val Ala Asn Pro Pro Asn Ala Ile Val Phe Ser Tyr Gly His
530 535 540

Leu Lys Val Ile Asp Met Val Lys Ala Gly Leu Gly Val Asn Ile Val
545 550 555 560

Gly Val Ala Val Val Met Leu Gly Ile Cys Thr Trp Ile Val Pro Met
565 570 575

Phe Asp Leu Tyr Thr Tyr Pro Ser Trp Ala Pro Ala Met Ser Asn Glu
580 585 590

Thr Met Pro
595

<210> 46

<211> 224

<212> PRT

<213> Homo sapiens

<400> 46

Arg Thr Met Lys Phe Phe Ser Tyr Ile Leu Val Tyr Arg Arg Phe Leu
1 5 10 15

Phe Val Val Phe Thr Val Leu Val Leu Leu Pro Leu Pro Ile Val Leu
20 25 30

His Thr Lys Glu Ala Glu Cys Ala Tyr Thr Leu Phe Val Val Ala Thr
35 40 45

Phe Trp Leu Thr Glu Ala Leu Pro Leu Ser Val Thr Ala Leu Leu Pro
50 55 60

Ser Leu Met Leu Pro Met Phe Gly Ile Met Pro Ser Lys Lys Val Ala
65 70 75 80

Ser Ala Tyr Phe Lys Asp Phe His Leu Leu Leu Ile Gly Val Ile Cys
85 90 95

Leu Ala Thr Ser Ile Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu
100 105 110

Lys Met Val Met Met Val Gly Val Asn Pro Ala Trp Leu Thr Leu Gly
115 120 125

Phe Met Ser Ser Thr Ala Phe Leu Ser Met Trp Leu Ser Asn Thr Ser
130 135 140

Thr Ala Ala Met Val Met Pro Ile Ala Glu Ala Val Val Gln Gln Ile
145 150 155 160

Ile Asn Ala Glu Ala Glu Val Glu Ala Thr Gln Met Thr Tyr Phe Asn
165 170 175

Gly Ser Thr Asn His Gly Leu Glu Ile Asp Glu Ser Val Asn Gly His
180 185 190

Glu Ile Asn Glu Arg Lys Glu Lys Thr Lys Pro Val Pro Gly Tyr Asn
195 200 205

Asn Asp Thr Gly Lys Ile Ser Ser Lys Val Glu Leu Glu Lys Thr Val
210 215 220

<210> 47

<211> 88

<212> PRT

<213> Homo sapiens

<400> 47

Ala Thr Gln Met Thr Tyr Phe Asn Gly Ser Thr Asn His Gly Leu Glu
1 5 10 15

Ile Asp Glu Ser Val Asn Gly His Glu Ile Asn Glu Arg Lys Glu Lys
20 25 30

Thr Lys Pro Val Pro Gly Tyr Asn Asn Asp Thr Gly Lys Ile Ser Ser
35 40 45

Lys Val Glu Leu Glu Lys His Trp Lys Leu Ala Val Gln Asp Gly Ser
50 55 60

Pro Ser Pro Ser Val His Ser Val Ser Gln Leu Ala Ala Gln Gly Lys
65 70 75 80

Glu Lys Val Glu Gly Ile Cys Thr
85

<210> 48

<211> 112

<212> PRT

<213> Homo sapiens

<400> 48

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Lys Tyr Arg Thr Lys Lys Gly His Val Thr Arg Lys Leu Thr Cys Leu
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Cys Ile Ala Tyr Ser Ser Thr Ile Gly Gly Leu Thr Thr Ile Thr Gly
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<210> 57

<211> 2572

<212> DNA

<213> Homo sapiens

<400> 57
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<210> 58

<211> 1324

<212> DNA

<213> Homo sapiens

<400> 58
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<210> 59

<211> 683

<212> DNA

<213> Homo sapiens

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gccgccgagc agaggaatca agacctgctc attctttcct cgggggatcc atccagcaat 180

gacatcatct catgctgcca caaggacccc aagtctgggc tgctggggac cagccacgct 240

ccccactgct cattccttca tcctagagac attctgactc tcctccgact gcgctgtgca 300

caggcgtgac aagctctttt acatctcagt ctgcacaact tcaggcactt agcagattga 360

tatgcatcca acaaatattg attgaatatc tgctaaatac ccagtaatgt ttcatgagtg 420

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gaaaaataaa ttgcactagc tgtggaataa tgtgaatccc aatgtcatct attgaaatat 540

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taatacagca tatcccctta ttcacggggg gtatgttcca agacccccgg tggatgcctg 660

aaactatgga taataccaga tcc 683

<210> 60

<211> 914

<212> PRT

<213> Homo sapiens

<400> 60

Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu
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Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Asn Gly Tyr
20 25 30

Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35 40 45

Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu
50 55 60

Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu

65 70 75 80

Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu
85 90 95

Glu Thr Tyr Lys Asn Ala Asp Val Leu Val Ala Glu Ser Thr Pro Pro
100 105 110

Gly Asn Asp Glu Pro Tyr Thr Glu Gln Met Gly Asn Cys Gly Glu Lys
115 120 125

Gly Glu Arg Ile His Leu Thr Pro Asp Phe Ile Ala Gly Lys Lys Leu
130 135 140

Ala Glu Tyr Gly Pro Gln Gly Lys Ala Phe Val His Glu Trp Ala His
145 150 155 160

Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Glu Lys Phe Tyr
165 170 175

Leu Ser Asn Gly Arg Ile Gln Ala Val Arg Cys Ser Ala Gly Ile Thr
180 185 190

Gly Thr Asn Val Val Lys Lys Cys Gln Gly Gly Ser Cys Tyr Thr Lys
195 200 205

Arg Cys Thr Phe Asn Lys Val Thr Gly Leu Tyr Glu Lys Gly Cys Glu
210 215 220

Phe Val Leu Gln Ser Arg Gln Thr Glu Lys Ala Ser Ile Met Phe Ala
225 230 235 240

Gln His Val Asp Ser Ile Val Glu Phe Cys Thr Glu Gln Asn His Asn
245 250 255

Lys Glu Ala Pro Asn Lys Gln Asn Gln Lys Cys Asn Leu Arg Ser Thr
260 265 270

Trp Glu Val Ile Arg Asp Ser Glu Asp Phe Lys Lys Thr Thr Pro Met
275 280 285

Thr Thr Gln Pro Pro Asn Pro Thr Phe Ser Leu Leu Gln Ile Gly Gln
290 295 300

Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ala Thr Gly
305 310 315 320

Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln
325 330 335

Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala
340 345 350

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Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg
        355                 360                 365

Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser
    370                 375                 380

Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr
385                 390                 395                 400

Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn
                405                 410                 415

Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile
            420                 425                 430

His Thr Val Ala Leu Gly Pro Ser Ala Ala Gln Glu Leu Glu Glu Leu
        435                 440                 445

Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln
    450                 455                 460

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly
465                 470                 475                 480

Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu
                485                 490                 495

Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val
            500                 505                 510

Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln
        515                 520                 525

Ile Leu Leu Trp Asp Pro Ser Gly Gln Lys Gln Gly Gly Phe Val Val
    530                 535                 540

Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys
545                 550                 555                 560

Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr
                565                 570                 575

Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr
            580                 585                 590

Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu
        595                 600                 605

Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala
    610                 615                 620
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Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu
625 630 635 640

Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
645 650 655

Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
660 665 670

Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
675 680 685

Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
690 695 700

Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp
705 710 715 720

Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
725 730 735

Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
740 745 750

Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
755 760 765

Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
770 775 780

Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785 790 795 800

Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
805 810 815

Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
820 825 830

Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
835 840 845

Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
850 855 860

Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865 870 875 880

Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
885 890 895

His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
900 905 910

Ile Ala

<210> 61

<211> 501

<212> PRT

<213> Homo sapiens

<400> 61

Met Lys Lys Glu Gly Arg Lys Arg Trp Lys Arg Lys Glu Asp Lys Lys
1 5 10 15

Arg Val Val Val Ser Asn Leu Leu Phe Glu Gly Trp Ser His Lys Glu
20 25 30

Asn Pro Asn Arg His His Arg Gly Asn Gln Ile Lys Thr Ser Lys Tyr
35 40 45

Thr Val Leu Ser Phe Val Pro Lys Asn Ile Phe Glu Gln Leu His Arg
50 55 60

Phe Ala Asn Leu Tyr Phe Val Gly Ile Ala Val Leu Asn Phe Ile Pro
65 70 75 80

Val Val Asn Ala Phe Gln Pro Glu Val Ser Met Ile Pro Ile Cys Val
85 90 95

Ile Leu Ala Val Thr Ala Ile Lys Asp Ala Trp Glu Asp Leu Arg Arg
100 105 110

Tyr Lys Ser Asp Lys Val Ile Asn Asn Arg Glu Cys Leu Ile Tyr Ser
115 120 125

Arg Lys Glu Gln Thr Tyr Val Gln Lys Cys Trp Lys Asp Val Arg Val
130 135 140

Gly Asp Phe Ile Gln Met Lys Cys Asn Glu Ile Val Pro Ala Asp Ile
145 150 155 160

Leu Leu Leu Phe Ser Ser Asp Pro Asn Gly Ile Cys His Leu Glu Thr
165 170 175

Ala Ser Leu Asp Gly Glu Thr Asn Leu Lys Gln Arg Arg Val Val Lys
180 185 190

Gly Phe Ser Gln Gln Glu Val Gln Phe Glu Pro Glu Leu Phe His Asn

195 200 205

Thr Ile Val Cys Glu Lys Pro Asn Asn His Leu Asn Lys Phe Lys Gly
210 215 220

Tyr Met Glu His Pro Asp Gln Thr Arg Thr Gly Phe Gly Cys Glu Ser
225 230 235 240

Leu Leu Leu Arg Gly Cys Thr Ile Arg Asn Thr Glu Met Ala Val Gly
245 250 255

Ile Val Ile Tyr Ala Gly His Glu Thr Lys Ala Met Leu Asn Asn Ser
260 265 270

Gly Pro Arg Tyr Lys Arg Ser Lys Ile Glu Arg Arg Met Asn Ile Asp
275 280 285

Ile Phe Phe Cys Ile Gly Ile Leu Ile Leu Met Cys Leu Ile Gly Ala
290 295 300

Val Gly His Ser Ile Trp Asn Gly Thr Phe Glu Glu His Pro Pro Phe
305 310 315 320

Asp Val Pro Asp Ala Asn Gly Ser Phe Leu Pro Ser Ala Leu Gly Gly
325 330 335

Phe Tyr Met Phe Leu Thr Met Ile Ile Leu Leu Gln Val Leu Ile Pro
340 345 350

Ile Ser Leu Tyr Val Ser Ile Glu Leu Val Lys Leu Gly Gln Val Phe
355 360 365

Phe Leu Ser Asn Asp Leu Asp Leu Tyr Asp Glu Glu Thr Asp Leu Ser
370 375 380

Ile Gln Cys Arg Ala Leu Asn Ile Ala Glu Asp Leu Gly Gln Ile Gln
385 390 395 400

Tyr Ile Phe Ser Asp Lys Thr Gly Thr Leu Thr Glu Asn Lys Met Val
405 410 415

Phe Arg Arg Cys Thr Ile Met Gly Ser Glu Tyr Ser His Gln Glu Asn
420 425 430

Gly Ile Glu Ala Pro Lys Gly Ser Ile Pro Leu Ser Lys Arg Lys Tyr
435 440 445

Pro Ala Leu Leu Arg Asn Glu Glu Ile Lys Asp Ile Leu Leu Ala Leu
450 455 460

Leu Glu Ala Val Trp His Phe His Lys Leu Leu Pro Val Ser Leu Trp
465 470 475 480

Ser Ser Leu Ser Gln Ile Arg Ala Val Pro Ile Thr Cys Lys Leu Ser
485 490 495

Phe Val Tyr Lys Gly
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<210> 62

<211> 154

<212> PRT

<213> Homo sapiens

<400> 62

Met Gly Arg Arg Ser Pro Phe Lys Pro Arg Asn Lys Val Phe Gly Phe
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Ser Tyr Pro Trp Cys Arg Ser Tyr Gln Pro Phe Pro Arg Lys Arg Ala
20 25 30

Trp Pro Pro Ser Arg Val Trp Leu Gly Ala Cys Cys Ala Ser Leu Ala
35 40 45

Ser Pro Pro Lys Gly Thr Ile Pro Ser Gly Glu Tyr Tyr Arg Pro Ala
50 55 60

Pro Ser Ser Ser Gly Asp Ser Leu Arg Arg Glu Ser Gly Ala Leu Leu
65 70 75 80

Gln Tyr Leu Pro Ser Leu Ala Ser Pro Cys Ala Asn His Ala Thr Arg
85 90 95

Cys Ser Leu Leu Phe Pro Ile Tyr Lys Ile Lys Met Thr Leu Leu Tyr
100 105 110

Leu Thr Gly Leu Ala Arg Thr His Cys Cys Cys Leu Ala Asp Arg Cys
115 120 125

Ala Glu Ala Val Glu Ser Ala Phe Tyr Leu Val Gly Ser Leu Cys Ile
130 135 140

Asn Ala Arg Gly Ala Ala His Leu Thr Asp
145 150

<210> 63

<211> 484

<212> PRT

<213> Homo sapiens

<400> 63

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

Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile Leu Gly
20 25 30

Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys Asp His Asn
35 40 45

Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser Ala Met Arg Glu
50 55 60

Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr Val
65 70 75 80

Leu Lys His Ile Ile Trp Leu Lys Val Ile Thr Ala Asn Ile Leu Gln
85 90 95

Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val Lys Ile
100 105 110

Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys Thr Ile
115 120 125

Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg Met Asp
130 135 140

Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
145 150 155 160

Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
165 170 175

Val Asn Ala Leu Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu
180 185 190

Pro Asn Leu Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe
195 200 205

Asn Gly Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser
210 215 220

Leu Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
225 230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser Gln
245 250 255

Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu Thr Met
260 265 270

Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser Gln Asp Val
275 280 285

Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu Glu Phe Met Val
290 295 300

Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His Arg Leu Lys Ser Ser
305 310 315 320

Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp Lys Leu Gly Ser Thr Gln
325 330 335

Ile Val Lys Ile Leu Thr Gln Asp Thr Pro Glu Phe Phe Ile Asp Gln
340 345 350

Gly His Ala Lys Val Ala Gln Leu Ile Val Leu Glu Val Phe Pro Ser
355 360 365

Ser Glu Ala Leu Arg Pro Leu Phe Thr Leu Gly Ile Glu Ala Ser Ser
370 375 380

Glu Ala Gln Phe Tyr Thr Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn
385 390 395 400

Asn Ile Ser Ser Asp Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp
405 410 415

Phe Gln Pro Asp Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser
420 425 430

Ile Leu Leu Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val
435 440 445

Ser Leu Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr
450 455 460

Lys Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
465 470 475 480

Pro Val Ser Gln

<210> 64

<211> 256

<212> PRT

<213> Homo sapiens

<400> 64

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Met Phe Gln Thr Gly Gly Leu Ile Val Phe Tyr Gly Leu Leu Ala Gln
1               5                  10                  15

Thr Met Ala Gln Phe Gly Gly Leu Pro Val Pro Leu Asp Gln Thr Leu
            20                  25                  30

Pro Leu Asn Val Asn Pro Ala Leu Pro Leu Ser Pro Thr Gly Leu Ala
        35                  40                  45

Gly Ser Leu Thr Asn Ala Leu Ser Asn Gly Leu Leu Ser Gly Gly Leu
    50                  55                  60

Leu Gly Ile Leu Glu Asn Leu Pro Leu Leu Asp Ile Leu Lys Pro Gly
65                  70                  75                  80

Gly Gly Thr Ser Gly Gly Leu Leu Gly Gly Leu Leu Gly Lys Val Thr
                85                  90                  95

Ser Val Ile Pro Gly Leu Asn Asn Ile Ile Asp Ile Lys Val Thr Asp
            100                 105                 110

Pro Gln Leu Leu Glu Leu Gly Leu Val Gln Ser Pro Asp Gly His Arg
        115                 120                 125

Leu Tyr Val Thr Ile Pro Leu Gly Ile Lys Leu Gln Val Asn Thr Pro
    130                 135                 140

Leu Val Gly Ala Ser Leu Leu Arg Leu Ala Val Lys Leu Asp Ile Thr
145                 150                 155                 160

Ala Glu Ile Leu Ala Val Arg Asp Lys Gln Glu Arg Ile His Leu Val
                165                 170                 175

Leu Gly Asp Cys Thr His Ser Pro Gly Ser Leu Gln Ile Ser Leu Leu
            180                 185                 190

Asp Gly Leu Gly Pro Leu Pro Ile Gln Gly Leu Leu Asp Ser Leu Thr
        195                 200                 205

Gly Ile Leu Asn Lys Val Leu Pro Glu Leu Val Gln Gly Asn Val Cys
    210                 215                 220

Pro Leu Val Asn Glu Val Leu Arg Gly Leu Asp Ile Thr Leu Val His
225                 230                 235                 240

Asp Ile Val Asn Met Leu Ile His Gly Leu Gln Phe Val Ile Lys Val
                245                 250                 255
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<210> 65

<211> 791

<212> PRT

<213> Homo sapiens

<400> 65

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Met Ser Gln Pro Arg Pro Arg Tyr Val Val Asp Arg Ala Ala Tyr Ser
1               5                  10                  15

Leu Thr Leu Phe Asp Asp Glu Phe Glu Lys Lys Asp Arg Thr Tyr Pro
            20                  25                  30

Val Gly Glu Lys Leu Arg Asn Ala Phe Arg Cys Ser Ser Ala Lys Ile
        35                  40                  45

Lys Ala Val Val Phe Gly Leu Leu Pro Val Leu Ser Trp Leu Pro Lys
    50                  55                  60

Tyr Lys Ile Lys Asp Tyr Ile Ile Pro Asp Leu Leu Gly Gly Leu Ser
65                  70                  75                  80

Gly Gly Ser Ile Gln Val Pro Gln Gly Met Ala Phe Ala Leu Leu Ala
                85                  90                  95

Asn Leu Pro Ala Val Asn Gly Leu Tyr Ser Ser Phe Phe Pro Leu Leu
            100                 105                 110

Thr Tyr Phe Phe Leu Gly Gly Val His Gln Met Val Pro Gly Thr Phe
        115                 120                 125

Ala Val Ile Ser Ile Leu Val Gly Asn Ile Cys Leu Gln Leu Ala Pro
    130                 135                 140

Glu Ser Lys Phe Gln Val Phe Asn Asn Ala Thr Asn Glu Ser Tyr Val
145                 150                 155                 160

Asp Thr Ala Ala Met Glu Ala Glu Arg Leu His Val Ser Ala Thr Leu
                165                 170                 175

Ala Cys Leu Thr Ala Ile Ile Gln Met Gly Leu Gly Phe Met Gln Phe
            180                 185                 190

Gly Phe Val Ala Ile Tyr Leu Ser Glu Ser Phe Ile Arg Gly Phe Met
        195                 200                 205

Thr Ala Ala Gly Leu Gln Ile Leu Ile Ser Val Leu Lys Tyr Ile Phe
    210                 215                 220

Gly Leu Thr Ile Pro Ser Tyr Thr Gly Pro Gly Ser Ile Val Phe Thr
225                 230                 235                 240
```

```
Phe Ile Asp Ile Cys Lys Asn Leu Pro His Thr Asn Ile Ala Ser Leu
                245                 250                 255

Ile Phe Ala Leu Ile Ser Gly Ala Phe Leu Val Leu Val Lys Glu Leu
            260                 265                 270

Asn Ala Arg Tyr Met His Lys Ile Arg Phe Pro Ile Pro Thr Glu Met
        275                 280                 285

Ile Val Val Val Val Ala Thr Ala Ile Ser Gly Gly Cys Lys Met Pro
    290                 295                 300

Lys Lys Tyr His Met Gln Ile Val Gly Glu Ile Gln Arg Gly Phe Pro
305                 310                 315                 320

Thr Pro Val Ser Pro Val Val Ser Gln Trp Lys Asp Met Ile Gly Thr
                325                 330                 335

Ala Phe Ser Leu Ala Ile Val Ser Tyr Val Ile Asn Leu Ala Met Gly
            340                 345                 350

Arg Thr Leu Ala Asn Lys His Gly Tyr Asp Val Asp Ser Asn Gln Glu
        355                 360                 365

Met Ile Ala Leu Gly Cys Ser Asn Phe Phe Gly Ser Phe Phe Lys Ile
    370                 375                 380

His Val Ile Cys Cys Ala Leu Ser Val Thr Leu Ala Val Asp Gly Ala
385                 390                 395                 400

Gly Gly Lys Ser Gln Val Ala Ser Leu Cys Val Ser Leu Val Val Met
                405                 410                 415

Ile Thr Met Leu Val Leu Gly Ile Tyr Leu Tyr Pro Leu Pro Lys Ser
            420                 425                 430

Val Leu Gly Ala Leu Ile Ala Val Asn Leu Lys Asn Ser Leu Lys Gln
        435                 440                 445

Leu Thr Asp Pro Tyr Tyr Leu Trp Arg Lys Ser Lys Leu Asp Cys Cys
    450                 455                 460

Ile Trp Val Val Ser Phe Leu Ser Ser Phe Phe Leu Ser Leu Pro Tyr
465                 470                 475                 480

Gly Val Ala Val Gly Val Ala Phe Ser Val Leu Val Val Val Phe Gln
                485                 490                 495

Thr Gln Phe Arg Asn Gly Tyr Ala Leu Ala Gln Val Met Asp Thr Asp
            500                 505                 510
```

```
Ile Tyr Val Asn Pro Lys Thr Tyr Asn Arg Ala Gln Asp Ile Gln Gly
        515                 520                 525

Ile Lys Ile Ile Thr Tyr Cys Ser Pro Leu Tyr Phe Ala Asn Ser Glu
    530                 535                 540

Ile Phe Arg Gln Lys Val Ile Ala Lys Thr Gly Met Asp Pro Gln Lys
545                 550                 555                 560

Val Leu Leu Ala Lys Gln Lys Tyr Leu Lys Lys Gln Glu Lys Arg Arg
                565                 570                 575

Met Arg Pro Thr Gln Gln Arg Arg Ser Leu Phe Met Lys Thr Lys Thr
            580                 585                 590

Val Ser Leu Gln Glu Leu Gln Gln Asp Phe Glu Asn Ala Pro Pro Thr
        595                 600                 605

Asp Pro Asn Asn Asn Gln Thr Pro Ala Asn Gly Thr Ser Val Ser Tyr
    610                 615                 620

Ile Thr Phe Ser Pro Asp Ser Ser Ser Pro Ala Gln Ser Glu Pro Pro
625                 630                 635                 640

Ala Ser Ala Glu Ala Pro Gly Glu Pro Ser Asp Met Leu Ala Ser Val
                645                 650                 655

Pro Pro Phe Val Thr Phe His Thr Leu Ile Leu Asp Met Ser Gly Val
            660                 665                 670

Ser Phe Val Asp Leu Met Gly Ile Lys Ala Leu Ala Lys Leu Ser Ser
        675                 680                 685

Thr Tyr Gly Lys Ile Gly Val Lys Val Phe Leu Val Asn Ile His Ala
    690                 695                 700

Gln Val Tyr Asn Asp Ile Ser His Gly Gly Val Phe Glu Asp Gly Ser
705                 710                 715                 720

Leu Glu Cys Lys His Val Phe Pro Ser Ile His Asp Ala Val Leu Phe
                725                 730                 735

Ala Gln Ala Asn Ala Arg Asp Val Thr Pro Gly His Asn Phe Gln Gly
            740                 745                 750

Ala Pro Gly Asp Ala Glu Leu Ser Leu Tyr Asp Ser Glu Glu Asp Ile
        755                 760                 765

Arg Ser Tyr Trp Asp Leu Glu Gln Glu Met Phe Gly Ser Met Phe His
    770                 775                 780

Ala Glu Thr Leu Thr Ala Leu
```

785 790

<210> 66

<211> 243

<212> PRT

<213> Homo sapiens

<400> 66

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe
1 5 10 15

Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp
20 25 30

Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly
35 40 45

Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly
50 55 60

Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser
65 70 75 80

Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu
85 90 95

Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu
100 105 110

Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro
115 120 125

Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr
130 135 140

Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val
145 150 155 160

Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met
165 170 175

Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala
180 185 190

Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp Gly Gly Asn His
195 200 205

Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu
210 215 220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser
225 230 235 240

Leu Pro Arg

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 67
acacgaatgg tagatacagt g 21

<210> 68

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 68
atacttgtga gctgttccat g 21

<210> 69

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 69
actgttacct tgcatggact g 21

<210> 70

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 70
caatgagaac acatggacat g 21

<210> 71

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 71
ccatgaaagc tccatgtcta c 21

<210> 72

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 72
agagatggca catattctgt c 21

<210> 73

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 73
atcggctgaa gtcaagcatc g 21

<210> 74

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 74
tggtcagtga ggactcagct g 21

<210> 75

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 75
tttctctgct tgatgcactt g 21

<210> 76

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 76
gtgagcactg ggaagcagct c 21

<210> 77

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 77
ggcaaatgct agagacgtga c 21

<210> 78

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 78
aggtgtcctt cagctgccaa g 21

<210> 79

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 79
gttaagtgct ctctggattt g 21

<210> 80

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 80
atcctgattg ctgtgtgcaa g 21

<210> 81

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 81
ctcttctagc tggtcaacat c 21

<210> 82

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 82
ccagcaacaa cttacgtggt c 21

<210> 83

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 83
cctttattca cccaatcact c 21

<210> 84

<211> 2165

<212> DNA

<213> Homo sapiens

<400> 84
agaacagcgc agtttgccct ccgctcacgc agagcctctc cgtggcctcc gcaccttgag 60

cattaggcca gttctcctct tctctctaat ccatccgtca cctctcctgt catccgtttc 120

catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt ttggttctga 180

gtctcctcaa gctgggatca gggcagtggc aggtgtttgg gccagacaag cctgtccagg 240

ccttggtggg ggaggacgca gcattctcct gtttcctgtc tcctaagacc aatgcagagg 300

ccatggaagt gcggttcttc aggggccagt tctctagcgt ggtccacctc tacagggacg 360

ggaaggacca gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 420

attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg ttggatgctg 480

gcctctatgg gtgcaggatt agttcccagt cttactacca gaaggccatc tgggagctac 540

aggtgtcagc actgggctca gttcctctca tttccatcac gggatatgtt gatagagaca 600
tccagctact ctgtcagtcc tcgggctggt tcccccggcc cacagcgaag tggaaaggtc 660
cacaaggaca ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 720
atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt tccatgcggc 780
atgctcatct gagccgagag gtggaatcca gggtacagat aggagatacc tttttcgagc 840
ctatatcgtg gcacctggct accaaagtac tgggaatact ctgctgtggc ctatttttg 900
gcattgttgg actgaagatt ttcttctcca aattccagtg taagcgagag agagaagcat 960
gggccggtgc cttattcatg gttccagcag ggacaggatc agagatgctc ccacatccag 1020
ctgcttctct tcttctagtc ctagcctcca ggggcccagg cccaaaaaag gaaaatccag 1080
gcggaactgg actggagaag aaagcacgga caggcagaat tgagagacgc ccggaaacac 1140
gcagtggagg tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1200
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa gagatttaca 1260
aggaagagtg tggtggcttc tcagagtttc caagcaggga aacattactg ggaggtggac 1320
ggaggacaca ataaaaggtg gcgcgtggga gtgtgccggg atgatgtgga caggaggaag 1380
gagtacgtga ctttgtctcc cgatcatggg tactgggtcc tcagactgaa tggagaacat 1440
ttgtatttca cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1500
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat aaatgaccag 1560
tcccttattt ataccctgac atgtcggttt gaaggcttat tgaggcccta cattgagtat 1620
ccgtcctata atgagcaaaa tggaactccc atagtcatct gcccagtcac ccaggaatca 1680
gagaaagagg cctcttggca aagggcctct gcaatcccag agacaagcaa cagtgagtcc 1740
tcctcacagg caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc 1800
acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg cagcagccgg 1860
ccaaggtggc ttccagatga agggggactg gcctgtccac atgggagtca ggtgtcatgg 1920
ctgccctgag ctgggaggga agaaggctga cattacattt agtttgctct cactccatct 1980
ggctaagtga tcttgaaata ccacctctca ggtgaagaac cgtcaggaat tcccatctca 2040
caggctgtgg tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2100
acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa aaaaaaaaaa 2160
aaaaa 2165

<210> 85
<211> 347
<212> PRT
<213> Homo sapiens

<400> 85

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Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly Ser
1               5                  10                  15

Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu Val
            20                  25                  30

Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys Thr Asn Ala
        35                  40                  45

Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe Ser Ser Val Val
    50                  55                  60

His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe Met Gln Met Pro Gln
65                  70                  75                  80

Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp Ser Ile Ala Glu Gly Arg
                85                  90                  95

Ile Ser Leu Arg Leu Glu Asn Ile Thr Val Leu Asp Ala Gly Leu Tyr
            100                 105                 110

Gly Cys Arg Ile Ser Ser Gln Ser Tyr Tyr Gln Lys Ala Ile Trp Glu
        115                 120                 125

Leu Gln Val Ser Ala Leu Gly Ser Val Pro Leu Ile Ser Ile Thr Gly
    130                 135                 140

Tyr Val Asp Arg Asp Ile Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe
145                 150                 155                 160

Pro Arg Pro Thr Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser
                165                 170                 175

Thr Asp Ser Arg Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu
            180                 185                 190

Ile Ser Leu Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met
        195                 200                 205

Arg His Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly
    210                 215                 220

Asp Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu
225                 230                 235                 240

Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys Ile
                245                 250                 255

Phe Phe Ser Lys Phe Gln Cys Lys Arg Glu Arg Glu Ala Trp Ala Gly
            260                 265                 270

Ala Leu Phe Met Val Pro Ala Gly Thr Gly Ser Glu Met Leu Pro His
```

275 280 285

Pro Ala Ala Ser Leu Leu Leu Val Leu Ala Ser Arg Gly Pro Gly Pro
290 295 300

Lys Lys Glu Asn Pro Gly Gly Thr Gly Leu Glu Lys Lys Ala Arg Thr
305 310 315 320

Gly Arg Ile Glu Arg Arg Pro Glu Thr Arg Ser Gly Gly Asp Ser Gly
325 330 335

Ser Arg Asp Gly Ser Pro Glu Ala Leu Arg Phe
340 345

<210> 86

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 86
attcatggtt ccagcaggga c 21

<210> 87

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 87
gggagacaaa gtcacgtact c 21

<210> 88
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 88
tcctggtgtt cgtggtctgc tt 22

<210> 89
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 89
gagagtcctg gcttttgtgg gc 22

<210> 90
<211> 15
<212> PRT
<213> Homo sapiens

<400> 90

Gly Ser Ser Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Cys
1 5 10 15

<210> 91
<211> 16
<212> PRT
<213> Homo sapiens

<400> 91

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
1 5 10 15

<210> 92
<211> 15
<212> PRT
<213> Homo sapiens

<400> 92

Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu Cys
1 5 10 15

<210> 93
<211> 13
<212> PRT
<213> Homo sapiens

<400> 93

Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg
1 5 10

<210> 94
<211> 22
<212> PRT
<213> Homo sapiens

<400> 94

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1 5 10 15

Pro Ala Ile Lys Leu Gly
20

<210> 95
<211> 14
<212> PRT
<213> Homo sapiens

<400> 95

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly
1 5 10

<210> 96
<211> 22
<212> PRT
<213> Homo sapiens

<400> 96

Gly Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe
1 5 10 15

Asn Ser Met Arg Phe Pro
20

<210> 97
<211> 30
<212> PRT
<213> Homo sapiens

<400> 97

Ala Lys Glu Phe Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Arg Ala
1 5 10 15

Lys Ala His Lys Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
20 25 30

<210> 98
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 98
tcctgctcgt cgctctcctg at 22

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 99

tcgctttttg tcgtatttgc 20

<210> 100
<211> 15
<212> PRT
<213> Homo sapiens

<400> 100

His Asn Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser
1 5 10 15

<210> 101
<211> 15
<212> PRT
<213> Homo sapiens

<400> 101

Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Ala
1 5 10 15

<210> 102
<211> 619
<212> PRT
<213> Homo sapiens

<400> 102

Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp Ser His
1 5 10 15

Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr Asn His
20 25 30

Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg
35 40 45

Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu
50 55 60

Lys His Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn
65 70 75 80

Lys Leu Leu Gln Ile Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr
85 90 95

Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg
100 105 110

Gly Ser Leu Arg Glu Val Leu Asn Asp Thr Ile Ser Tyr Pro Asp Gly
115 120 125

Thr Phe Met Asp Trp Glu Phe Lys Ile Ser Val Leu Tyr Asp Ile Ala
130 135 140

Lys Gly Met Ser Tyr Leu His Ser Ser Lys Thr Glu Val His Gly Arg

```
145                 150                 155                 160

Leu Lys Ser Thr Asn Cys Val Val Asp Ser Arg Met Val Val Lys Ile
                165                 170                 175

Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro Pro Lys Lys Asp Leu Trp
            180                 185                 190

Thr Ala Pro Glu His Leu Arg Gln Ala Asn Ile Ser Gln Lys Gly Asp
        195                 200                 205

Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu Ile Ile Leu Arg Lys Glu
    210                 215                 220

Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg Asn Glu Lys Ile Phe Arg
225                 230                 235                 240

Val Glu Asn Ser Asn Gly Met Lys Pro Phe Arg Pro Asp Leu Phe Leu
                245                 250                 255

Glu Thr Ala Glu Glu Lys Glu Leu Glu Val Tyr Leu Leu Val Lys Asn
            260                 265                 270

Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro Asp Phe Lys Lys Ile Glu
        275                 280                 285

Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe His Asp Gln Lys Asn Glu
    290                 295                 300

Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu Gln Leu Tyr Ser Arg Asn
305                 310                 315                 320

Leu Glu His Leu Val Glu Glu Arg Thr Gln Leu Tyr Lys Ala Glu Arg
                325                 330                 335

Asp Arg Ala Asp Arg Leu Asn Phe Met Leu Leu Pro Arg Leu Val Val
            340                 345                 350

Lys Ser Leu Lys Glu Lys Gly Phe Val Glu Pro Glu Leu Tyr Glu Glu
        355                 360                 365

Val Thr Ile Tyr Phe Ser Asp Ile Val Gly Phe Thr Thr Ile Cys Lys
    370                 375                 380

Tyr Ser Thr Pro Met Glu Val Val Asp Met Leu Asn Asp Ile Tyr Lys
385                 390                 395                 400

Ser Phe Asp His Ile Val Asp His His Asp Val Tyr Lys Val Glu Thr
                405                 410                 415

Ile Gly Asp Ala Tyr Met Val Ala Ser Gly Leu Pro Lys Arg Asn Gly
            420                 425                 430
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Asn Arg His Ala Ile Asp Ile Ala Lys Met Ala Leu Glu Ile Leu Ser
435 440 445

Phe Met Gly Thr Phe Glu Leu Glu His Leu Pro Gly Leu Pro Ile Trp
450 455 460

Ile Arg Ile Gly Val His Ser Gly Pro Cys Ala Ala Gly Val Val Gly
465 470 475 480

Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly Asp Thr Val Asn Thr Ala
485 490 495

Ser Arg Met Glu Ser Thr Gly Leu Pro Leu Arg Ile His Val Ser Gly
500 505 510

Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu Cys Gln Phe Leu Tyr Glu
515 520 525

Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg Gly Asn Glu Thr Thr Tyr
530 535 540

Trp Leu Thr Gly Met Lys Asp Gln Lys Phe Asn Leu Pro Thr Pro Pro
545 550 555 560

Thr Val Glu Asn Gln Gln Arg Leu Gln Ala Glu Phe Ser Asp Met Ile
565 570 575

Ala Asn Ser Leu Gln Lys Arg Gln Ala Ala Gly Ile Arg Ser Gln Lys
580 585 590

Pro Arg Arg Val Ala Ser Tyr Lys Lys Gly Thr Leu Glu Tyr Leu Gln
595 600 605

Leu Asn Thr Thr Asp Lys Glu Ser Thr Tyr Phe
610 615

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 103
gctggtaact atcttcctgc 20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: Oligonucleotide

<400> 104
gaagaatgtt gtccagaggt 20

<210> 105
<211> 15
<212> PRT
<213> Homo sapiens

<400> 105

Leu Ile Asn Lys Val Pro Leu Pro Val Asp Lys Leu Ala Pro Leu
1 5 10 15

<210> 106
<211> 15
<212> PRT
<213> Homo sapiens

<400> 106

Ser Glu Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
1 5 10 15

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 107
tgttttcaac taccaggggc 20

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 108
tgttggcttt ggcagagtcc 20

<210> 109
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 109
gaggcagagt tcaggcttca ccga 24

<210> 110

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

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 110
tgttggcttt ggcagagtcc 20

<210> 111
<211> 56
<212> PRT
<213> Homo sapiens

<400> 111

Thr Gly Met Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val
1 5 10 15

Thr Ser Val Phe Gln Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln
20 25 30

Ser Ser Gly Phe Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu
35 40 45

Pro Ala Met Leu Gln Ala Val Arg
50 55

<210> 112
<211> 53
<212> PRT
<213> Homo sapiens

<400> 112

Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val
1 5 10 15

Phe Asn Tyr Gln Gly Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly
20 25 30

Phe Thr Glu Cys Arg Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met
35 40 45

Leu Gln Ala Val Arg
50

<210> 113
<211> 14
<212> PRT
<213> Homo sapiens

<400> 113

Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe
1 5 10

<210> 114
<211> 12
<212> PRT
<213> Homo sapiens

<400> 114

Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro
1 5 10

<210> 115
<211> 12
<212> PRT
<213> Homo sapiens

<400> 115

Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala
1 5 10

<210> 116
<211> 13
<212> PRT
<213> Homo sapiens

<400> 116

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly
1 5 10

<210> 117
<211> 816
<212> DNA
<213> Homo sapiens

<400> 117
gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg 60

ctggccggct gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 120

aaccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt 180

tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag 240

gcagtgcgag ccctgatgat cgtaggcatc gtcctgggtg ccattggcct cctggtatcc 300

atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg 360

acactgacct ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 420

gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc 480

atgggtggga tggtgcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg 540

ggctgggtcg ctggaggcct cacactaatt gggggtgtga tgatgtgcat cgcctgccgg 600

ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt 660

gttgcctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 720

aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta tccttccaag 780

cacgactatg tgtaatgctc taagacctct cagcac 816

<210> 118

<211> 261
<212> PRT
<213> Homo sapiens

<400> 118

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Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1               5                  10                  15

Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
            20                  25                  30

Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
        35                  40                  45

Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
    50                  55                  60

Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65                  70                  75                  80

Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
                85                  90                  95

Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
            100                 105                 110

Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
        115                 120                 125

Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
    130                 135                 140

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145                 150                 155                 160

Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
                165                 170                 175

Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
            180                 185                 190

Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
        195                 200                 205

Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
    210                 215                 220

Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225                 230                 235                 240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
                245                 250                 255
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Lys His Asp Tyr Val
260

<210> 119
<211> 227
<212> DNA
<213> Homo sapiens

<400> 119
gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg 60

ctggccggct gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 120

aaccccgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt 180

tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttcc 227

<210> 120
<211> 69
<212> PRT
<213> Homo sapiens

<400> 120

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15

Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30

Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35 40 45

Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60

Pro Tyr Phe Thr Ile
65

<210> 121
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 121
aatgagagga aagagaaaac 20

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 122
atggtagaag agtaggcaat 20

<210> 123
<211> 15
<212> PRT
<213> Homo sapiens

<400> 123

Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Lys Met Val Cys
1 5 10 15

<210> 124
<211> 11
<212> PRT
<213> Homo sapiens

<400> 124

Cys Leu Gly Phe Asn Phe Lys Glu Met Phe Lys
1 5 10

<210> 125
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 125
taatgatgaa ccctacactg agc 23

<210> 126
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 126
atggacaaat gccctacctt 20

<210> 127
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 127
agtgctggaa ggatgtgcgt gt 22

<210> 128
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 128
ttgaggtggt tgttgggttt 20

<210> 129
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 129
agatgtgctg aggctgtaga 20

<210> 130
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 130
atgaaggttg attatttgag 20

<210> 131
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 131
agccgcatac tcccttaccc tct 23

<210> 132
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 132
gcagcagccc aaacaccaca 20

<210> 133
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 133
ctgagccgag aggtggaatc 20

<210> 134
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Oligonucleotide

<400> 134
ctctctcgct tacactggaa 20

<210> 135
<211> 14
<212> PRT
<213> Homo sapiens

<400> 135

Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu
1 5 10

<210> 136
<211> 15
<212> PRT
<213> Homo sapiens

<400> 136

Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser
1 5 10 15

<210> 137
<211> 32
<212> PRT
<213> Homo sapiens

<400> 137

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

Gly Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly
20 25 30