-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala G
1               5                   10                  15

Leu Thr Met Gly
            20
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: <Unknown>
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
Gly Asn His Ala Ala Gly Ile Leu Thr
1               5
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
ATGAACCTTC CTTCTACAAA GGTTCCCTGG GCCGCCGTGA CGCTGCTGCT GCTGC60

CTGCCGCCGG CGCTGCTGTC GCTTGGGGTG GACGCGCAGC CTCTGCCCGA CTGC120

CAGAAGACGT GTTCCTGCCG TCTCTACGAA CTGTTGCACG GAGCTGGCAA CCAC180

GGCATCCTCA CTCTGGGAAA GCGGCGACCT GGACCCCCAG GCCTCCAAGG ACGG240

CGCCTCCTTC AGGCCAACGG TAACCACGCA GCTGGCATCC TGACCATGGG CCGC300

GGCGCAGAGC TAGAGCCATA TCCCTGCCCT GGTCGCCGCT GTCCGACTGC AACC360

GCTTTAGCGC CCCGGGGCGG ATCCAGAGTC TGA                       393
```

(2) INFORMATION FOR SEQ ID NO: 15: