-continued

```
atgtgtacct ataaccagac cgttcagctg gatattacgg ccttttaaa gaccgtaaag     60

aaaaataagc acaagtttta tccggccttt attcacattc ttgcccgcct gatgaatgct    120

catccggaat tccgtatggc aatgaaagac ggtgagctgg tgatatggga tagtgttcac    180

ccttgttaca ccgttttcca tgagcaaact gaaacgtttt catcgctctg gagtgaatac    240

cacgacgatt tccggcagtt tctacacata tattcgcaag atgtggcgtg ttacggtgaa    300

aacctggcct atttccctaa agggtttatt gagaatatgt ttttcgtctc agccaatccc    360

tgggtgagtt tcaccagttt tgatttaaac gtggccaata tggacaactt cttcgccccc    420

gttttcacca tgggcaaata ttatacgcaa ggcgacaagg tgctgatgcc gctggcgatt    480

caggttcatc atgccgtctg tgatggcttc catgtcggca gaatgcttaa tgaattacaa    540

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<210> SEQ ID NO 67
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: CAT N-terminal fragment amino acid sequence

<400> SEQUENCE: 67

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
1               5                   10                  15

His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln
            20                  25                  30


<210> SEQ ID NO 68
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: CAT C-terminal fragment  amino acid sequence

<400> SEQUENCE: 68

Met Cys Thr Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu
1               5                   10                  15

Lys Thr Val Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His
            20                  25                  30

Ile Leu Ala Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met
        35                  40                  45

Lys Asp Gly Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr
    50                  55                  60

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

His Asp Asp Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala
                85                  90                  95

Cys Tyr Gly Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn
            100                 105                 110

Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp
        115                 120                 125

Leu Asn Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met
    130                 135                 140

Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
145                 150                 155                 160
```