FIGURE 1. FUP MSP-1 p42 amino acid sequence

AISVTMDNIL SGFENEYDVI YLKPLAGVYR SLKKQIEKNI FTFNLNLNDI LNSRLKKRKY 60
FLDVLESDLM QFKHISSNEY IIEDSFKLLN SEQKNTLLKS YKYIKESVEN DIKEAQEGIS 120
YYEKVLAKYK DDLESIKKVI KEEKEKFPSS PPTTPPSPAK TDEQKKESKF LPFLTNIETL 180
YNNLVNKIDD YLINLKAKIN DCNVEKDEAH VKITKLSDLK AIDDKIDLFK NHNDFEAIKK 240
LINDDTKKDM LGKLLSTGLV QNFPNTIISK LIEGKFQDML ***NISQHQCVKK QCPENSGCFR*** ***300***
HLDEREECKC LLNYKQEGDK CVENPNPTCN ENNGGCDADA KCTEEDSGSN GKKITCECTK ***360***
PDSYPLFDGI FCS 373

FIGURE 2. Alignment of the MSP-1 p42 amino acid sequences from the three *P. falciparum* strains FUP, 3D7, and FVO.

```
            10         20         30         40         50
   --- ------+---------+---------+---------+---------+---------
   1 AIS-VTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRK FUP_P42
   1 +++-++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
   1 +VTPSVI+++++KI++++E+L+++++++++++++++L+++VM+++V+VK+++++++N++E FVO_P42

   60         70         80         90         100        110
   +---------+---------+---------+---------+---------+----------
  60 YFLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGI FUP_P42
  60 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
  61 N+KN++++++IPYKDLT+SN+VVK+PY+F++K+KRDKF+S++N+++DSIDT++N++NDVL FVO_P42

   120        130        140        150        160        170
   +---------+---------+---------+---------+---------+---------
 120 SYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIET FUP_P42
 120 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
 121 G++KILSE+++S++D++++Y+N--------------------+K+GENE+Y++++N++++ FVO_P42

   180        190        200        210        220        230
   +---------+---------+---------+---------+---------+---------
 180 LYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIK FUP_P42
 180 +++++++++++++++++++++++++++++++++++++++++++++++++++++++++E+++ 3D7_P42
 161 ++KTVND+++LFV+H+E++VLNYTY++SNVE+++KELNY++TIQ++LAD++KN+N+VG+A FVO_P42

   240        250        260        270        280        290
   +---------+---------+ ---------+---------+---------+--------
 240 KLINDDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDML***NISQHQCVKKQCPENSGC*** FUP_P42
 240 ++++++++++++++++++++-++++++++++++++++++++++++++++++++++++++++ 3D7_P42
 221 D+ST+YNHNNL+TKF++++M+FENLAKTVL+N+LD+NL+G++++++++++++++***Q***++++ FVO_P42

    300        310        320        330        340        350
   -+---------+---------+---------+---------+---------+--------
 299 ***FRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCEC*** FUP_P42
 299 ++++++++++++++++++++++++++++++++++***T***++++++++***SR***+++++++ 3D7_P42
 281 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ FVO_P42

    360        370
   -+---------+---
 359 ***TKPDSYPLFDGIFCS*** FUP_P42
 359 +++++++++++++++++ 3D7_P42
 341 +++++++++++++++++ FVO_P42
```

FIGURE 3. Alignment of the amino acid sequences from the three N-terminally truncated subunits of Construct A, Construct B, and Construct C relative to the FUP MSP-1 p42 sequence.

```
          10         20         30         40         50         60
    ---------+---------+---------+---------+---------+---------+
1   AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  FUP_p42

          70         80         90         100        110        120
    ---------+---------+---------+---------+---------+---------+
61  FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  FUP_p42

          130        140        150        160        170        180
    ---------+---------+---------+---------+---------+---------+
121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  FUP_p42

          190        200        210        220        230        240
    ---------+---------+---------+---------+---------+---------+
181 YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  FUP_p42

  1                   garsggggtAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  Construct A
  1       garsLKPLAGVYRSLKKQggggtAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  Construct B

          250        260        270        280        290        300
    ---------+---------+ ---------+---------+---------+---------+
241 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  FUP_p42

 42 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct A
 59 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct B
  1 garsggggtMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct C

          310        320        330        340        350        360
    ---------+---------+---------+--------+---------+---------+
301 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK  FUP_p42

102 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK  Construct A
119 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK  Construct B
 61 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK  Construct C

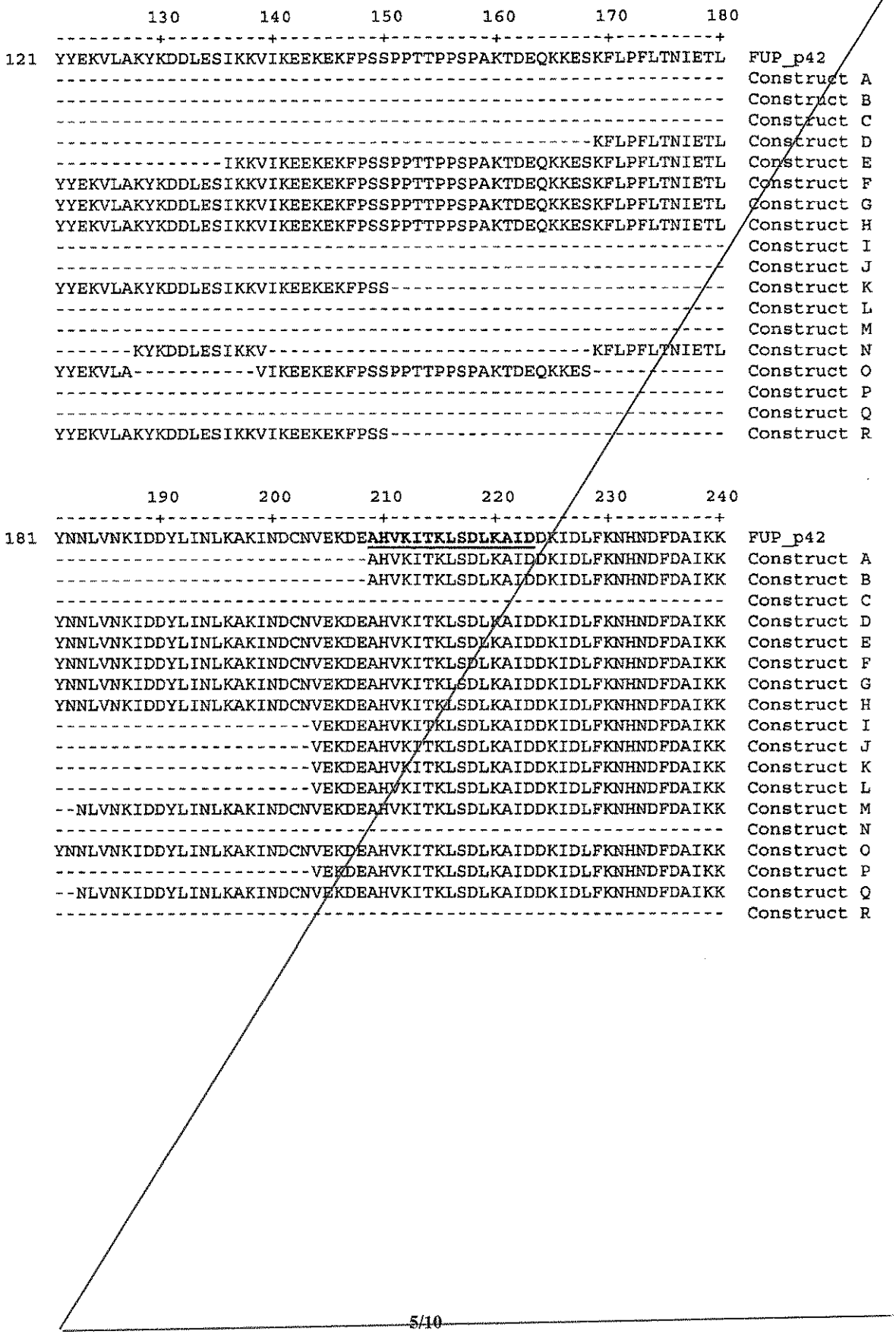
          370
    ---------+---
361 PDSYPLFDGIFCS   FUP_p42

162 PDSYPLFDGIFCS   Construct A
179 PDSYPLFDGIFCS   Construct B
121 PDSYPLFDGIFCS   Construct C
```

FIGURE 4. Alignment of the amino acid sequences from all MSP-1 C-terminal subunit protein Constructs relative to the FUP MSP-1 p33 sequence.

```
          10        20        30        40        50        60
          +---------+---------+---------+---------+---------+
1   AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  FUP_p42
    ------------------------------------------------------------  Construct A
    ----------LKPLAGVYRSLKKQ------------------------------------  Construct B
    ------------------------------------------------------------  Construct C
    ------------------------------------------------------------  Construct D
    ------------------------------------------------------------  Construct E
    ------------------------------------------------------------  Construct F
    ------------------------------------------------------------  Construct G
    AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  Construct H
    AISVTMDNILSGFENEYDVI--------------------------------------  Construct I
    AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNI-----------------  Construct J
    ------------------------------------------------------------  Construct K
    ------------------------------------------------------------  Construct L
    ------------------------------------------------------------  Construct M
    ------DNILS---------YLKPLAGVYRSLKKQI-------------LNSRL-----  Construct N
    AISVTM-----GFENEYDVI---------------EKNIFTFNLNLNDI-----KKRKY  Construct O
    ------------------------------------------------------------  Construct P
    ------------------------------------------------------------  Construct Q
    AISVTMDNILSGFENEYDVI--------------------------------------  Construct R


          70        80        90        100       110       120
          +---------+---------+---------+---------+---------+
61  FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  FUP_p42
    ------------------------------------------------------------  Construct A
    ------------------------------------------------------------  Construct B
    ------------------------------------------------------------  Construct C
    ------------------------------------------------------------  Construct D
    ------------------------------------------------------------  Construct E
    ------------------------------------------KFAQEGIS  Construct F
    ----------------------------NTLLKSYKYIKESVENDIKFAQEGIS  Construct G
    FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  Construct H
    ------------------------------------------------------------  Construct I
    ------------------------------------------------------------  Construct J
    ------------------------------------------------AQEGIS  Construct K
    ----------ISSNEYIIEDSFKLLNSEQKNTL----------------------  Construct L
    ------------------------------------------------------------  Construct M
    ---VLESDL------------------------------------------------  Construct N
    FLD------MQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  Construct O
    ------------------------------------------------------------  Construct P
    ------------------------------------------------------------  Construct Q
    ----------ISSNEYIIEDSFKLLNSEQKNTL----------------AQEGIS  Construct R
```


130 140 150 160 170 180
121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL FUP_p42
Construct A
Construct B
Construct C
KFLPFLTNIETL Construct D
IKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL Construct E
YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL Construct F
YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL Construct G
YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL Construct H
Construct I
Construct J
YYEKVLAKYKDDLESIKKVIKEEKEKFPSS Construct K
Construct L
Construct M
KYKDDLESIKKV KFLPFLTNIETL Construct N
YYEKVLA VIKEEKEKFPSSPPTTPPSPAKTDEQKKES Construct O
Construct P
Construct Q
YYEKVLAKYKDDLESIKKVIKEEKEKFPSS Construct R
190 200 210 220 230 240
181 YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK FUP_p42
AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct A
AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct B
Construct C
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct D
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct E
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct F
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct G
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct H
VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct I
VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct J
VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct K
VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct L
NLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct M
Construct N
YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct O
VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct P
NLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK Construct Q
Construct R

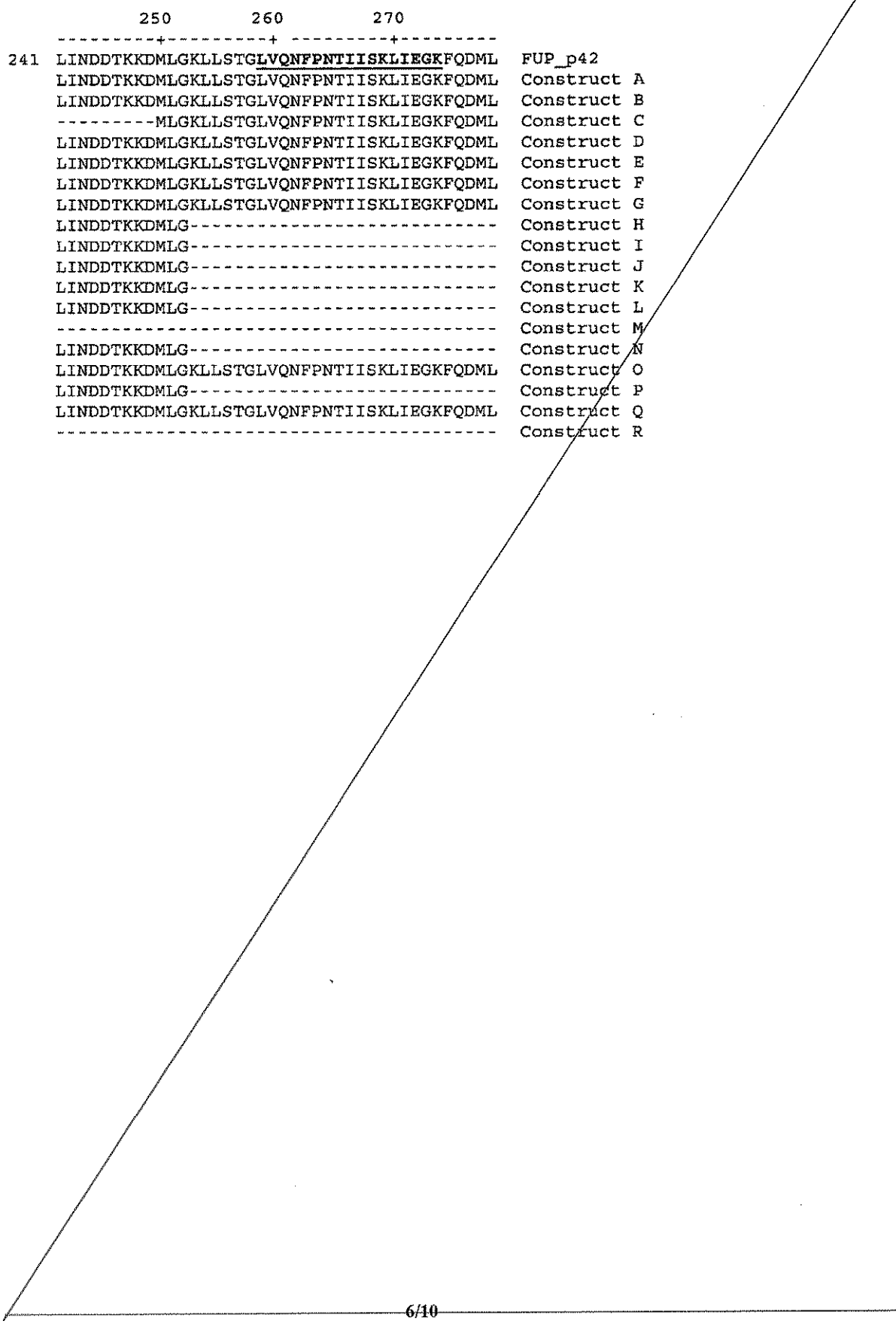

250
260
270
241 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML FUP_p42
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct A
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct B
MLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct C
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct D
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct E
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct F
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct G
LINDDTKKDMLG Construct H
LINDDTKKDMLG Construct I
LINDDTKKDMLG Construct J
LINDDTKKDMLG Construct K
LINDDTKKDMLG Construct L
Construct M
LINDDTKKDMLG Construct N
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct O
LINDDTKKDMLG Construct P
LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML Construct Q
Construct R

FIGURE 1. FUP MSP-1 p42 amino acid sequence SEQ ID NO: 19

AISVTMDNIL SGFENEYDVI YLKPLAGVYR SLKKQIEKNI FTFNLNLNDI LNSRLKKRKY 60

FLDVLESDLM QFKHISSNEY IIEDSFKLLN SEQKNTLLKS YKYIKESVEN DIKFAQEGIS 120

YYEKVLAKYK DDLESIKKVI KEEKEKFPSS PPTTPPSPAK TDEQKKESKF LPFLTNIETL 180

YNNLVNKIDD YLINLKAKIN DCNVEKDEAH VKITKLSDLK AIDDKIDLFK NHNDFEAIKK 240

LINDDTKKDM LGKLLSTGLV QNFPNTIISK LIEGKFQDML ***NISQHQCVKK QCPENSGCFR*** ***300***

HLDEREECKC LLNYKQEGDK CVENPNPTCN ENNGGCDADA KCTEEDSGSN GKKITCECTK ***360***

PDSYPLFDGI FCS 373

FIGURE 2. Alignment of the MSP-1 p42 amino acid sequences from the three *P. falciparum* strains FUP SEQ ID NO:19, 3D7 SEQ ID NO:20, and FVO SEQ ID NO:21.

```
            10         20         30         40         50
    --- ------+---------+---------+---------+---------+---------
  1 AIS-VTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRK FUP_P42
  1 +++-++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
  1 +VTPSVI+++++KI++++E+L+++++++++++++L+++VM+++V+VK+++++++N++E FVO_P42

    60         70         80         90         100        110
    +---------+---------+---------+---------+---------+---------
 60 YFLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGI FUP_P42
 60 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
 61 N+KN++++++IPYKDLT+SN+VVK+PY+F++K+KRDKF+S++N+++DSIDT++N++NDVL FVO_P42

    120        130        140        150        160        170
    +---------+---------+---------+---------+---------+---------
120 SYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIET FUP_P42
120 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ 3D7_P42
121 G++KILSE+++S++D++++Y+N--------------------+K+GENE+Y++++N++++ FVO_P42

    180        190        200        210        220        230
    +---------+---------+---------+---------+---------+---------
180 LYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIK FUP_P42
180 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++E+++ 3D7_P42
161 ++KTVND+++LFV+H+E++VLNYTY++SNVE+++KELNY++TIQ++LAD++KN+N+VG+A FVO_P42

    240        250        260         270        280        290
    +---------+---------+ ---------+---------+---------+--------
240 KLINDDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDML***NISQHQCVKKQCPENSGC*** FUP_P42
240 ++++++++++++++++++++-++++++++++++++++++++++++++++++++++++++++ 3D7_P42
221 D+ST+YNHNNL+TKF++++M+FENLAKTVL+N+LD+NL+G+++++++++++++***Q++++*** FVO_P42

     300        310        320        330        340        350
    -+---------+---------+---------+---------+---------+--------
299 ***FRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCEC*** FUP_P42
299 ++++++++++++++++++++++++++++++++++++++++***T***++++++++***SR***+++++++ 3D7_P42
281 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ FVO_P42

     360        370
    -+---------+---
359 ***TKPDSYPLFDGIFCS*** FUP_P42
359 +++++++++++++++ 3D7_P42
341 +++++++++++++++ FVO_P42
```

FIGURE 3. Alignment of the amino acid sequences from the three N-terminally truncated subunits of Construct A SEQ ID NO:1, Construct B SEQ ID NO:2, and Construct C SEQ ID NO:3 relative to the FUP MSP-1 p42 sequence SEQ ID NO:19.

```
            10        20        30        40        50        60
    ---------+---------+---------+---------+---------+---------+
1   AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  FUP_p42

            70        80        90        100       110       120
    ---------+---------+---------+---------+---------+---------+
61  FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  FUP_p42

            130       140       150       160       170       180
    ---------+---------+---------+---------+---------+---------+
121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  FUP_p42

            190       200       210       220       230       240
    ---------+---------+---------+---------+---------+---------+
181 YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  FUP_p42

  1                   garsggggtAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  Construct A
  1       garsLKPLAGVYRSLKKQggggtAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  Construct B

          250       260       270       280       290       300
    ---------+---------+ ---------+---------+---------+---------+
241 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  FUP_p42

 42 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct A
 59 LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct B
  1 garsggggtMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR  Construct C

          310       320       330       340       350       360
    ---------+---------+---------+---------+---------+---------+
301 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK  FUP_p42

102 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK  Construct A
119 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTK  Construct B
 61 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTK  Construct C

          370
    ---------+---
361 PDSYPLFDGIFCS   FUP_p42

162 PDSYPLFDGIFCS   Construct A
179 PDSYPLFDGIFCS   Construct B
121 PDSYPLFDGIFCS   Construct C
```

FIGURE 4. Alignment of the amino acid sequences from all MSP-1 C-terminal subunit protein Constructs relative to the FUP MSP-1 p33 sequence (1-280 of SEQ ID NO:19).

```
          10         20         30         40         50         60
     ---------+---------+---------+---------+---------+---------+
1    AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  FUP_p42
     ------------------------------------------------------------  SEQ ID NO:1(A)
     --------------------LKPLAGVYRSLKKQ------------------------  SEQ ID NO:2(B)
     ------------------------------------------------------------  SEQ ID NO:3(C)
     ------------------------------------------------------------  SEQ ID NO:4(D)
     ------------------------------------------------------------  SEQ ID NO:5(E)
     ------------------------------------------------------------  SEQ ID NO:6(F)
     ------------------------------------------------------------  SEQ ID NO:7(G)
     AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTFNLNLNDILNSRLKKRKY  SEQ ID NO:8(H)
     AISVTMDNILSGFENEYDVI------------------------------------------  SEQ ID NO:9(I)
     AISVTMDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNI--------------------  SEQ ID NO:10(J)
     ------------------------------------------------------------  SEQ ID NO:11(K)
     ------------------------------------------------------------  SEQ ID NO:12(L)
     ------------------------------------------------------------  SEQ ID NO:13(M)
     ------DNILS---------YLKPLAGVYRSLKKQI--------------LNSRL-----  SEQ ID NO:14(N)
     AISVTM-----GFENEYDVI----------------EKNIFTFNLNLNDI-----KKRKY  SEQ ID NO:15(O)
     ------------------------------------------------------------  SEQ ID NO:16(P)
     ------------------------------------------------------------  SEQ ID NO:17(Q)
     AISVTMDNILSGFENEYDVI------------------------------------------  SEQ ID NO:18(R)

          70         80         90         100        110        120
     ---------+---------+---------+---------+---------+---------+
61   FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  FUP_p42
     ------------------------------------------------------------  SEQ ID NO:(A)
     ------------------------------------------------------------  SEQ ID NO:(B)
     ------------------------------------------------------------  SEQ ID NO:(C)
     ------------------------------------------------------------  SEQ ID NO:(D)
     ------------------------------------------------------------  SEQ ID NO:(E)
     ------------------------------------------------KFAQEGIS  SEQ ID NO:(F)
     --------------------------------NTLLKSYKYIKESVENDIKFAQEGIS  SEQ ID NO:(G)
     FLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  SEQ ID NO:(H)
     ------------------------------------------------------------  SEQ ID NO:(I)
     ------------------------------------------------------------  SEQ ID NO:(J)
     ------------------------------------------------AQEGIS  SEQ ID NO:(K)
     -------------ISSNEYIIEDSFKLLNSEQKNTL----------------------  SEQ ID NO:(L)
     ------------------------------------------------------------  SEQ ID NO:(M)
     ---VLESDL----------------------------------------------------  SEQ ID NO:(N)
     FLD------MQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGIS  SEQ ID NO:(O)
     ------------------------------------------------------------  SEQ ID NO:(P)
     ------------------------------------------------------------  SEQ ID NO:(Q)
     -------------ISSNEYIIEDSFKLLNSEQKNTL----------------AQEGIS  SEQ ID NO:(R)
```

```
          130       140       150       160       170       180
     ---------+---------+---------+---------+---------+---------+
121  YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  FUP_p42
     ------------------------------------------------------------  SEQ ID NO:(A)
     ------------------------------------------------------------  SEQ ID NO:(B)
     ------------------------------------------------------------  SEQ ID NO:(C)
     ----------------------------------------------KFLPFLTNIETL  SEQ ID NO:(D)
     --------------IKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  SEQ ID NO:(E)
     YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  SEQ ID NO:(F)
     YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  SEQ ID NO:(G)
     YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETL  SEQ ID NO:(H)
     ------------------------------------------------------------  SEQ ID NO:(I)
     ------------------------------------------------------------  SEQ ID NO:(J)
     YYEKVLAKYKDDLESIKKVIKEEKEKFPSS----------------------------  SEQ ID NO:(K)
     ------------------------------------------------------------  SEQ ID NO:(L)
     ------------------------------------------------------------  SEQ ID NO:(M)
     -------KYKDDLESIKKV-----------------------------KFLPFLTNIETL  SEQ ID NO:(N)
     YYEKVLA----------VIKEEKEKFPSSPPTTPPSPAKTDEQKKES------------  SEQ ID NO:(O)
     ------------------------------------------------------------  SEQ ID NO:(P)
     ------------------------------------------------------------  SEQ ID NO:(Q)
     YYEKVLAKYKDDLESIKKVIKEEKEKFPSS----------------------------  SEQ ID NO:(R)

          190       200       210       220       230       240
     ---------+---------+---------+---------+---------+---------+
181  YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  FUP_p42
     ----------------------------AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(A)
     ----------------------------AHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(B)
     ------------------------------------------------------------  SEQ ID NO:(C)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(D)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(E)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(F)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(G)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(H)
     ----------------------VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(I)
     ----------------------VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(J)
     ----------------------VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(K)
     ----------------------VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(L)
     --NLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(M)
     ------------------------------------------------------------  SEQ ID NO:(N)
     YNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(O)
     ----------------------VEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(P)
     --NLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNHNDFDAIKK  SEQ ID NO:(Q)
     ------------------------------------------------------------  SEQ ID NO:(R)
```

```
          250        260        270
     ---------+---------+ ---------+---------
241  LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  FUP_p42
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:1(A)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:2(B)
     ---------MLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:3(C)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:4(D)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:5(E)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:6(F)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:7(G)
     LINDDTKKDMLG----------------------------  SEQ ID NO:8(H)
     LINDDTKKDMLG----------------------------  SEQ ID NO:9(I)
     LINDDTKKDMLG----------------------------  SEQ ID NO:10(J)
     LINDDTKKDMLG----------------------------  SEQ ID NO:11(K)
     LINDDTKKDMLG----------------------------  SEQ ID NO:12(L)
     ----------------------------------------  SEQ ID NO:13(M)
     LINDDTKKDMLG----------------------------  SEQ ID NO:14(N)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:15(O)
     LINDDTKKDMLG----------------------------  SEQ ID NO:16(P)
     LINDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDML  SEQ ID NO:17(Q)
     ----------------------------------------  SEQ ID NO:18(R)
```