SEQUENCE LISTING

<110> BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM
COOPER, LAURENCE JN
BELOUSOVA, NATALYA

<120> TRANSPOSASE POLYPEPTIDES AND USES THEREOF

<130> UTFC.P1256WO

<150> US 62/131,827
<151> 2015-03-11

<160> 7

<170> PatentIn version 3.5

<210> 1
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 1

```
Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Arg Ile Val
1               5                   10                  15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
            20                  25                  30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
        35                  40                  45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
    50                  55                  60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65                  70                  75                  80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
                85                  90                  95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100                 105                 110

Lys Gly His Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115                 120                 125

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

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
```

```
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

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

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys His Val Arg Lys
                245                 250                 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Asn Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335

Ala Thr Lys Tyr
            340
```

<210> 2
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 2
atgggcaaga gcaaagagat cagccaggac ctgcggaagc ggatcgtgga cctgcacaag 60

agcggctcta gcctgggcgc catcagcaag agactggccg tgcctagaag cagcgtgcag 120

accatcgtgc ggaagtacaa gcaccacggc accacccagc ccagctacag atctggaagg 180

cggagagtgc tgagccccag ggacgagaga acactcgtgc gcaaggtgca gatcaacccc 240

cggaccaccg ccaaggacct cgtgaagatg ctggaagaga caggcaccaa ggtgtccatc 300

agcaccgtga agcgggtgct gtaccggcac aacctgaagg gccacagcgc cagaaagaag 360

cccctgctgc agaacagaca caagaaggcc cggctgagat tcgccagagc ccacggcgac 420

aaggacagaa ccttctggcg gaacgtgctg tggagcgacg agacaaagat cgagctgttc 480

ggccacaacg accacagata cgtgtggcgg aagaagggcg aggcctgcaa gcccaagaac 540

accatcccca cagtgaagca cggcggaggc agcatcatgc tgtggggctg ttttgccgct 600

ggcggcacag gcgccctgca caaaatcgac ggcatcatgg acgccgtgca gtacgtggac 660

atcctgaagc agcacctgaa aacctctgtg cggaagctga agctgggccg gaaatgggtg 720

ttccagcacg acaacgaccc caagcacacc agcaagcacg tgcggaaatg gctgaaggac 780

aacaaagtga aagtgctgga atggcccagc cagtcccccg acctgaaccc catcgaaaac 840

ctgtgggccg agctgaagaa aagagtgcgg gccagacggc ccaccaacct gacacagctg 900

caccagctgt gccaggaaga gtgggccaag atccacccca actactgcgg caagctggtg 960

gaaggctacc ccaagaggct gacccaagtg aaacagttca agggcaacgc caccaagtac 1020

tga 1023

<210> 3
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 3

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Arg Ile Val
1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
50 55 60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr

```
                85                  90                  95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100                 105                 110

Lys Gly His Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115                 120                 125

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

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

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

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys His Val Arg Lys
                245                 250                 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335

Ala Thr Lys Tyr
```

340

<210> 4
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide

<400> 4
atgggcaaga gcaaagagat cagccaggac ctgcggaagc ggatcgtgga cctgcacaag 60

agcggctcta gcctgggcgc catcagcaag agactggccg tgcctagaag cagcgtgcag 120

accatcgtgc ggaagtacaa gcaccacggc accacccagc ccagctacag atctggaagg 180

cggagagtgc tgagccccag ggacgagaga acactcgtgc gcaaggtgca gatcaacccc 240

cggaccaccg ccaaggacct cgtgaagatg ctggaagaga caggcaccaa ggtgtccatc 300

agcaccgtga agcgggtgct gtaccggcac aacctgaagg gccacagcgc cagaaagaag 360

cccctgctgc agaacagaca caagaaggcc cggctgagat tcgccagagc ccacggcgac 420

aaggacagaa ccttctggcg gaacgtgctg tggagcgacg agacaaagat cgagctgttc 480

ggccacaacg accacagata cgtgtggcgg aagaagggcg aggcctgcaa gcccaagaac 540

accatcccca cagtgaagca cggcggaggc agcatcatgc tgtggggctg ttttgccgct 600

ggcggcacag gcgccctgca caaaatcgac ggcatcatgg acgccgtgca gtacgtggac 660

atcctgaagc agcacctgaa aacctctgtg cggaagctga agctgggccg gaaatgggtg 720

ttccagcacg acaacgaccc caagcacacc agcaagcacg tgcggaaatg gctgaaggac 780

aacaaagtga aagtgctgga atggcccagc cagtcccccg acctgaaccc catcgaaaac 840

ctgtgggccg agctgaagaa aagagtgcgg gccagacggc ccaccaacct gacacagctg 900

caccagctgt gccaggaaga gtgggccaag atccacccca cctactgcgg caagctggtg 960

gaaggctacc ccaagaggct gacccaagtg aaacagttca agggcaacgc caccaagtac 1020

tga 1023

<210> 5
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 5

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu

```
            20                  25                  30

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

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
    50                  55                  60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65                  70                  75                  80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
                85                  90                  95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100                 105                 110

Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115                 120                 125

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

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
    210                 215                 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln Gln Asp Asn Asp Pro Lys His Thr Ser Lys His Val Arg Lys
                245                 250                 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
```

275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305 310 315 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
325 330 335

Ala Thr Lys Tyr
340

<210> 6
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 6

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

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

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
50 55 60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
100 105 110

Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
115 120 125

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

```
Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
    210                 215                 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
                245                 250                 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335

Ala Thr Lys Tyr
            340
```

<210> 7
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 7

```
Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Arg Ile Val
```

```
1               5                   10                  15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
            20                  25                  30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
        35                  40                  45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
    50                  55                  60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65                  70                  75                  80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
                85                  90                  95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
            100                 105                 110

Lys Gly His Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
        115                 120                 125

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

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145                 150                 155                 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
                165                 170                 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
            180                 185                 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
        195                 200                 205

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

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225                 230                 235                 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
                245                 250                 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
```

```
            260                 265                 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
        275                 280                 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
    290                 295                 300

Gln Glu Glu Trp Ala Lys Ile His Pro Asn Tyr Cys Gly Lys Leu Val
305                 310                 315                 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
                325                 330                 335

Ala Thr Lys Tyr
            340
```