SEQUENCE LISTING

<110> BioNTech RNA Pharmaceuticals GmbH et al.

<120> THERAPEUTIC RNA FOR PROSTATE CANCER

<130> 674-273 PCT2

<150> PCT/EP2019/056185
<151> 2019-03-12

<160> 31

<170> PatentIn version 3.5

<210> 1
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<220>
<223> KLK2

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Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15

Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
35 40 45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
85 90 95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
100 105 110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu

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        115                 120                 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
    130                 135                 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
                165                 170                 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
            180                 185                 190

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

Cys Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
    210                 215                 220

Gly Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro
225                 230                 235                 240

Ala Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
                245                 250                 255

Ile Ala Ala Asn Pro
            260


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<223>  KLK2 fusion

<400>  2

Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
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Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
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            20                  25                  30

Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
        35                  40                  45

His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60

His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65                  70                  75                  80

Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
                85                  90                  95

Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
            100                 105                 110

Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115                 120                 125

Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
    130                 135                 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160

Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
                165                 170                 175

His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
            180                 185                 190

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

Cys Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
    210                 215                 220

Gly Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro
225                 230                 235                 240
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Ala Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
                245                 250                 255

Ile Ala Ala Asn Pro Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Lys
            260                 265                 270

Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
        275                 280                 285

Lys Lys Leu Gly Gly Gly Lys Arg Gly Gly Gly Lys Lys Met Thr Asn
    290                 295                 300

Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe
305                 310                 315                 320

Pro Ser Val Ile Ser Lys Val Asn Gln Gly Ala Gln Gly Lys Lys Leu
                325                 330                 335

Gly Ser Ser Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Ser Ile Val
            340                 345                 350

Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile Gly Ala
        355                 360                 365

Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly Lys Gly
    370                 375                 380

Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp
385                 390                 395                 400

Val Ser Leu Thr Ala
                405
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<212> RNA
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gcuguguaca gucauggaug ggcacacugu gggggugucc uggugcaccc ccagugggug 180

cucacagcug cccauugccu aaagaagaau agccaggucu ggcugggucg gcacaaccug 240

uuugagccug aagacacagg ccagaggguc ccugucagcc acagcuuccc acacccgcuc 300

uacaauauga gccuucugaa gcaucaaagc cuuagaccag augaagacuc cagccaugac 360

cucaugcugc uccgccuguc agagccugcc aagaucacag auguugugaa gguccugggc 420

cugcccaccc aggagccagc acuggggacc accugcuacg ccucaggcug gggcagcauc 480

gaaccagagg aguucuugcg ccccaggagu cuucagugug ugagccucca ucuccugucc 540

aaugacaugu gugcuagagc uuacucugag aaggugacag aguucauguu gugugcuggg 600

cucuggacag gugguaaaga cacuuguggg ggugauucug gggguccacu ugucuguaau 660

ggugugcuuc aagguaucac aucaugggge ccugagccau gugcccugcc ugaaaagccu 720

gcuguguaca ccaagguggu gcauuaccgg aaguggauca aggacaccau cgcagccaac 780

ccc 783

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ucggauugug ggaggcuggg agugugagaa gcauucccaa cccuggcagg uggcugugua 180

cagucaugga ugggcacacu gugggggugu ccuggugcac ccccaguggg ugcucacagc 240

ugcccauugc cuaaagaaga auagccaggu cuggcugggu cggcacaacc uguuugagcc 300

ugaagacaca ggccagaggg ucccugucag ccacagcuuc ccacacccgc ucuacaauau 360

gagccuucug aagcaucaaa gccuuagacc agaugaagac uccagccaug accucaugcu 420

gcuccgccug ucagagccug ccaagaucac agauguugug aagguccugg gccugcccac 480

ccaggagcca gcacugggga ccaccugcua cgccucaggc uggggcagca ucgaaccaga 540

ggaguucuug cgccccagga gucuucagug ugugagccuc caucuccugu ccaaugacau 600

gugugcuaga gcuuacucug agaaggugac agaguucaug uugugugcug ggcucuggac 660

aggugguaaa gacacuugug ggggugauuc ugggggucca cuugucugua auggugugcu 720

ucaagguauc acaucauggg gcccugagcc augugcccug ccugaaaagc cugcugugua 780

caccaaggug gugcauuacc ggaaguggau caaggacacc aucgcagcca accccggagg 840

auccgguggu ggcggcagcg gcggcaagaa gcaguacauc aaggccaaca gcaaguucau 900

cggcaucacc gagcugaaga agcugggagg gggcaaacgg ggaggcggca aaaagaugac 960

caacagcgug gacgacgccc ugaucaacag caccaagauc uacagcuacu uccccagcgu 1020

gaucagcaaa gugaaccagg gcgcucaggg caagaaacug ggcucuagcg gaggggggagg 1080

cucuccuggc gggggaucua gcaucguggg aauuguggca ggacuggcag ugcuggccgu 1140

gguggugauc ggagccgugg uggcuaccgu gaugugcaga cggaagucca gcggaggcaa 1200

gggcggcagc uacagccagg ccgccagcuc ugauagcgcc cagggcagcg acgugucacu 1260

gacagccuag uaacucgagc ugguacugca ugcacgcaau gcuagcugcc ccuuucccgu 1320

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cccacucacc accucugcua guuccagaca ccucccaagc acgcagcaau gcagcucaaa 1440

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aaaguuuaac uaagcuauac uaaccccagg guuggucaau uucgugccag ccacaccgag 1560

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<400> 5

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
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Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20                  25                  30

Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
        35                  40                  45

Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60

His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
65                  70                  75                  80

Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
                85                  90                  95

Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
            100                 105                 110

Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115                 120                 125

Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
    130                 135                 140

Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160

Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu
                165                 170                 175

His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val
            180                 185                 190

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

Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
    210                 215                 220

Gly Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro
225                 230                 235                 240
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Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
245 250 255

Ile Val Ala Asn Pro
260

<210> 6
<211> 405
<212> PRT
<213> Artificial Sequence

<220>
<223> PSA fusion

<400> 6

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
1 5 10 15

Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
35 40 45

Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
65 70 75 80

Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
85 90 95

Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
100 105 110

Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125

Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
130 135 140

```
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160

Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu
                165                 170                 175

His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val
            180                 185                 190

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

Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
    210                 215                 220

Gly Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro
225                 230                 235                 240

Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
                245                 250                 255

Ile Val Ala Asn Pro Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Lys
            260                 265                 270

Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
        275                 280                 285

Lys Lys Leu Gly Gly Gly Lys Arg Gly Gly Gly Lys Lys Met Thr Asn
    290                 295                 300

Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe
305                 310                 315                 320

Pro Ser Val Ile Ser Lys Val Asn Gln Gly Ala Gln Gly Lys Lys Leu
                325                 330                 335

Gly Ser Ser Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Ser Ile Val
            340                 345                 350
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```
Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile Gly Ala
        355                 360                 365

Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly Lys Gly
    370                 375                 380

Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp
385                 390                 395                 400

Val Ser Leu Thr Ala
                405
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<212> RNA
<213> Artificial Sequence

<220>
<223> PSA CDS

<400> 7

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cuuguggccu cucguggcag ggcagucugc ggcgguguuc uggugcaccc ccaguggguc      180

cucacagcug cccacugcau caggaacaaa agcgugaucu ugcugggucg gcacagccug      240

uuucauccug aagacacagg ccagguauuu caggucagcc acagcuuccc acacccgcuc      300

uacgauauga gccuccugaa gaaucgauuc cucaggccag gugaugacuc cagccacgac      360

cucaugcugc uccgccuguc agagccugcc gagcucacgg augcugugaa ggucauggac      420

cugcccaccc aggagccagc acuggggacc accugcuacg ccucaggcug gggcagcauu      480

gaaccagagg aguucuugac cccaaagaaa cuucagugug uggaccucca uguuauuucc      540

aaugacgugu gugcgcaagu ucacccucag aaggugacca aguucaugcu gugugcugga      600

cgcuggacag ggggcaaaag caccugcucg ggugauucug ggggcccacu ugucuguaau      660

ggugugcuuc aagguaucac gucaugggge agugaaccau gugcccugcc cgaaaggccu      720

ucccuguaca ccaaggguggu gcauuaccgg aaguggauca aggacaccau cguggccaac      780

ccc                                                                    783
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<210> 8
<211> 1700
<212> RNA
<213> Artificial Sequence

<220>
<223> PSA RNA

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cccgguuguc uuccucaccc uguccgugac guggauuggu gcugcacccc ucauccuguc 120

ucggauugug ggaggcuggg agugcgagaa gcauucccaa cccuggcagg ugcuuguggc 180

cucucguggc agggcagucu gcggcggugu ucuggugcac ccccaguggg uccucacagc 240

ugcccacugc aucaggaaca aaagcgugau cuugcugggu cggcacagcc uguuucaucc 300

ugaagacaca ggccagguau uucaggucag ccacagcuuc ccacacccgc ucuacgauau 360

gagccuccug aagaaucgau uccucaggcc aggugaugac uccagccacg accucaugcu 420

gcuccgccug ucagagccug ccgagcucac ggaugcugug aaggucaugg accugcccac 480

ccaggagcca gcacuggggа ccaccugcua cgccucaggc uggggcagca uugaaccaga 540

ggaguucuug accccaaaga aacuucagug uguggaccuc cauguuauuu ccaaugacgu 600

gugugcgcaa guucacccuc agaaggugac caaguucaug cugugugcug gacgcuggac 660

agggggcaaa agcaccugcu cgggugauuc ugggggccca cuugucugua augguguгcu 720

ucaagguauc acgucauggg gcagugaacc augugcccug cccgaaaggc cuucccugua 780

caccaaggug gugcauuacc ggaaguggau caaggacacc aucguggcca accccggagg 840

auccgguggu ggcggcagcg gcggcaagaa gcaguacauc aaggccaaca gcaaguucau 900

cggcaucacc gagcugaaga agcugggagg gggcaaacgg ggaggcggca aaaagaugac 960

caacagcgug gacgacgccc ugaucaacag caccaagauc uacagcuacu uccccagcgu 1020

gaucagcaaa gugaaccagg gcgcucaggg caagaaacug ggcucuagcg gagggggagg 1080

cucuccuggc gggggaucua gcaucguggg aauuguggca ggacuggcag ugcuggccgu 1140

gguggugauc ggagccgugg uggcuaccgu gaugugcaga cggaagucca gcggaggcaa 1200

gggcggcagc uacagccagg ccgccagcuc ugauagcgcc cagggcagcg acgugucacu 1260

gacagccuag uaacucgagc ugguacugca ugcacgcaau gcuagcugcc ccuuucccgu 1320

ccuggguacc ccgagucucc cccgaccucg gguccccaggu augcucccac cuccaccugc 1380

cccacucacc accucugcua guuccagaca ccucccaagc acgcagcaau gcagcucaaa 1440

acgcuuagcc uagccacacc cccacgggaa acagcaguga uuaaccuuua gcaauaaacg 1500

aaaguuuaac uaagcuauac uaaccccagg guuggucaau uucgugccag ccacaccgag 1560

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aaaaaaaaaa aaaaaaaaaa 1700

<210> 9
<211> 418
<212> PRT
<213> Artificial Sequence

<220>
<223> PAP

<400> 9

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
20 25 30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
35 40 45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
50 55 60

Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65 70 75 80

Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
85 90 95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
100 105 110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
115 120 125

```
Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130                 135                 140

Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
145                 150                 155                 160

Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
                165                 170                 175

Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
            180                 185                 190

Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
        195                 200                 205

Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
    210                 215                 220

Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
225                 230                 235                 240

Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
                245                 250                 255

Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
            260                 265                 270

Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
        275                 280                 285

His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
    290                 295                 300

Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
305                 310                 315                 320

Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln
                325                 330                 335
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```
His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
            340                 345                 350

Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
        355                 360                 365

Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Val Leu Lys Val Ile
    370                 375                 380

Phe Ala Val Ala Phe Cys Leu Ile Ser Ala Val Leu Met Val Leu Leu
385                 390                 395                 400

Phe Ile His Ile Arg Arg Gly Leu Cys Trp Gln Arg Glu Ser Tyr Gly
                405                 410                 415

Asn Ile
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<210> 10
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> PAP fusion

<400> 10

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Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
            20                  25                  30

Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
        35                  40                  45

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
    50                  55                  60

Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
65                  70                  75                  80
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```
Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
                85                  90                  95

Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
            100                 105                 110

Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
        115                 120                 125

Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
    130                 135                 140

Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
145                 150                 155                 160

Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
                165                 170                 175

Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
            180                 185                 190

Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
        195                 200                 205

Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro
    210                 215                 220

Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu
225                 230                 235                 240

Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser
                245                 250                 255

Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys
            260                 265                 270

Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala
        275                 280                 285

His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn
    290                 295                 300
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```
Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe
305                 310                 315                 320

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

His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro
            340                 345                 350

Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp
        355                 360                 365

Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Val Leu Lys Val Ile
    370                 375                 380

Phe Ala Val Ala Phe Cys Leu Ile Ser Ala Val Leu Met Val Leu Leu
385                 390                 395                 400

Phe Ile His Ile Arg Arg Gly Leu Cys Trp Gln Arg Glu Ser Tyr Gly
                405                 410                 415

Asn Ile Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Lys Lys Gln Tyr
            420                 425                 430

Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys Lys Leu
        435                 440                 445

Gly Gly Gly Lys Arg Gly Gly Gly Lys Lys Met Thr Asn Ser Val Asp
    450                 455                 460

Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe Pro Ser Val
465                 470                 475                 480

Ile Ser Lys Val Asn Gln Gly Ala Gln Gly Lys Lys Leu Gly Ser Ser
                485                 490                 495

Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Ser Ile Val Gly Ile Val
            500                 505                 510
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Ala Gly Leu Ala Val Leu Ala Val Val Val Ile Gly Ala Val Val Ala
515 520 525

Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr
530 535 540

Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu
545 550 555 560

Thr Ala

<210> 11
<211> 1254
<212> RNA
<213> Artificial Sequence

<220>
<223> PAP CDS

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guguuuagac acggagacag aucucccauu gauaccuuuc ccaccgaucc caucaaagaa 180

ucuucuuggc cacagggauu uggacagcug acccagcugg gaauggagca gcacuacgaa 240

cugggagaau acaucagaaa aagauacaga aaauuucuga augaaucuua caaacacgaa 300

cagguguaca ucagaucuac cgauguggau agaacccuga ugucugcaau gaccaaucug 360

gcugcucugu uucccccaga aggagugagc aucuggaauc ccauccugcu guggcagccc 420

aucccugugc acaccgugcc ucugucugaa gaucagcugc uguaccugcc uuuuagaaau 480

ugcccaagau uucaggaacu ugaaucugaa acccugaaau cugaagaauu ucagaaaaga 540

cugcacccuu acaaagauuu uaucgcaacc cugggaaaac ugucuggacu gcacggacag 600

gaucucuuug gaauuugguc aaaaguguac gauccucugu acugugaauc ugugcacaau 660

uuuacccugc ccucuugggc aaccgaagau accaugacca aacugagaga acugucugaa 720

cugucucugc ugucucugua cggaauccac aaacagaaag aaaaaucaag acugcaggga 780

ggagugcugg ugaaugaaau ccugaaucac augaaaagag caacccagau cccaucuuac 840

aagaagcuga ucauguacuc ugcucacgau accacagugu cuggacugca gauggcucug 900

gauguguaca auggacugcu gccucccuac gcuucuugcc accugaccga acuguacuuu 960

gaaaaaggag aauacuuugu ggaaauguac uacagaaaug aaacccagca cgaaccuuac 1020

ccccugaugc ugccuggaug cucucccucu ugcccucugg aaagauuugc ugaacuggug 1080

ggaccuguga ucccucagga uugguccaca gaaugcauga ccaccaauuc ucaccaggug 1140

cugaaaguga ucuuugcugu ggcuuuuugc cugaucucug cugugcugau ggugcugcug 1200

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uuucuggcug gauagaucug ugcuggcaaa agaacugaaa uuugugaccc ugguguuuag 180

acacggagac agaucuccca uugauaccuu ucccaccgau cccaucaaag aaucuucuug 240

gccacaggga uuuggacagc ugacccagcu gggaauggag cagcacuacg aacugggaga 300

auacaucaga aaaagauaca gaaaauuucu gaaugaaucu uacaaacacg aacaggugua 360

caucagaucu accgaugugg auagaacccu gaugucugca augaccaauc uggcugcucu 420

guuuccccca gaaggaguga gcaucuggaa ucccauccug cuguggcagc ccaucccugu 480

gcacaccgug ccucugucug aagaucagcu gcuguaccug ccuuuuagaa auugcccaag 540

auuucaggaa cuugaaucug aaacccugaa aucugaagaa uuucagaaaa gacugcaccc 600

uuacaaagau uuuaucgcaa cccugggaaa acugucugga cugcacggac aggaucucuu 660

uggaauuugg ucaaaagugu acgauccucu guacugugaa ucugugcaca auuuuacccu 720

gcccucuugg gcaaccgaag auaccaugac caaacugaga gaacugucug aacugucucu 780

gcugucucug uacggaaucc acaaacagaa agaaaaauca agacugcagg gaggagugcu 840

ggugaaugaa auccugaauc acaugaaaag agcaacccag aucccaucuu acaagaagcu 900

gaucauguac ucugcucacg auaccacagu gucuggacug cagauggcuc uggaugugua 960

caauggacug cugccucccu acgcuucuug ccaccugacc gaacuguacu uugaaaaagg 1020

agaauacuuu guggaaaugu acuacagaaa ugaaacccag cacgaaccuu acccccugau 1080

gcugccugga ugcucucccu cuugcccucu ggaaagauuu gcugaacugg ugggaccugu 1140

gaucccucag gauugqucca cagaaugcau gaccaccaau ucucaccagg ugcugaaagu 1200

gaucuuugcu guggcuuuuu gccugaucuc ugcugugcug auggugcugc uguuuaucca 1260

caucaggaga ggacugugcu ggcagagaga aucuuacgga aauaucggag gauccggugg 1320

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agugaaccag ggcgcucagg gcaagaaacu gggcucuagc ggaggggggag gcucuccugg 1560

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cuaagcuaua cuaaccccag gguuggucaa uuucgugcca gccacaccga gaccuggucc 2040

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aaaaaaaaaa a 2171

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<211> 284
<212> PRT
<213> Artificial Sequence

<220>
<223> HOXB13

<400> 13

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Gly Leu Leu Gly Ala Gly Gly Gly Arg Asn Leu Val Ala His Ser Pro
            20                  25                  30

Leu Thr Ser His Pro Ala Ala Pro Thr Leu Met Pro Ala Val Asn Tyr
        35                  40                  45

Ala Pro Leu Asp Leu Pro Gly Ser Ala Glu Pro Pro Lys Gln Cys His
    50                  55                  60

Pro Cys Pro Gly Val Pro Gln Gly Thr Ser Pro Ala Pro Val Pro Tyr
65                  70                  75                  80

Gly Tyr Phe Gly Gly Gly Tyr Tyr Ser Cys Arg Val Ser Arg Ser Ser
                85                  90                  95

Leu Lys Pro Cys Ala Gln Ala Ala Thr Leu Ala Ala Tyr Pro Ala Glu
            100                 105                 110

Thr Pro Thr Ala Gly Glu Glu Tyr Pro Ser Arg Pro Thr Glu Phe Ala
        115                 120                 125

Phe Tyr Pro Gly Tyr Pro Gly Thr Tyr Gln Pro Met Ala Ser Tyr Leu
    130                 135                 140

Asp Val Ser Val Val Gln Thr Leu Gly Ala Pro Gly Glu Pro Arg His
145                 150                 155                 160

Asp Ser Leu Leu Pro Val Asp Ser Tyr Gln Ser Trp Ala Leu Ala Gly
                165                 170                 175

Gly Trp Asn Ser Gln Met Cys Cys Gln Gly Glu Gln Asn Pro Pro Gly
            180                 185                 190

Pro Phe Trp Lys Ala Ala Phe Ala Asp Ser Ser Gly Gln His Pro Pro
        195                 200                 205

Asp Ala Cys Ala Phe Arg Arg Gly Arg Lys Lys Arg Ile Pro Tyr Ser
    210                 215                 220
```

```
Lys Gly Gln Leu Arg Glu Leu Glu Arg Glu Tyr Ala Ala Asn Lys Phe
225                 230                 235                 240


Ile Thr Lys Asp Lys Arg Arg Lys Ile Ser Ala Ala Thr Ser Leu Ser
                245                 250                 255


Glu Arg Gln Ile Thr Ile Trp Phe Gln Asn Arg Arg Val Lys Glu Lys
            260                 265                 270


Lys Val Leu Ala Lys Val Lys Asn Ser Ala Thr Pro
        275                 280


<210>  14
<211>  464
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  HOXB13 fusion

<400>  14

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1               5                   10                  15


Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Gly Gly Ser Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Met Glu Pro Gly Asn Tyr Ala Thr Leu Asp Gly Ala
        35                  40                  45


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


Ala His Ser Pro Leu Thr Ser His Pro Ala Ala Pro Thr Leu Met Pro
65                  70                  75                  80


Ala Val Asn Tyr Ala Pro Leu Asp Leu Pro Gly Ser Ala Glu Pro Pro
                85                  90                  95


Lys Gln Cys His Pro Cys Pro Gly Val Pro Gln Gly Thr Ser Pro Ala
            100                 105                 110
```

```
Pro Val Pro Tyr Gly Tyr Phe Gly Gly Gly Tyr Tyr Ser Cys Arg Val
        115                 120                 125

Ser Arg Ser Ser Leu Lys Pro Cys Ala Gln Ala Ala Thr Leu Ala Ala
    130                 135                 140

Tyr Pro Ala Glu Thr Pro Thr Ala Gly Glu Glu Tyr Pro Ser Arg Pro
145                 150                 155                 160

Thr Glu Phe Ala Phe Tyr Pro Gly Tyr Pro Gly Thr Tyr Gln Pro Met
                165                 170                 175

Ala Ser Tyr Leu Asp Val Ser Val Val Gln Thr Leu Gly Ala Pro Gly
            180                 185                 190

Glu Pro Arg His Asp Ser Leu Leu Pro Val Asp Ser Tyr Gln Ser Trp
        195                 200                 205

Ala Leu Ala Gly Gly Trp Asn Ser Gln Met Cys Cys Gln Gly Glu Gln
    210                 215                 220

Asn Pro Pro Gly Pro Phe Trp Lys Ala Ala Phe Ala Asp Ser Ser Gly
225                 230                 235                 240

Gln His Pro Pro Asp Ala Cys Ala Phe Arg Arg Gly Arg Lys Lys Arg
                245                 250                 255

Ile Pro Tyr Ser Lys Gly Gln Leu Arg Glu Leu Glu Arg Glu Tyr Ala
            260                 265                 270

Ala Asn Lys Phe Ile Thr Lys Asp Lys Arg Arg Lys Ile Ser Ala Ala
        275                 280                 285

Thr Ser Leu Ser Glu Arg Gln Ile Thr Ile Trp Phe Gln Asn Arg Arg
    290                 295                 300

Val Lys Glu Lys Lys Val Leu Ala Lys Val Lys Asn Ser Ala Thr Pro
305                 310                 315                 320
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Lys Lys Gln Tyr Ile Lys
                325                 330                 335

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

Gly Lys Arg Gly Gly Gly Lys Lys Met Thr Asn Ser Val Asp Asp Ala
        355                 360                 365

Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr Phe Pro Ser Val Ile Ser
    370                 375                 380

Lys Val Asn Gln Gly Ala Gln Gly Lys Lys Leu Gly Ser Ser Gly Gly
385                 390                 395                 400

Gly Gly Ser Pro Gly Gly Gly Ser Ser Ile Val Gly Ile Val Ala Gly
                405                 410                 415

Leu Ala Val Leu Ala Val Val Val Ile Gly Ala Val Val Ala Thr Val
            420                 425                 430

Met Cys Arg Arg Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr Ser Gln
        435                 440                 445

Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu Thr Ala
    450                 455                 460
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<210> 15
<211> 852
<212> RNA
<213> Artificial Sequence

<220>
<223> HOXB13 CDS

<400> 15

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gcgggagggg ggcggaaucu ggucgcccac uccccucuga ccagccaccc agcggcgccu      120

acgcugaugc cugcugucaa cuaugccccc uuggaucugc caggcucggc ggagccgcca      180

aagcaaugcc acccaugccc uggggugccc caggggacgu ccccagcucc cgugccuuau      240

gguuacuuug gaggcgggua cuacuccugc cgaguguccc ggaguucgcu gaaacccugu      300
```

gcccaggcag ccacccuggc cgcguacccc gcggagacuc ccacggccgg ggaggaguac 360

cccagccgcc ccacugaguu ugccuucuau ccgggauauc cgggaaccua ccagccuaug 420

gccaguuacc uggacguguc uguggugcag acucugggug cuccuggaga accgcgacau 480

gacucccugu ugccugugga caguuaccag ucuugggcuc ucgcuggugg cuggaacagc 540

cagauguguu gccagggaga acagaaccca ccaggucccu uuuggaaggc agcauuugca 600

gacuccagcg ggcagcaccc uccugacgcc ugcgccuuuc gucgcggccg caagaaacgc 660

auuccguaca gcaaggggca guugcgggag cuggagcggg aguaugcggc uaacaaguuc 720

aucaccaagg acaagaggcg caagaucucg gcagccacca gccucucgga gcgccagauu 780

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agcgcuaccc cu 852

<210> 16
<211> 1877
<212> RNA
<213> Artificial Sequence

<220>
<223> HOXB13 RNA

<400> 16
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gauggccccc agaacccuga uccugcugcu gucuggcgcc cuggcccuga cagagacaug 120

ggccggaagc ggcggcucug gaggaggcgg cuccggaggc auggagcccg gcaauuaugc 180

caccuuggau ggagccaagg auaucgaagg cuugcuggga gcgggagggg ggcggaaucu 240

ggucgcccac uccccucuga ccagccaccc agcggcgccu acgcugaugc cugcugucaa 300

cuaugccccc uuggaucugc caggcucggc ggagccgcca aagcaaugcc acccaugccc 360

uggggugccc caggggacgu ccccagcucc cgugccuuau gguuacuuug gaggcgggua 420

cuacuccugc cgaguguccc ggaguucgcu gaaacccugu gcccaggcag ccacccuggc 480

cgcguacccc gcggagacuc ccacggccgg ggaggaguac cccagccgcc ccacugaguu 540

ugccuucuau ccgggauauc cgggaaccua ccagccuaug gccaguuacc uggacguguc 600

uguggugcag acucugggug cuccuggaga accgcgacau gacucccugu ugccugugga 660

caguuaccag ucuugggcuc ucgcuggugg cuggaacagc cagauguguu gccagggaga 720

acagaaccca ccaggucccu uuuggaaggc agcauuugca gacuccagcg ggcagcaccc 780

uccugacgcc ugcgccuuuc gucgcggccg caagaaacgc auuccguaca gcaaggggca 840

guugcgggag cuggagcggg aguaugcggc uaacaaguuc aucaccaagg acaagaggcg 900

caagaucucg gcagccacca gccucucgga gcgccagauu accaucuggu uucagaaccg 960

ccgggucaaa gagaagaagg uucucgccaa ggugaagaac agcgcuaccc cuggaggauc 1020

cggugguggc ggcagcggcg gcaagaagca guacaucaag gccaacagca aguucaucgg 1080

caucaccgag cugaagaagc ugggaggggg caaacgggga ggcggcaaaa agaugaccaa 1140

cagcguggac gacgcccuga ucaacagcac caagaucuac agcuacuucc ccagcgugau 1200

cagcaaagug aaccagggcg cucagggcaa gaaacugggc ucuagcggag ggggaggcuc 1260

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ggugaucgga gccguggugg cuaccgugau gugcagacgg aaguccagcg gaggcaaggg 1380

cggcagcuac agccaggccg ccagcucuga uagcgcccag ggcagcgacg ugucacugac 1440

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acucaccacc ucugcuaguu ccagacaccu cccaagcacg cagcaaugca gcucaaaacg 1620

cuuagccuag ccacaccccc acgggaaaca gcagugauua accuuuagca auaaacgaaa 1680

guuuaacuaa gcuauacuaa ccccaggguu ggucaauuuc gugccagcca caccgagacc 1740

ugguccagag ucgcuagccg cgucgcuaaa aaaaaaaaaa aaaaaaaaaa aaaaaaagca 1800

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aaaaaaaaaa aaaaaa 1877

<210> 17
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> NKX3-1

<400> 17

Met Leu Arg Val Pro Glu Pro Arg Pro Gly Glu Ala Lys Ala Glu Gly
1 5 10 15

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Ala Ala Pro Pro Thr Pro Ser Lys Pro Leu Thr Ser Phe Leu Ile Gln
            20                  25                  30

Asp Ile Leu Arg Asp Gly Ala Gln Arg Gln Gly Gly Arg Thr Ser Ser
        35                  40                  45

Gln Arg Gln Arg Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Gly
    50                  55                  60

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

Arg Ala Ala Pro Glu Glu Ala Glu Thr Leu Ala Glu Thr Glu Pro Glu
                85                  90                  95

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

Leu Pro Arg Leu Pro Gln Thr Pro Lys Gln Pro Gln Lys Arg Ser Arg
        115                 120                 125

Ala Ala Phe Ser His Thr Gln Val Ile Glu Leu Glu Arg Lys Phe Ser
    130                 135                 140

His Gln Lys Tyr Leu Ser Ala Pro Glu Arg Ala His Leu Ala Lys Asn
145                 150                 155                 160

Leu Lys Leu Thr Glu Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg
                165                 170                 175

Tyr Lys Thr Lys Arg Lys Gln Leu Ser Ser Glu Leu Gly Asp Leu Glu
            180                 185                 190

Lys His Ser Ser Leu Pro Ala Leu Lys Glu Glu Ala Phe Ser Arg Ala
        195                 200                 205

Ser Leu Val Ser Val Tyr Asn Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr
    210                 215                 220
```

Cys Val Gly Ser Trp Ser Pro Ala Phe Trp
225 230

<210> 18
<211> 414
<212> PRT
<213> Artificial Sequence

<220>
<223> NKX3-1 fusion

<400> 18

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Gly Gly Ser Gly Gly Gly
20 25 30

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

Lys Ala Glu Gly Ala Ala Pro Pro Thr Pro Ser Lys Pro Leu Thr Ser
50 55 60

Phe Leu Ile Gln Asp Ile Leu Arg Asp Gly Ala Gln Arg Gln Gly Gly
65 70 75 80

Arg Thr Ser Ser Gln Arg Gln Arg Asp Pro Glu Pro Glu Pro Glu Pro
85 90 95

Glu Pro Glu Gly Gly Arg Ser Arg Ala Gly Ala Gln Asn Asp Gln Leu
100 105 110

Ser Thr Gly Pro Arg Ala Ala Pro Glu Glu Ala Glu Thr Leu Ala Glu
115 120 125

Thr Glu Pro Glu Arg His Leu Gly Ser Tyr Leu Leu Asp Ser Glu Asn
130 135 140

Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr Pro Lys Gln Pro Gln
145 150 155 160

```
Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile Glu Leu Glu
                165                 170                 175

Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu Arg Ala His
            180                 185                 190

Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys Ile Trp Phe
        195                 200                 205

Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln Leu Ser Ser Glu Leu
    210                 215                 220

Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala Leu Lys Glu Glu Ala
225                 230                 235                 240

Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn Ser Tyr Pro Tyr Tyr
                245                 250                 255

Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro Ala Phe Trp Gly Gly
            260                 265                 270

Ser Gly Gly Gly Gly Ser Gly Gly Lys Lys Gln Tyr Ile Lys Ala Asn
        275                 280                 285

Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys Lys Leu Gly Gly Gly Lys
    290                 295                 300

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

Asn Ser Thr Lys Ile Tyr Ser Tyr Phe Pro Ser Val Ile Ser Lys Val
                325                 330                 335

Asn Gln Gly Ala Gln Gly Lys Lys Leu Gly Ser Ser Gly Gly Gly Gly
            340                 345                 350

Ser Pro Gly Gly Gly Ser Ser Ile Val Gly Ile Val Ala Gly Leu Ala
        355                 360                 365

Val Leu Ala Val Val Val Ile Gly Ala Val Val Ala Thr Val Met Cys
    370                 375                 380
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Arg Arg Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr Ser Gln Ala Ala
385 390 395 400

Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu Thr Ala
405 410

<210> 19
<211> 702
<212> RNA
<213> Artificial Sequence

<220>
<223> NKX3-1 CDS

<400> 19
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agacaaggcg gcagaacaag cucucagaga cagagagauc ccgagccuga gccugaacca 180

gaaccugaag gcggaagauc uagagccggc gcucagaacg aucagcugag cacaggaccu 240

agagccgcuc cugaggaagc cgaaacacug gccgaaaccg agccagagag acaccugggc 300

agcuaccugc uggacagcga gaauacuucu ggcgcccugc cuagacugcc ccagacaccu 360

aaacagccuc agaagcggag cagagccgcc uuuagccaca cacaagugau cgagcuggaa 420

cggaaguuca gccaccagaa guaccugagc gccccugaaa gagcccaccu ggccaagaau 480

cugaagcuga ccgagacuca agugaagauc ugguuccaga accggcggua caagaccaag 540

cggaagcagc ugucaagcga gcugggcgac cuggaaaagc acagcucucu gcccgcucug 600

aaagaggaag ccuucuccag agccagccug guguccgugu acaacagcua cccuuacuac 660

cccuaccugu acugcgucgg cucuuggagc ccugccuuuu gg 702

<210> 20
<211> 1727
<212> RNA
<213> Artificial Sequence

<220>
<223> NKX3-1 RNA

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ggccggaagc ggcggcucug gaggaggcgg cuccggaggc augcugagag ugcccgaacc 180

uagaccuggc gaggcuaaag cugaaggcgc ugcuccuccu acaccuagca agccucugac 240

cagcuuccug auccaagaca uccugagaga uggcgcccag agacaaggcg gcagaacaag 300

cucucagaga cagagagauc ccgagccuga gccugaacca gaaccugaag gcggaagauc 360

uagagccggc gcucagaacg aucagcugag cacaggaccu agagccgcuc cugaggaagc 420

cgaaacacug gccgaaaccg agccagagag acaccugggc agcuaccugc uggacagcga 480

gaauacuucu ggcgcccugc cuagacugcc ccagacaccu aaacagccuc agaagcggag 540

cagagccgcc uuuagccaca cacaagugau cgagcuggaa cggaaguuca gccaccagaa 600

guaccugagc gccccugaaa gagcccaccu ggccaagaau cugaagcuga ccgagacuca 660

agugaagauc ugguuccaga accggcggua caagaccaag cggaagcagc ugucaagcga 720

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caagaucuac agcuacuucc ccagcgugau cagcaaagug aaccagggcg cucagggcaa 1080

gaaacugggc ucuagcggag ggggaggcuc uccuggcggg ggaucuagca ucgugggaau 1140

uguggcagga cuggcagugc uggccguggu ggugaucgga gccguggugg cuaccgugau 1200

gugcagacgg aaguccagcg gaggcaaggg cggcagcuac agccaggccg ccagcucuga 1260

uagcgcccag ggcagcgacg ugucacugac agccuaguaa cucgagcugg uacugcaugc 1320

acgcaaugcu agcugccccu uucccguccu ggguaccccg agucucccc gaccucgggu 1380

cccagguaug cucccaccuc caccugcccc acucaccacc ucugcuaguu ccagacaccu 1440

cccaagcacg cagcaaugca gcucaaaacg cuuagccuag ccacaccccc acgggaaaca 1500

gcagugauua accuuuagca auaaacgaaa guuuaacuaa gcuauacuaa ccccaggguu 1560

ggucaauuuc gugccagcca caccgagacc ugguccagag ucgcuagccg cgucgcuaaa 1620

aaaaaaaaaa aaaaaaaaaa aaaaaaagca uaugacuaaa aaaaaaaaaa aaaaaaaaaa 1680

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1727

<210> 21
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> 5' UTR

<400> 21
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<210> 22
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Secretory signal

<400> 22

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser
20 25

<210> 23
<211> 78
<212> RNA
<213> Artificial Sequence

<220>
<223> Secretory signal

<400> 23
augagaguga uggcccccag aacccugauc cugcugcugu cuggcgcccu ggcccugaca 60

gagacauggg ccggaagc 78

<210> 24
<211> 55
<212> PRT
<213> Artificial Sequence

<220>

<223> MITD

<400> 24

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile
1   5   10   15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly
            20   25   30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly
        35   40   45

Ser Asp Val Ser Leu Thr Ala
    50   55

<210> 25
<211> 171
<212> RNA
<213> Artificial Sequence

<220>
<223> MITD

<400> 25
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Leu Lys Lys Leu Gly Gly Gly Lys Arg Gly Gly Gly Lys Lys Met Thr
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Asn Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr Ser Tyr
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Leu
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ucugcuaguu ccagacaccu cccaagcacg cagcaaugca gcucaaaacg cuuagccuag 180

ccacaccccc acgggaaaca gcagugauua accuuuagca auaaacgaaa guuuaacuaa 240

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Met Thr Asn Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile Tyr
1 5 10 15

Ser Tyr Phe Pro Ser Val Ile Ser Lys Val Asn Gln Gly Ala Gln Gly
20 25 30