SEQUENCE LISTING

<110> WANG, Xiao-Jing
ZHANG, Qinghong
REFAELI, Yosef

<120> PTD-SMAD7 THERAPEUTICS

<130> UTEC.P0037US.P1

<160> 39

<170> PatentIn version 3.5

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        35                  40                  45

Gly Glu Gly Ala Thr Asp Ser Arg Ala His Gly Ala Gly Gly Gly Gly
    50                  55                  60

Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys Ala Val Arg Gly Ala Lys
65                  70                  75                  80

Gly His His His Pro His Pro Pro Ala Ala Gly Ala Gly Ala Ala Gly
                85                  90                  95

Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr His Ser Val Leu Lys Lys
            100                 105                 110

Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu Gln Ala Val Glu Ser Arg
        115                 120                 125

Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu Pro Gly Arg Leu Asp Cys
    130                 135                 140

Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala Gln Pro Ala Gln Pro Pro
145                 150                 155                 160

Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys Lys Val Phe Arg Trp Pro
                165                 170                 175

Asp Leu Arg His Ser Ser Glu Val Lys Arg Leu Cys Cys Cys Glu Ser
            180                 185                 190

Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys Cys Asn Pro His His Leu
        195                 200                 205

Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro Pro Pro Tyr Ser Arg Tyr
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Pro Met Asp Phe Leu Lys Pro Thr Ala Asp Cys Pro Asp Ala Val Pro
225                 230                 235                 240

Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr Leu Ala Pro Gly Gly Leu
                245                 250                 255

Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly Asp Arg Ser His Trp Cys
            260                 265                 270
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Val Val Ala Tyr Trp Glu Glu Lys Thr Arg Val Gly Arg Leu Tyr Cys
275 280 285

Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr Asp Leu Pro Gln Gly Asn
290 295 300

Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp Asn Lys Ser Gln Leu Val
305 310 315 320

Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu Thr Arg Glu
325 330 335

Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro Ile Phe Ile
340 345 350

Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu Leu Val His
355 360 365

Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr Glu Lys Ala
370 375 380

Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln Gln Pro Trp
385 390 395 400

Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp Gly Gln Cys
405 410 415

Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu Glu Val Ile
420 425 430

Phe Asn Ser Arg Lys Gly Glu Leu Asn Ser Lys Leu Glu Gly Lys Pro
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His His His His
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            20                  25                  30

Gly Glu Asp Glu Glu Glu Gly Ala Gly Gly Gly Gly Gly Gly Gly Glu
        35                  40                  45

Leu Arg Gly Glu Gly Ala Thr Asp Ser Arg Ala His Gly Ala Gly Gly
    50                  55                  60

Gly Gly Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys Ala Val Arg Gly
65                  70                  75                  80

Ala Lys Gly His His His Pro His Pro Pro Ala Ala Gly Ala Gly Ala
                85                  90                  95

Ala Gly Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr His Ser Val Leu
            100                 105                 110

Lys Lys Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu Gln Ala Val Glu
        115                 120                 125

Ser Arg Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu Pro Gly Arg Leu
    130                 135                 140

Asp Cys Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala Gln Pro Ala Gln
145                 150                 155                 160

Pro Pro Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys Lys Val Phe Arg
                165                 170                 175

Trp Pro Asp Leu Arg His Ser Ser Glu Val Lys Arg Leu Cys Cys Cys
            180                 185                 190

Glu Ser Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys Cys Asn Pro His
        195                 200                 205

His Leu Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro Pro Pro Tyr Ser
    210                 215                 220

Arg Tyr Pro Met Asp Phe Leu Lys Pro Thr Ala Asp Cys Pro Asp Ala
225                 230                 235                 240

Val Pro Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr Leu Ala Pro Gly
                245                 250                 255
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Gly Leu Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly Asp Arg Ser His
            260                 265                 270

Trp Cys Val Val Ala Tyr Trp Glu Glu Lys Thr Arg Val Gly Arg Leu
        275                 280                 285

Tyr Cys Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr Asp Leu Pro Gln
    290                 295                 300

Gly Asn Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp Asn Lys Ser Gln
305                 310                 315                 320

Leu Val Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu Thr
                325                 330                 335

Arg Glu Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro Ile
            340                 345                 350

Phe Ile Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu Leu
        355                 360                 365

Val His Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr Glu
    370                 375                 380

Lys Ala Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln Gln
385                 390                 395                 400

Pro Trp Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp Gly
                405                 410                 415

Gln Cys Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu Glu
            420                 425                 430

Val Ile Phe Asn Ser Arg Lys Gly Glu Leu Asn Ser Lys Leu Glu Gly
        435                 440                 445

Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
    450                 455                 460


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Gly Gly Gly Glu Leu Arg Gly Glu Gly Ala Thr Asp Ser Arg Ala His
        35                  40                  45

Gly Ala Gly Gly Gly Gly Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys
    50                  55                  60

Ala Val Arg Gly Ala Lys Gly His His His Pro His Pro Pro Ala Ala
65                  70                  75                  80

Gly Ala Gly Ala Ala Gly Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr
                85                  90                  95

His Ser Val Leu Lys Lys Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu
            100                 105                 110

Gln Ala Val Glu Ser Arg Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu
        115                 120                 125

Pro Gly Arg Leu Asp Cys Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala
    130                 135                 140

Gln Pro Ala Gln Pro Pro Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys
145                 150                 155                 160

Lys Val Phe Arg Trp Pro Asp Leu Arg His Ser Ser Glu Val Lys Arg
                165                 170                 175

Leu Cys Cys Cys Glu Ser Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys
            180                 185                 190

Cys Asn Pro His His Leu Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro
        195                 200                 205

Pro Pro Tyr Ser Arg Tyr Pro Met Asp Phe Leu Lys Pro Thr Ala Asp
    210                 215                 220

Cys Pro Asp Ala Val Pro Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr
225                 230                 235                 240

Leu Ala Pro Gly Gly Leu Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly
                245                 250                 255

Asp Arg Ser His Trp Cys Val Val Ala Tyr Trp Glu Glu Lys Thr Arg
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260 265 270

Val Gly Arg Leu Tyr Cys Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr
275 280 285

Asp Leu Pro Gln Gly Asn Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp
290 295 300

Asn Lys Ser Gln Leu Val Gln Lys Val Arg Ser Lys Ile Gly Cys Gly
305 310 315 320

Ile Gln Leu Thr Arg Glu Val Asp Gly Val Trp Val Tyr Asn Arg Ser
325 330 335

Ser Tyr Pro Ile Phe Ile Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser
340 345 350

Arg Thr Leu Leu Val His Lys Val Phe Pro Gly Phe Ser Ile Lys Ala
355 360 365

Phe Asp Tyr Glu Lys Ala Tyr Ser Leu Gln Arg Pro Asn Asp His Glu
370 375 380

Phe Met Gln Gln Pro Trp Thr Gly Phe Thr Val Gln Ile Ser Phe Val
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Lys Gly Trp Gly Gln Cys Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro
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gcgaaaggtc atcaccatcc gcacccgccg gcagcaggtg caggtgcagc tggcggtgcg 300

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ccgccgtatt ctcgttaccc gatggatttc ctgaaaccga ctgcagattg cccggacgca 720

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cgtcagttta tctcgtcctg tccgtgctgg ctggaagtga ttttcaatag ccgcaagggc 1320

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acgtgagtcg ac 1392

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tcgcagctgg tgcaaaaagt tcgctcaaaa attggctgcg gtatccagct gacccgtgaa 240

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tacacccgtc agtttatctc gtcctgtccg tgctggctgg aagtgatttt caatagccgc 540

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gattctacgt gagtcgac 618

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Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr Asp Leu Pro Gln Gly Asn
35 40 45

Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp Asn Lys Ser Gln Leu Val
50 55 60

Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu Thr Arg Glu
65 70 75 80

Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro Ile Phe Ile
85 90 95

Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu Leu Val His
100 105 110

Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr Glu Lys Ala
115 120 125

Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln Gln Pro Trp
130 135 140

Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp Gly Gln Cys
145 150 155 160

Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu Glu Val Ile
165 170 175

Phe Asn Ser Arg Lys Gly Glu Leu Asn Ser Lys Leu Glu Gly Lys Pro
180 185 190

Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
195 200

<210> 26
<211> 861
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<213> Artificial Sequence

<220>
<223> Tat-Smad7-N

<400> 26
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ggcggcggtg gcggtggcgg tgaactgcgt ggcgagggtg caaccgatag tcgtgcacac 180

ggtgcaggcg gtggcggtcc gggtcgtgct ggttgctgtc tgggtaaagc tgtgcgcggc 240

gcgaaaggtc atcaccatcc gcacccgccg gcagcaggtg caggtgcagc tggcggtgcg 300

gaagccgatc tgaaagccct gacccatagt gtcctgaaaa aactgaaaga acgtcagctg 360

gagctgctgc tgcaagcagt agaatcccgt ggcggtaccc gtacggcttg tctgctgctg 420

ccgggtcgtc tggattgccg tctgggtccg ggtgcaccgg ctggtgcgca gccggcacaa 480

ccgccgagct cttacagcct gccgctgctg ctgtgtaaag tgtttcgttg gccggacctg 540

cgccacagtt ccgaagttaa acgcctgtgc tgttgcgaga gctatggcaa aattaacccg 600

gaactggttt gttgcaatcc gcaccatctg tctcgtctgt gtgaactgga gagcccgccg 660

ccgccgtatt ctcgttaccc gatggatttc ctgaaaccga ctgcagattg cccggacgca 720

gtcccgtcat cggctgagac cggcggcacc aactatctgg caccgggcgg tctgagtgat 780

tcccagctgc tgctggaacc gggcgaccgt ggtaagccta tccctaaccc tctcctcggt 840

ctcgattcta cgtgagtcga c 861

<210> 27

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

<220>
<223> Synthetic peptide

<400> 27

Gly Ser Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Phe Arg Thr
1 5 10 15

Lys Arg Ser Ala Leu Val Arg Arg Leu Trp Arg Ser Arg Ala Pro Gly
20 25 30

Gly Glu Asp Glu Glu Glu Gly Ala Gly Gly Gly Gly Gly Gly Gly Glu
35 40 45

Leu Arg Gly Glu Gly Ala Thr Asp Ser Arg Ala His Gly Ala Gly Gly
50 55 60

Gly Gly Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys Ala Val Arg Gly
65 70 75 80

Ala Lys Gly His His His Pro His Pro Pro Ala Ala Gly Ala Gly Ala
85 90 95

Ala Gly Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr His Ser Val Leu
100 105 110

Lys Lys Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu Gln Ala Val Glu
115 120 125

Ser Arg Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu Pro Gly Arg Leu
130 135 140

Asp Cys Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala Gln Pro Ala Gln
145 150 155 160

Pro Pro Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys Lys Val Phe Arg
165 170 175

Trp Pro Asp Leu Arg His Ser Ser Glu Val Lys Arg Leu Cys Cys Cys
180 185 190

Glu Ser Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys Cys Asn Pro His
195 200 205

His Leu Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro Pro Pro Tyr Ser
210 215 220

```
Arg Tyr Pro Met Asp Phe Leu Lys Pro Thr Ala Asp Cys Pro Asp Ala
225                 230                 235                 240

Val Pro Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr Leu Ala Pro Gly
                245                 250                 255

Gly Leu Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly Asp Arg Gly Lys
            260                 265                 270

Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
        275                 280
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<210> 28
<211> 1442
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-Smad7-V5

<400> 28

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ggcggcggtg gcggtggcgg tgaactgcgt aagatgaaga agaaggtgct ggcggcggtg      180

gcggtggcgg tgaactgcgt ggcgagggtg caaccgatag tcgtgcacac ggtgcaggcg      240

gtggcggtcc gggtcgtgct ggttgctgtc tgggtaaagc tgtgcgcggc gcgaaaggtc      300

atcaccatcc gcacccgccg gcagcaggtg caggtgcagc tggcggtgcg gaagccgatc      360

tgaaagccct gacccatagt gtcctgaaaa aactgaaaga acgtcagctg gagctgctgc      420

tgcaagcagt agaatcccgt ggcggtaccc gtacggcttg tctgctgctg ccgggtcgtc      480

tggattgccg tctgggtccg ggtgcaccgg ctggtgcgca gccggcacaa ccgccgagct      540

cttacagcct gccgctgctg ctgtgtaaag tgtttcgttg gccggacctg cgccacagtt      600

ccgaagttaa acgcctgtgc tgttgcgaga gctatggcaa aattaacccg gaactggttt      660

gttgcaatcc gcaccatctg tctcgtctgt gtgaactgga gagcccgccg ccgccgtatt      720

ctcgttaccc gatggatttc ctgaaaccga ctgcagattg cccggacgca gtcccgtcat      780

cggctgagac cggcggcacc aactatctgg caccgggcgg tctgagtgat tcccagctgc      840

tgctggaacc gggcgaccgt tcacattggt gtgtggttgc ctattgggaa gagaaaacgc      900

gtgtcggtcg cctgtactgc gtacaggaac cgtcgctgga tatcttttat gacctgccgc      960

agggcaatgg tttctgtctg ggccaactga actcagataa taaatcgcag ctggtgcaaa     1020

aagttcgctc aaaaattggc tgcggtatcc agctgacccg tgaagttgac ggtgtctggg     1080
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tatataaccg cagctcttac ccgattttta tcaaaagtgc caccctggat aatccggact 1140

cccgtacgct gctggtccac aaagtatttc cgggcttctc aatcaaagcg ttcgattacg 1200

agaaagccta ctcgctgcag cgcccgaacg accatgaatt catgcagcaa ccgtggacgg 1260

gttttactgt gcagatctct ttcgttaaag gctggggtca atgctacacc cgtcagttta 1320

tctcgtcctg tccgtgctgg ctggaagtga ttttcaatag ccgcaagggc gagctcaatt 1380

cgaagcttga aggtaagcct atccctaacc ctctcctcgg tctcgattct acgtgagtcg 1440

ac 1442

<210> 29
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> optimized Tat-Smad7-V5

<400> 29
agcagctttc agtcagtagc agccagcagc cagagcagca gccagtagca gcagcagcag 60

agcagc 66

<210> 30
<211> 1392
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-Smad7M216L -V5

<400> 30
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ctggtccgtc gcctgtggcg cagccgtgct ccgggtggtg aagatgaaga agaaggtgct 120

ggcggcggtg gcggtggcgg tgaactgcgt ggcgagggtg caaccgatag ccgtgcacat 180

ggtgcaggcg gtggcggtcc gggtcgtgct ggttgctgtc tgggtaaagc tgtgcgcggc 240

gcgaaaggtc atcatcatcc gcatccgccg gcagcaggtg caggtgcagc tggcggtgcg 300

gaagccgatc tgaaagccct gacccatagc gtcctgaaaa aactgaaaga acgtcagctg 360

gagctgctgc tgcaagcagt agaaagccgt ggcggtaccc gtacggcttg tctgctgctg 420

ccgggtcgtc tggattgccg tctgggtccg ggtgcaccgg ctggtgcgca gccggcacaa 480

ccgccgagca gctacagcct gccgctgctg ctgtgtaaag tgtttcgttg gccggacctg 540

cgccatagca gcgaagttaa acgcctgtgc tgttgcgaga gctatggcaa aattaacccg 600

gaactggttt gttgcaatcc gcatcatctg agccgtctgt gtgaactgga gagcccgccg 660

ccgccgtata gccgttaccc gctggatttc ctgaaaccga ctgcagattg cccggacgca 720

gtcccgagca gcgctgagac cggcggcacc aactatctgg caccgggcgg tctgagcgat 780

agccagctgc tgctggaacc gggcgaccgt agccattggt gtgtggttgc ctattgggaa 840

gagaaaacgc gtgtcggtcg cctgtactgc gtacaggaac cgagcctgga tatcttttat 900

gacctgccgc agggcaatgg tttctgtctg ggccaactga acagcgataa taaaagccag 960

ctggtgcaaa aagttcgcag caaaattggc tgcggtatcc agctgacccg tgaagttgac 1020

ggtgtctggg tatataaccg cagcagctac ccgattttta tcaaaagcgc caccctggat 1080

aatccggaca gccgtacgct gctggtccat aaagtatttc cgggcttcag catcaaagcg 1140

ttcgattacg agaaagccta cagcctgcag cgcccgaacg accatgaatt catgcagcaa 1200

ccgtggacgg gttttactgt gcagatcagc ttcgttaaag gctggggtca atgctacacc 1260

cgtcagttta tcagcagctg tccgtgctgg ctggaagtga ttttcaatag ccgcaagggc 1320

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acgtgagtcg ac 1392

<210> 31
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> Tat-Smad7M216L -V5

<400> 31

Gly Ser Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Phe Arg Thr
1 5 10 15

Lys Arg Ser Ala Leu Val Arg Arg Leu Trp Arg Ser Arg Ala Pro Gly
20 25 30

Gly Glu Asp Glu Glu Glu Gly Ala Gly Gly Gly Gly Gly Gly Gly Glu
35 40 45

Leu Arg Gly Glu Gly Ala Thr Asp Ser Arg Ala His Gly Ala Gly Gly
50 55 60

Gly Gly Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys Ala Val Arg Gly
65 70 75 80

Ala Lys Gly His His His Pro His Pro Pro Ala Ala Gly Ala Gly Ala
85 90 95

Ala Gly Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr His Ser Val Leu
100 105 110

Lys Lys Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu Gln Ala Val Glu

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        115                 120                 125

Ser Arg Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu Pro Gly Arg Leu
    130                 135                 140

Asp Cys Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala Gln Pro Ala Gln
145                 150                 155                 160

Pro Pro Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys Lys Val Phe Arg
                165                 170                 175

Trp Pro Asp Leu Arg His Ser Ser Glu Val Lys Arg Leu Cys Cys Cys
            180                 185                 190

Glu Ser Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys Cys Asn Pro His
        195                 200                 205

His Leu Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro Pro Pro Tyr Ser
    210                 215                 220

Arg Tyr Pro Leu Asp Phe Leu Lys Pro Thr Ala Asp Cys Pro Asp Ala
225                 230                 235                 240

Val Pro Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr Leu Ala Pro Gly
                245                 250                 255

Gly Leu Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly Asp Arg Ser His
            260                 265                 270

Trp Cys Val Val Ala Tyr Trp Glu Glu Lys Thr Arg Val Gly Arg Leu
        275                 280                 285

Tyr Cys Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr Asp Leu Pro Gln
    290                 295                 300

Gly Asn Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp Asn Lys Ser Gln
305                 310                 315                 320

Leu Val Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu Thr
                325                 330                 335

Arg Glu Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro Ile
            340                 345                 350

Phe Ile Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu Leu
        355                 360                 365
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Val His Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr Glu
370 375 380

Lys Ala Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln Gln
385 390 395 400

Pro Trp Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp Gly
405 410 415

Gln Cys Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu Glu
420 425 430

Val Ile Phe Asn Ser Arg Lys Gly Glu Leu Asn Ser Lys Leu Glu Gly
435 440 445

Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
450 455 460

<210> 32
<211> 861
<212> DNA
<213> Artificial Sequence

<220>
<223> N-Tat-Smad7-V5

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ggcggcggtg gcggtggcgg tgaactgcgt ggcgagggtg caaccgatag ccgtgcacat 180

ggtgcaggcg gtggcggtcc gggtcgtgct ggttgctgtc tgggtaaagc tgtgcgcggc 240

gcgaaaggtc atcatcatcc gcatccgccg gcagcaggtg caggtgcagc tggcggtgcg 300

gaagccgatc tgaaagccct gacccatagc gtcctgaaaa aactgaaaga acgtcagctg 360

gagctgctgc tgcaagcagt agaaagccgt ggcggtaccc gtacggcttg tctgctgctg 420

ccgggtcgtc tggattgccg tctgggtccg ggtgcaccgg ctggtgcgca gccggcacaa 480

ccgccgagca gctacagcct gccgctgctg ctgtgtaaag tgtttcgttg gccggacctg 540

cgccatagca gcgaagttaa acgcctgtgc tgttgcgaga gctatggcaa aattaacccg 600

gaactggttt gttgcaatcc gcatcatctg agccgtctgt gtgaactgga gagcccgccg 660

ccgccgtata gccgttaccc gatggatttc ctgaaaccga ctgcagattg cccggacgca 720

gtcccgagca gcgctgagac cggcggcacc aactatctgg caccgggcgg tctgagcgat 780

agccagctgc tgctggaacc gggcgaccgt ggtaagccta tccctaaccc tctcctcggt 840

ctcgattcta cgtgagtcga c 861

<210> 33
<211> 558
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-C-terminal-Smad7-V5

<400> 33
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tgggaagaga aaacgcgtgt cggtcgcctg tactgcgtac aggaaccgag cctggatatc 120

ttttatgacc tgccgcaggg caatggtttc tgtctgggcc aactgaacag cgataataaa 180

agccagctgg tgcaaaaagt tcgcagcaaa attggctgcg gtatccagct gacccgtgaa 240

gttgacggtg tctgggtata taaccgcagc agctacccga tttttatcaa aagcgccacc 300

ctggataatc cggacagccg tacgctgctg gtccataaag tatttccggg cttcagcatc 360

aaagcgttcg attacgagaa agcctacagc ctgcagcgcc cgaacgacca tgaattcatg 420

cagcaaccgt ggacgggttt tactgtgcag atcagcttcg ttaaaggctg gggtcaatgc 480

aagggcgagc tcaatagcaa gcttgaaggt aagcctatcc ctaaccctct cctcggtctc 540

gatagcacgt gagtcgac 558

<210> 34
<211> 618
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-C-Smad7

<400> 34
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ttttatgacc tgccgcaggg caatggtttc tgtctgggcc aactgaacag cgataataaa 180

agccagctgg tgcaaaaagt tcgcagcaaa attggctgcg gtatccagct gacccgtgaa 240

gttgacggtg tctgggtata taaccgcagc agctacccga tttttatcaa aagcgccacc 300

ctggataatc cggacagccg tacgctgctg gtccataaag tatttccggg cttcagcatc 360

aaagcgttcg attacgagaa agcctacagc ctgcagcgcc cgaacgacca tgaattcatg 420

cagcaaccgt ggacgggttt tactgtgcag atcagcttcg ttaaaggctg gggtcaatgc 480

tacacccgtc agtttatcag cagctgtccg tgctggctgg aagtgatttt caatagccgc 540

aagggcgagc tcaatagcaa gcttgaaggt aagcctatcc ctaaccctct cctcggtctc 600

gatagcacgt gagtcgac 618

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-C-termal

<400> 35
tcgtcatcgt catctttcct catcgtcttc gtctcgtct 39

<210> 36
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic pirmier

<400> 36
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ctggttcgtc gtctgtggcg ttctcgtgcg ccgggtggtg aagacgaaga agaaggtgcg 120

ggtggtggtg gtggtggtgg tgaactgcgt ggtgaaggtg cgaccgactc tcgtgcgcac 180

ggtgcgggtg gtggtggtcc gggtcgtgcg ggttgctgcc tgggtaaagc ggttcgtggt 240

gcgaaaggtc accaccaccc gcacccgccg gcggcgggtg cgggtgcggc gggtggtgcg 300

gaagcggacc tgaaagcgct gacccactct gttctgaaaa aactgaaaga acgtcagctg 360

gaactgctgc tgcaggcggt tgaatctcgt ggtggtaccc gtaccgcgtg cctgctgctg 420

ccgggtcgtc tggactgccg tctgggtccg ggtgcgccgg cgggtgcgca gccggcgcag 480

ccgccgtctt cttactctct gccgctgctg ctgtgcaaag ttttccgttg gccggacctg 540

cgtcactctt ctgaagttaa acgtctgtgc tgctgcgaat cttacggtaa aatcaacccg 600

gaactggttt gctgcaaccc gcaccacctg tctcgtctgt gcgaactgga atctccgccg 660

ccgccgtact ctcgttaccc gctggacttc ctgaaaccga ccgcggactg cccggacgcg 720

gttccgtctt ctgcggaaac cggtggtacc aactacctgg cgccgggtgg tctgtctgac 780

tctcagctgc tgctggaacc gggtgaccgt tctcactggt gcgttgttgc gtactgggaa 840

gaaaaaaccc gtgttggtcg tctgtactgc gttcaggaac cgtctctgga catcttctac 900

gacctgccgc agggtaacgg tttctgcctg ggtcagctga actctgacaa caaatctcag 960

ctggttcaga aagttcgttc taaaatcggt tgcggtatcc agctgacccg tgaagttgac 1020

ggtgtttggg tttacaaccg ttcttcttac ccgatcttca tcaaatctgc gaccctggac 1080

aacccggact ctcgtaccct gctggttcac aaagttttcc cgggtttctc tatcaaagcg 1140

ttcgactacg aaaaagcgta ctctctgcag cgtccgaacg accacgaatt catgcagcag 1200

ccgtggaccg gtttcaccgt tcagatctct ttcgttaaag gttggggtca gtgctacacc 1260

cgtcagttca tctcttcttg cccgtgctgg ctggaagtta tcttcaactc tcgtggtaaa 1320

ccgatcccga acccgctgct gggtctggac tctacctgag tcgac 1365

<210> 37
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<400> 37

Gly Ser Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Phe Arg Thr
1 5 10 15

Lys Arg Ser Ala Leu Val Arg Arg Leu Trp Arg Ser Arg Ala Pro Gly
20 25 30

Gly Glu Asp Glu Glu Glu Gly Ala Gly Gly Gly Gly Gly Gly Gly Glu
35 40 45

Leu Arg Gly Glu Gly Ala Thr Asp Ser Arg Ala His Gly Ala Gly Gly
50 55 60

Gly Gly Pro Gly Arg Ala Gly Cys Cys Leu Gly Lys Ala Val Arg Gly
65 70 75 80

Ala Lys Gly His His His Pro His Pro Pro Ala Ala Gly Ala Gly Ala
85 90 95

Ala Gly Gly Ala Glu Ala Asp Leu Lys Ala Leu Thr His Ser Val Leu
100 105 110

Lys Lys Leu Lys Glu Arg Gln Leu Glu Leu Leu Leu Gln Ala Val Glu
115 120 125

Ser Arg Gly Gly Thr Arg Thr Ala Cys Leu Leu Leu Pro Gly Arg Leu
130 135 140

Asp Cys Arg Leu Gly Pro Gly Ala Pro Ala Gly Ala Gln Pro Ala Gln
145 150 155 160

Pro Pro Ser Ser Tyr Ser Leu Pro Leu Leu Leu Cys Lys Val Phe Arg
165 170 175

Trp Pro Asp Leu Arg His Ser Ser Glu Val Lys Arg Leu Cys Cys Cys
180 185 190

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Glu Ser Tyr Gly Lys Ile Asn Pro Glu Leu Val Cys Cys Asn Pro His
        195                 200                 205

His Leu Ser Arg Leu Cys Glu Leu Glu Ser Pro Pro Pro Pro Tyr Ser
    210                 215                 220

Arg Tyr Pro Leu Asp Phe Leu Lys Pro Thr Ala Asp Cys Pro Asp Ala
225                 230                 235                 240

Val Pro Ser Ser Ala Glu Thr Gly Gly Thr Asn Tyr Leu Ala Pro Gly
                245                 250                 255

Gly Leu Ser Asp Ser Gln Leu Leu Leu Glu Pro Gly Asp Arg Ser His
            260                 265                 270

Trp Cys Val Val Ala Tyr Trp Glu Glu Lys Thr Arg Val Gly Arg Leu
        275                 280                 285

Tyr Cys Val Gln Glu Pro Ser Leu Asp Ile Phe Tyr Asp Leu Pro Gln
    290                 295                 300

Gly Asn Gly Phe Cys Leu Gly Gln Leu Asn Ser Asp Asn Lys Ser Gln
305                 310                 315                 320

Leu Val Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu Thr
                325                 330                 335

Arg Glu Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro Ile
            340                 345                 350

Phe Ile Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu Leu
        355                 360                 365

Val His Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr Glu
    370                 375                 380

Lys Ala Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln Gln
385                 390                 395                 400

Pro Trp Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp Gly
                405                 410                 415

Gln Cys Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu Glu
            420                 425                 430

Val Ile Phe Asn Ser Arg Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
        435                 440                 445
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Leu Asp Ser Thr
450

<210> 38
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Tat-Smad7-21

<400> 38
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ctggttcgtc gtctgtggcg ttctcgtgcg ccgggtggtg aagacgaaga agaaggtgcg 120

ggtggtggtg gtggtggtgg tgaactgcgt ggtgaaggtg cgaccgactc tcgtgcgcac 180

ggtgcgggtg gtggtggtcc gggtcgtgcg ggttgctgcc tgggtaaagc ggttcgtggt 240

gcgaaaggtc accaccaccc gcacccgccg gcggcgggtg cgggtgcggc gggtggtgcg 300

gaagcggacc tgaaagcgct gacccactct gttctgaaaa aactgaaaga acgtcagctg 360

gaactgctgc tgcaggcggt tgaatctcgt ggtggtaccc gtaccgcgtg cctgctgctg 420

ccgggtcgtc tggactgccg tctgggtccg ggtgcgccgg cgggtgcgca gccggcgcag 480

ccgccgtctt cttactctct gccgctgctg ctgtgcaaag ttttccgttg gccggacctg 540

cgtcactctt ctgaagttaa acgtctgtgc tgctgcgaat cttacggtaa aatcaacccg 600

gaactggttt gctgcaaccc gcaccacctg tctcgtctgt gcgaactgga atctccgccg 660

ccgccgtact ctcgttaccc gctggacttc ctgaaaccga ccgcggactg cccggacgcg 720

gttccgtctt ctgcggaaac cggtggtacc aactacctgg cgccgggtgg tctgtctgac 780

tctcagctgc tgctggaacc gggtgaccgt tctcactggt gcgttgttgc gtactgggaa 840

gaaaaaaccc gtgttggtcg tctgtactgc gttcaggaac cgtctctgga catcttctac 900

gacctgccgc agggtaacgg tttctgcctg ggtcagctga actctgacaa caaatctcag 960

ctggttcaga aagttcgttc taaaatcggt tgcggtatcc agctgacccg tgaagttgac 1020

ggtgtttggg tttacaaccg ttcttcttac ccgatcttca tcaaatctgc gaccctggac 1080

aacccggact ctcgtaccct gctggttcac aaagttttcc cgggtttctc tatcaaagcg 1140

ttcgactacg aaaaagcgta ctctctgcag cgtccgaacg accacgaatt catgcagcag 1200

ccgtggaccg gtttcaccgt tcagatctct ttcgttaaag gttggggtca gtgctacacc 1260

cgtcagttca tctcttcttg cccgtgctgg ctggaagtta tcttcaactc tcgtggtaaa 1320

ccgatcccga acccgctgct gggtctggac tctacctgag tcgac 1365

<210> 39
<211> 1392

<212> DNA
<213> Artificial Sequence

<220>
<223> TatSmad7 Ser

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