SEQUENCE LISTING

<110> Adamed Sp. z o.o.
Pieczykolan, Jerzy Szczepan
Pawlak, Sebastian Dominik
¯erek , Bart³omiej Maciej
Rózga, Piotr Kamil

<120> Anticancer fusion protein

<130> KP4

<150> PL393578
<151> 2010-01-05

<160> 56

<170> PatentIn version 3.5

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Arg Lys Arg Lys Lys Ser Arg Gly Gly Gly Gly Gly Arg Val Ala Ala
1 5 10 15

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
20 25 30

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
35 40 45

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
50 55 60

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
65 70 75 80

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
85 90 95

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
100 105 110

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
115 120 125

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
130 135 140

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
145 150 155 160

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
165 170

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Arg Lys Arg Lys Lys Ser Arg Gly Gly Gly Gly Gly Thr Ser Glu Glu
1 5 10 15

Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val
20 25 30

Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg
35 40 45

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

Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser
65 70 75 80

Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu
85 90 95

Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu
100 105 110

Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
115 120 125

Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala
130 135 140

Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile
145 150 155 160

Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val
165 170 175

Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe
180 185 190

Phe Gly Ala Phe Leu Val Gly
195

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<400> 3

Arg Lys Arg Lys Lys Ser Arg Gly Gly Gly Gly Gly Arg Val Ala Ala
1 5 10 15

His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
20 25 30

Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
35 40 45

Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
50 55 60

Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
65 70 75 80

Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
85 90 95

Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
100 105 110

Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
115 120 125

Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
130 135 140

Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
145 150 155 160

Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly
165 170 175

Pro Leu Gly Leu Ala Gly Arg Val Val Arg Thr Met Pro Phe Leu Phe
180 185 190

Cys Asn Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
195 200 205

Tyr Trp Leu Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
210 215 220

Ser Leu Asn Pro Glu Arg
225 230

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<400> 4

Arg Lys Arg Lys Lys Ser Arg Pro Leu Gly Leu Ala Gly Glu Arg Lys
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Arg Lys Lys Ser Arg Gly Gly Gly Gly Gly Arg Val Ala Ala His Ile
20 25 30

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
35 40 45

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
50 55 60

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
65 70 75 80

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
85 90 95

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
100 105 110

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
115 120 125

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
130 135 140

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
145 150 155 160

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
165 170 175

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
180 185

<210> 5
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<220>
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<400> 5

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Arg Lys Arg Lys Lys Ser Arg Val Val Arg Pro Leu Gly Leu Ala Gly
1               5                  10                  15

Glu Arg Lys Arg Lys Lys Ser Arg Gly Gly Arg Val Ala Ala His Ile
            20                  25                  30

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
        35                  40                  45

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
    50                  55                  60

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
65                  70                  75                  80

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
                85                  90                  95

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
            100                 105                 110

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
        115                 120                 125

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
    130                 135                 140

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
145                 150                 155                 160

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
                165                 170                 175

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            180                 185
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<211> 222
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<400> 6

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1               5                  10                  15

Glu Arg Lys Arg Lys Lys Ser Arg Gly Gly Gly Cys Ala Ala Ala Cys
            20                  25                  30

Ala Ala Cys Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln
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35 40 45

Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala
50 55 60

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
65 70 75 80

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
85 90 95

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
100 105 110

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
115 120 125

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
130 135 140

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
145 150 155 160

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
165 170 175

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
180 185 190

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
195 200 205

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
210 215 220

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<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein sequence

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Cys Asn Gly Arg Cys Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
1 5 10 15

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
20 25 30

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
35 40 45

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
50 55 60

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
65 70 75 80

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
85 90 95

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
100 105 110

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
115 120 125

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
130 135 140

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
145 150 155 160

Phe Phe Gly Ala Phe Leu Val Gly
165

<210> 8
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<220>
<223> fusion protein sequence

<400> 8

Cys Asp Cys Arg Gly Asp Cys Phe Cys Gly Gly Gly Gly Ser Thr Ser
1 5 10 15

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
20 25 30

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
35 40 45

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
50 55 60

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
65 70 75 80

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
85 90 95

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe

100 105 110

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
115 120 125

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
130 135 140

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
145 150 155 160

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
165 170 175

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
180 185 190

Ser Phe Phe Gly Ala Phe Leu Val Gly
195 200

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<213> Artificial Sequence

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Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu
1 5 10 15

Lys Pro Thr Arg Val Val Arg Pro Leu Gly Leu Ala Gly Pro Gln Arg
20 25 30

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
35 40 45

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
50 55 60

Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
65 70 75 80

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

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
100 105 110

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
115 120 125

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
130 135 140

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
145 150 155 160

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
165 170 175

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
180 185 190

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<212> PRT
<213> Artificial Sequence

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Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu
1 5 10 15

Lys Pro Thr Arg Val Val Arg Pro Leu Gly Leu Ala Gly Thr Ser Glu
20 25 30

Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu
35 40 45

Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
50 55 60

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
65 70 75 80

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
85 90 95

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
100 105 110

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
115 120 125

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
130 135 140

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
145 150 155 160

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser

165 170 175

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
180 185 190

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
195 200 205

Phe Phe Gly Ala Phe Leu Val Gly
210 215

<210> 11
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<212> PRT
<213> Artificial Sequence

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<223> fusion protein sequence

<400> 11

Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu
1 5 10 15

Lys Pro Thr Arg Val Val Arg Pro Leu Gly Leu Ala Gly Gly Gly Cys
20 25 30

Ala Ala Ala Cys Ala Ala Cys Thr Ser Glu Glu Thr Ile Ser Thr Val
35 40 45

Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro
50 55 60

Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
65 70 75 80

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
85 90 95

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
100 105 110

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
115 120 125

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
130 135 140

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
145 150 155 160

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
165 170 175

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
180 185 190

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
195 200 205

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
210 215 220

Val Gly
225

<210> 12
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<400> 12

Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys Asn Phe Ala
1 5 10 15

Ser Arg Asn Asp Tyr Ser Tyr Trp Leu Cys Asn Tyr Tyr Ser Asn Ser
20 25 30

Tyr Ser Phe Trp Leu Ala Ser Leu Asn Pro Glu Arg Val Val Arg Pro
35 40 45

Leu Gly Leu Ala Gly Gly Gly Gly Arg Val Ala Ala His Ile Thr Gly
50 55 60

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
65 70 75 80

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
85 90 95

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
100 105 110

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
115 120 125

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
130 135 140

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
145 150 155 160

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr

165 170 175

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
180 185 190

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
195 200 205

Ser Phe Phe Gly Ala Phe Leu Val Gly
210 215

<210> 13
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<213> Artificial Sequence

<220>
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<400> 13

Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn
1 5 10 15

Pro Glu Arg Val Val Arg Pro Leu Gly Leu Ala Gly Gly Gly Gly Arg
20 25 30

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
35 40 45

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
50 55 60

Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
65 70 75 80

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

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
100 105 110

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
115 120 125

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
130 135 140

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
145 150 155 160

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
165 170 175

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Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
            180                 185                 190

Gly Gly Gly Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys
        195                 200                 205

Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp Leu
    210                 215                 220
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<400> 14

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Leu Gly Leu Arg Ser Leu Arg Glu Arg Val Val Arg Pro Leu Gly Leu
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Ala Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg
            20                  25                  30

Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly
        35                  40                  45

Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu
    50                  55                  60

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

Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile
                85                  90                  95

Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys
            100                 105                 110

Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn
        115                 120                 125

Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln
    130                 135                 140

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

Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly
                165                 170                 175

Ala Phe Leu Val Gly
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180

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<400> 15

Leu Gly Leu Arg Ser Leu Arg Glu Arg Val Val Arg Pro Leu Gly Leu
1 5 10 15

Ala Gly Pro Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Thr Ser
20 25 30

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
35 40 45

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
50 55 60

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
65 70 75 80

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
85 90 95

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
100 105 110

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
115 120 125

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
130 135 140

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
145 150 155 160

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
165 170 175

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
180 185 190

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
195 200 205

Ser Phe Phe Gly Ala Phe Leu Val Gly
210 215

<210> 16
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<300>
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<309> 1996-10-01
<313> (1)..(281)

<400> 16

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Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1               5                  10                  15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
            20                  25                  30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
        35                  40                  45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
    50                  55                  60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65                  70                  75                  80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
                85                  90                  95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
            100                 105                 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
        115                 120                 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
    130                 135                 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145                 150                 155                 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
                165                 170                 175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
            180                 185                 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
        195                 200                 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
    210                 215                 220
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```
Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225                 230                 235                 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
                245                 250                 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
            260                 265                 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
        275                 280
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<210> 17
<211> 7
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<300>
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<309> 2009-03-16
<313> (333)..(339)

<400> 17

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1               5
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<210> 18
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<213> Homo sapiens

<300>
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<309> 2000-05-30
<313> (74)..(98)

<400> 18

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Thr Met Pro Phe Leu Phe Cys Asn Val Asn Asp Val Cys Asn Phe Ala
1               5                   10                  15

Ser Arg Asn Asp Tyr Ser Tyr Trp Leu
            20                  25
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<210> 19
<211> 18
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<213> Homo sapiens

<300>
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<400> 19

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Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn
1               5                   10                  15
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Pro Glu

<210> 20
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<223> synthetic peptide

<300>
<301> Arap W., Pasqualini R., Ruoslahti E.
<302> Cancer treatment by targeted drug delivery to tumor vasculature
<303> Science (Washington DC)
<304> 279
<305> 5349
<306> 377-380
<307> 1998-01-16
<313> (1)..(5)

<400> 20

Cys Asn Gly Arg Cys
1 5

<210> 21
<211> 9
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<220>
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<300>
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<400> 21

Cys Asp Cys Arg Gly Asp Cys Phe Cys
1 5

<210> 22
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<213> Homo sapiens

<300>
<301> Khachigian LM, Owensby DA, Chesterman CN.
<302> A tyrosinated peptide representing the alternatively spliced exon of the platelet-derived growth factor A-chain binds specifically to cultured cells and interferes with binding of several growth factors.
<303> Journal of Biological Chemistry
<304> 25
<305> 267
<306> 1660-1666
<307> 1992-01-25

<300>
<301> Khachigian LM, Field SL, Crouch R, Chesterman CN
<302> Platelet-derived growth factor A-chain synthetic peptide inhibits

human glioma xenograft proliferation in nude mice.
<303> Anticancer Res
<304> 15
<305> 2
<306> 337-41
<307> 1995-04-05

<400> 22

Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu
1 5 10 15

Lys Pro Thr

<210> 23
<211> 8
<212> PRT
<213> Homo sapiens

<300>
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<309> 2008-05-05
<313> (453)..(460)

<400> 23

Leu Gly Leu Arg Ser Leu Arg Glu
1 5

<210> 24
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<220>
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<400> 24

Pro Leu Gly Leu Ala Gly
1 5

<210> 25
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<212> PRT
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<223> protease cutting sequence

<400> 25

Arg Val Val Arg
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<210> 26
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<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence of steric linker

<400> 26

Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys
1 5 10

<210> 27
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence of steric linker

<400> 27

Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys
1 5 10

<210> 28
<211> 5
<212> PRT
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<223> artificial sequence of steric linker

<400> 28

Gly Gly Gly Gly Gly
1 5

<210> 29
<211> 4
<212> PRT
<213> Mus musculus

<300>
<308> GenBank/CAA94521.1
<309> 1996-06-13
<313> (122)..(124)

<400> 29

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<210> 30
<211> 5
<212> PRT
<213> Mus musculus

<300>
<308> GenBank/CAA94521.1
<309> 1996-06-13
<313> (122)..(126)

<400> 30

Gly Gly Gly Gly Ser
1 5

<210> 31

<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 31
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acccgtggcc gcagcaacac gctgagctct ccgaattcga aaaatgaaaa agcactgggc 120

cgcaaaatta actcgtggga aagcagtcgt tctggtcaca gctttctgtc gaatctgcac 180

ctgcgcaatg gtgaactggt gattcatgaa aaaggctttt actatatcta ttctcagacg 240

tattttcgtt ttcaggaaga aattaaagaa aacaccaaaa atgacaaaca gatggtgcag 300

tacatttaca aatacaccag ttacccggac ccgattctgc tgatgaaaag cgcccgtaac 360

tcatgctgga gcaaagacgc tgaatatggc ctgtattcta tttatcaggg tggcatcttc 420

gaactgaaag aaaacgatcg tatttttgtt tcggtgacca acgaacacct gattgatatg 480

gatcatgaag catcgttttt cggcgcgttt ctggtcggc 519

<210> 32
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 32
cgcaaacgta aaaaaagccg tggtggtggc ggtggcacca gcgaagaaac cattagcacc 60

gttcaggaaa aacagcagaa tattagtccg ctggttcgtg aacgtggtcc gcagcgtgtt 120

gcagcacata ttaccggcac ccgtggtcgt agcaataccc tgagcagccc gaatagcaaa 180

aatgaaaaag cactgggtcg caaaattaat agctgggaaa gcagccgtag cggtcatagc 240

tttctgagca atctgcatct gcgtaatggt gaactggtga ttcatgaaaa aggcttttat 300

tatatttata gccagaccta ttttcgcttt caggaagaaa ttaaagaaaa taccaaaaat 360

gataaacaaa tggtgcagta tatctataaa tacaccagct atccggatcc gattctgctg 420

atgaaaagcg cacgtaatag ctgttggagc aaagatgcag aatatggtct gtatagcatt 480

tatcagggtg gcatttttga actgaaagaa aatgatcgca tttttgtgag cgtgaccaat 540

gaacatctga ttgatatgga tcatgaagcc agctttttg gtgcatttct ggtgggt 597

<210> 33
<211> 690
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 33
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acccgtggtc gtagcaatac cctgagcagc ccgaatagca aaaatgaaaa agcactgggt 120

cgcaaaatta atagctggga aagcagccgt agcggtcata gctttctgag caatctgcat 180

ctgcgtaatg gtgaactggt gattcatgaa aaaggctttt attatattta tagccagacc 240

tattttcgct ttcaggaaga aattaaagaa aataccaaaa atgataaaca aatggtgcag 300

tacatttaca aatataccag ctatccggat ccgattctgc tgatgaaaag cgcacgtaat 360

agctgttgga gcaaagatgc agaatatggt ctgtatagca tttatcaggg tggcatttt 420

gaactgaaag aaaatgatcg catttttgtg agcgtgacca atgaacatct gattgatatg 480

gatcatgaag ccagcttttt tggtgcattt ctggttggtg gcggtggtcc gctgggtctg 540

gcaggtcgtg ttgttcgtac catgccgttt ctgttttgca atgttaatga tgtgtgcaat 600

tttgccagcc gcaatgatta tagctattgg ctgtgcaatt attatagcaa tagctatagc 660

ttttggctgg ctagtctgaa tccggaacgt 690

<210> 34
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 34
cgcaaacgta aaaaaagccg tccgctgggt attgccggtg aacgtaaacg caaaaaatct 60

cgtggtggtg gtggcggtcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagccctgg gtcgcaaaat taatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaggaa 300

gaaattaaag aaaacaccaa aaatgataaa caaatggtgc agtatatcta taaatacacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gcctgtatag catttatcag ggtggcattt ttgaactgaa agaaaatgat 480

cgcatttttg tgagcgtgac caatgaacat ctgattgata tggatcatga agccagcttt 540

tttggtgcat ttctggtggg t 561

<210> 35
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 35
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aaaaaatcac gtggtggtcg tgttgcagca catattaccg gcacccgtgg tcgtagcaat 120

accctgagca gcccgaatag caaaaatgaa aaagcactgg gtcgcaaaat taatagctgg 180

gaaagcagcc gtagcggtca tagctttctg agcaatctgc atctgcgtaa tggtgaactg 240

gtgattcatg aaaaaggctt ttattatatt tatagccaga cctattttcg ctttcaggaa 300

gaaattaaag aaaataccaa aaatgataaa caaatggtgc agtacattta caaatatacc 360

agctatccgg atccgattct gctgatgaaa agcgcacgta atagctgttg gagcaaagat 420

gcagaatatg gtctgtatag catttatcag ggtggcattt ttgaactgaa agaaaatgat 480

cgcatttttg tgagcgtgac caatgaacat ctgattgata tggatcatga agccagcttt 540

tttggtgcat ttctggttgg t 561

<210> 36
<211> 666
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 36
cgtaaacgta aaaaaagccg tgttgttcgt ccgctgggta ttgcaggtga acgtaaacgt 60

aaaaaaagcc gtggtggtgg ttgtgcagca gcatgtgcag catgtaccag cgaagaaacc 120

attagcaccg ttcaggaaaa acagcagaat attagcccgc tggttcgtga acgtggtccg 180

cagcgtgttg cagcacatat taccggtacc cgtggtcgta gcaataccct gagcagcccg 240

aatagcaaaa atgaaaaagc actgggtcgt aaaattaata gctgggaaag cagccgtagc 300

ggtcatagct ttctgagcaa tctgcatctg cgtaatggtg aactggttat tcatgaaaaa 360

ggtttttatt atatttatag ccagacctat tttcgttttc aggaagaaat taaagaaaat 420

accaaaaatg ataaacagat ggttcagtat atttataaat ataccagcta tccggatccg 480

attctgctga tgaaaagcgc acgtaatagc tgttggagca aagatgcaga atatggtctg 540

tatagcattt atcagggtgg tatttttgaa ctgaaagaaa atgatcgtat ttttgttagc 600

gttaccaatg aacatctgat tgatatggat catgaagcaa gctttttgg tgcatttctg 660

gttggt 666

<210> 37
<211> 505
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 37
tgtaatggtc gttgtccgca gcgtgttgca gcacatatta ccggcacccg tggtcgtagc 60

aataccctga gcagcccgaa tagcaaaaat gaaaaagccc tgggtcgcaa aattaatagc 120

tgggaaagca gccgtagcgg tcatagcttt ctgagcaatc tgcatctgcg taatggtgaa 180

ctggtgattc atgaaaaagg cttttattat atttatagcc agacctattt tcgctttcag 240

gaagaaatta aagaaaacac caaaaatgat aaacaaatgg tgcagtatat ctataaatac 300

accagctatc cggatccgat tctgctgatg aaaagcgcac gtaatagctg ttggagcaaa 360

gatgcagaat atggcctgta tagcatttat cagggtggca tttttgaact gaaagaaaat 420

gatcgcattt ttgtgagcgt gaccaatgaa catctgattg atatggatca tgaaagccag 480

ctttttggt gcatttctgg tgggt 505

<210> 38
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 38
tgtgaatgtg gcggtgaatg tttttgtggt ggcggtagca ccagtgaaga aaccattagc 60

accgttcaag aaaaacagca gaatattagt ccgctggttc gtgaacgtgg tccgcagcgt 120

gttgcagcac atattaccgg cacccgtggt cgtagcaata ccctgagcag cccgaatagc 180

aaaaatgaaa aagcactggg tcgcaaaatc aatagctggg aaagcagccg tagcggtcat 240

agctttctga gcaatctgca tctgcgtaat ggtgaactgg tgattcatga aaaaggcttc 300

tactatatct acagccagac ctattttcgc ttccaagaag aaatcaaaga gaacaccaaa 360

aacgacaaac aaatggtgca gtacatctac aaatatacca gctatccgga tccgattctg 420

ctgatgaaaa gcgcacgtaa tagctgttgg agcaaagatg cagaatatgg tctgtatagc 480

atttatcagg gtggcatctt tgagctgaaa gaaaatgatc gcatctttgt tagcgtgacc 540

aacgaacatc tgatcgatat ggatcatgaa gccagctttt ttggtgcatt tctggtgggt 600

<210> 39
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 39
tatggtcgtc cgcgtcagag cggtaaaaaa cgtaaacgta aacgcctgaa accgacccgt 60

gttgttcgtc cgctgggtct ggcaggtccg cagcgtgttg cagcacatat taccggcacc 120

cgtggtcgta gcaataccct gagcagcccg aatagcaaaa atgaaaaagc cctgggtcgt 180

aaaattaata gctgggaaag cagccgtagc ggtcatagct ttctgagcaa tctgcatctg 240

cgtaatggcg aactggtgat tcatgaaaaa ggcttttatt atatttatag ccagacctat 300

tttcgctttc aggaagaaat taaagaaaat accaaaaatg ataaacaaat ggtgcagtat 360

atctataaat ataccagcta tccggatccg attctgctga tgaaaagcgc acgtaatagc 420

tgttggagca aagatgccga atatggtctg tatagcattt atcagggtgg cattttgaa 480

ctgaaagaaa atgatcgcat ttttgtgagc gtgaccaatg aacatctgat tgatatggat 540

catgaagcca gctttttttgg tgcatttctg gttggt 576

<210> 40
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 40
tatggtcgtc cgcgtcagag cggtaaaaaa cgtaaacgta aacgcctgaa accgacccgt 60

gttgttcgtc cgctgggtct ggcaggcacc agcgaagaaa ccattagcac cgttcaggaa 120

aaacagcaga atattagtcc gctggttcgt gaacgtggtc cgcagcgtgt tgcagcacat 180

attaccggca cccgtggtcg tagcaatacc ctgagcagcc cgaatagcaa aaatgaaaaa 240

gcactgggtc gcaaaattaa tagctgggaa agcagccgta gcggtcatag ctttctgagc 300

aatctgcatc tgcgtaatgg tgaactggtg attcatgaaa aaggctttta ttatatttat 360

agccagacct attttcgctt tcaggaagaa attaaagaaa ataccaaaaa tgataaacaa 420

atggtgcagt atatctataa atacaccagc tatccggatc cgattctgct gatgaaaagc 480

gcacgtaata gctgttggag caaagatgca gaatatggtc tgtatagcat ttatcagggt 540

ggcatttttg aactgaaaga aaatgatcgc atttttgtga gcgtgaccaa tgaacatctg 600

attgatatgg atcatgaagc cagcttttt ggtgcatttc tggtgggt 648

<210> 41
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 41
tatggtcgtc cgcgtcagag cggtaaaaaa cgtaaacgta aacgtctgaa accgacccgt 60

gttgttcgtc cgctgggtct ggcaggtggt ggttgtgcag cagcatgtgc agcatgtacc 120

agcgaagaaa ccattagcac cgttcaggaa aaacagcaga atattagccc gctggttcgt 180

gaacgtggtc cgcagcgtgt tgcagcacat attaccggta cccgtggtcg tagcaatacc 240

ctgagcagcc cgaatagcaa aaatgaaaaa gcactgggtc gtaaaattaa tagctgggaa 300

agcagccgta gcggtcatag ctttctgagc aatctgcatc tgcgtaatgg tgaactggtt 360

attcatgaaa aaggttttta ttatatttat agccagacct attttcgttt tcaggaagaa 420

attaaagaaa ataccaaaaa tgataaacag atggttcagt atatttataa atataccagc 480

tatccggatc cgattctgct gatgaaaagc gcacgtaata gctgttggag caaagatgca 540

gaatatggtc tgtatagcat ttatcagggt ggtatttttg aactgaaaga aaatgatcgt 600

atttttgtta gcgttaccaa tgaacatctg attgatatgg atcatgaagc aagcttttt 660

ggtgcatttc tggttggt 678

<210> 42

<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 42
accatgccgt ttctgttttg caatgttaat gatgtgtgca attttgccag ccgcaatgat 60

tatagctatt ggctgtgcaa ttattatagc aatagctata gcttttggct ggcttctctg 120

aatccggaac gtgttgttcg tccgctgggt ctggcaggcg gtggtggtcg tgttgcagca 180

catattaccg gcacccgtgg tcgtagcaat accctgagca gcccgaatag caaaaatgaa 240

aaagcactgg gtcgcaaaat taatagctgg gaaagcagcc gtagcggtca tagctttctg 300

agcaatctgc atctgcgtaa tggtgaactg gtgattcatg aaaaaggctt ttattatatt 360

tatagccaga cctattttcg ctttcaggaa gaaattaaag aaaataccaa aaatgataaa 420

caaatggtgc agtacattta caaatatacc agctatccgg atccgattct gctgatgaaa 480

agcgcacgta atagctgttg gagcaaagat gcagaatatg gtctgtatag catttatcag 540

ggtggcattt ttgaactgaa agaaaatgat cgcatttttg tgagcgtgac caatgaacat 600

ctgattgata tggatcatga agccagcttt tttggtgcat ttctggttgg t 651

<210> 43
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 43
tgcaattatt atagcaatag ctatagcttt tggctggcaa gcctgaatcc ggaacgtgtt 60

gttcgtccgc tgggtctggc tgggggtggc ggtcgtgttg cagcacatat taccggcacc 120

cgtggtcgta gcaataccct gagcagcccg aatagcaaaa atgaaaaagc actgggtcgc 180

aaaattaata gctgggaaag cagccgtagc ggtcatagct ttctgagcaa tctgcatctg 240

cgtaatggtg aactggtgat tcatgaaaaa ggcttttatt atatttatag ccagacctat 300

tttcgctttc aggaagaaat taaagaaaat accaaaaatg ataaacaaat ggtgcagtac 360

atttacaaat ataccagcta tccggatccg attctgctga tgaaaagcgc acgtaatagc 420

tgttggagca aagatgcaga atatggtctg tatagcattt atcagggtgg cattttgaa 480

ctgaaagaaa atgatcgcat ttttgtgagc gtgaccaatg aacatctgat tgatatggat 540

catgaagcca gctttttgg tgcatttctg gttggtggcg gtggtactat gccgtttctg 600

ttttgcaatg ttaatgatgt gtgcaatttt gccagccgca atgattatag ctattggctg 660

<210> 44
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 44
ctgggtctgc gtagcctgcg tgaacgtgtt gttcgtccgc tgggtctggc aggtccgcag 60

cgtgttgcag cacatattac cggcacccgt ggtcgtagca ataccctgag cagcccgaat 120

agcaaaaatg aaaaagccct gggtcgtaaa attaatagct gggaaagcag ccgtagcggt 180

catagctttc tgagcaatct gcatctgcgt aatggcgaac tggtgattca tgaaaaaggc 240

ttttattata tttatagcca gacctatttt cgctttcagg aagaaattaa agaaaatacc 300

aaaaatgata aacaaatggt gcagtatatc tataaatata ccagctatcc ggatccgatt 360

ctgctgatga aaagcgcacg taatagctgt tggagcaaag atgccgaata tggtctgtat 420

agcatttatc agggtggcat ttttgaactg aaagaaaatg atcgcatttt tgtgagcgtg 480

accaatgaac atctgattga tatggatcat gaagccagct ttttggtgc atttctggtt 540

ggt 543

<210> 45
<211> 651
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial construct

<400> 45
ctgggtctgc gtagcctgcg tgaacgtgtt gttcgtccgc tgggtctggc aggtccgggt 60

ggtggttgtg cagcagcatg tgcagcatgt accagcgaag aaaccattag caccgttcag 120

gaaaaacagc agaatattag cccgctggtt cgtgaacgtg gtccgcagcg tgttgcagca 180

catattaccg gtacccgtgg tcgtagcaat accctgagca gcccgaatag caaaaatgaa 240

aaagcactgg gtcgtaaaat taatagctgg gaaagcagcc gtagcggtca tagctttctg 300

agcaatctgc atctgcgtaa tggtgaactg gttattcatg aaaaaggttt ttattatatt 360

tatagccaga cctattttcg ttttcaggaa gaaattaaag aaaataccaa aaatgataaa 420

cagatggttc agtatattta taaatatacc agctatccgg atccgattct gctgatgaaa 480

agcgcacgta atagctgttg gagcaaagat gcagaatatg gtctgtatag catttatcag 540

ggtggtattt ttgaactgaa agaaaatgat cgtatttttg ttagcgttac caatgaacat 600

ctgattgata tggatcatga agcaagcttt tttggtgcat ttctggttgg t 651

<210> 46
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence

<400> 46

Arg Lys Arg Lys Lys Ser Arg Val Val Arg Pro Leu Gly Ile Ala Gly

1 5 10 15

Glu Arg Lys Arg Lys Lys Ser Arg Thr Ser Glu Glu Thr Ile Ser Thr
20 25 30

Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly
35 40 45

Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
50 55 60

Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
65 70 75 80

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
85 90 95

Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
100 105 110

Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
115 120 125

Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
130 135 140

Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
145 150 155 160

Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
165 170 175

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
180 185 190

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
195 200 205

Leu Val Gly
210

<210> 47
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence

<400> 47

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

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Glu Arg Lys Arg Lys Lys Ser Arg Gly Gly Gly Cys Ala Ala Ala Cys
            20                  25                  30

Ala Ala Cys Gly Ser Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr
        35                  40                  45

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
    50                  55                  60

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
65                  70                  75                  80

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
                85                  90                  95

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
            100                 105                 110

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
        115                 120                 125

Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
    130                 135                 140

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
145                 150                 155                 160

Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
                165                 170                 175

Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
            180                 185                 190

Phe Phe Gly Ala Phe Leu Val Gly
        195                 200
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<210> 48
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence

<400> 48

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Arg Lys Arg Lys Lys Ser Arg Val Val Arg Lys Arg Lys Lys Ser Arg
1               5                   10                  15

Gly Gly Gly Cys Ala Ala Ala Cys Ala Ala Cys Gly Ser Gly Gln Arg
            20                  25                  30

Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
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35 40 45

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
50 55 60

Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
65 70 75 80

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

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
100 105 110

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
115 120 125

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
130 135 140

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
145 150 155 160

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
165 170 175

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
180 185 190

<210> 49
<211> 206
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence

<400> 49

Tyr Gly Arg Pro Arg Gln Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu
1 5 10 15

Lys Pro Thr Arg Val Val Arg Pro Leu Gly Ile Ala Gly Glu Gly Gly
20 25 30

Gly Cys Ala Ala Ala Cys Ala Ala Cys Gly Ser Gly Gln Arg Val Ala
35 40 45

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
50 55 60

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
65 70 75 80

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
85 90 95

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
100 105 110

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
115 120 125

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
130 135 140

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
145 150 155 160

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
165 170 175

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
180 185 190

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
195 200 205

<210> 50
<211> 633
<212> DNA
<213> Artificial Sequence

<220>
<223> artificial sequence

<400> 50
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aaaaaaagcc gtaccagcga agaaaccatt agcaccgtgc aggaaaaaca gcagaacatt 120

agcccgctgg tgcgtgaacg tggcccgcag cgtgtggcgg cgcatattac cggcacccgt 180

ggccgtagca acaccctgag cagcccgaac agcaaaaacg aaaaagcgct gggccgtaaa 240

attaacagct gggaaagcag ccgtagcggc catagctttc tgagcaacct gcatctgcgt 300

aacggcgaac tggtgattca tgaaaaaggc ttttattata tttatagcca gacctatttt 360

cgttttcagg aagaaattaa agaaaacacc aaaaacgata aacagatggt gcagtatatt 420

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