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<110> NGM BIOPHARMACEUTICALS, INC.

<120> BINDING PROTEINS AND METHODS OF USE THEREOF

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<151> 2014-01-24

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Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr
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Ser Tyr Asp Ile Asn
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Gly Tyr Thr Phe Thr Ser Tyr
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Pro Gly Asp Gly
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Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys
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Ser Thr Ser Gly Tyr Val Tyr Met His Trp Asn
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Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu
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Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Arg Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
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Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Ile Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

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Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
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Tyr Ile Asn Tyr Asp Gly Asn Ser Asn Tyr Thr Pro Ser Leu Lys Asn

1 5 10 15

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Lys Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val
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Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser
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Arg Ala Asn Arg Leu Val Asp
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Leu Gln Tyr Asp Glu Phe Pro Phe Thr
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Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
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Ala Arg Lys Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val
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Gly Tyr Ser Ile Thr Ser Gly Tyr
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Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp
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Tyr Asp Glu Phe Pro Phe
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Ala Arg Lys Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp
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Asn Ser Tyr Leu Ser Trp Val
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Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val
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Tyr Ile Asn Tyr Asp Gly Asn Ser Asn
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20 25 30
Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45
Met Gly Tyr Ile Asn Tyr Asp Gly Asn Ser Asn Tyr Thr Pro Ser Leu
50 55 60
Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80
Leu Lys Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95
Ala Arg Lys Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val Trp
100 105 110
Gly Thr Gly Thr Thr Val Thr Val Ser Ser
115 120

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Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Ser Trp Val Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Phe
85 90 95
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

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Gly Tyr Thr Phe Thr Arg Tyr Asp Ile Asn
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Trp Ile Tyr Pro Gly Asp Ser Ser Thr Lys Phe Asn Glu Asn Phe Lys
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Asp

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<400> 55
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Thr Tyr
 1   5   10

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Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
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Leu Ala Ser Asn Leu Glu Ser
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Gln His Ser Arg Glu Leu Pro Tyr Thr
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Gly Tyr Thr Phe Thr Arg Tyr Asp
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 1   5   10

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Arg Tyr Asp Ile Asn
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Gly Tyr Thr Phe Thr Arg Tyr
 1   5

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Asp Tyr Tyr Gly Ser Arg Ser Phe Thr
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Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
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Ser Arg Glu Leu Pro Tyr
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Thr Arg Tyr Asp Ile Asn
 1   5

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Trp Ile Gly Trp Ile Tyr Pro Gly Asp Ser Ser Thr Lys
 1   5   10

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Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Thr
 1   5   10

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<400> 73

Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
 1   5   10

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<400> 74
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1   5   10

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<400> 75
Gln His Ser Arg Glu Leu Pro Tyr
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<400> 76
Trp Ile Tyr Pro Gly Asp Ser Ser Thr Lys
 1   5   10

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Gln Val Gln Pro Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
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Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Asp Ile Asn Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Ser Ser Thr Lys Phe Asn Glu Asn Phe
    50   55   60
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Thr Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Thr Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

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<400> 79
Gly Tyr Thr Phe Thr Arg Tyr Asp Ile Asn
 1   5   10

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Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys Tyr Asn Glu Lys Phe Lys
 1   5   10   15
Gly

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<400> 81
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

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<400> 82
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Leu His
 1   5   10   15

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<400> 83
Leu Ala Ser Asn Leu Glu Ser
 1   5

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<400> 84
Gln His Ser Gly Glu Leu Pro Tyr Thr
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Gly Tyr Thr Phe Thr Arg Tyr Asp
 1   5

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<400> 86
Ile Tyr Pro Gly Asp Asp Ser Thr
 1   5

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<400> 87
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
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Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

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Leu Ala Ser
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<400> 90
Arg Tyr Asp Ile Asn
 1   5

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<220>
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<400> 91
Gly Tyr Thr Phe Thr Arg Tyr
 1   5

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<400> 93
Asp Tyr Tyr Gly Ser Arg Ser Phe Val
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Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

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<400> 95
Ser Gly Glu Leu Pro Tyr
 1   5

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VH CDR1 - Contact

<400> 96
Thr Arg Tyr Asp Ile Asn
 1   5

<210> 97
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VH CDR2 - Contact

<400> 97

Trp Ile Gly Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys
 1   5   10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VH CDR3 - Contact

<400> 98
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5   10

<210> 99
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VL CDR1 - Contact

<400> 99
Ser Thr Ser Gly Tyr Ser Tyr Leu His Trp Tyr
 1   5   10

<210> 100
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VL CDR2 - Contact

<400> 100
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1   5   10

<210> 101
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VL CDR3 - Contact

<400> 101
Gln His Ser Gly Glu Leu Pro Tyr
 1   5

<210> 102
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VH CDR2 - AbM

<400> 102
Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys
 1   5   10

<210> 103
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VH Sequence

<400> 103
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Lys Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 104
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 2L12 VL Sequence

<400> 104
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Pro Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Gly
                85   90   95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 105
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR1 - Exemplary

<400> 105
Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn
 1   5   10

<210> 106
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR2 - Exemplary
<400> 106
Trp Ile Tyr Pro Gly Asp Gly Ser Pro Lys Tyr Asp Glu Lys Phe Lys
 1   5   10   15
Gly

<210> 107
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR3 - Exemplary

<400> 107
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 108
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR1- Exemplary

<400> 108
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Val His
 1   5   10   15

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR2- Exemplary

<400> 109
Leu Ala Ser Asn Leu Glu Ser
 1   5

<210> 110
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR3- Exemplary

<400> 110
Gln His Ser Gly Glu Leu Pro Tyr Thr
 1   5

<210> 111
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR1 - IMGT

<400> 111
Gly Tyr Thr Phe Thr Ser Tyr Asp
 1   5

<210> 112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR2 - IMGT

<400> 112
Ile Tyr Pro Gly Asp Gly Ser Pro
 1   5

<210> 113
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR3 - IMGT

<400> 113
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR1- IMGT

<400> 114
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 115
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR2- IMGT

<400> 115
Leu Ala Ser
 1

<210> 116
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR1 - Kabat

<400> 116
Ser Tyr Asp Ile Asn
 1   5

<210> 117
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR1 - Chothia

<400> 117
Gly Tyr Thr Phe Thr Ser Tyr
 1   5

<210> 118
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR2 - Chothia

<400> 118
Pro Gly Asp Gly
 1

<210> 119
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR3 - Chothia

<400> 119
Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5

<210> 120
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR1- Chothia

<400> 120
Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 121
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR3- Chothia

<400> 121
Ser Gly Glu Leu Pro Tyr

1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR1 - Contact

<400> 122
Thr Ser Tyr Asp Ile Asn
1 5

<210> 123
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR2 - Contact

<400> 123
Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Pro Lys
1 5 10

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR3 - Contact

<400> 124
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val
1 5 10

<210> 125
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR1- Contact

<400> 125
Ser Thr Ser Gly Tyr Ser Tyr Val His Trp Tyr
1 5 10

<210> 126
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR2- Contact

<400> 126
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
1 5 10

<210> 127
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL CDR3- Contact

<400> 127
Gln His Ser Gly Glu Leu Pro Tyr
 1   5

<210> 128
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH CDR2 - AbM

<400> 128
Trp Ile Tyr Pro Gly Asp Gly Ser Pro Lys
 1   5   10

<210> 129
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VH Sequence

<400> 129
Gln Val Gln Pro Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Pro Lys Tyr Asp Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 130
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 3L3 VL Sequence

<400> 130
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Val His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60
Arg Phe Ser Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Gly
85 90 95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR1- Exemplary

<400> 131
Gly Tyr Ile Phe Thr Asn Tyr Gly Ile Ser
1 5 10

<210> 132
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR2- Exemplary

<400> 132
Glu Ile Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 133
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR3- Exemplary

<400> 133
His Trp Asp Gly Val Leu Asp Tyr Phe Asp Tyr
1 5 10

<210> 134
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR1- Exemplary

<400> 134
Lys Ser Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu
1 5 10 15
Ala

<210> 135
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR2- Exemplary

<400> 135
Gly Ala Ser Thr Arg Glu Ser
 1   5

<210> 136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR3- Exemplary

<400> 136
Leu Asn Asp His Ser Tyr Pro Phe Thr
 1   5

<210> 137
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR1 - IMGT

<400> 137
Gly Tyr Ile Phe Thr Asn Tyr Gly
 1   5

<210> 138
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR2 - IMGT

<400> 138
Ile Tyr Pro Arg Ser Gly Asn Thr
 1   5

<210> 139
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR3 - IMGT

<400> 139
Ala Arg His Trp Asp Gly Val Leu Asp Tyr Phe Asp Tyr
 1   5   10

<210> 140
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR1 - IMGT

<400> 140
Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr
 1   5   10

<210> 141
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR2 - IMGT

<400> 141
Gly Ala Ser
 1

<210> 142
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR1 - Kabat

<400> 142
Asn Tyr Gly Ile Ser
 1   5

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR1 - Chothia

<400> 143
Gly Tyr Ile Phe Thr Asn Tyr
 1   5

<210> 144
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR2 - Chothia

<400> 144
Pro Arg Ser Gly
 1

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR3 - Chothia

<400> 145
Trp Asp Gly Val Leu Asp Tyr Phe Asp
 1   5

<210> 146
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR1- Chothia

<400> 146
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr
 1   5   10

<210> 147
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR3- Chothia

<400> 147
Asp His Ser Tyr Pro Phe
 1   5

<210> 148
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR1 - Contact

<400> 148
Thr Asn Tyr Gly Ile Ser
 1   5

<210> 149
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR2 - Contact

<400> 149
Trp Ile Gly Glu Ile Tyr Pro Arg Ser Gly Asn Thr Tyr
 1   5   10

<210> 150
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR3 - Contact

<400> 150
Ala Arg His Trp Asp Gly Val Leu Asp Tyr Phe Asp
 1   5   10

<210> 151
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR1 - Contact

<400> 151
Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
 1   5   10

<210> 152
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR2 - Contact

<400> 152
Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu
 1   5   10

<210> 153
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL CDR3 - Contact

<400> 153
Leu Asn Asp His Ser Tyr Pro Phe
 1   5

<210> 154
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH CDR2 - AbM

<400> 154
Glu Ile Tyr Pro Arg Ser Gly Asn Thr Tyr
 1   5   10

<210> 155
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VH Sequence

<400> 155
Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1   5   10   15
Ser Val Lys Leu Ser Cys Lys Val Ser Gly Tyr Ile Phe Thr Asn Tyr
            20   25   30
Gly Ile Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile

35 40 45
Gly Glu Ile Tyr Pro Arg Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Met Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Asp Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg His Trp Asp Gly Val Leu Asp Tyr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Ser Leu Thr Val Ser Ser
115 120

<210> 156
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> 3N20 VL Sequence

<400> 156
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Val Ser Ala Gly
1 5 10 15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30
Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Leu Asn
85 90 95
Asp His Ser Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
100 105 110
Lys

<210> 157
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR1 - Exemplary

<400> 157
Gly Tyr Thr Phe Thr Arg Tyr Asp Ile Asn
1 5 10

<210> 158
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR2 - Exemplary

<400> 158
Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 159
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR3 - Exemplary

<400> 159
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR1 - Exemplary

<400> 160
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
 1   5   10   15

<210> 161
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR2 - Exemplary

<400> 161
Leu Ala Ser Asn Leu Glu Ser
 1   5

<210> 162
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR3 - Exemplary

<400> 162
His His Ser Gly Glu Leu Pro Tyr Thr
 1   5

<210> 163
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR1 - IMGT

<400> 163
Gly Tyr Thr Phe Thr Arg Tyr Asp
 1   5

<210> 164
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> 4P5 VH CDR2 - IMGT

<400> 164
Ile Tyr Pro Gly Asp Asp Ser Thr
 1   5

<210> 165
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR3 - IMGT

<400> 165
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 166
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR1- IMGT

<400> 166
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 167
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR2- IMGT

<400> 167
Leu Ala Ser
 1

<210> 168
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR1 - Kabat

<400> 168
Arg Tyr Asp Ile Asn
 1   5

<210> 169
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> 4P5 VH CDR1 - Chothia

<400> 169
Gly Tyr Thr Phe Thr Arg Tyr
 1   5

<210> 170
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR2 - Chothia

<400> 170
Pro Gly Asp Asp
 1

<210> 171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR3 - Chothia

<400> 171
Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5

<210> 172
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR1- Chothia

<400> 172
Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 173
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR3- Chothia

<400> 173
Ser Gly Glu Leu Pro Tyr
 1   5

<210> 174
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR1 - Contact

<400> 174

Thr Arg Tyr Asp Ile Asn
 1   5

<210> 175
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR2 - Contact

<400> 175
Trp Ile Gly Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys
 1   5   10

<210> 176
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR3 - Contact

<400> 176
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5   10

<210> 177
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR1- Contact

<400> 177
Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
 1   5   10

<210> 178
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR2- Contact

<400> 178
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1   5   10

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL CDR3- Contact

<400> 179
His His Ser Gly Glu Leu Pro Tyr
 1   5

<210> 180
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH CDR2 - AbM

<400> 180
Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys
 1   5   10

<210> 181
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VH Sequence

<400> 181
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Lys Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Asp Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 182
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 4P5 VL Sequence

<400> 182
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys His His Ser Gly
                85   90   95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 183
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR1- Exemplary

<400> 183
Gly Tyr Thr Phe Thr Arg Tyr Asp Ile Asn
 1   5   10

<210> 184
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR2- Exemplary

<400> 184
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Glu
 1   5   10   15
Gly

<210> 185
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR3- Exemplary

<400> 185
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 186
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR1- Exemplary

<400> 186
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
 1   5   10   15

<210> 187
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR2- Exemplary

<400> 187
Leu Ala Ser Asn Leu Glu Ser
 1   5

<210> 188
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> 5C23 VL CDR3- Exemplary

<400> 188
Gln His Ser Arg Glu Leu Pro Tyr Thr
 1   5

<210> 189
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR1 - IMGT

<400> 189
Gly Tyr Thr Phe Thr Arg Tyr Asp
 1   5

<210> 190
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR2 - IMGT

<400> 190
Ile Tyr Pro Gly Asp Gly Ser Thr
 1   5

<210> 191
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR3 - IMGT

<400> 191
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 192
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR1- IMGT

<400> 192
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 193
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> 5C23 VL CDR2- IMGT

<400> 193
Leu Ala Ser
 1

<210> 194
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR1 - Kabat

<400> 194
Arg Tyr Asp Ile Asn
 1   5

<210> 195
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR1 - Chothia

<400> 195
Gly Tyr Thr Phe Thr Arg Tyr
 1   5

<210> 196
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR2 - Chothia

<400> 196
Pro Gly Asp Gly
 1

<210> 197
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR3 - Chothia

<400> 197
Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5

<210> 198
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR1- Chothia

<400> 198

Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 199
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR3- Chothia

<400> 199
Ser Arg Glu Leu Pro Tyr
 1   5

<210> 200
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR1 - Contact

<400> 200
Thr Arg Tyr Asp Ile Asn
 1   5

<210> 201
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR2 - Contact

<400> 201
Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys
 1   5   10

<210> 202
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR3 - Contact

<400> 202
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5   10

<210> 203
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR1 - Contact

<400> 203
Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
 1   5   10

<210> 204
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR2 - Contact

<400> 204
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1   5   10

<210> 205
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL CDR3 - Contact

<400> 205
Gln His Ser Arg Glu Leu Pro Tyr
 1   5

<210> 206
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH CDR2 - AbM

<400> 206
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys
 1   5   10

<210> 207
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VH Sequence

<400> 207
Gln Val Gln Pro Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Lys Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Glu Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 208

<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 5C23 VL Sequence

<400> 208
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 209
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR1 - Exemplary

<400> 209
Gly Tyr Thr Phe Thr Arg Tyr Asp Ile Asn
 1   5   10

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

<220>
<223> 5F7 VH CDR2 - Exemplary

<400> 210
Trp Ile Tyr Pro Gly Asp Ile Ser Thr Lys Tyr Asn Glu Lys Phe Lys
 1   5   10   15
Gly

<210> 211
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR3 - Exemplary

<400> 211
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 212
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> 5F7 VL CDR1- Exemplary

<400> 212
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met His
 1   5   10   15

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

<220>
<223> 5F7 VL CDR2- Exemplary

<400> 213
Leu Ala Ser Asn Leu Glu Ser
 1   5

<210> 214
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR3- Exemplary

<400> 214
Gln His Ser Arg Glu Leu Pro Tyr Thr
 1   5

<210> 215
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR1 - IMGT

<400> 215
Gly Tyr Thr Phe Thr Arg Tyr Asp
 1   5

<210> 216
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR2 - IMGT

<400> 216
Ile Tyr Pro Gly Asp Ile Ser Thr
 1   5

<210> 217
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> 5F7 VH CDR3 - IMGT

<400> 217
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr
 1   5   10

<210> 218
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR1- IMGT

<400> 218
Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 219
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR2- IMGT

<400> 219
Leu Ala Ser
 1

<210> 220
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR1 - Kabat

<400> 220
Arg Tyr Asp Ile Asn
 1   5

<210> 221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR1 - Chothia

<400> 221
Gly Tyr Thr Phe Thr Arg Tyr
 1   5

<210> 222
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR2 - Chothia

<400> 222

Pro Gly Asp Ile
 1

<210> 223
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR3 - Chothia

<400> 223
Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5

<210> 224
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR1 - Chothia

<400> 224
Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 1   5   10

<210> 225
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR3 - Chothia

<400> 225
Ser Arg Glu Leu Pro Tyr
 1   5

<210> 226
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR1 - Contact

<400> 226
Thr Arg Tyr Asp Ile Asn
 1   5

<210> 227
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR2 - Contact

<400> 227
Trp Ile Gly Trp Ile Tyr Pro Gly Asp Ile Ser Thr Lys
 1   5   10

<210> 228
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR3 - Contact

<400> 228
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val
 1   5   10

<210> 229
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR1- Contact

<400> 229
Ser Thr Ser Gly Tyr Ser Tyr Met His Trp Tyr
 1   5   10

<210> 230
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR2- Contact

<400> 230
Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu
 1   5   10

<210> 231
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL CDR3- Contact

<400> 231
Gln His Ser Arg Glu Leu Pro Tyr
 1   5

<210> 232
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH CDR2 - AbM

<400> 232
Trp Ile Tyr Pro Gly Asp Ile Ser Thr Lys
 1   5   10

<210> 233
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VH Sequence

<400> 233
Gln Val Gln Pro Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Ile Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Val Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 234
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F7 VL Sequence

<400> 234
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65   70   75   80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 235
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR1- Exemplary

<400> 235
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr Trp Asn
 1   5   10

<210> 236
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR2- Exemplary

<400> 236
Tyr Ile Asn Tyr Gly Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
 1   5   10   15

<210> 237
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR3- Exemplary

<400> 237
Arg Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val
 1   5   10

<210> 238
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR1- Exemplary

<400> 238
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser
 1   5   10

<210> 239
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR2- Exemplary

<400> 239
Arg Ala Asn Arg Leu Val Asp
 1   5

<210> 240
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR3- Exemplary

<400> 240
Leu Gln Tyr Asp Glu Phe Pro Tyr Thr
 1   5

<210> 241
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR1 - IMGT

<400> 241
Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
 1   5

<210> 242
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR2 - IMGT

<400> 242
Ile Asn Tyr Gly Gly Ser Asn
 1   5

<210> 243
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR3 - IMGT

<400> 243
Ala Arg Arg Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val
 1   5   10   15

<210> 244
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR1 - IMGT

<400> 244
Gln Asp Ile Asn Ser Tyr
 1   5

<210> 245
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR2 - IMGT

<400> 245
Arg Ala Asn
 1

<210> 246
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR1 - Kabat

<400> 246
Ser Gly Tyr Tyr Trp Asn
 1   5

<210> 247
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR1 - Chothia

<400> 247
Gly Tyr Ser Ile Thr Ser Gly Tyr
 1   5

<210> 248
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR2 - Chothia

<400> 248
Tyr Gly Gly
 1

<210> 249
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR3 - Chothia

<400> 249
Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp
 1   5   10

<210> 250
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR1- Chothia

<400> 250
Ser Gln Asp Ile Asn Ser Tyr
 1   5

<210> 251
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR3- Chothia

<400> 251
Tyr Asp Glu Phe Pro Tyr
 1   5

<210> 252

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

<220>
<223> 1G19 VH CDR1 - Contact

<400> 252
Thr Ser Gly Tyr Tyr Trp Asn
 1   5

<210> 253
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR2 - Contact

<400> 253
Trp Met Gly Tyr Ile Asn Tyr Gly Gly Ser Asn Asn
 1   5   10

<210> 254
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR3 - Contact

<400> 254
Ala Arg Arg Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp
 1   5   10

<210> 255
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR1 - Contact

<400> 255
Asn Ser Tyr Leu Ser Trp Phe
 1   5

<210> 256
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR2 - Contact

<400> 256
Thr Leu Ile Tyr Arg Ala Asn Arg Leu Val
 1   5   10

<210> 257
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL CDR3 - Contact
<400> 257
Leu Gln Tyr Asp Glu Phe Pro Tyr
 1   5

<210> 258
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH CDR2 - AbM

<400> 258
Tyr Ile Asn Tyr Gly Gly Ser Asn Asn
 1   5

<210> 259
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VH Sequence

<400> 259
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1   5   10   15
Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
            20   25   30
Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
        35   40   45
Met Gly Tyr Ile Asn Tyr Gly Gly Ser Asn Asn Tyr Asn Pro Ser Leu
    50   55   60
Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65   70   75   80
Leu Lys Leu Thr Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85   90   95
Ala Arg Arg Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val Trp
            100   105   110
Gly Thr Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 260
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 1G19 VL Sequence

<400> 260
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
 1   5   10   15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
            20   25   30
Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
        35   40   45
Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
65   70   75   80
Glu Glu Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Tyr

85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 261
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR1 sequence of anti-beta klotho antibodies
VH domain

<220>
<221> VARIANT
<222> 6
<223> Xaa = Arg or Ser

<400> 261
Gly Tyr Thr Phe Thr Xaa Tyr Asp Ile Asn
1 5 10

<210> 262
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR2 sequence of anti-beta klotho antibodies
VH domain

<220>
<221> VARIANT
<222> 7
<223> Xaa = Gly, Asp, Ser or Ile

<400> 262
Trp Ile Tyr Pro Gly Asp Xaa Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15
Gly

<210> 263
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR2 sequence of anti-beta klotho antibodies
VH domain

<220>
<221> VARIANT
<222> 10
<223> Xaa = Val, Thr or Ala

<400> 263
Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Xaa Tyr
1 5 10

<210> 264
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR3 sequence of anti-beta klotho antibodies
VH domain

<220>
<221> VARIANT
<222> 5
<223> Xaa = Asp or Gly

<220>
<221> VARIANT
<222> 7
<223> Xaa = Asn or Ser

<220>
<221> VARIANT
<222> 8
<223> Xaa = Ser or Asn

<220>
<221> VARIANT
<222> 11
<223> Xaa = Thr or Asn

<400> 264
Tyr Ile Asn Tyr Xaa Gly Xaa Xaa Asn Tyr Xaa Pro Ser Leu Lys Asn
1 5 10 15

<210> 265
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR3 sequence of anti-beta klotho antibodies
VH domain

<220>
<221> VARIANT
<222> 1
<223> Xaa = Lys or Arg

<400> 265
Xaa Gly Ala Tyr Tyr Ser Asn Tyr Asp Ser Phe Asp Val
1 5 10

<210> 266
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR1 sequence of anti-beta klotho antibodies
VL domain

<220>
<221> VARIANT
<222> 14
<223> Xaa = Met, Leu or Val

<400> 266
Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Xaa His
1 5 10 15

<210> 267
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR3 sequence of anti-beta klotho antibodies
VL domain

<220>
<221> VARIANT
<222> 1
<223> Xaa = Gln or His

<220>
<221> VARIANT
<222> 4
<223> Xaa = Arg or Gly

<400> 267
Xaa His Ser Xaa Glu Leu Pro Tyr Thr
1 5

<210> 268
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus CDR3 sequence of anti-beta klotho antibodies
VL domain

<220>
<221> VARIANT
<222> 8
<223> Xaa = Phe or Tyr

<400> 268
Leu Gln Tyr Asp Glu Phe Pro Xaa Thr
1 5

<210> 269
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH1

<400> 269
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 270
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH2

<400> 270
Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Arg Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 271
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH3

<400> 271
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 272
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH4

<400> 272
Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

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            20                  25                  30
Asp Ile Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Arg Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 273
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH5

<400> 273
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asn Thr Ala Val Tyr Phe Cys
                85                  90                  95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 274
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH6

<400> 274
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30
Asp Ile Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Arg Thr Ala Tyr
65                  70                  75                  80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asn Thr Ala Val Tyr Phe Cys
                85                  90                  95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 275
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> vL1

<400> 275
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Ala Glu Asp Ala Ala Ile Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 276
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> vL2

<400> 276
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 277
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> vL3

<400> 277
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Val Gln Ala Glu Asp Val Ala Ile Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 278
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR1

<400> 278
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 279
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR1

<400> 279
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 280
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR1

<400> 280
Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 281
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR2

<400> 281
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 282
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR2

<400> 282
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 1   5   10

<210> 283
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR2

<400> 283
Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
 1   5   10

<210> 284
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 284
Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 285
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 285
Lys Ala Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg
            20   25   30

<210> 286
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 286
Lys Ala Thr Leu Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asn Thr Ala Val Tyr Phe Cys Ala Arg
            20   25   30

<210> 287
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 287
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ala Arg Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asn Thr Ala Val Tyr Phe Cys Ala Arg
            20   25   30

<210> 288
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR4

<400> 288
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1   5   10

<210> 289
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR1

<400> 289
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys
            20

<210> 290
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR1

<400> 290
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys
            20

<210> 291
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 291

Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 292
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 292
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 293
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 293
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Ile Tyr Tyr Cys
            20   25   30

<210> 294
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 294
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            20   25   30

<210> 295
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 295
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Ile Tyr Tyr Cys
            20   25   30

<210> 296
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized Anti-Beta Klotho VL FR4

<400> 296
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 1   5   10

<210> 297
<211> 1044
<212> PRT
<213> Homo sapiens

<220>
<223> human beta klotho

<400> 297
Met Lys Pro Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Ile Phe
 1   5   10   15
Phe Ser Thr Asp Glu Ile Thr Thr Arg Tyr Arg Asn Thr Met Ser Asn
            20   25   30
Gly Gly Leu Gln Arg Ser Val Ile Leu Ser Ala Leu Ile Leu Leu Arg
        35   40   45
Ala Val Thr Gly Phe Ser Gly Asp Gly Arg Ala Ile Trp Ser Lys Asn
    50   55   60
Pro Asn Phe Thr Pro Val Asn Glu Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Ile Gly Thr Gly Ala Leu Gln Val
                85   90   95
Glu Gly Ser Trp Lys Lys Asp Gly Lys Gly Pro Ser Ile Trp Asp His
            100   105   110
Phe Ile His Thr His Leu Lys Asn Val Ser Ser Thr Asn Gly Ser Ser
        115   120   125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Ser Ala Leu Asp Phe Ile
    130   135   140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asp Gly Ile Val Thr Val Ala Asn Ala Lys Gly Leu Gln Tyr Tyr Ser
                165   170   175
Thr Leu Leu Asp Ala Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
            180   185   190
Leu Tyr His Trp Asp Leu Pro Leu Ala Leu Gln Glu Lys Tyr Gly Gly
        195   200   205
Trp Lys Asn Asp Thr Ile Ile Asp Ile Phe Asn Asp Tyr Ala Thr Tyr
    210   215   220
Cys Phe Gln Met Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225   230   235   240
Asn Pro Tyr Leu Val Ala Trp His Gly Tyr Gly Thr Gly Met His Ala
                245   250   255
Pro Gly Glu Lys Gly Asn Leu Ala Ala Val Tyr Thr Val Gly His Asn
            260   265   270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asn Thr His Phe
        275   280   285
Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
    290   295   300
Ile Glu Pro Asn Arg Ser Glu Asn Thr Met Asp Ile Phe Lys Cys Gln
305   310   315   320
Gln Ser Met Val Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
                325   330   335
Asp Gly Asp Tyr Pro Glu Gly Met Arg Lys Lys Leu Phe Ser Val Leu
            340   345   350
Pro Ile Phe Ser Glu Ala Glu Lys His Glu Met Arg Gly Thr Ala Asp
        355   360   365
Phe Phe Ala Phe Ser Phe Gly Pro Asn Asn Phe Lys Pro Leu Asn Thr
    370   375   380
Met Ala Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Glu Ala Leu
385   390   395   400
Asn Trp Ile Lys Leu Glu Tyr Asn Asn Pro Arg Ile Leu Ile Ala Glu
                405   410   415

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Asn Gly Trp Phe Thr Asp Ser Arg Val Lys Thr Glu Asp Thr Thr Ala
            420                 425                 430
Ile Tyr Met Met Lys Asn Phe Leu Ser Gln Val Leu Gln Ala Ile Arg
        435                 440                 445
Leu Asp Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp
    450                 455                 460
Gly Phe Glu Trp Gln Asp Ala Tyr Thr Ile Arg Arg Gly Leu Phe Tyr
465                 470                 475                 480
Val Asp Phe Asn Ser Lys Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala
                485                 490                 495
His Tyr Tyr Lys Gln Ile Ile Arg Glu Asn Gly Phe Ser Leu Lys Glu
            500                 505                 510
Ser Thr Pro Asp Val Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly
        515                 520                 525
Val Thr Glu Ser Val Leu Lys Pro Glu Ser Val Ala Ser Ser Pro Gln
    530                 535                 540
Phe Ser Asp Pro His Leu Tyr Val Trp Asn Ala Thr Gly Asn Arg Leu
545                 550                 555                 560
Leu His Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ala Gln Cys
                565                 570                 575
Thr Asp Phe Val Asn Ile Lys Lys Gln Leu Glu Met Leu Ala Arg Met
            580                 585                 590
Lys Val Thr His Tyr Arg Phe Ala Leu Asp Trp Ala Ser Val Leu Pro
        595                 600                 605
Thr Gly Asn Leu Ser Ala Val Asn Arg Gln Ala Leu Arg Tyr Tyr Arg
    610                 615                 620
Cys Val Val Ser Glu Gly Leu Lys Leu Gly Ile Ser Ala Met Val Thr
625                 630                 635                 640
Leu Tyr Tyr Pro Thr His Ala His Leu Gly Leu Pro Glu Pro Leu Leu
                645                 650                 655
His Ala Asp Gly Trp Leu Asn Pro Ser Thr Ala Glu Ala Phe Gln Ala
            660                 665                 670
Tyr Ala Gly Leu Cys Phe Gln Glu Leu Gly Asp Leu Val Lys Leu Trp
        675                 680                 685
Ile Thr Ile Asn Glu Pro Asn Arg Leu Ser Asp Ile Tyr Asn Arg Ser
    690                 695                 700
Gly Asn Asp Thr Tyr Gly Ala Ala His Asn Leu Leu Val Ala His Ala
705                 710                 715                 720
Leu Ala Trp Arg Leu Tyr Asp Arg Gln Phe Arg Pro Ser Gln Arg Gly
                725                 730                 735
Ala Val Ser Leu Ser Leu His Ala Asp Trp Ala Glu Pro Ala Asn Pro
            740                 745                 750
Tyr Ala Asp Ser His Trp Arg Ala Ala Glu Arg Phe Leu Gln Phe Glu
        755                 760                 765
Ile Ala Trp Phe Ala Glu Pro Leu Phe Lys Thr Gly Asp Tyr Pro Ala
    770                 775                 780
Ala Met Arg Glu Tyr Ile Ala Ser Lys His Arg Arg Gly Leu Ser Ser
785                 790                 795                 800
Ser Ala Leu Pro Arg Leu Thr Glu Ala Glu Arg Arg Leu Leu Lys Gly
                805                 810                 815
Thr Val Asp Phe Cys Ala Leu Asn His Phe Thr Thr Arg Phe Val Met
            820                 825                 830
His Glu Gln Leu Ala Gly Ser Arg Tyr Asp Ser Asp Arg Asp Ile Gln
        835                 840                 845
Phe Leu Gln Asp Ile Thr Arg Leu Ser Ser Pro Thr Arg Leu Ala Val
    850                 855                 860
Ile Pro Trp Gly Val Arg Lys Leu Leu Arg Trp Val Arg Arg Asn Tyr
865                 870                 875                 880
Gly Asp Met Asp Ile Tyr Ile Thr Ala Ser Gly Ile Asp Asp Gln Ala
                885                 890                 895
Leu Glu Asp Asp Arg Leu Arg Lys Tyr Tyr Leu Gly Lys Tyr Leu Gln
            900                 905                 910
Glu Val Leu Lys Ala Tyr Leu Ile Asp Lys Val Arg Ile Lys Gly Tyr
        915                 920                 925
Tyr Ala Phe Lys Leu Ala Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe
    930                 935                 940
Phe Thr Ser Asp Phe Lys Ala Lys Ser Ser Ile Gln Phe Tyr Asn Lys
945                 950                 955                 960
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Val Ile Ser Ser Arg Gly Phe Pro Phe Glu Asn Ser Ser Ser Arg Cys
965 970 975
Ser Gln Thr Gln Glu Asn Thr Glu Cys Thr Val Cys Leu Phe Leu Val
980 985 990
Gln Lys Lys Pro Leu Ile Phe Leu Gly Cys Cys Phe Phe Ser Thr Leu
995 1000 1005
Val Leu Leu Leu Ser Ile Ala Ile Phe Gln Arg Gln Lys Arg Arg Lys
1010 1015 1020
Phe Trp Lys Ala Lys Asn Leu Gln His Ile Pro Leu Lys Lys Gly Lys
1025 1030 1035 1040
Arg Val Val Ser

<210> 298
<211> 3132
<212> DNA
<213> Homo sapiens

<220>
<223> human beta klotho coding sequence

<400> 298
atgaagccag gctgtgcggc aggatctcca gggaatgaat ggattttctt cagcactgat 60
gaaataacca cacgctatag gaatacaatg tccaacgggg gattgcaaag atctgtcatc 120
ctgtcagcac ttattctgct acgagctgtt actggattct ctggagatgg aagagctata 180
tggtctaaaa atcctaattt tactccggta aatgaaagtc agctgtttct ctatgacact 240
ttccctaaaa actttttctg gggtattggg actggagcat tgcaagtgga agggagttgg 300
aagaaggatg gaaaaggacc ttctatatgg gatcatttca tccacacaca ccttaaaaat 360
gtcagcagca cgaatggttc cagtgacagt tatatttttc tggaaaaaga cttatcagcc 420
ctggatttta taggagtttc tttttatcaa ttttcaattt cctggccaag gcttttcccc 480
gatggaatag taacagttgc caacgcaaaa ggtctgcagt actacagtac tcttctggac 540
gctctagtgc ttagaaacat tgaacctata gttactttat accactggga tttgcctttg 600
gcactacaag aaaaatatgg ggggtggaaa aatgatacca taatagatat cttcaatgac 660
tatgccacat actgtttcca gatgtttggg gaccgtgtca aatattggat tacaattcac 720
aacccatatc tagtggcttg gcatgggtat gggacaggta tgcatgcccc tggagagaag 780
ggaaatttag cagctgtcta cactgtggga cacaacttga tcaaggctca ctcgaaagtt 840
tggcataact acaacacaca tttccgccca catcagaagg gttggttatc gatcacgttg 900
ggatctcatt ggatcgagcc aaaccggtcg gaaaacacga tggatatatt caaatgtcaa 960
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catgagatga gaggcacagc tgatttcttt gccttttctt ttggacccaa caacttcaag 1140
cccctaaaca ccatggctaa aatgggacaa aatgtttcac ttaatttaag agaagcgctg 1200
aactggatta aactggaata caacaaccct cgaatcttga ttgctgagaa tggctggttc 1260
acagacagtc gtgtgaaaac agaagacacc acggccatct acatgatgaa gaatttcctc 1320
agccaggtgc ttcaagcaat aaggttagat gaaatacgag tgtttggtta tactgcctgg 1380
tctctcctgg atggctttga atggcaggat gcttacacca tccgccgagg attattttat 1440
gtggatttta acagtaaaca gaaagagcgg aaacctaagt cttcagcaca ctactacaaa 1500
cagatcatac gagaaaatgg tttttcttta aaagagtcca cgccagatgt gcagggccag 1560
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ttgcaccgag tggaaggggt gaggctgaaa acacgacccg ctcaatgcac agattttgta 1740
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tggctgaacc catcgacggc cgaggccttc caggcctacg ctgggctgtg cttccaggag 2040
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gactaccccg cggccatgag ggaatacatt gcctccaagc accgacgggg gctttccagc 2400
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tgcgcgctca accacttcac cactaggttc gtgatgcacg agcagctggc cggcagccgc 2520
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ggcgacatgg acatttacat caccgccagt ggcatcgacg accaggctct ggaggatgac 2700

cggctccgga agtactacct agggaagtac cttcaggagg tgctgaaagc atacctgatt 2760
gataaagtca gaatcaaagg ctattatgca ttcaaactgg ctgaagagaa atctaaaccc 2820
agatttggat tcttcacatc tgattttaaa gctaaatcct caatacaatt ttacaacaaa 2880
gtgatcagca gcaggggctt ccctttgag aacagtagtt ctagatgcag tcagacccaa 2940
gaaaatacag agtgcactgt ctgcttattc cttgtgcaga agaaaccact gatattcctg 3000
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agagttgtta gc 3132

<210> 299
<211> 1044
<212> PRT
<213> Macaca fascicularis

<220>
<223> cynomolgus monkey (cyno) beta klotho

<400> 299
Met Lys Pro Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Ile Phe
 1   5   10   15
Phe Ser Thr Asp Glu Ile Thr Ile Arg Tyr Arg Asn Thr Met Ser Asn
            20   25   30
Gly Gly Leu Gln Arg Ser Val Ile Leu Ser Ala Leu Thr Leu Leu Arg
        35   40   45
Ala Val Thr Gly Phe Ser Gly Asp Gly Arg Ala Val Trp Ser Lys Asn
    50   55   60
Pro Asn Phe Thr Pro Val Asn Glu Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Val Gly Thr Gly Ala Leu Gln Val
                85   90   95
Glu Gly Ser Trp Lys Lys Asp Gly Lys Gly Pro Ser Ile Trp Asp His
            100   105   110
Phe Val His Thr His Leu Lys Asn Val Ser Ser Thr Asn Gly Ser Ser
        115   120   125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Ser Ala Leu Asp Phe Ile
    130   135   140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asp Gly Ile Val Thr Val Ala Asn Ala Lys Gly Leu Gln Tyr Tyr Asn
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Thr Leu Leu Asp Ser Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
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Leu Tyr His Trp Asp Leu Pro Leu Ala Leu Gln Glu Lys Tyr Gly Gly
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Trp Lys Asn Asp Thr Ile Ile Asp Ile Phe Asn Asp Tyr Ala Thr Tyr
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Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225   230   235   240
Asn Pro Tyr Leu Val Ala Trp His Gly Tyr Gly Thr Gly Met His Ala
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Pro Gly Glu Lys Gly Asn Leu Ala Ala Val Tyr Thr Val Gly His Asn
            260   265   270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asn Thr His Phe
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Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
    290   295   300
Ile Glu Pro Asn Arg Ser Glu Asn Thr Met Asp Ile Leu Lys Cys Gln
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Gln Ser Met Val Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
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Asp Gly Asp Tyr Pro Glu Gly Met Lys Lys Lys Leu Leu Ser Ile Leu
            340   345   350
Pro Leu Phe Ser Glu Ala Glu Lys Asn Glu Val Arg Gly Thr Ala Asp
        355   360   365
Phe Phe Ala Phe Ser Phe Gly Pro Asn Asn Phe Lys Pro Leu Asn Thr
    370   375   380
Met Ala Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Glu Ala Leu
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Leu Asp Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp
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Gly Phe Glu Trp Gln Asp Ala Tyr Thr Ile Arg Arg Gly Leu Phe Tyr
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Val Asp Phe Asn Ser Lys Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala
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His Tyr Tyr Lys Gln Ile Ile Arg Glu Asn Gly Phe Ser Leu Lys Glu
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Ala Thr Pro Asp Val Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly
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Thr Asp Phe Val Asn Ile Lys Lys Gln Leu Glu Met Leu Ala Arg Met
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Lys Val Thr His Tyr Arg Phe Ala Leu Asp Trp Ala Ser Val Leu Pro
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Cys Val Val Ser Glu Gly Leu Lys Leu Gly Ile Ser Ala Met Val Thr
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Tyr Ala Gly Leu Cys Phe Gln Glu Leu Gly Asp Leu Val Lys Leu Trp
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Ile Thr Ile Asn Glu Pro Asn Arg Leu Ser Asp Ile Tyr Asn Arg Ser
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Ala Val Ser Leu Ser Leu His Ala Asp Trp Ala Glu Pro Ala Asn Pro
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Tyr Ala Asp Ser His Trp Arg Ala Ala Glu Arg Phe Leu Gln Phe Glu
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Glu Val Leu Lys Ala Tyr Leu Ile Asp Lys Val Arg Ile Lys Gly Tyr
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Tyr Ala Phe Lys Leu Ala Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe
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Gln Lys Lys Pro Leu Ile Phe Leu Gly Cys Cys Phe Phe Ser Thr Leu
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Ala Val Thr Gly Phe Ser Gly Asp Gly Lys Ala Ile Trp Asp Lys Lys
    50   55   60
Gln Tyr Val Ser Pro Val Asn Pro Ser Gln Leu Phe Leu Tyr Asp Thr
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Phe Pro Lys Asn Phe Ser Trp Gly Val Gly Thr Gly Ala Phe Gln Val
                85   90   95
Glu Gly Ser Trp Lys Thr Asp Gly Arg Gly Pro Ser Ile Trp Asp Arg
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Tyr Val Tyr Ser His Leu Arg Gly Val Asn Gly Thr Asp Arg Ser Thr
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Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Leu Ala Leu Asp Phe Leu
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Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asn Gly Thr Val Ala Ala Val Asn Ala Gln Gly Leu Arg Tyr Tyr Arg
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Ala Leu Leu Asp Ser Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
            180   185   190
Leu Tyr His Trp Asp Leu Pro Leu Thr Leu Gln Glu Glu Tyr Gly Gly
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Trp Lys Asn Ala Thr Met Ile Asp Leu Phe Asn Asp Tyr Ala Thr Tyr
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Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
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Asn Pro Tyr Leu Val Ala Trp His Gly Phe Gly Thr Gly Met His Ala
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Pro Gly Glu Lys Gly Asn Leu Thr Ala Val Tyr Thr Val Gly His Asn
            260   265   270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asp Lys Asn Phe
        275   280   285
Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
    290   295   300
Ile Glu Pro Asn Arg Thr Asp Asn Met Glu Asp Val Ile Asn Cys Gln
305   310   315   320
His Ser Met Ser Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
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Asp Gly Asp Tyr Pro Glu Phe Met Lys Thr Gly Ala Met Ile Pro Glu
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Phe Ser Glu Ala Glu Lys Glu Glu Val Arg Gly Thr Ala Asp Phe Phe
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Ala Phe Ser Phe Gly Pro Asn Asn Phe Arg Pro Ser Asn Thr Val Val
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Trp Phe Thr Asp Ser Tyr Ile Lys Thr Glu Asp Thr Thr Ala Ile Tyr
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Met Met Lys Asn Phe Leu Asn Gln Val Leu Gln Ala Ile Lys Phe Asp
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Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Thr Leu Leu Asp Gly Phe
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Glu Trp Gln Asp Ala Tyr Thr Thr Arg Arg Gly Leu Phe Tyr Val Asp
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Tyr Lys Gln Ile Ile Gln Asp Asn Gly Phe Pro Leu Lys Glu Ser Thr
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Thr His Tyr Gln Phe Ala Leu Asp Trp Thr Ser Ile Leu Pro Thr Gly
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Val Ser Glu Gly Leu Lys Leu Gly Val Phe Pro Met Val Thr Leu Tyr
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His Pro Thr His Ser His Leu Gly Leu Pro Leu Pro Leu Leu Ser Ser
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Gly Gly Trp Leu Asn Met Asn Thr Ala Lys Ala Phe Gln Asp Tyr Ala
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Glu Leu Cys Phe Arg Glu Leu Gly Asp Leu Val Lys Leu Trp Ile Thr
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Ile Asn Glu Pro Asn Arg Leu Ser Asp Met Tyr Asn Arg Thr Ser Asn
    690                 695                 700
Asp Thr Tyr Arg Ala Ala His Asn Leu Met Ile Ala His Ala Gln Val
705                 710                 715                 720
Trp His Leu Tyr Asp Arg Gln Tyr Arg Pro Val Gln His Gly Ala Val
                725                 730                 735
Ser Leu Ser Leu His Cys Asp Trp Ala Glu Pro Ala Asn Pro Phe Val
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Asp Ser His Trp Lys Ala Ala Glu Arg Phe Leu Gln Phe Glu Ile Ala
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Trp Phe Ala Asp Pro Leu Phe Lys Thr Gly Asp Tyr Pro Ser Val Met
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Lys Glu Tyr Ile Ala Ser Lys Asn Gln Arg Gly Leu Ser Ser Ser Val
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Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Ile His Lys
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Gln Leu Asn Thr Asn Arg Ser Val Ala Asp Arg Asp Val Gln Phe Leu
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Gln Asp Ile Thr Arg Leu Ser Ser Pro Ser Arg Leu Ala Val Thr Pro
    850                 855                 860
Trp Gly Val Arg Lys Leu Leu Ala Trp Ile Arg Arg Asn Tyr Arg Asp
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Arg Asp Ile Tyr Ile Thr Ala Asn Gly Ile Asp Asp Leu Ala Leu Glu
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Asp Asp Gln Ile Arg Lys Tyr Tyr Leu Glu Lys Tyr Val Gln Glu Ala
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Leu Lys Ala Tyr Leu Ile Asp Lys Val Lys Ile Lys Gly Tyr Tyr Ala
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Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe Phe Thr
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Ser Ser Ser Gly Leu Pro Ala Glu Asn Arg Ser Pro Ala Cys Gly Gln
965 970 975
Pro Ala Glu Asp Thr Asp Cys Thr Ile Cys Ser Phe Leu Val Glu Lys
980 985 990
Lys Pro Leu Ile Phe Phe Gly Cys Cys Phe Ile Ser Thr Leu Ala Val
995 1000 1005
Leu Leu Ser Ile Thr Val Phe His His Gln Lys Arg Arg Lys Phe Gln
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gggcttgtca ccggactgga ggccgtgagg agtcccagct ttgagaagta a 651

<210> 304
<211> 194
<212> PRT
<213> Artificial Sequence

<220>
<223> full length FGF19 (NP_005108.1)

<400> 304
Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro His Val His Tyr Gly Trp
 1   5   10   15
Gly Asp Pro Ile Arg Leu Arg His Leu Tyr Thr Ser Gly Pro His Gly
            20   25   30
Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala Asp Gly Val Val Asp Cys
        35   40   45
Ala Arg Gly Gln Ser Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala
    50   55   60
Leu Arg Thr Val Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys
65   70   75   80
Met Gly Ala Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu
                85   90   95
Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr
            100   105   110
Arg Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln
        115   120   125
Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe Leu
    130   135   140
Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg Gly His
145   150   155   160
Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp Ser Met Asp
                165   170   175
Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg Ser Pro Ser Phe
            180   185   190
Glu Lys

<210> 305
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> A full length FGF21

<400> 305
atggactcgg acgagaccgg gttcgagcac tcaggactgt gggtttctgt gctggctggt 60
cttctgctgg gagcctgcca ggcacacccc atccctgact ccagtcctct cctgcaattc 120
gggggccaag tccggcagcg gtacctctac acagatgatg cccagcagac agaagcccac 180
ctggagatca gggaggatgg gacggtgggg ggcgctgctg accagagccc cgaaagtctc 240
ctgcagctga aagccttgaa gccgggagtt attcaaatct tgggagtcaa gacatccagg 300
ttcctgtgcc agcggccaga tggggccctg tatggatcgc tccactttga ccctgaggcc 360
tgcagcttcc gggagctgct tcttgaggac ggatacaatg tttaccagtc cgaagcccac 420
ggcctcccgc tgcacctgcc agggaacaag tccccacacc gggaccctgc accccgagga 480
ccagctcgct tcctgccact accaggcctg ccccccgcac ccccggagcc acccggaatc 540
ctggcccccc agccccccga tgtgggctcc tcggaccctc tgagcatggt gggaccttcc 600
cagggccgaa gccccagcta cgcttcctga 630

<210> 306
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> A full length FGF21

<400> 306
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
 1   5   10   15
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20   25   30
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35   40   45
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50   55   60
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65   70   75   80
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85   90   95
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100   105   110
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115   120   125
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130   135   140
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145   150   155   160
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165   170   175
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180   185   190
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195   200   205
Ser

<210> 307
<211> 2469
<212> DNA
<213> Homo sapiens

<220>
<223> human FGFR1c NM_023110.2 (also designated FGFR alpha-IIIc)

<400> 307
atgtggagct ggaagtgcct cctcttctgg gctgtgctgg tcacagccac actctgcacc 60
gctaggccgt ccccgacctt gcctgaacaa gcccagccct ggggagcccc tgtggaagtg 120
gagtccttcc tggtccaccc cggtgacctg ctgcagcttc gctgtcggct gcgggacgat 180
gtgcagagca tcaactggct gcgggacggg gtgcagctgg cggaaagcaa ccgcacccgc 240
atcacagggg aggaggtgga ggtgcaggac tccgtgcccg cagactccgg cctctatgct 300
tgcgtaacca gcagcccctc gggcagtgac accacctact tctccgtcaa tgtttcagat 360
gctctccccc cctcggagga tgatgatgat gatgatgact cctcttcaga ggagaaagaa 420
acagataaca ccaaaccaaa ccgtatgccc gtagctccat attggacatc accagaaaag 480
atggaaaaga aattgcatgc agtgccggct gccaagacag tgaagttcaa atgcccttcc 540
agtgggacac caaacccaac actgcgctgg ttgaaaaatg gcaaagaatt caaacctgac 600
cacagaattg gaggctacaa ggtccgttat gccacctgga gcatcataat ggactctgtg 660
gtgccctctg acaagggcaa ctacacctgc attgtggaga atgagtacgg cagcatcaac 720
cacacatacc agctggatgt cgtggagcgg tcccctcacc ggcccatcct gcaagcaggg 780
ttgcccgcca acaaaacagt ggccctgggt agcaacgtgg agttcatgtg taaggtgtac 840
agtgacccgc agccgcacat ccagtggcta aagcacatcg aggtgaatgg gagcaagatt 900
ggcccagaca acctgcctta tgtccagatc ttgaagactg ctggagttaa taccaccgac 960
aaagagatgg aggtgcttca cttaagaaat gtctcctttg aggacgcagg ggagtatacg 1020
tgcttggcgg gtaactctat cggactctcc catcactctg catggttgac cgttctggaa 1080
gccctggaag agaggccggc agtgatgacc tcgcccctgt acctggagat catcatctat 1140
tgcacagggg ccttcctcat ctcctgcatg gtggggtcgg tcatcgtcta caagatgaag 1200
agtggtacca agaagagtga cttccacagc cagatggctg tgcacaagct ggccaagagc 1260
atccctctgc gcagacaggt aacagtgtct gctgactcca gtgcatccat gaactctggg 1320
gttcttctgg ttcggccatc acggctctcc tccagtggga ctcccatgct agcaggggtc 1380
tctgagtatg agcttcccga agaccctcgc tgggagctgc ctcgggacag actggtctta 1440
ggcaaacccc tgggagaggg ctgctttggg caggtggtgt tggcagaggc tatcgggctg 1500
gacaaggaca aacccaaccg tgtgaccaaa gtggctgtga agatgttgaa gtcggacgca 1560
acagagaaag acttgtcaga cctgatctca gaaatggaga tgatgaagat gatcgggaag 1620
cataagaata tcatcaacct gctgggggcc tgcacgcagg atggtccctt gtatgtcatc 1680
gtggagtatg cctccaaggg caacctgcgg gagtacctgc aggcccggag gcccccaggg 1740
ctggaatact gctacaaccc cagccacaac ccagaggagc agctctcctc caaggacctg 1800
gtgtcctgcg cctaccaggt ggcccgaggc atggagtatc tggcctccaa gaagtgcata 1860
caccgagacc tggcagccag gaatgtcctg gtgacagagg acaatgtgat gaagatagca 1920
gactttggcc tcgcacggga cattcaccac atcgactact ataaaaagac aaccaacggc 1980
cgactgcctg tgaagtggat ggcacccgag gcattatttg accggatcta cacccaccag 2040
agtgatgtgt ggtctttcgg ggtgctcctg tgggagatct tcactctggg cggctcccca 2100
taccccggtg tgcctgtgga ggaacttttc aagctgctga aggagggtca ccgcatggac 2160
aagcccagta actgcaccaa cgagctgtac atgatgatgc gggactgctg gcatgcagtg 2220
ccctcacaga gacccacctt caagcagctg gtggaagacc tggaccgcat cgtggccttg 2280
acctccaacc aggagtacct ggacctgtcc atgcccctgg accagtactc ccccagcttt 2340
cccgacaccc ggagctctac gtgctcctca ggggaggatt ccgtcttctc tcatgagccg 2400
ctgcccgagg agccctgcct gccccgacac ccagcccagc ttgccaatgg cggactcaaa 2460
cgccgctga 2469

<210> 308
<211> 822
<212> PRT
<213> Homo sapiens

<220>
<223> human FGFR1c NP_075598.2 (also designated FGFR alpha-IIIc)

<400> 308
Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
 1   5   10   15
Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln
            20   25   30
Pro Trp Gly Ala Pro Val Glu Val Glu Ser Phe Leu Val His Pro Gly
        35   40   45
Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
    50   55   60
Asn Trp Leu Arg Asp Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg
65   70   75   80
Ile Thr Gly Glu Glu Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser
                85   90   95

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Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
            100                 105                 110
Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
        115                 120                 125
Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
    130                 135                 140
Lys Pro Asn Arg Met Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
145                 150                 155                 160
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
                165                 170                 175
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
            180                 185                 190
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
        195                 200                 205
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
    210                 215                 220
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
225                 230                 235                 240
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
                245                 250                 255
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
            260                 265                 270
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
        275                 280                 285
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
    290                 295                 300
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
305                 310                 315                 320
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
                325                 330                 335
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
            340                 345                 350
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
        355                 360                 365
Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
    370                 375                 380
Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
385                 390                 395                 400
Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
                405                 410                 415
Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
            420                 425                 430
Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
        435                 440                 445
Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
    450                 455                 460
Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
465                 470                 475                 480
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
                485                 490                 495
Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
            500                 505                 510
Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
        515                 520                 525
Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
    530                 535                 540
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
545                 550                 555                 560
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
                565                 570                 575
Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
            580                 585                 590
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
        595                 600                 605
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
    610                 615                 620
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
625                 630                 635                 640
```

Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
645 650 655
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
660 665 670
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
675 680 685
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
690 695 700
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
705 710 715 720
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
725 730 735
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
740 745 750
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
755 760 765
Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
770 775 780
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
785 790 795 800
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
805 810 815
Gly Gly Leu Lys Arg Arg
820

<210> 309
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> example of extracellular region of FGFR1c

<400> 309
Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
1 5 10 15
Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln
20 25 30
Pro Trp Gly Ala Pro Val Glu Val Glu Ser Phe Leu Val His Pro Gly
35 40 45
Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
50 55 60
Asn Trp Leu Arg Asp Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg
65 70 75 80
Ile Thr Gly Glu Glu Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser
85 90 95
Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
100 105 110
Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
115 120 125
Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
130 135 140
Lys Pro Asn Arg Met Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
145 150 155 160
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
165 170 175
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
180 185 190
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
195 200 205
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
210 215 220
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
225 230 235 240
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
245 250 255
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn

```
            260                 265                 270
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
        275                 280                 285
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
    290                 295                 300
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
305                 310                 315                 320
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
                325                 330                 335
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
            340                 345                 350
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
        355                 360                 365
Met Thr Ser Pro Leu Tyr
    370
```

<210> 310
<211> 2466
<212> DNA
<213> Homo sapiens

<220>
<223> Coding sequence of human FGFR2c (NM_000141.4)

<400> 310

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atggtcagct ggggtcgttt catctgcctg gtcgtggtca ccatggcaac cttgtccctg 60
gcccggccct ccttcagttt agttgaggat accacattag agccagaaga gccaccaacc 120
aaataccaaa tctctcaacc agaagtgtac gtggctgcgc caggggagtc gctagaggtg 180
cgctgcctgt tgaaagatgc cgccgtgatc agttggacta aggatggggt gcacttgggg 240
cccaacaata ggacagtgct tattggggag tacttgcaga taaagggcgc cacgcctaga 300
gactccggcc tctatgcttg tactgccagt aggactgtag acagtgaaac ttggtacttc 360
atggtgaatg tcacagatgc catctcatcc ggagatgatg aggatgacac cgatggtgcg 420
gaagattttg tcagtgagaa cagtaacaac aagagagcac catactggac caacacagaa 480
aagatggaaa agcggctcca tgctgtgcct gcggccaaca ctgtcaagtt tcgctgccca 540
gccgggggga acccaatgcc aaccatgcgg tggctgaaaa acgggaagga gtttaagcag 600
gagcatcgca ttggaggcta caaggtacga aaccagcact ggagcctcat tatggaaagt 660
gtggtcccat ctgacaaggg aaattatacc tgtgtagtgg agaatgaata cgggtccatc 720
aatcacacgt accacctgga tgttgtggag cgatcgcctc accggcccat cctccaagcc 780
ggactgccgg caaatgcctc cacagtggtc ggaggagacg tagagtttgt ctgcaaggtt 840
tacagtgatg cccagcccca catccagtgg atcaagcacg tggaaaagaa cggcagtaaa 900
tacgggcccg acgggctgcc ctacctcaag gttctcaagg ccgccggtgt taacaccacg 960
gacaaagaga ttgaggttct ctatattcgg aatgtaactt ttgaggacgc tggggaatat 1020
acgtgcttgg cgggtaattc tattgggata tcctttcact ctgcatggtt gacagttctg 1080
ccagcgcctg gaagagaaaa ggagattaca gcttccccag actacctgga gatagccatt 1140
tactgcatag gggtcttctt aatcgcctgt atggtggtaa cagtcatcct gtgccgaatg 1200
aagaacacga ccaagaagcc agacttcagc agccagccgg ctgtgcacaa gctgaccaaa 1260
cgtatccccc tgcggagaca ggtaacagtt tcggctgagt ccagctcctc catgaactcc 1320
aacaccccgc tggtgaggat aacaacacgc ctctcttcaa cggcagacac ccccatgctg 1380
gcaggggtct ccgagtatga acttccagag gacccaaaat gggagtttcc aagagataag 1440
ctgacactgg gcaagccccct gggagaaggt tgctttgggc aagtggtcat ggcggaagca 1500
gtgggaattg acaaagacaa gcccaaggag gcggtcaccg tggccgtgaa gatgttgaaa 1560
gatgatgcca cagagaaaga cctttctgat ctggtgtcag agatggagat gatgaagatg 1620
attgggaaac acaagaatat cataaatctt cttggagcct gcacacagga tgggcctctc 1680
tatgtcatag ttgagtatgc ctctaaaggc aacctccgag aatacctccg agcccggagg 1740
ccacccggga tggagtactc ctatgacatt aaccgtgttc ctgaggagca gatgaccttc 1800
aaggacttgg tgtcatgcac ctaccagctg gccagaggca tggagtactt ggcttcccaa 1860
aaatgtattc atcgagattt agcagccaga aatgttttgg taacagaaaa caatgtgatg 1920
aaaatagcag actttggact cgccagagat atcaacaata tagactatta caaaaagacc 1980
accaatgggc ggcttccagt caagtggatg gctccagaag ccctgtttga tagagtatac 2040
actcatcaga gtgatgtctg gtccttcggg gtgttaatgt gggagatctt cactttaggg 2100
ggctcgccct acccagggat tcccgtggag gaacttttta agctgctgaa ggaaggacac 2160
agaatggata agccagccaa ctgcaccaac gaactgtaca tgatgatgag ggactgttgg 2220
catgcagtgc cctcccagag accaacgttc aagcagttgg tagaagactt ggatcgaatt 2280
ctcactctca caaccaatga ggaatacttg gacctcagcc aacctctcga acagtattca 2340
cctagttacc ctgacacaag aagttcttgt tcttcaggag atgattctgt tttttctcca 2400
gaccccatgc cttacgaacc atgccttcct cagtatccac acataaacgg cagtgttaaa 2460
acatga                                                          2466
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<210> 311
<211> 800
<212> PRT
<213> Homo sapiens

<220>
<223> human FGFR2c (NP_000132.3)

<400> 311
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Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu
 1               5                  10                  15
Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala
            20                  25                  30
Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val
        35                  40                  45
Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr
    50                  55                  60
Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp
65                  70                  75                  80
Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr
                85                  90                  95
Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp
            100                 105                 110
Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn
        115                 120                 125
Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg
    130                 135                 140
Leu His Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala
145                 150                 155                 160
Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu
                165                 170                 175
Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His
            180                 185                 190
Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr
        195                 200                 205
Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His
    210                 215                 220
Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly
225                 230                 235                 240
Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val
                245                 250                 255
Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His
            260                 265                 270
Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu
        275                 280                 285
Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu
    290                 295                 300
Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
305                 310                 315                 320
Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu
                325                 330                 335
Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro
            340                 345                 350
Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala
        355                 360                 365
Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys
    370                 375                 380
Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg
385                 390                 395                 400
Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser
                405                 410                 415
Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser
            420                 425                 430
Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro
        435                 440                 445
Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys
    450                 455                 460
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Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val
465                 470                 475                 480
Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys
                485                 490                 495
Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser
            500                 505                 510
Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn
        515                 520                 525
Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu
    530                 535                 540
Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
545                 550                 555                 560
Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu Gln
                565                 570                 575
Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala Arg Gly
            580                 585                 590
Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala
        595                 600                 605
Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys Ile Ala Asp Phe
    610                 615                 620
Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr Tyr Lys Lys Thr Thr
625                 630                 635                 640
Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp
                645                 650                 655
Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Met
            660                 665                 670
Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val
        675                 680                 685
Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro
    690                 695                 700
Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys Trp His
705                 710                 715                 720
Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu
                725                 730                 735
Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu Tyr Leu Asp Leu Ser
            740                 745                 750
Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro Asp Thr Arg Ser Ser
        755                 760                 765
Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro Asp Pro Met Pro Tyr
    770                 775                 780
Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn Gly Ser Val Lys Thr
785                 790                 795                 800
```

<210> 312
<211> 2421
<212> DNA
<213> Homo sapiens

<220>
<223> human FGFR3c (NM_000142.4)

<400> 312

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atgggcgccc ctgcctgcgc cctcgcgctc tgcgtggccg tggccatcgt ggccggcgcc 60
tcctcggagt ccttggggac ggagcagcgc gtcgtggggc gagcggcaga agtcccgggc 120
ccagagcccg gccagcagga gcagttggtc ttcggcagcg gggatgctgt ggagctgagc 180
tgtcccccgc ccgggggtgg tcccatgggg cccactgtct gggtcaagga tggcacaggg 240
ctggtgccct cggagcgtgt cctggtgggg ccccagcggc tgcaggtgct gaatgcctcc 300
cacgaggact ccggggccta cagctgccgg cagcggctca cgcagcgcgt actgtgccac 360
ttcagtgtgc gggtgacaga cgctccatcc tcgggagatg acgaagacgg ggaggacgag 420
gctgaggaca caggtgtgga cacaggggcc ccttactgga cacggcccga gcggatggac 480
aagaagctgc tggccgtgcc ggccgccaac accgtccgct tccgctgccc agccgctggc 540
aaccccactc cctccatctc ctggctgaag aacggcaggg agttccgcgg cgagcaccgc 600
attggaggca tcaagctgcg gcatcagcag tggagcctgg tcatggaaag cgtggtgccc 660
tcggaccgcg gcaactacac ctgcgtcgtg gagaacaagt ttggcagcat ccggcagacg 720
tacacgctgg acgtgctgga gcgctccccg caccggccca tcctgcaggc ggggctgccg 780
gccaaccaga cggcggtgct gggcagcgac gtggagttcc actgcaaggt gtacagtgac 840
gcacagcccc acatccagtg gctcaagcac gtggaggtga atggcagcaa ggtgggcccg 900
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gacggcacac cctacgttac cgtgctcaag acggcgggcg ctaacaccac cgacaaggag 960
ctagaggttc tctccttgca caacgtcacc tttgaggacg ccggggagta cacctgcctg 1020
gcgggcaatt ctattgggtt ttctcatcac tctgcgtggc tggtggtgct gccagccgag 1080
gaggagctgg tggaggctga cgaggcgggc agtgtgtatg caggcatcct cagctacggg 1140
gtgggcttct tcctgttcat cctggtggtg gcggctgtga cgctctgccg cctgcgcagc 1200
ccccccaaga aaggcctggg ctcccccacc gtgcacaaga tctcccgctt cccgctcaag 1260
cgacaggtgt ccctggagtc caacgcgtcc atgagctcca acacaccact ggtgcgcatc 1320
gcaaggctgt cctcagggga gggccccacg ctggccaatg tctccgagct cgagctgcct 1380
gccgacccca aatgggagct gtctcgggcc cggctgaccc tgggcaagcc ccttggggag 1440
ggctgcttcg gccaggtggt catggcggag gccatcggca ttgacaagga ccgggccgcc 1500
aagcctgtca ccgtagccgt gaagatgctg aaagacgatg ccactgacaa ggacctgtcg 1560
gacctggtgt ctgagatgga gatgatgaag atgatcggga aacacaaaaa catcatcaac 1620
ctgctgggcg cctgcacgca gggcgggccc ctgtacgtgc tggtggagta cgcggccaag 1680
ggtaacctgc gggagtttct gcgggcgcgg cggcccccgg gcctggacta ctccttcgac 1740
acctgcaagc cgcccgagga gcagctcacc ttcaaggacc tggtgtcctg tgcctaccag 1800
gtggcccggg gcatggagta cttggcctcc cagaagtgca tccacaggga cctggctgcc 1860
cgcaatgtgc tggtgaccga ggacaacgtg atgaagatcg cagacttcgg gctggcccgg 1920
gacgtgcaca acctcgacta ctacaagaag acaaccaacg gccggctgcc cgtgaagtgg 1980
atggcgcctg aggccttgtt tgaccgagtc tacactcacc agagtgacgt ctggtccttt 2040
ggggtcctgc tctgggagat cttcacgctg gggggctccc cgtaccccgg catccctgtg 2100
gaggagctct tcaagctgct gaaggagggc caccgcatgg acaagcccgc caactgcaca 2160
cacgacctgt acatgatcat gcgggagtgc tggcatgccg cgccctccca gaggcccacc 2220
ttcaagcagc tggtggagga cctggaccgt gtccttaccg tgacgtccac cgacgagtac 2280
ctggacctgt cggcgccttt cgagcagtac tccccgggtg gccaggacac ccccagctcc 2340
agctcctcag gggacgactc cgtgtttgcc cacgacctgc tgccccggc cccacccagc 2400
agtgggggct cgcggacgtg a                                          2421

<210> 313
<211> 784
<212> PRT
<213> Homo sapiens

<220>
<223> human FGFR3c (NP_000133.1)

<400> 313
Glu Ser Leu Gly Thr Glu Gln Arg Val Val Gly Arg Ala Ala Glu Val
 1               5                  10                  15
Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln Leu Val Phe Gly Ser Gly
            20                  25                  30
Asp Ala Val Glu Leu Ser Cys Pro Pro Pro Gly Gly Gly Pro Met Gly
        35                  40                  45
Pro Thr Val Trp Val Lys Asp Gly Thr Gly Leu Val Pro Ser Glu Arg
    50                  55                  60
Val Leu Val Gly Pro Gln Arg Leu Gln Val Leu Asn Ala Ser His Glu
65                  70                  75                  80
Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg Leu Thr Gln Arg Val Leu
                85                  90                  95
Cys His Phe Ser Val Arg Val Thr Asp Ala Pro Ser Ser Gly Asp Asp
            100                 105                 110
Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr Gly Val Asp Thr Gly Ala
        115                 120                 125
Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp Lys Lys Leu Leu Ala Val
    130                 135                 140
Pro Ala Ala Asn Thr Val Arg Phe Arg Cys Pro Ala Ala Gly Asn Pro
145                 150                 155                 160
Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly Arg Glu Phe Arg Gly Glu
                165                 170                 175
His Arg Ile Gly Gly Ile Lys Leu Arg His Gln Gln Trp Ser Leu Val
            180                 185                 190
Met Glu Ser Val Val Pro Ser Asp Arg Gly Asn Tyr Thr Cys Val Val
        195                 200                 205
Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr Tyr Thr Leu Asp Val Leu
    210                 215                 220
Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn
225                 230                 235                 240
Gln Thr Ala Val Leu Gly Ser Asp Val Glu Phe His Cys Lys Val Tyr
                245                 250                 255
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Ser Asp Ala Gln Pro His Ile Gln Trp Leu Lys His Val Glu Val Asn
            260                 265                 270
Gly Ser Lys Val Gly Pro Asp Gly Thr Pro Tyr Val Thr Val Leu Lys
        275                 280                 285
Thr Ala Gly Ala Asn Thr Thr Asp Lys Glu Leu Glu Val Leu Ser Leu
    290                 295                 300
His Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly
305                 310                 315                 320
Asn Ser Ile Gly Phe Ser His His Ser Ala Trp Leu Val Val Leu Pro
                325                 330                 335
Ala Glu Glu Glu Leu Val Glu Ala Asp Glu Ala Gly Ser Val Tyr Ala
            340                 345                 350
Gly Ile Leu Ser Tyr Gly Val Gly Phe Phe Leu Phe Ile Leu Val Val
        355                 360                 365
Ala Ala Val Thr Leu Cys Arg Leu Arg Ser Pro Pro Lys Lys Gly Leu
    370                 375                 380
Gly Ser Pro Thr Val His Lys Ile Ser Arg Phe Pro Leu Lys Arg Gln
385                 390                 395                 400
Val Ser Leu Glu Ser Asn Ala Ser Met Ser Ser Asn Thr Pro Leu Val
                405                 410                 415
Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly Pro Thr Leu Ala Asn Val
            420                 425                 430
Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys Trp Glu Leu Ser Arg Ala
        435                 440                 445
Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
    450                 455                 460
Val Met Ala Glu Ala Ile Gly Ile Asp Lys Asp Arg Ala Ala Lys Pro
465                 470                 475                 480
Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Asp Lys Asp
                485                 490                 495
Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
            500                 505                 510
His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Gly Gly Pro
        515                 520                 525
Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys Gly Asn Leu Arg Glu Phe
    530                 535                 540
Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp Tyr Ser Phe Asp Thr Cys
545                 550                 555                 560
Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys Asp Leu Val Ser Cys Ala
                565                 570                 575
Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
            580                 585                 590
His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val
        595                 600                 605
Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Val His Asn Leu Asp
    610                 615                 620
Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
625                 630                 635                 640
Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
                645                 650                 655
Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
            660                 665                 670
Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
        675                 680                 685
His Arg Met Asp Lys Pro Ala Asn Cys Thr His Asp Leu Tyr Met Ile
    690                 695                 700
Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe Lys
705                 710                 715                 720
Gln Leu Val Glu Asp Leu Asp Arg Val Leu Thr Val Thr Ser Thr Asp
                725                 730                 735
Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu Gln Tyr Ser Pro Gly Gly
            740                 745                 750
Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly Asp Asp Ser Val Phe Ala
        755                 760                 765
His Asp Leu Leu Pro Pro Ala Pro Pro Ser Ser Gly Gly Ser Arg Thr
    770                 775                 780
```

<210> 314
<211> 2409
<212> DNA
<213> Homo sapiens

<220>
<223> human FGFR4 (NM_002011.4)

<400> 314
atgcggctgc tgctggccct gttgggggtc ctgctgagtg tgcctgggcc tccagtcttg 60
tccctggagg cctctgagga agtggagctt gagccctgcc tggctcccag cctggagcag 120
caagagcagg agctgacagt agcccttggg cagcctgtgc gtctgtgctg tgggcgggct 180
gagcgtggtg gccactggta caaggagggc agtcgcctgg cacctgctgg ccgtgtacgg 240
ggctggaggg gccgcctaga gattgccagc ttcctacctg aggatgctgg ccgctacctc 300
tgcctggcac gaggctccat gatcgtcctg cagaatctca ccttgattac aggtgactcc 360
ttgacctcca gcaacgatga tgaggacccc aagtcccata gggacccctc gaataggcac 420
agttaccccc agcaagcacc ctactggaca cacccccagc gcatggagaa gaaactgcat 480
gcagtacctg cggggaacac cgtcaagttc cgctgtccag ctgcaggcaa ccccacgccc 540
accatccgct ggcttaagga tggacaggcc tttcatgggg agaaccgcat tggaggcatt 600
cggctgcgcc atcagcactg gagtctcgtg atggagagcg tggtgccctc ggaccgcggc 660
acatacacct gcctggtaga gaacgctgtg ggcagcatcc gctataacta cctgctagat 720
gtgctggagc ggtccccgca ccggcccatc ctgcaggccg ggctcccggc caacaccaca 780
gccgtggtgg gcagcgacgt ggagctgctg tgcaaggtgt acagcgatgc ccagccccac 840
atccagtggc tgaagcacat cgtcatcaac ggcagcagct tcggagccga cggtttcccc 900
tatgtgcaag tcctaaagac tgcagacatc aatagctcag aggtggaggt cctgtacctg 960
cggaacgtgt cagccgagga cgcaggcgag tacacctgcc tcgcaggcaa ttccatcggc 1020
ctctcctacc agtctgcctg gctcacggtg ctgccagagg aggaccccac atggaccgca 1080
gcagcgcccg aggccaggta tacggacatc atcctgtacg cgtcgggctc cctggccttg 1140
gctgtgctcc tgctgctggc cgggctgtat cgagggcagg cgctccacgg ccggcacccc 1200
cgcccgcccg ccactgtgca gaagctctcc cgcttccctc tggcccgaca gttctccctg 1260
gagtcaggct cttccggcaa gtcaagctca tccctggtac gaggcgtgcg tctctcctcc 1320
agcggccccg ccttgctcgc cggcctcgtg agtctagatc tacctctcga cccactatgg 1380
gagttccccc gggacaggct ggtgcttggg aagcccctag gcgagggctg ctttggccag 1440
gtagtacgtg cagaggcctt tggcatggac cctgcccggc ctgaccaagc cagcactgtg 1500
gccgtcaaga tgctcaaaga caacgcctct gacaaggacc tggccgacct ggtctcggag 1560
atggaggtga tgaagctgat cggccgacac aagaacatca tcaacctgct tggtgtctgc 1620
acccaggaag ggcccctgta cgtgatcgtg gagtgcgccg ccaagggaaa cctgcgggag 1680
ttcctgcggg cccggcgccc cccaggcccc gacctcagcc ccgacggtcc tcggagcagt 1740
gaggggccgc tctccttccc agtcctggtc tcctgcgcct accaggtggc ccgaggcatg 1800
cagtatctgg agtcccggaa gtgtatccac cgggacctgg ctgcccgcaa tgtgctggtg 1860
actgaggaca atgtgatgaa gattgctgac tttgggctgg cccgcggcgt ccaccacatt 1920
gactactata agaaaaccag caacggccgc ctgcctgtga agtggatggc gcccgaggcc 1980
ttgtttgacc gggtgtacac acaccagagt gacgtgtggt cttttgggat cctgctatgg 2040
gagatcttca ccctcggggg ctccccgtat cctggcatcc cggtggagga gctgttctcg 2100
ctgctgcggg agggacatcg gatggaccga cccccacact gccccccaga gctgtacggg 2160
ctgatgcgtg agtgctggca cgcagcgccc tcccagaggc ctaccttcaa gcagctggtg 2220
gaggcgctgg acaaggtcct gctggccgtc tctgaggagt acctcgacct ccgcctgacc 2280
ttcggaccct attccccctc tggtggggac gccagcagca cctgctcctc cagcgattct 2340
gtcttcagcc acgacccccc gccattggga tccagctcct tccccttcgg gtctggggtg 2400
cagacatga 2409

<210> 315
<211> 781
<212> PRT
<213> Homo sapiens

<220>
<223> human FGFR4 (NP_002002.3)

<400> 315
Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro Cys Leu Ala Pro Ser
 1   5   10   15
Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala Leu Gly Gln Pro Val
            20   25   30
Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly His Trp Tyr Lys Glu
        35   40   45
Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg Gly Trp Arg Gly Arg
    50   55   60

```
Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala Gly Arg Tyr Leu Cys
65                  70                  75                  80
Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn Leu Thr Leu Ile Thr
                85                  90                  95
Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu Asp Pro Lys Ser His
            100                 105                 110
Arg Asp Pro Ser Asn Arg His Ser Tyr Pro Gln Gln Ala Pro Tyr Trp
        115                 120                 125
Thr His Pro Gln Arg Met Glu Lys Lys Leu His Ala Val Pro Ala Gly
    130                 135                 140
Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly Asn Pro Thr Pro Thr
145                 150                 155                 160
Ile Arg Trp Leu Lys Asp Gly Gln Ala Phe His Gly Glu Asn Arg Ile
                165                 170                 175
Gly Gly Ile Arg Leu Arg His Gln His Trp Ser Leu Val Met Glu Ser
            180                 185                 190
Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys Leu Val Glu Asn Ala
        195                 200                 205
Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp Val Leu Glu Arg Ser
    210                 215                 220
Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Thr Thr Ala
225                 230                 235                 240
Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys Val Tyr Ser Asp Ala
                245                 250                 255
Gln Pro His Ile Gln Trp Leu Lys His Ile Val Ile Asn Gly Ser Ser
            260                 265                 270
Phe Gly Ala Asp Gly Phe Pro Tyr Val Gln Val Leu Lys Thr Ala Asp
        275                 280                 285
Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu Arg Asn Val Ser Ala
    290                 295                 300
Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu
305                 310                 315                 320
Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro Glu Glu Asp Pro Thr
                325                 330                 335
Trp Thr Ala Ala Ala Pro Glu Ala Arg Tyr Thr Asp Ile Ile Leu Tyr
            340                 345                 350
Ala Ser Gly Ser Leu Ala Leu Ala Val Leu Leu Leu Leu Ala Gly Leu
        355                 360                 365
Tyr Arg Gly Gln Ala Leu His Gly Arg His Pro Arg Pro Pro Ala Thr
    370                 375                 380
Val Gln Lys Leu Ser Arg Phe Pro Leu Ala Arg Gln Phe Ser Leu Glu
385                 390                 395                 400
Ser Gly Ser Ser Gly Lys Ser Ser Ser Ser Leu Val Arg Gly Val Arg
                405                 410                 415
Leu Ser Ser Ser Gly Pro Ala Leu Leu Ala Gly Leu Val Ser Leu Asp
            420                 425                 430
Leu Pro Leu Asp Pro Leu Trp Glu Phe Pro Arg Asp Arg Leu Val Leu
        435                 440                 445
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Arg Ala Glu
    450                 455                 460
Ala Phe Gly Met Asp Pro Ala Arg Pro Asp Gln Ala Ser Thr Val Ala
465                 470                 475                 480
Val Lys Met Leu Lys Asp Asn Ala Ser Asp Lys Asp Leu Ala Asp Leu
                485                 490                 495
Val Ser Glu Met Glu Val Met Lys Leu Ile Gly Arg His Lys Asn Ile
            500                 505                 510
Ile Asn Leu Leu Gly Val Cys Thr Gln Glu Gly Pro Leu Tyr Val Ile
        515                 520                 525
Val Glu Cys Ala Ala Lys Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg
    530                 535                 540
Arg Pro Pro Gly Pro Asp Leu Ser Pro Asp Gly Pro Arg Ser Ser Glu
545                 550                 555                 560
Gly Pro Leu Ser Phe Pro Val Leu Val Ser Cys Ala Tyr Gln Val Ala
                565                 570                 575
Arg Gly Met Gln Tyr Leu Glu Ser Arg Lys Cys Ile His Arg Asp Leu
            580                 585                 590
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
        595                 600                 605
```

Asp Phe Gly Leu Ala Arg Gly Val His His Ile Asp Tyr Tyr Lys Lys
610 615 620
Thr Ser Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
625 630 635 640
Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Ile
645 650 655
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile
660 665 670
Pro Val Glu Glu Leu Phe Ser Leu Leu Arg Glu Gly His Arg Met Asp
675 680 685
Arg Pro Pro His Cys Pro Pro Glu Leu Tyr Gly Leu Met Arg Glu Cys
690 695 700
Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
705 710 715 720
Ala Leu Asp Lys Val Leu Leu Ala Val Ser Glu Glu Tyr Leu Asp Leu
725 730 735
Arg Leu Thr Phe Gly Pro Tyr Ser Pro Ser Gly Gly Asp Ala Ser Ser
740 745 750
Thr Cys Ser Ser Ser Asp Ser Val Phe Ser His Asp Pro Leu Pro Leu
755 760 765
Gly Ser Ser Ser Phe Pro Phe Gly Ser Gly Val Gln Thr
770 775 780

<210> 316
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1 Fc with two amino acid changes to alanine

<400> 316
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110
Pro Ala Pro Ala Leu Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275 280 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 317
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5H23-vH3-human IgG1 (E233A)(L235A)

<400> 317
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Ala Leu Ala Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 318
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> Human kappa constant region of light chain

<400> 318
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 319
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized 5H23-vL2-human kappa constant region of light chain

<400> 319
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Val Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 320
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH7

<400> 320
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 321
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH8

<400> 321
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Arg Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 322
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> vH9

<400> 322
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 323
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H23v1-3

<400> 323
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 324
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H23v1-46

<400> 324
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 325
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> vL4

<400> 325
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 326
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> vL5

<400> 326
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 327
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39a

<400> 327
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser

20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 328
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39b

<400> 328
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 329
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39c

<400> 329
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 330
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39d

<400> 330
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 331
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39e

<400> 331
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 332
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39f

<400> 332
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 333
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39g

<400> 333
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 334
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39h

<400> 334
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 335
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39i

<400> 335
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser

```
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Leu Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 336
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39j

<400> 336

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Val Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 337
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39k

<400> 337

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Lys Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Val Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 338
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39l

<400> 338

```
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Lys Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Val Gln Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 339
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39m

<400> 339

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Val Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 340
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39n

<400> 340

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80
Ser Val Gln Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 341
<211> 111

<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39o

<400> 341
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gln Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 342
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v1-39p

<400> 342
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Val Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gln Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 343
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20a

<400> 343
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg

85 90 95
Asp Leu Thr Phe Pro Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 344
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20b

<400> 344
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 345
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20c

<400> 345
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 346
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20d

<400> 346
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 347
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20e

<400> 347
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Leu Glu Pro Glu Asp Ala Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 348
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20f

<400> 348
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 349
<211> 111
<212> PRT
<213> Artificial Sequence

<220>

<223> v3-20g

<400> 349
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Arg Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 350
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20h

<400> 350
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Arg Leu Glu Glu Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 351
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20i

<400> 351
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Arg Val Glu Glu Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 352
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> v3-20j

<400> 352
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Arg Val Glu Glu Glu Asp Ala Ala Val Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 353
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> hz5H23v1-39

<400> 353
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
        35   40   45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
    50   55   60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 354
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> hz5H23v3-20

<400> 354
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        35   40   45
Arg Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Ile Pro Ala
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 355
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> hz5H23v4-1

<400> 355
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Asp
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 356
<211> 1043
<212> PRT
<213> Rattus

<220>
<223> Rat beta klotho

<400> 356
Met Lys Thr Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Val Phe
1 5 10 15
Phe Ser Ser Asp Glu Arg Ser Thr Arg Ser Arg Lys Thr Met Ser Asn
20 25 30
Gly Ala Leu Gln Arg Ser Ala Val Leu Ser Ala Leu Val Leu Leu Arg
35 40 45
Ala Val Thr Gly Phe Ser Gly Asp Gly Lys Ala Ile Trp Asp Lys Lys
50 55 60
Gln Tyr Val Ser Pro Val Asn Pro Gly Gln Leu Phe Leu Tyr Asp Thr
65 70 75 80
Phe Pro Lys Asn Phe Ser Trp Gly Val Gly Thr Gly Ala Phe Gln Val
85 90 95
Glu Gly Ser Trp Lys Ala Asp Gly Arg Gly Pro Ser Ile Trp Asp Arg
100 105 110
Tyr Val Asp Ser His Leu Arg Gly Val Asn Ser Thr Asp Arg Ser Thr
115 120 125
Asp Ser Tyr Val Phe Leu Glu Lys Asp Leu Leu Ala Leu Asp Phe Leu
130 135 140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145 150 155 160
Asn Gly Thr Val Ala Ala Val Asn Ala Lys Gly Leu Gln Tyr Tyr Arg
165 170 175
Ala Leu Leu Asp Ser Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
180 185 190
Leu Tyr His Trp Asp Leu Pro Leu Thr Leu Gln Glu Glu Tyr Gly Gly
195 200 205

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Trp Lys Asn Ala Thr Met Ile Asp Leu Phe Asn Asp Tyr Ala Thr Tyr
    210                 215                 220
Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225                 230                 235                 240
Asn Pro Tyr Leu Val Ala Trp His Gly Phe Gly Thr Gly Met His Ala
                245                 250                 255
Pro Gly Glu Lys Gly Asn Leu Thr Ala Val Tyr Thr Val Gly His Asn
            260                 265                 270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asp Lys Asn Phe
        275                 280                 285
Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
    290                 295                 300
Ile Glu Pro Asn Arg Thr Glu Asn Met Glu Asp Val Ile Asn Cys Gln
305                 310                 315                 320
His Ser Met Ser Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
                325                 330                 335
Asp Gly Asp Tyr Pro Glu Phe Met Lys Thr Ser Ser Val Ile Pro Glu
            340                 345                 350
Phe Ser Glu Ala Glu Lys Glu Glu Val Arg Gly Thr Ala Asp Phe Phe
        355                 360                 365
Ala Phe Ser Phe Gly Pro Asn Asn Phe Arg Pro Ser Asn Thr Val Val
    370                 375                 380
Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Gln Val Leu Asn Trp
385                 390                 395                 400
Ile Lys Leu Glu Tyr Asp Asn Pro Arg Ile Leu Ile Ser Glu Asn Gly
                405                 410                 415
Trp Phe Thr Asp Ser Tyr Ile Lys Thr Glu Asp Thr Thr Ala Ile Tyr
            420                 425                 430
Met Met Lys Asn Phe Leu Asn Gln Val Leu Gln Ala Ile Lys Phe Asp
        435                 440                 445
Glu Ile Gln Val Phe Gly Tyr Thr Ala Trp Thr Leu Leu Asp Gly Phe
    450                 455                 460
Glu Trp Gln Asp Ala Tyr Thr Thr Arg Arg Gly Leu Phe Tyr Val Asp
465                 470                 475                 480
Phe Asn Ser Glu Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala His Tyr
                485                 490                 495
Tyr Lys Gln Ile Ile Gln Asp Asn Gly Phe Pro Leu Gln Glu Ser Thr
            500                 505                 510
Pro Asp Met Lys Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly Val Thr
        515                 520                 525
Glu Ser Val Leu Lys Pro Glu Phe Thr Val Ser Ser Pro Gln Phe Thr
    530                 535                 540
Asp Pro His Leu Tyr Val Trp Asn Val Thr Gly Asn Arg Leu Leu Tyr
545                 550                 555                 560
Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ser Gln Cys Thr Asp
                565                 570                 575
Tyr Val Ser Ile Lys Lys Arg Val Glu Met Leu Ala Lys Met Lys Val
            580                 585                 590
Thr His Tyr Gln Phe Ala Leu Asp Trp Thr Ser Ile Leu Pro Thr Gly
        595                 600                 605
Asn Leu Ser Lys Ile Asn Arg Gln Val Leu Arg Tyr Tyr Arg Cys Val
    610                 615                 620
Val Ser Glu Gly Leu Lys Leu Gly Ile Ser Pro Met Val Thr Leu Tyr
625                 630                 635                 640
His Pro Thr His Ser His Leu Gly Leu Pro Met Pro Leu Leu Ser Ser
                645                 650                 655
Gly Gly Trp Leu Asn Thr Asn Thr Ala Lys Ala Phe Gln Asp Tyr Ala
            660                 665                 670
Gly Leu Cys Phe Lys Glu Leu Gly Asp Leu Val Lys Leu Trp Ile Thr
        675                 680                 685
Ile Asn Glu Pro Asn Arg Leu Ser Asp Met Tyr Asn Arg Thr Ser Asn
    690                 695                 700
Asp Thr Tyr Arg Ala Ala His Asn Leu Met Ile Ala His Ala Gln Val
705                 710                 715                 720
Trp His Leu Tyr Asp Arg Gln Tyr Arg Pro Val Gln His Gly Ala Val
                725                 730                 735
Ser Leu Ser Leu His Ser Asp Trp Ala Glu Pro Ala Asn Pro Tyr Val
            740                 745                 750
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Glu Ser His Trp Lys Ala Ala Glu Arg Phe Leu Gln Phe Glu Ile Ala
        755                 760                 765
Trp Phe Ala Asp Pro Leu Phe Lys Thr Gly Asp Tyr Pro Leu Ala Met
    770                 775                 780
Lys Glu Tyr Ile Ala Ser Lys Lys Gln Arg Gly Leu Ser Ser Ser Val
785                 790                 795                 800
Leu Pro Arg Phe Thr Leu Lys Glu Ser Arg Leu Val Lys Gly Thr Ile
                805                 810                 815
Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Ile His Lys
            820                 825                 830
Gln Leu Asn Thr Asn Cys Ser Val Ala Asp Arg Asp Val Gln Phe Leu
        835                 840                 845
Gln Asp Ile Thr Arg Leu Ser Ser Pro Ser Arg Leu Ala Val Thr Pro
    850                 855                 860
Trp Gly Met Arg Lys Leu Leu Gly Trp Ile Arg Arg Asn Tyr Arg Asp
865                 870                 875                 880
Met Asp Ile Tyr Val Thr Ala Asn Gly Ile Asp Asp Leu Ala Leu Glu
                885                 890                 895
Asp Asp Gln Ile Arg Lys Tyr Tyr Leu Glu Lys Tyr Val Gln Glu Ala
            900                 905                 910
Leu Lys Ala Tyr Leu Ile Asp Lys Val Lys Ile Lys Gly Tyr Tyr Ala
        915                 920                 925
Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe Phe Thr
    930                 935                 940
Ser Asp Phe Lys Ala Lys Ser Ser Val Gln Phe Tyr Ser Lys Leu Ile
945                 950                 955                 960
Ser Ser Ser Gly Phe Ser Ser Glu Asn Arg Ser Pro Ala Cys Gly Gln
                965                 970                 975
Pro Pro Glu Asp Thr Glu Cys Ala Ile Cys Ser Phe Leu Thr Gln Lys
            980                 985                 990
Lys Pro Leu Ile Phe Phe Gly Cys Cys Phe Ile Ser Thr Leu Ala Ala
        995                 1000                1005
Leu Leu Ser Ile Thr Ile Phe His His Arg Lys Arg Arg Lys Phe Gln
    1010                1015                1020
Lys Ala Arg Asn Leu Gln Asn Ile Pro Leu Lys Lys Gly His Ser Arg
1025                1030                1035                1040
Val Phe Ser
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<210> 357
<211> 3132
<212> DNA
<213> Rattus

<220>
<223> Rat beta klotho

<400> 357

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atgaagacag gctgtgcagc agggtctcca gggaatgaat gggttttctt cagctctgat 60
gaaagaagca cacgctctag gaaaacaatg tccaacggag cactgcaaag atctgccgtg 120
ctgtctgcat tggttctgct gcgagctgtt accggcttct ctggagacgg aaaagcaata 180
tgggataaaa aacaatacgt gagtccggta aacccaggtc agctgttcct ctatgacact 240
ttccctaaaa acttttcctg gggcgttggg accggagcat ttcaagtgga agggagttgg 300
aaggcagatg gaagaggacc ctcgatctgg gaccgttatg tcgactcaca cctgagaggt 360
gtcaacagca cagacagatc cactgacagt tatgtctttc tggaaaagga cttgctggct 420
ctggattttt taggagtttc tttttatcag ttctcaatct cctggccgcg gttgttcccc 480
aacggaacag tagcagctgt gaatgcaaaa ggtctccagt actacagagc acttctggac 540
tcgctggtac ttaggaatat cgaacccatt gttaccttat accattggga tttgcctttg 600
acgctacagg aagaatatgg gggctggaaa aatgcaacta tgatagatct cttcaatgac 660
tatgccacat actgcttcca gacctttgga gaccgtgtca aatattggat tacaattcac 720
aacccttacc tcgttgcttg gcatgggttt ggcacaggta tgcatgcgcc aggagagaag 780
ggaaatttaa cagctgtcta cactgtggga cacaacctga tcaaggcgca ttcgaaagtg 840
tggcataact acgacaaaaa cttccgccct catcagaagg gttggctctc catcaccttg 900
gggtcccatt ggatagaacc aaacagaaca gaaaacatgg aggacgtgat caactgccag 960
cactccatgt cttctgtgct cggatggttt gccaacccca tccacggaga cggcgactac 1020
cccgagttca tgaagacgag ctccgtaatc cctgagttct ctgaggcaga gaaggaggag 1080
gtgcggggca ctgctgactt ctttgccttt tccttcgggc ccaacaattt caggccctcg 1140
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aacaccgtgg taaaaatggg acaaaatgta tcactcaact taagacaggt gctgaactgg 1200
attaaactag aatatgacaa ccctcgaatc ttgatttcgg agaacggctg gttcacagat 1260
agttatataa agacggaaga taccacggcc atctacatga tgaagaattt cctcaaccag 1320
gttcttcaag caataaagtt tgatgaaata caagtgtttg gttatacggc ttggactctc 1380
ctggatggct ttgagtggca ggatgcctac acgacccgac gagggctgtt ttatgtggac 1440
tttaatagtg agcagaaaga gaggaaaccc aagtcctccg ctcattacta caaacagatt 1500
atacaagaca acggtttccc tttgcaagaa tccacaccag acatgaaggg tcagtttccc 1560
tgtgacttct cctggggagt cactgagtct gttcttaagc cggagtttac ggtgtcctcc 1620
ccacagttta ctgatcctca cctgtatgtg tggaatgtca ctggcaacag attgctatac 1680
cgagtggaag gagtcaggct aaaaacaaga ccgtcccaat gcacagatta tgtgagcatc 1740
aaaaaacgag ttgaaatgtt ggccaaaatg aaagtcaccc actaccagtt tgctctggac 1800
tggacctcta tcctccctac cggaaatctg tctaaaatta atagacaagt gttgaggtac 1860
tataggtgtg tggtgagcga aggactgaag ctgggcatct cccctatggt gacgttgtac 1920
cacccgaccc actcccatct aggcctcccc atgccacttc tgagcagtgg gggatggcta 1980
aacaccaaca cagccaaggc cttccaggac tacgcaggcc tgtgcttcaa ggagctgggg 2040
gacttggtaa agctctggat caccatcaat gaacccaata ggctgagtga catgtacaac 2100
cgcacgagta acgacaccta ccgtgcggcc cacaacctga tgatcgccca tgcccaggtc 2160
tggcacctct atgataggca gtataggccg gtccagcacg gggctgtgtc gctgtcctta 2220
cattccgact gggcagaacc tgccaacccc tatgtggagt ctcactggaa ggcagccgag 2280
cgcttcctcc agtttgagat cgcctggttt gcggatccac tcttcaagac tggtgactac 2340
ccgctggcca tgaaggaata catcgcctcc aagaagcagc gagggctgtc tagctcagtc 2400
ctgccgcgct ttaccttgaa ggagagcagg ctggtgaagg ggaccatcga cttttacgca 2460
ctgaaccact tcactactag attcgtgata cacaagcagt tgaataccaa ctgctcagtg 2520
gcagacaggg acgtccagtt cctgcaggac atcacccgcc tgagctcgcc cagtcgccta 2580
gccgtaacgc cctggggaat gcgcaagctc cttgggtgga tccggaggaa ctacagagac 2640
atggatatct acgtcacagc caatggcatt gatgatcttg ctctagagga cgatcagatt 2700
agaaagtact acttggagaa gtacgtccag gaggctctga aagcatatct gattgacaag 2760
gtcaaaatca aaggctacta tgcattcaaa ctgactgaag agaaatctaa gcctagattt 2820
ggatttttca catctgactt caaagctaaa tcttctgtac agttttatag caagctgatc 2880
agcagcagcg gcttctcctc tgagaacaga agtcctgcct gtggtcagcc tccagaagac 2940
acagaatgcg ccatttgctc cttccttaca cagaagaaac cactcatctt ctttggttgt 3000
tgcttcatct ccactctggc tgcactgcta tcaatcacta tttttcatca tcggaagaga 3060
agaaaattcc agaaagcaag gaacttacaa aatataccat tgaagaaagg gcacagcaga 3120
gtttttagct aa 3132

<210> 358
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain SEQ ID NO: 32 in U.S. Publication US20110135657

<400> 358
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Arg Gly Ala Arg Cys Gln Val Thr Leu Lys Glu Ser Gly Pro Val
            20   25   30
Leu Val Lys Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Val Ser Gly
        35   40   45
Phe Ser Leu Asn Asn Ala Arg Met Gly Val Ser Trp Ile Arg Gln Pro
    50   55   60
Pro Gly Lys Ala Leu Glu Trp Leu Ala His Ile Phe Ser Asn Asp Glu
65   70   75   80
Lys Ser Tyr Ser Thr Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp
                85   90   95
Thr Ser Lys Ser Gln Val Val Leu Ile Met Thr Asn Met Asp Pro Val
            100   105   110
Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Val Val Thr Gly Gly Tyr
        115   120   125
Tyr Tyr Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
    130   135   140
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
145   150   155   160
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
                165   170   175
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
            180   185   190

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Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
        195                 200                 205
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
    210                 215                 220
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
225                 230                 235                 240
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
                245                 250                 255
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
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<210> 359
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Heavy Chain SEQ ID NO: 32 in U.S. Publication US20110135657

<400> 359
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atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtcagg tgacgctgaa agagtccgga ccggtcctgg tgaaaccaac tgaaacccta 120
actctcacgt gcactgtcag cggcttctct ctcaacaacg caagaatggg tgtgtcttgg 180
atcagacagc caccaggtaa agcgcttgag tggctggcac acatcttctc caacgatgag 240
aagagctact ctaccagcct caagtctcgt ctgaccatca gtaaagatac gtccaagtcc 300
caagtagtcc tcatcatgac taacatggac cccgtggata ccgcgaccta ctactgtgcg 360
aggagcgtcg tgaccggtgg ctactactac gacggcatgg atgtgtgggg tcagggtacg 420
acggtgaccg tcagcagcgc gagcaccaag ggtccgtccg tgtttccgct cgccccttgt 480
agccggagca cctcagagtc tactgccgca ctaggctgcc tggtgaagga ctacttccct 540
gaacccgtga cagtgagctg gaactccgga gcactgacta gcggcgtgca caccttcccc 600
gctgtcttgc agtctagcgg cctgtattcg ctctccagcg tggtcactgt accgtccagc 660
aatttcggaa cccagaccta cacatgtaac gtcgatcata aaccgtccaa cactaaggta 720
gacaaaaccg tggaaaggaa atgctgcgtg gagtgtcccc cctgcccagc tccgccagtg 780
gcaggcccca gcgtgttcct gttcccccca aagccaaaag acaccctgat gatctcgaga 840
acccccgagg tgacttgcgt cgtcgtcgat gtctcccatg aggatccaga agtacagttc 900
aactggtacg tggacggcgt ggaagtgcac aatgcaaaaa cgaagccccg agaagagcag 960
ttcaactcca cattccgggt ggtatcagtc ctgactgtgg tccaccagga ttggctgaac 1020
gggaaggaat acaaatgtaa agtgagcaat aagggtctgc ccgcaccgat cgagaaaact 1080
atctcaaaaa ctaagggtca gcctcgcgag cctcaagtgt atacgctgcc gccaagtagg 1140
gaggagatga ccaaaaacca ggtgtcactg acatgtctgg tgaaaggctt ctaccccagc 1200
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gacatcgccg tggagtggga gtcaaatggc cagccggaga acaactacaa gaccacaccg 1260
ccgatgctgg actcagacgg gtccttttc ctctattcca agctcaccgt cgacaaaagc 1320
cgttggcagc agggaaacgt attctcatgc tctgtgatgc acgaggccct tcacaaccat 1380
tacactcaga aatcgttgtc cctttctccc ggaaaatga 1419

<210> 360
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain SEQ ID No: 14 in U.S. Publication US20110135657

<400> 360
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1   5   10   15
Leu Arg Gly Ala Arg Cys Ser Tyr Val Leu Thr Gln Pro Pro Ser Val
            20   25   30
Ser Val Ala Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn
        35   40   45
Ile Gly Ser Glu Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala
    50   55   60
Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro
65   70   75   80
Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile
                85   90   95
Ser Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp
            100   105   110
Asp Gly Asn Ser Asp His Val Val Phe Gly Gly Gly Thr Lys Leu Thr
        115   120   125
Val Leu Gly Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro
    130   135   140
Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
145   150   155   160
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly
                165   170   175
Ser Pro Val Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser
            180   185   190
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
        195   200   205
Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
    210   215   220
Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225   230   235

<210> 361
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for Light Chain SEQ ID No: 14 in U.S.
      Publication US20110135657

<400> 361
atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgttcat acgtgctgac tcagccccca tccgtgtctg tggcacccgg acaaactgcc 120
aggatcactt gcggagggaa taacatcggt agcgagagcg tccactggta ccagcaaaaa 180
ccaggccagg caccggtcct cgtggtatac gacgattctg accgaccgtc cggcatccca 240
gaaagattct cgggtagcaa ctctggcaac acggctaccc tgaccatcag ccgtgtcgag 300
gccggtgacg aggcggatta ctactgccag gtgtgggacg ggaactccga tcatgtggtg 360
ttcggcggag gcactaagct gaccgtattg ggtcagccca aagcaaatcc caccgtgacg 420
ctctttcccc ctagctccga ggagctgcag gcgaacaagg caactcttgt ctgtctcatc 480
tcggacttct atccgggagc ggtgaccgtc gcatggaaag cagatggttc tccggtcaaa 540
gcaggcgtgg aaacgaccaa gccttccaaa cagagtaaca acaagtatgc tgccagctcc 600
tacctaagcc tgacaccgga gcagtggaag agccaccggt catacagctg ccaggtaact 660
catgaaggct caacagtgga gaaaaccgtg gcgccaaccg agtgttcctg a 711

<210> 362
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV1-3

<400> 362
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45
Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Lys Tyr Ser Gln Lys Phe
    50   55   60
Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg

<210> 363
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV1-18

<400> 363
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50   55   60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65   70   75   80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85   90   95
Ala Arg

<210> 364
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV1-46

<400> 364
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg

<210> 365
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IGHV1-69

<400> 365
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg

<210> 366
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> U00583

<400> 366
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Asp Ile Leu Thr Gly Leu Asn Trp Phe Asp Pro Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 367
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKV4-1

<400> 367
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20   25   30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85   90   95
Tyr Tyr Ser Thr Pro
            100

<210> 368
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKV1-39

<400> 368
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20   25   30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro
                85   90   95

<210> 369
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> IGKV3-20

<400> 369
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20   25   30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50   55   60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
                85   90

<210> 370
<211> 450
<212> PRT
<213> Artificial Sequence

<220>

<223> hIgK-5H23(VH)-hIgG1(E233A)(L235A) (5H23 chimera)

<400> 370
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15
Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Arg Thr Ala Tyr
65   70   75   80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val Tyr Phe Cys
                85   90   95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115   120   125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130   135   140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145   150   155   160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165   170   175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180   185   190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195   200   205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210   215   220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Ala Leu Ala Gly Gly
225   230   235   240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245   250   255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260   265   270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275   280   285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    290   295   300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305   310   315   320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325   330   335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340   345   350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355   360   365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370   375   380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385   390   395   400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405   410   415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420   425   430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445
Gly Lys
    450

<210> 371
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of hIgK-5H23(VH)-hIgG1(E233A)(L235A)
(5H23 chimera)

<400> 371
atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtcaag tgcaacttca acagtcaggc ccagaactcg tcaaacccgg agcactcgtg 120
aagatctcgt gcaaggcgtc gggttacact ttcacgtcct acgacatcaa ttgggtgaag 180
cagaggcctg gacagggcct ggagtggatt ggatggatct acccggggga tgggtctacc 240
aagtacaacg aaaagttcaa aggcaaagcc actctgaccg cagacaagag cagcagaacc 300
gcgtacatgc agttgtcatc cctgaccagc gagaactcgg ccgtctactt ttgtgctcgc 360
tccgattact atggatcccg gagcttcgcc tactggggac agggaactct ggtgactgtg 420
tcatcggcta gcaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgcactcgcg 780
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 840
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 900
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 960
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1020
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1080
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1140
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1200
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1260
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1320
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1380
tacacgcaga agagcctctc cctgtctccg ggtaaatga 1419

<210> 372
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK-5H23(VL)-hIgK (5H23 chimera)

<400> 372
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30
Gly Tyr Val Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Leu Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80
Pro Val Glu Glu Glu Asp Ala Ala Ile Tyr Tyr Cys Gln His Ser Arg
85 90 95
Asp Leu Thr Phe Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 373
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of hIgK-5H23(VL)-hIgK (5H23 chimera)

<400> 373
atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtgaca tcgtcctgac tcagagcccc gcatccctcg ccgtgtcact tggtcaaaga 120
gctaccattt cctgccgcgc atcgaagtct gtgagcactt ccggctacgt ctacatgcac 180
tggaaccagc agaagccagg acaaccgccg aagctgctga tctatctcgc gtcatacctg 240
gaatcgggag tgccggcgag gttttcggga tcgggctccg gaaccgactt caccctgaat 300
atccatccag tggaagagga ggatgccgcc atctactact gtcagcacag ccgggatctc 360
actttccctt tcggcggagg gacgaaattg gaaatcaaac gtacggtggc tgcaccatct 420
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 540
caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600
ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720
tag 723

<210> 374
<211> 1045
<212> PRT
<213> Artificial Sequence

<220>
<223> human KLB (M1-F508)- mouse KLB (P507-S1043)

<400> 374
Met Lys Pro Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Ile Phe
 1   5   10   15
Phe Ser Thr Asp Glu Ile Thr Thr Arg Tyr Arg Asn Thr Met Ser Asn
            20   25   30
Gly Gly Leu Gln Arg Ser Val Ile Leu Ser Ala Leu Ile Leu Leu Arg
        35   40   45
Ala Val Thr Gly Phe Ser Gly Asp Gly Arg Ala Ile Trp Ser Lys Asn
    50   55   60
Pro Asn Phe Thr Pro Val Asn Glu Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Ile Gly Thr Gly Ala Leu Gln Val
                85   90   95
Glu Gly Ser Trp Lys Lys Asp Gly Lys Gly Pro Ser Ile Trp Asp His
            100   105   110
Phe Ile His Thr His Leu Lys Asn Val Ser Ser Thr Asn Gly Ser Ser
        115   120   125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Ser Ala Leu Asp Phe Ile
    130   135   140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asp Gly Ile Val Thr Val Ala Asn Ala Lys Gly Leu Gln Tyr Tyr Ser
                165   170   175
Thr Leu Leu Asp Ala Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
            180   185   190
Leu Tyr His Trp Asp Leu Pro Leu Ala Leu Gln Glu Lys Tyr Gly Gly
        195   200   205
Trp Lys Asn Asp Thr Ile Ile Asp Ile Phe Asn Asp Tyr Ala Thr Tyr
    210   215   220
Cys Phe Gln Met Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225   230   235   240
Asn Pro Tyr Leu Val Ala Trp His Gly Tyr Gly Thr Gly Met His Ala
                245   250   255
Pro Gly Glu Lys Gly Asn Leu Ala Ala Val Tyr Thr Val Gly His Asn
            260   265   270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asn Thr His Phe

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        275                 280                 285
Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
    290                 295                 300
Ile Glu Pro Asn Arg Ser Glu Asn Thr Met Asp Ile Phe Lys Cys Gln
305                 310                 315                 320
Gln Ser Met Val Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
                325                 330                 335
Asp Gly Asp Tyr Pro Glu Gly Met Arg Lys Lys Leu Phe Ser Val Leu
            340                 345                 350
Pro Ile Phe Ser Glu Ala Glu Lys His Glu Met Arg Gly Thr Ala Asp
        355                 360                 365
Phe Phe Ala Phe Ser Phe Gly Pro Asn Asn Phe Lys Pro Leu Asn Thr
    370                 375                 380
Met Ala Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Glu Ala Leu
385                 390                 395                 400
Asn Trp Ile Lys Leu Glu Tyr Asn Asn Pro Arg Ile Leu Ile Ala Glu
                405                 410                 415
Asn Gly Trp Phe Thr Asp Ser Arg Val Lys Thr Glu Asp Thr Thr Ala
            420                 425                 430
Ile Tyr Met Met Lys Asn Phe Leu Ser Gln Val Leu Gln Ala Ile Arg
        435                 440                 445
Leu Asp Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp
    450                 455                 460
Gly Phe Glu Trp Gln Asp Ala Tyr Thr Ile Arg Arg Gly Leu Phe Tyr
465                 470                 475                 480
Val Asp Phe Asn Ser Lys Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala
                485                 490                 495
His Tyr Tyr Lys Gln Ile Ile Arg Glu Asn Gly Phe Pro Leu Lys Glu
            500                 505                 510
Ser Thr Pro Asp Met Lys Gly Arg Phe Pro Cys Asp Phe Ser Trp Gly
        515                 520                 525
Val Thr Glu Ser Val Leu Lys Pro Glu Phe Thr Val Ser Ser Pro Gln
    530                 535                 540
Phe Thr Asp Pro His Leu Tyr Val Trp Asn Val Thr Gly Asn Arg Leu
545                 550                 555                 560
Leu Tyr Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ser Gln Cys
                565                 570                 575
Thr Asp Tyr Val Ser Ile Lys Lys Arg Val Glu Met Leu Ala Lys Met
            580                 585                 590
Lys Val Thr His Tyr Gln Phe Ala Leu Asp Trp Thr Ser Ile Leu Pro
        595                 600                 605
Thr Gly Asn Leu Ser Lys Val Asn Arg Gln Val Leu Arg Tyr Tyr Arg
    610                 615                 620
Cys Val Val Ser Glu Gly Leu Lys Leu Gly Val Phe Pro Met Val Thr
625                 630                 635                 640
Leu Tyr His Pro Thr His Ser His Leu Gly Leu Pro Leu Pro Leu Leu
                645                 650                 655
Ser Ser Gly Gly Trp Leu Asn Met Asn Thr Ala Lys Ala Phe Gln Asp
            660                 665                 670
Tyr Ala Glu Leu Cys Phe Arg Glu Leu Gly Asp Leu Val Lys Leu Trp
        675                 680                 685
Ile Thr Ile Asn Glu Pro Asn Arg Leu Ser Asp Met Tyr Asn Arg Thr
    690                 695                 700
Ser Asn Asp Thr Tyr Arg Ala Ala His Asn Leu Met Ile Ala His Ala
705                 710                 715                 720
Gln Val Trp His Leu Tyr Asp Arg Gln Tyr Arg Pro Val Gln His Gly
                725                 730                 735
Ala Val Ser Leu Ser Leu His Cys Asp Trp Ala Glu Pro Ala Asn Pro
            740                 745                 750
Phe Val Asp Ser His Trp Lys Ala Ala Glu Arg Phe Leu Gln Phe Glu
        755                 760                 765
Ile Ala Trp Phe Ala Asp Pro Leu Phe Lys Thr Gly Asp Tyr Pro Ser
    770                 775                 780
Val Met Lys Glu Tyr Ile Ala Ser Lys Asn Gln Arg Gly Leu Ser Ser
785                 790                 795                 800
Ser Val Leu Pro Arg Phe Thr Ala Lys Glu Ser Arg Leu Val Lys Gly
                805                 810                 815
Thr Val Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Ile
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            820                 825                 830
His Lys Gln Leu Asn Thr Asn Arg Ser Val Ala Asp Arg Asp Val Gln
        835                 840                 845
Phe Leu Gln Asp Ile Thr Arg Leu Ser Ser Pro Ser Arg Leu Ala Val
    850                 855                 860
Thr Pro Trp Gly Val Arg Lys Leu Leu Ala Trp Ile Arg Arg Asn Tyr
865                 870                 875                 880
Arg Asp Arg Asp Ile Tyr Ile Thr Ala Asn Gly Ile Asp Asp Leu Ala
                885                 890                 895
Leu Glu Asp Asp Gln Ile Arg Lys Tyr Tyr Leu Glu Lys Tyr Val Gln
            900                 905                 910
Glu Ala Leu Lys Ala Tyr Leu Ile Asp Lys Val Lys Ile Lys Gly Tyr
        915                 920                 925
Tyr Ala Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe
    930                 935                 940
Phe Thr Ser Asp Phe Arg Ala Lys Ser Ser Val Gln Phe Tyr Ser Lys
945                 950                 955                 960
Leu Ile Ser Ser Ser Gly Leu Pro Ala Glu Asn Arg Ser Pro Ala Cys
                965                 970                 975
Gly Gln Pro Ala Glu Asp Thr Asp Cys Thr Ile Cys Ser Phe Leu Val
            980                 985                 990
Glu Lys Lys Pro Leu Ile Phe Phe Gly Cys Cys Phe Ile Ser Thr Leu
        995                 1000                1005
Ala Val Leu Leu Ser Ile Thr Val Phe His His Gln Lys Arg Arg Lys
    1010                1015                1020
Phe Gln Lys Ala Arg Asn Leu Gln Asn Ile Pro Leu Lys Lys Gly His
1025                1030                1035                1040
Ser Arg Val Phe Ser
                1045
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<210> 375
<211> 3138
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of human KLB (M1-F508)- mouse KLB (P507-S1043)

<400> 375

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atgaagccag gctgtgcggc aggatctcca gggaatgaat ggattttctt cagcactgat 60
gaaataacca cacgctatag gaatacaatg tccaacgggg gattgcaaag atctgtcatc 120
ctgtcagcac ttattctgct acgagctgtt actggattct ctggagatgg aagagctata 180
tggtctaaaa atcctaattt tactccggta aatgaaagtc agctgtttct ctatgacact 240
ttccctaaaa acttttctg gggtattggg actggagcat tgcaagtgga agggagttgg 300
aagaaggatg gaaaaggacc ttctatatgg gatcatttca tccacacaca ccttaaaaat 360
gtcagcagca cgaatggttc cagtgacagt tatatttttc tggaaaaaga cttatcagcc 420
ctggatttta taggagtttc tttttatcaa ttttcaattt cctggccaag gcttttcccc 480
gatggaatag taacagttgc caacgcaaaa ggtctgcagt actacagtac tcttctggac 540
gctctagtgc ttagaaacat tgaacctata gttactttat accactggga tttgcctttg 600
gcactacaag aaaaatatgg ggggtggaaa aatgatacca taatagatat cttcaatgac 660
tatgccacat actgtttcca gatgtttggg gaccgtgtca aatattggat tacaattcac 720
aacccatatc tagtggcttg gcatgggtat gggacaggta tgcatgcccc tggagagaag 780
ggaaatttag cagctgtcta cactgtggga cacaacttga tcaaggctca ctcgaaagtt 840
tggcataact acaacacaca tttccgccca catcagaagg gttggttatc gatcacgttg 900
ggatctcatt ggatcgagcc aaaccggtcg gaaaacacga tggatatatt caaatgtcaa 960
caatccatgg tttctgtgct tggatggttt gccaacccta tccatgggga tggcgactat 1020
ccagagggga tgagaaagaa gttgttctcc gttctaccca ttttctctga agcagagaag 1080
catgagatga gaggcacagc tgatttcttt gccttttctt ttggacccaa caacttcaag 1140
cccctaaaca ccatggctaa aatgggacaa aatgtttcac ttaatttaag agaagcgctg 1200
aactggatta aactggaata caacaaccct cgaatcttga ttgctgagaa tggctggttc 1260
acagacagtc gtgtgaaaac agaagacacc acggccatct acatgatgaa gaatttcctc 1320
agccaggtgc ttcaagcaat aaggttagat gaaatacgag tgtttggtta tactgcctgg 1380
tctctcctgg atggctttga atggcaggat gcttacacca tccgccgagg attattttat 1440
gtggatttta acagtaaaca gaaagagcgg aaacctaagt cttcagcaca ctactacaaa 1500
cagatcatac gagaaaatgg ttttcctttg aaagagtcca cgccagacat gaagggtcgg 1560
ttcccctgtg atttctcttg gggagtcact gagtctgttc ttaagcccga gtttacggtc 1620
tcctccccgc agtttaccga tcctcacctg tatgtgtgga atgtcactgg caacagattg 1680
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ctctaccgag tggaaggggt aaggctgaaa acaagaccat cccagtgcac agattatgtg 1740
agcatcaaaa aacgagttga aatgttggca aaaatgaaag tcacccacta ccagtttgct 1800
ctggactgga cctctatcct tcccactggc aatctgtcca aagttaacag acaagtgtta 1860
aggtactata ggtgtgtggt gagcgaagga ctgaagctgg gcgtcttccc catggtgacg 1920
ttgtaccacc caacccactc ccatctcggc ctccccctgc cacttctgag cagtgggggg 1980
tggctaaaca tgaacacagc caaggccttc caggactacg ctgagctgtg cttccgggag 2040
ttgggggact tggtgaagct ctggatcacc atcaatgagc ctaacaggct gagtgacatg 2100
tacaaccgca cgagtaatga cacctaccgt gcagcccaca acctgatgat cgcccatgcc 2160
caggtctggc acctctatga taggcagtat aggccggtcc agcatggggc tgtgtcgctg 2220
tccttacatt gcgactgggc agaacctgcc aacccctttg tggattcaca ctggaaggca 2280
gccgagcgct tcctccagtt tgagatcgcc tggtttgcag atccgctctt caagactggc 2340
gactatccat cggttatgaa ggaatacatc gcctccaaga accagcgagg gctgtctagc 2400
tcagtcctgc cgcgcttcac cgcgaaggag agcaggctgg tgaagggtac cgtcgacttc 2460
tacgcactga accacttcac tacgaggttc gtgatacaca agcagctgaa caccaaccgc 2520
tcagttgcag acagggacgt ccagttcctg caggacatca cccgcctaag ctcgcccagc 2580
cgcctggctg taacaccctg gggagtgcgc aagctccttg cgtggatccg gaggaactac 2640
agagacaggg atatctacat cacagccaat ggcatcgatg acctggctct agaggatgat 2700
cagatccgaa agtactactt ggagaagtat gtccaggagg ctctgaaagc atatctcatt 2760
gacaaggtca aaatcaaagg ctactatgca ttcaaactga ctgaagagaa atctaagcct 2820
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ctgatcagca gcagtggcct ccccgctgag aacagaagtc ctgcgtgtgg tcagcctgcg 2940
gaagacacag actgcaccat ttgctcattt ctcgtggaga agaaaccact catcttcttc 3000
ggttgctgct tcatctccac tctggctgta ctgctatcca tcaccgtttt tcatcatcaa 3060
aagagaagaa aattccagaa agcaaggaac ttacaaaata taccattgaa gaaaggccac 3120
agcagagttt tcagctga 3138

<210> 376
<211> 1042
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse KLB (M1-F506) - human KLB(S509-S1044)

<400> 376
Met Lys Thr Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Ile Phe
 1   5   10   15
Phe Ser Ser Asp Glu Arg Asn Thr Arg Ser Arg Lys Thr Met Ser Asn
            20   25   30
Arg Ala Leu Gln Arg Ser Ala Val Leu Ser Ala Phe Val Leu Leu Arg
        35   40   45
Ala Val Thr Gly Phe Ser Gly Asp Gly Lys Ala Ile Trp Asp Lys Lys
    50   55   60
Gln Tyr Val Ser Pro Val Asn Pro Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Ser Trp Gly Val Gly Thr Gly Ala Phe Gln Val
                85   90   95
Glu Gly Ser Trp Lys Thr Asp Gly Arg Gly Pro Ser Ile Trp Asp Arg
            100   105   110
Tyr Val Tyr Ser His Leu Arg Gly Val Asn Gly Thr Asp Arg Ser Thr
        115   120   125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Leu Ala Leu Asp Phe Leu
    130   135   140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asn Gly Thr Val Ala Ala Val Asn Ala Gln Gly Leu Arg Tyr Tyr Arg
                165   170   175
Ala Leu Leu Asp Ser Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
            180   185   190
Leu Tyr His Trp Asp Leu Pro Leu Thr Leu Gln Glu Glu Tyr Gly Gly
        195   200   205
Trp Lys Asn Ala Thr Met Ile Asp Leu Phe Asn Asp Tyr Ala Thr Tyr
    210   215   220
Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225   230   235   240
Asn Pro Tyr Leu Val Ala Trp His Gly Phe Gly Thr Gly Met His Ala
                245   250   255
Pro Gly Glu Lys Gly Asn Leu Thr Ala Val Tyr Thr Val Gly His Asn

260 265 270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asp Lys Asn Phe
275 280 285
Arg Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp
290 295 300
Ile Glu Pro Asn Arg Thr Asp Asn Met Glu Asp Val Ile Asn Cys Gln
305 310 315 320
His Ser Met Ser Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
325 330 335
Asp Gly Asp Tyr Pro Glu Phe Met Lys Thr Gly Ala Met Ile Pro Glu
340 345 350
Phe Ser Glu Ala Glu Lys Glu Glu Val Arg Gly Thr Ala Asp Phe Phe
355 360 365
Ala Phe Ser Phe Gly Pro Asn Asn Phe Arg Pro Ser Asn Thr Val Val
370 375 380
Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Gln Val Leu Asn Trp
385 390 395 400
Ile Lys Leu Glu Tyr Asp Asp Pro Gln Ile Leu Ile Ser Glu Asn Gly
405 410 415
Trp Phe Thr Asp Ser Tyr Ile Lys Thr Glu Asp Thr Thr Ala Ile Tyr
420 425 430
Met Met Lys Asn Phe Leu Asn Gln Val Leu Gln Ala Ile Lys Phe Asp
435 440 445
Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Thr Leu Leu Asp Gly Phe
450 455 460
Glu Trp Gln Asp Ala Tyr Thr Thr Arg Arg Gly Leu Phe Tyr Val Asp
465 470 475 480
Phe Asn Ser Glu Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala His Tyr
485 490 495
Tyr Lys Gln Ile Ile Gln Asp Asn Gly Phe Ser Leu Lys Glu Ser Thr
500 505 510
Pro Asp Val Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly Val Thr
515 520 525
Glu Ser Val Leu Lys Pro Glu Ser Val Ala Ser Ser Pro Gln Phe Ser
530 535 540
Asp Pro His Leu Tyr Val Trp Asn Ala Thr Gly Asn Arg Leu Leu His
545 550 555 560
Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ala Gln Cys Thr Asp
565 570 575
Phe Val Asn Ile Lys Lys Gln Leu Glu Met Leu Ala Arg Met Lys Val
580 585 590
Thr His Tyr Arg Phe Ala Leu Asp Trp Ala Ser Val Leu Pro Thr Gly
595 600 605
Asn Leu Ser Ala Val Asn Arg Gln Ala Leu Arg Tyr Tyr Arg Cys Val
610 615 620
Val Ser Glu Gly Leu Lys Leu Gly Ile Ser Ala Met Val Thr Leu Tyr
625 630 635 640
Tyr Pro Thr His Ala His Leu Gly Leu Pro Glu Pro Leu Leu His Ala
645 650 655
Asp Gly Trp Leu Asn Pro Ser Thr Ala Glu Ala Phe Gln Ala Tyr Ala
660 665 670
Gly Leu Cys Phe Gln Glu Leu Gly Asp Leu Val Lys Leu Trp Ile Thr
675 680 685
Ile Asn Glu Pro Asn Arg Leu Ser Asp Ile Tyr Asn Arg Ser Gly Asn
690 695 700
Asp Thr Tyr Gly Ala Ala His Asn Leu Leu Val Ala His Ala Leu Ala
705 710 715 720
Trp Arg Leu Tyr Asp Arg Gln Phe Arg Pro Ser Gln Arg Gly Ala Val
725 730 735
Ser Leu Ser Leu His Ala Asp Trp Ala Glu Pro Ala Asn Pro Tyr Ala
740 745 750
Asp Ser His Trp Arg Ala Ala Glu Arg Phe Leu Gln Phe Glu Ile Ala
755 760 765
Trp Phe Ala Glu Pro Leu Phe Lys Thr Gly Asp Tyr Pro Ala Ala Met
770 775 780
Arg Glu Tyr Ile Ala Ser Lys His Arg Arg Gly Leu Ser Ser Ser Ala
785 790 795 800
Leu Pro Arg Leu Thr Glu Ala Glu Arg Arg Leu Leu Lys Gly Thr Val

805 810 815
Asp Phe Cys Ala Leu Asn His Phe Thr Thr Arg Phe Val Met His Glu
820 825 830
Gln Leu Ala Gly Ser Arg Tyr Asp Ser Asp Arg Asp Ile Gln Phe Leu
835 840 845
Gln Asp Ile Thr Arg Leu Ser Ser Pro Thr Arg Leu Ala Val Ile Pro
850 855 860
Trp Gly Val Arg Lys Leu Leu Arg Trp Val Arg Arg Asn Tyr Gly Asp
865 870 875 880
Met Asp Ile Tyr Ile Thr Ala Ser Gly Ile Asp Asp Gln Ala Leu Glu
885 890 895
Asp Asp Arg Leu Arg Lys Tyr Tyr Leu Gly Lys Tyr Leu Gln Glu Val
900 905 910
Leu Lys Ala Tyr Leu Ile Asp Lys Val Arg Ile Lys Gly Tyr Tyr Ala
915 920 925
Phe Lys Leu Ala Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe Phe Thr
930 935 940
Ser Asp Phe Lys Ala Lys Ser Ser Ile Gln Phe Tyr Asn Lys Val Ile
945 950 955 960
Ser Ser Arg Gly Phe Pro Phe Glu Asn Ser Ser Ser Arg Cys Ser Gln
965 970 975
Thr Gln Glu Asn Thr Glu Cys Thr Val Cys Leu Phe Leu Val Gln Lys
980 985 990
Lys Pro Leu Ile Phe Leu Gly Cys Cys Phe Phe Ser Thr Leu Val Leu
995 1000 1005
Leu Leu Ser Ile Ala Ile Phe Gln Arg Gln Lys Arg Arg Lys Phe Trp
1010 1015 1020
Lys Ala Lys Asn Leu Gln His Ile Pro Leu Lys Lys Gly Lys Arg Val
1025 1030 1035 1040
Val Ser

<210> 377
<211> 3129
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Mouse KLB (M1-F506) - human KLB(S509-S1044)

<400> 377
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gaaagaaaca cacgctctag gaaaacaatg tccaacaggg cactgcaaag atctgccgtg 120
ctgtctgcgt ttgttctgct gcgagctgtt accggcttct ccggagacgg gaaagcaata 180
tgggataaaa aacagtacgt gagtccggta aacccaagtc agctgttcct ctatgacact 240
ttccctaaaa acttttcctg gggcgttggg accggagcat ttcaagtgga agggagttgg 300
aagacagatg gaagaggacc ctcgatctgg gatcggtacg tctactcaca cctgagaggt 360
gtcaacggca cagacagatc cactgacagt tacatctttc tggaaaaaga cttgttggct 420
ctggattttt taggagtttc tttttatcag ttctcaatct cctggccacg gttgtttccc 480
aatggaacag tagcagcagt gaatgcgcaa ggtctccggt actaccgtgc acttctggac 540
tcgctggtac ttaggaatat cgagcccatt gttaccttgt accattggga tttgcctctg 600
acgctccagg aagaatatgg gggctggaaa aatgcaacta tgatagatct cttcaacgac 660
tatgccacat actgcttcca gacctttgga gaccgtgtca aatattggat tacaattcac 720
aacccttacc ttgttgcttg gcatgggttt ggcacaggta tgcatgcacc aggagagaag 780
ggaaatttaa cagctgtcta cactgtggga cacaacctga tcaaggcaca ttcgaaagtg 840
tggcataact acgacaaaaa cttccgccct catcagaagg gttggctctc catcaccttg 900
gggtcccatt ggatagagcc aaacagaaca gacaacatgg aggacgtgat caactgccag 960
cactccatgt cctctgtgct tggatggttc gccaacccca tccacgggga cggcgactac 1020
cctgagttca tgaagacggg cgccatgatc cccgagttct ctgaggcaga gaaggaggag 1080
gtgaggggca cggctgattt ctttgccttt tccttcgggc ccaacaactt caggccctca 1140
aacaccgtgg tgaaaatggg acaaaatgta tcactcaact taaggcaggt gctgaactgg 1200
attaaactgg aatacgatga ccctcaaatc ttgatttcgg agaacggctg gttcacagat 1260
agctatataa agacagagga caccacggcc atctacatga tgaagaattt cctaaaccag 1320
gttcttcaag caataaaatt tgatgaaatc cgcgtgtttg gttatacggc ctggactctc 1380
ctggatggct ttgagtggca ggatgcctat acgacccgac gagggctgtt ttatgtggac 1440
tttaacagtg agcagaaaga gaggaaaccc aagtcctcgg ctcattacta caagcagatc 1500
atacaagaca acggcttctc tttaaaagag tccacgccag atgtgcaggg ccagtttccc 1560
tgtgacttct cctggggtgt cactgaatct gttcttaagc ccgagtctgt ggcttcgtcc 1620

ccacagttca gcgatcctca tctgtacgtg tggaacgcca ctggcaacag actgttgcac 1680
cgagtggaag gggtgaggct gaaaacacga cccgctcaat gcacagattt tgtaaacatc 1740
aaaaaacaac ttgagatgtt ggcaagaatg aaagtcaccc actaccggtt tgctctggat 1800
tgggcctcgg tccttcccac tggcaacctg tccgcggtga accgacaggc cctgaggtac 1860
tacaggtgcg tggtcagtga ggggctgaag cttggcatct ccgcgatggt caccctgtat 1920
tatccgaccc acgcccacct aggcctcccc gagcctctgt tgcatgccga cgggtggctg 1980
aacccatcga cggccgaggc cttccaggcc tacgctgggc tgtgcttcca ggagctgggg 2040
gacctggtga agctctggat caccatcaac gagcctaacc ggctaagtga catctacaac 2100
cgctctggca acgacaccta cggggcggcg cacaacctgc tggtggccca cgccctggcc 2160
tggcgcctct acgaccggca gttcaggccc tcacagcgcg gggccgtgtc gctgtcgctg 2220
cacgcggact gggcggaacc cgccaacccc tatgctgact cgcactggag ggcggccgag 2280
cgcttcctgc agttcgagat cgcctggttc gccgagccgc tcttcaagac cggggactac 2340
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atggacattt acatcaccgc cagtggcatc gacgaccagg ctctggagga tgaccggctc 2700
cggaagtact acctagggaa gtaccttcag gaggtgctga aagcatacct gattgataaa 2760
gtcagaatca aaggctatta tgcattcaaa ctggctgaag agaaatctaa acccagattt 2820
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agcagcaggg gcttcccttt tgagaacagt agttctagat gcagtcagac ccaagaaaat 2940
acagagtgca ctgtctgctt attccttgtg cagaagaaac cactgatatt cctgggttgt 3000
tgcttcttct ccaccctggt tctactctta tcaattgcca tttttcaaag gcagaagaga 3060
agaaagtttt ggaaagcaaa aaacttacaa cacataccat taaagaaagg caagagagtt 3120
gttagctag 3129

<210> 378
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR1

<400> 378
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1   5   10   15
Ser Val Lys Val Ser Cys Lys Ala Ser
            20   25

<210> 379
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 379
Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 380
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 380
Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Arg Thr Ala Tyr Met Glu

 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 381
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VH FR3

<400> 381
Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
 1   5   10   15
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            20   25   30

<210> 382
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR1

<400> 382
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys
            20

<210> 383
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR1

<400> 383
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys
            20

<210> 384
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR1

<400> 384
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1   5   10   15
Glu Arg Ala Thr Leu Ser Cys
            20

<210> 385
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 385
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 386
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 386
Trp Asn Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 387
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 387
Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 388
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 388
Trp Asn Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 389
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 389
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 1   5   10   15

<210> 390
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized Anti-Beta Klotho VL FR2

<400> 390
Trp Asn Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 1   5   10   15

<210> 391
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 391
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
 1   5   10   15

<210> 392
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR2

<400> 392
Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr
 1   5   10   15

<210> 393
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 393
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            20   25   30

<210> 394
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 394
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
            20   25   30

<210> 395
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 395
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
            20   25   30

<210> 396
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 396
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys
            20   25   30

<210> 397
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 397
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Glu Glu Asp Phe Ala Thr Tyr Tyr Cys
            20   25   30

<210> 398
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 398
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Val Gln Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
            20   25   30

<210> 399
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 399
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 400
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 400
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 401
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 401
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Ala Ala Val Tyr Tyr Cys
            20   25   30

<210> 402
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 402
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Leu Glu Glu Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 403
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR3

<400> 403
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Val Glu Glu Glu Asp Phe Ala Val Tyr Tyr Cys
            20   25   30

<210> 404
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> Humanized Anti-Beta Klotho VL FR3

<400> 404
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Arg Val Glu Glu Glu Asp Ala Ala Val Tyr Tyr Cys
            20   25   30

<210> 405
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR4

<400> 405
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 1   5   10

<210> 406
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR4

<400> 406
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 1   5   10

<210> 407
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized Anti-Beta Klotho VL FR4

<400> 407
Phe Gly Gly Gln Thr Lys Leu Glu Ile Lys
 1   5   10

<210> 408
<211> 1042
<212> PRT
<213> Cricetulus griseus

<220>
<223> hamster beta klotho

<400> 408
Met Lys Ala Gly Cys Ala Ala Gly Ser Pro Gly Asn Glu Trp Ile Phe
 1   5   10   15
Leu Ser Ser Tyr Glu Arg Asn Thr Arg Ser Lys Lys Thr Met Ser Asn
            20   25   30
Arg Ala Leu Gln Arg Ser Val Val Leu Ser Ala Phe Val Leu Leu Arg
        35   40   45
Ala Val Thr Gly Leu Ser Gly Asp Gly Lys Ala Ile Trp Asp Lys Lys
    50   55   60
Gln Tyr Val Ser Pro Val Asn Ala Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Val Gly Thr Gly Ala Phe Gln Val

```
                85                  90                  95
Glu Gly Asn Trp Gln Ala Asp Gly Arg Gly Pro Ser Ile Trp Asp Arg
            100                 105                 110
Phe Ile Tyr Thr His Leu Arg Asp Val Ser Ile Thr Glu Lys Ser Ala
        115                 120                 125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Leu Ala Leu Asp Phe Leu
    130                 135                 140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145                 150                 155                 160
Asn Gly Thr Val Ala Ser Val Asn Ala Lys Gly Leu Gln Tyr Tyr Asn
                165                 170                 175
Lys Leu Leu Asp Ser Leu Ile Leu Arg Asn Ile Glu Pro Val Val Thr
            180                 185                 190
Leu Tyr His Trp Asp Leu Pro Leu Ala Leu Gln Glu Asp Tyr Gly Gly
        195                 200                 205
Trp Lys Asn Ala Thr Met Ile Asp Leu Phe Asn Asp Tyr Ala Thr Tyr
    210                 215                 220
Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225                 230                 235                 240
Asn Pro Tyr Leu Val Ala Trp His Gly Phe Ala Thr Gly Met His Ala
                245                 250                 255
Pro Gly Glu Thr Gly Asn Leu Thr Ala Val Tyr Ile Val Gly His Asn
            260                 265                 270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asp Lys Asn Phe
        275                 280                 285
Arg Pro His Gln Lys Gly Leu Leu Ser Ile Thr Leu Gly Ser His Trp
    290                 295                 300
Ile Glu Pro Asn Lys Thr Glu Asn Met Ala Asp Thr Ile Ser Cys Gln
305                 310                 315                 320
His Ser Met Ala Phe Val Leu Gly Trp Phe Ala Asn Pro Ile His Ala
                325                 330                 335
Asp Gly Asp Tyr Pro Glu Phe Met Lys Thr Leu Ser Thr Met Pro Val
            340                 345                 350
Phe Ser Glu Ala Glu Lys Glu Glu Val Arg Gly Thr Ala Asp Phe Phe
        355                 360                 365
Ala Phe Ser Phe Gly Pro Asn Asn Phe Arg Pro Ser Asn Thr Val Val
    370                 375                 380
Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Gln Val Leu Asn Trp
385                 390                 395                 400
Ile Lys Leu Glu Tyr Asp Asn Pro Arg Ile Leu Ile Ser Glu Asn Gly
                405                 410                 415
Trp Phe Thr Asp Ser Asp Ile Lys Thr Glu Asp Thr Thr Ala Ile Tyr
            420                 425                 430
Met Met Lys His Phe Leu Asn Gln Val Leu Gln Ala Ile Gln Phe Asp
        435                 440                 445
Glu Ile Arg Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp Gly Phe
    450                 455                 460
Glu Trp Gln Tyr Ala Tyr Thr Ser Arg Arg Gly Leu Phe Tyr Val Asp
465                 470                 475                 480
Phe Asn Ser Glu Gln Lys Glu Arg Lys Pro Lys Thr Ser Ala His Tyr
                485                 490                 495
Tyr Lys Gln Ile Ile Gln Glu Asn Gly Phe Pro Leu Lys Glu Ser Thr
            500                 505                 510
Pro Asp Met Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly Val Thr
        515                 520                 525
Glu Ser Val Leu Lys Pro Glu Phe Met Val Ser Ser Pro Gln Phe Thr
    530                 535                 540
Asp Pro His Leu Tyr Val Trp Asn Ala Thr Gly Asn Arg Leu Leu Gln
545                 550                 555                 560
Arg Val Glu Gly Val Arg Leu Lys Thr Lys Pro Ser His Cys Thr Asp
                565                 570                 575
Tyr Val Ser Ile Lys Lys Arg Val Glu Met Leu Ala Lys Met Lys Val
            580                 585                 590
Thr His Tyr Gln Phe Ala Leu Asp Trp Ala Thr Ile Leu Pro Thr Gly
        595                 600                 605
Asn Leu Ser Glu Val Asn Arg Gln Val Leu Arg Tyr Tyr Arg Cys Val
    610                 615                 620
Val Ser Glu Gly Leu Lys Leu Gly Val Ser Pro Met Val Thr Leu Tyr
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625 630 635 640
His Pro Thr His Ser His Leu Gly Leu Pro Glu Pro Leu Leu Asn Ser
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Gly Gly Trp Leu Asn Thr Tyr Thr Ala Lys Ala Phe Gln Asp Tyr Ala
660 665 670
Gly Leu Cys Phe Gln Glu Leu Gly Asp Leu Val Lys Leu Trp Ile Thr
675 680 685
Ile Asn Glu Pro Asn Arg Leu Ser Asp Met Tyr Asn Arg Thr Ser Asn
690 695 700
Asp Thr Tyr Arg Ala Ala His Asn Leu Met Ile Ala His Ala Gln Val
705 710 715 720
Trp Arg Leu Tyr Asp Arg Gln Tyr Arg Pro Val Gln His Gly Ala Val
725 730 735
Ser Leu Ser Leu His Ser Asp Trp Val Glu Pro Ala Asn Pro Tyr Val
740 745 750
Asp Ser His Trp Lys Ala Ala Glu Arg Phe Leu Leu Phe Glu Ile Ala
755 760 765
Trp Phe Ala Asp Pro Leu Phe Lys Thr Gly Asp Tyr Pro Leu Ala Met
770 775 780
Lys Glu Tyr Ile Ala Ser Lys Asn Gln Gln Gly Leu Ser Arg Ser Val
785 790 795 800
Leu Pro Arg Phe Thr Pro Glu Glu Ser Arg Leu Val Lys Gly Thr Ile
805 810 815
Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Ile His Lys
820 825 830
Gln Leu Asn Ser Ser Arg Ser Met Ala Asp Arg Asp Val Gln Phe Leu
835 840 845
Gln Asp Ile Thr Arg Leu Ser Ser Pro Ser Arg Leu Ala Val Met Pro
850 855 860
Trp Gly Ala Arg Lys Leu Leu Gly Trp Ile Gln Arg Asn Tyr Gly Asp
865 870 875 880
Met Asp Ile Tyr Ile Thr Ala Asn Gly Ile Asp Asp Leu Ala Leu Glu
885 890 895
Asn Asp Gly Ile Arg Lys Tyr Tyr Leu Glu Lys Tyr Ile Gln Glu Ala
900 905 910
Leu Lys Ala Tyr Leu Ile Asp Lys Val Lys Ile Lys Gly Tyr Tyr Ala
915 920 925
Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe Phe Thr
930 935 940
Ser Asp Phe Lys Ala Lys Ser Ser Val Glu Phe Tyr Ser Lys Leu Ile
945 950 955 960
Ser Arg Ser Gly Phe Pro Ser Glu Thr Ser Asn Pro Ala Cys Gly Gln
965 970 975
Pro Pro Glu Asp Thr Asp Cys Thr Ile Cys Ser Phe Phe Thr Gln Lys
980 985 990
Lys Ser Leu Ile Phe Phe Gly Cys Cys Phe Ile Ser Thr Leu Ala Val
995 1000 1005
Leu Leu Ser Ile Thr Ile Phe His His Arg Lys Arg Arg Phe His Lys
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Ser Lys Asn Leu Glu Asn Ile Pro Leu Lys Glu Gly His Ser Arg Val
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Leu Ser

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<211> 3042
<212> DNA
<213> Cricetulus griseus

<220>
<223> Coding sequence of hamster beta klotho

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ggaactggag catttcaagt ggaagggaat tggcaggcag acggaagagg accctcgatt 240

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aatataccat tgaaggaagg ccacagtaga gttcttagct aa 3042

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<211> 1044
<212> PRT
<213> Oryctolagus cuniculus

<220>
<223> Rabbit beta klotho

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Gly Arg Leu Arg Arg Ser Val Met Leu Ser Ala Phe Ile Leu Leu Arg
        35   40   45
Ala Val Thr Gly Phe Pro Gly Asp Gly Arg Ala Val Trp Ser Gln Asn
    50   55   60
Pro Asn Leu Ser Pro Val Asn Glu Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Val Gly Thr Gly Ala Phe Gln Val

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Glu Gly Ser Trp Lys Lys Asp Gly Lys Gly Leu Ser Val Trp Asp His
            100                 105                 110
Phe Ile Ala Thr His Leu Asn Val Ser Ser Arg Asp Gly Ser Ser Asp
        115                 120                 125
Ser Tyr Ile Phe Leu Glu Lys Asp Leu Ser Ala Leu Asp Phe Leu Gly
    130                 135                 140
Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro Asp
145                 150                 155                 160
Gly Thr Val Ala Val Ala Asn Ala Lys Gly Leu Gln Tyr Tyr Asn Arg
                165                 170                 175
Leu Leu Asp Ser Leu Leu Leu Arg Asn Ile Glu Pro Val Val Thr Leu
            180                 185                 190
Tyr His Trp Asp Leu Pro Trp Ala Leu Gln Glu Lys Tyr Gly Gly Trp
        195                 200                 205
Lys Asn Glu Thr Leu Ile Asp Leu Phe Asn Asp Tyr Ala Thr Tyr Cys
    210                 215                 220
Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His Asn
225                 230                 235                 240
Pro Tyr Leu Val Ala Trp His Gly Tyr Gly Thr Gly Leu His Ala Pro
                245                 250                 255
Gly Glu Lys Gly Asn Val Ala Ala Val Tyr Thr Val Gly His Asn Leu
            260                 265                 270
Leu Lys Ala His Ser Lys Val Trp His Asn Tyr Asn Arg Asn Phe Arg
        275                 280                 285
Pro His Gln Lys Gly Trp Leu Ser Ile Thr Leu Gly Ser His Trp Ile
    290                 295                 300
Glu Pro Asn Arg Ala Glu Ser Ile Val Asp Ile Leu Lys Cys Gln Gln
305                 310                 315                 320
Ser Met Val Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly Asp
                325                 330                 335
Gly Asp Tyr Pro Glu Val Met Thr Lys Lys Leu Leu Ser Val Leu Pro
            340                 345                 350
Ala Phe Ser Glu Ala Glu Lys Asn Glu Val Arg Gly Thr Ala Asp Phe
        355                 360                 365
Phe Ala Phe Ser Phe Gly Pro Asn Asn Phe Lys Pro Leu Asn Thr Met
    370                 375                 380
Ala Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Gln Val Leu Asn
385                 390                 395                 400
Trp Ile Lys Leu Glu Tyr Gly Asn Pro Arg Ile Leu Ile Ala Glu Asn
                405                 410                 415
Gly Trp Phe Thr Asp Ser Tyr Val Gln Thr Glu Asp Thr Thr Ala Ile
            420                 425                 430
Tyr Met Met Lys Asn Phe Leu Asn Gln Val Leu Gln Ala Ile Arg Leu
        435                 440                 445
Asp Gly Val Arg Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp Gly
    450                 455                 460
Phe Glu Trp Gln Asp Ala Tyr Asn Thr Arg Arg Gly Leu Phe Tyr Val
465                 470                 475                 480
Asp Phe Asn Ser Glu Gln Arg Glu Arg Arg Pro Lys Ser Ser Ala His
                485                 490                 495
Tyr Tyr Lys Gln Val Ile Gly Glu Asn Gly Phe Thr Leu Arg Glu Ala
            500                 505                 510
Thr Pro Asp Leu Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly Val
        515                 520                 525
Thr Glu Ser Val Leu Lys Pro Glu Ser Val Ala Ser Ser Pro Gln Phe
    530                 535                 540
Ser Asp Pro His Leu Tyr Val Trp Asn Ala Thr Gly Asn Arg Met Leu
545                 550                 555                 560
His Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ala Gln Cys Thr
                565                 570                 575
Asp Phe Ile Thr Ile Lys Lys Gln Leu Glu Met Leu Ala Arg Met Lys
            580                 585                 590
Val Thr His Phe Arg Phe Ala Leu Asp Trp Ala Ser Val Leu Pro Thr
        595                 600                 605
Gly Asn Leu Ser Glu Val Asn Arg Gln Ala Leu Arg Tyr Tyr Arg Cys
    610                 615                 620
Val Val Thr Glu Gly Leu Lys Leu Asn Ile Ser Pro Met Val Thr Leu
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625 630 635 640
Tyr Tyr Pro Thr His Ala His Leu Gly Leu Pro Ala Pro Leu Leu His
645 650 655
Ser Gly Gly Trp Leu Asp Pro Ser Thr Ala Lys Ala Phe Arg Asp Tyr
660 665 670
Ala Gly Leu Cys Phe Arg Glu Leu Gly Asp Leu Val Lys Leu Trp Ile
675 680 685
Thr Ile Asn Glu Pro Asn Arg Leu Ser Asp Val Tyr Asn Arg Thr Ser
690 695 700
Asn Asp Thr Tyr Gln Ala Ala His Asn Leu Leu Ile Ala His Ala Leu
705 710 715 720
Val Trp His Leu Tyr Asp Arg Gln Tyr Arg Pro Ser Gln Arg Gly Ala
725 730 735
Leu Ser Leu Ser Leu His Ser Asp Trp Ala Glu Pro Ala Asn Pro Tyr
740 745 750
Val Ala Ser His Trp Gln Ala Ala Glu Arg Phe Leu Gln Phe Glu Ile
755 760 765
Ala Trp Phe Ala Glu Pro Leu Phe Lys Thr Gly Asp Tyr Pro Val Ala
770 775 780
Met Arg Glu Tyr Ile Ala Ser Lys Thr Arg Arg Gly Leu Ser Ser Ser
785 790 795 800
Val Leu Pro Arg Phe Ser Asp Ala Glu Arg Arg Leu Val Lys Gly Ala
805 810 815
Ala Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Met His
820 825 830
Glu Gln Gln Asn Gly Ser Arg Tyr Asp Ser Asp Arg Asp Val Gln Phe
835 840 845
Leu Gln Asp Ile Thr Arg Leu Ala Ser Pro Ser Arg Leu Ala Val Met
850 855 860
Pro Trp Gly Glu Gly Lys Leu Leu Arg Trp Met Arg Asn Asn Tyr Gly
865 870 875 880
Asp Leu Asp Val Tyr Ile Thr Ala Asn Gly Ile Asp Asp Gln Ala Leu
885 890 895
Gln Asn Asp Gln Leu Arg Gln Tyr Tyr Leu Glu Lys Tyr Val Gln Glu
900 905 910
Ala Leu Lys Ala Tyr Leu Ile Asp Lys Ile Lys Ile Lys Gly Tyr Tyr
915 920 925
Ala Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe Phe
930 935 940
Thr Ser Asp Phe Lys Ala Lys Ser Ser Ile Gln Phe Tyr Asn Lys Leu
945 950 955 960
Ile Thr Ser Asn Gly Phe Pro Ser Glu Asn Gly Gly Pro Arg Cys Asn
965 970 975
Gln Thr Gln Gly Asn Pro Glu Cys Thr Val Cys Leu Leu Leu Leu Gln
980 985 990
Lys Lys Pro Leu Ile Phe Phe Ser Cys Cys Phe Phe Cys Thr Leu Val
995 1000 1005
Leu Leu Ser Ser Ile Thr Ile Phe His Arg Arg Lys Arg Arg Lys Phe
1010 1015 1020
Trp Lys Ala Lys Asp Leu Gln His Ile Pro Leu Lys Lys Gly His Lys
1025 1030 1035 1040
Arg Val Leu Ser

<210> 411
<211> 5737
<212> DNA
<213> Oryctolagus cuniculus

<220>
<223> Coding sequence of Rabbit beta klotho

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aacgatgtcc agcggacgcc tgcggagatc tgtcatgctg tcagccttca tcctgctgcg 180
agccgtgact gggttccccg gagacggaag agctgtatgg tcgcaaaatc ctaatttgag 240

tccggtaaac gaaagtcagc tgtttctcta tgacactttc ccaaaaaact ttttctgggg 300
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gtctaattta ttccaaataa actgatttac gccaata 5737

<210> 412
<211> 1045
<212> PRT
<213> Canis lupus familiaris

<220>
<223> Dog beta klotho

<400> 412
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Leu Ser Thr Asp Glu Ser Asn Thr His Tyr Arg Lys Thr Met Cys Asn
            20   25   30
His Gly Leu Gln Arg Ser Val Ile Leu Ser Ala Phe Ile Leu Leu Gly
        35   40   45
Ala Val Pro Gly Phe Ser Gly Asp Gly Arg Ala Ile Trp Ser Lys Asn
    50   55   60
Pro His Phe Ser Pro Val Asn Glu Ser Gln Leu Phe Leu Tyr Asp Thr
65   70   75   80
Phe Pro Lys Asn Phe Phe Trp Gly Val Gly Thr Gly Ala Phe Gln Val
                85   90   95
Glu Gly Asn Trp Lys Thr Asp Gly Lys Gly Pro Ser Ile Trp Asp His
            100   105   110
Phe Ile His Thr His Leu Lys Asn Val Asn Ser Met Asn Ser Ser Ser
        115   120   125
Asp Ser Tyr Ile Phe Leu Glu Lys Asp Leu Ser Ala Leu Asp Phe Ile
    130   135   140
Gly Val Ser Phe Tyr Gln Phe Ser Ile Ser Trp Pro Arg Leu Phe Pro
145   150   155   160
Asp Gly Ile Ala Ala Val Ala Asn Ala Lys Gly Leu Gln Tyr Tyr Asn
                165   170   175
Ser Leu Leu Asp Ala Leu Val Leu Arg Asn Ile Glu Pro Ile Val Thr
            180   185   190
Leu Tyr His Trp Asp Leu Pro Leu Ala Leu Gln Glu Lys Tyr Gly Gly
        195   200   205
Trp Lys Asn Glu Thr Ile Thr Asp Ile Phe Asn Asp Tyr Ala Thr Tyr
    210   215   220
Cys Phe Gln Thr Phe Gly Asp Arg Val Lys Tyr Trp Ile Thr Ile His
225   230   235   240
Asn Pro Tyr Leu Val Ala Trp His Gly Tyr Gly Thr Gly Met His Ala
                245   250   255

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Pro Gly Glu Lys Gly Asn Leu Ala Ala Val Tyr Thr Val Gly His Asn
            260                 265                 270
Leu Ile Lys Ala His Ser Lys Val Trp His Asn Tyr Asn Thr Asn Phe
        275                 280                 285
Arg Pro Tyr Gln Lys Gly Leu Leu Ser Ile Thr Leu Gly Ser His Trp
    290                 295                 300
Ile Glu Pro Asn Arg Ser Glu Asn Met Met Asp Ile Leu Lys Cys Gln
305                 310                 315                 320
Gln Ser Met Val Ser Val Leu Gly Trp Phe Ala Asn Pro Ile His Gly
                325                 330                 335
Asn Gly Asp Tyr Pro Glu Val Met Lys Lys Lys Leu Leu Ser Thr Leu
            340                 345                 350
Pro Leu Phe Ser Glu Ala Glu Lys Asn Glu Val Arg Gly Thr Ala Asp
        355                 360                 365
Phe Phe Ala Phe Ser Phe Gly Pro Asn Asn Phe Lys Pro Gln Asn Thr
    370                 375                 380
Met Ala Lys Met Gly Gln Asn Val Ser Leu Asn Leu Arg Glu Val Leu
385                 390                 395                 400
Asn Trp Ile Lys Leu Glu Tyr Gly Asn Pro Arg Ile Leu Ile Ala Glu
                405                 410                 415
Asn Gly Trp Phe Thr Asp Ser His Val Lys Thr Glu Asp Thr Thr Ala
            420                 425                 430
Ile Tyr Met Met Lys Asn Phe Leu Asn Gln Val Leu Gln Ala Ile Arg
        435                 440                 445
Phe Asp Glu Ile Gln Val Phe Gly Tyr Thr Ala Trp Ser Leu Leu Asp
    450                 455                 460
Gly Phe Glu Trp Gln Asp Ala Tyr Ser Thr Arg Arg Gly Leu Phe Tyr
465                 470                 475                 480
Val Asp Phe Asn Ser Lys Gln Lys Glu Arg Lys Pro Lys Ser Ser Ala
                485                 490                 495
Tyr Tyr Tyr Lys Gln Ile Ile Gln Glu Asn Gly Phe Thr Phe Lys Glu
            500                 505                 510
Ser Thr Pro Asp Val Gln Gly Gln Phe Pro Cys Asp Phe Ser Trp Gly
        515                 520                 525
Val Thr Glu Ser Val Leu Lys Pro Lys Val Val Ala Ser Ser Pro Gln
    530                 535                 540
Phe Ser Asp Pro His Leu Tyr Val Trp Asn Val Thr Gly Asn Arg Leu
545                 550                 555                 560
Leu His Arg Val Glu Gly Val Arg Leu Lys Thr Arg Pro Ala Gln Cys
                565                 570                 575
Thr Asp Phe Val Ser Ile Lys Arg Gln Leu Glu Met Leu Ala Arg Met
            580                 585                 590
Asn Val Thr His Tyr Arg Phe Ala Leu Asp Trp Pro Ser Ile Leu Pro
        595                 600                 605
Thr Gly Asn Leu Ser Thr Val Asn Arg Gln Ala Leu Arg Tyr Tyr Arg
    610                 615                 620
Cys Val Val Ser Glu Ser Leu Lys Leu Ser Ile Ser Pro Met Val Thr
625                 630                 635                 640
Leu Tyr Tyr Pro Thr His Ala His Leu Gly Leu Pro Ser Pro Leu Leu
                645                 650                 655
His Ser Gly Gly Trp Leu Asn Ala Ser Thr Ala Arg Ala Phe Gln Asp
            660                 665                 670
Tyr Ala Gly Leu Cys Phe Gln Glu Leu Gly Asp Leu Val Lys Leu Trp
        675                 680                 685
Ile Thr Ile Asn Glu Pro Asn Arg Leu Ser Asp Val Tyr Ser His Thr
    690                 695                 700
Ser Ser Asp Thr Tyr Arg Ala Ala His Asn Leu Leu Ile Ala His Ala
705                 710                 715                 720
Leu Val Trp His Leu Tyr Asp Arg Arg Tyr Arg Pro Ala Gln Arg Gly
                725                 730                 735
Ala Val Ser Leu Ser Leu His Ser Asp Trp Ala Glu Pro Ala Asn Pro
            740                 745                 750
Tyr Ala Asp Ser His Trp Lys Ala Ala Glu Arg Phe Leu Gln Phe Glu
        755                 760                 765
Ile Ala Trp Phe Ala Glu Pro Leu Phe Lys Thr Gly Asp Tyr Pro Pro
    770                 775                 780
Ala Met Arg Glu Tyr Ile Ala Ser Lys Asn Arg Gln Gly Leu Ser Arg
785                 790                 795                 800
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Ser Thr Leu Pro Arg Phe Thr Asp Glu Glu Arg Arg Leu Val Lys Gly
                805                 810                 815
Ala Ala Asp Phe Tyr Ala Leu Asn His Phe Thr Thr Arg Phe Val Met
            820                 825                 830
His Ala Arg Gln Asn Gly Ser Arg Tyr Asp Ala Asp Arg Asp Val Gln
        835                 840                 845
Phe Leu Gln Asp Ile Thr Cys Leu Ser Ser Pro Ser Arg Leu Ala Val
    850                 855                 860
Leu Pro Trp Gly Glu Arg Lys Val Leu Arg Trp Ile Gln Lys Asn Tyr
865                 870                 875                 880
Gly Asp Val Asp Val Tyr Ile Thr Ala Ser Gly Ile Asp Asp Gln Ser
                885                 890                 895
Leu Glu Asn Asp Glu Leu Arg Lys Tyr Tyr Leu Glu Lys Tyr Ile Gln
            900                 905                 910
Glu Ala Leu Lys Ala His Leu Ile Asp Lys Val Lys Val Lys Gly Tyr
        915                 920                 925
Tyr Ala Phe Lys Leu Thr Glu Glu Lys Ser Lys Pro Arg Phe Gly Phe
    930                 935                 940
Phe Thr Ser Glu Phe Lys Ala Lys Ser Ser Val Gln Leu Tyr Asn Lys
945                 950                 955                 960
Leu Ile Ser Asn Ser Gly Phe Pro Ser Glu Asn Arg Ser Pro Arg Cys
                965                 970                 975
Ser Glu Thr Gln Arg Asn Thr Glu Cys Met Val Cys Leu Phe Leu Val
            980                 985                 990
Gln Lys Lys Pro Leu Ile Phe Phe Ser Cys Cys Phe Phe Ser Thr Leu
        995                 1000                1005
Val Leu Leu Ser Ser Ile Thr Ile Leu His Lys Arg Lys Arg Arg Lys
    1010                1015                1020
Ile Trp Lys Ala Lys Asn Leu Gln His Ile Pro Leu Lys Lys Ser Lys
1025                1030                1035                1040
Asn Ser Leu Gln Ser
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<210> 413
<211> 4350
<212> DNA
<213> Canis lupus familiaris

<220>
<223> Coding sequence of dog beta klotho

<400> 413
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caacacacac tataggaaaa caatgtgcaa ccacgggcta cagagatctg tcatcctgtc 180
agcatttatt ctcctaggag ctgttcctgg attctctgga gacggaagag ctatatggtc 240
taaaaatcct cattttagtc cggtaaatga aagtcagctg tttctctatg acacttttcc 300
taaaaacttt ttttggggcg ttgggactgg agcatttcaa gtggaaggga attggaagac 360
agatggaaaa ggaccctcta tatgggatca tttcatccac acacacctta aaaatgtcaa 420
cagcatgaat agttccagtg acagttacat ttttctggaa aaagacctat cagccctgga 480
ttttatcgga gtttcttttt atcaattttc aatttcctgg ccaaggcttt tccccgatgg 540
aatagcagca gttgccaacg caaaaggtct ccagtactac aattctcttc tcgatgctct 600
agtacttagg aacattgaac ctatagttac tttataccat tgggatttgc ctttggcact 660
acaagaaaaa tatgggggt ggaaaaatga aaccataacg gatatcttca atgactatgc 720
cacctactgt ttccagacgt tcggggatcg tgtcaaatac tggattacaa ttcacaatcc 780
atatctagtt gcttggcatg ggtatgggac aggtatgcac gcgcctggag agaagggaaa 840
cttagcagct gtctacactg tgggacacaa cctaatcaag gctcattcga aagtttggca 900
taactacaac acaaatttcc gcccatatca gaagggtttg ttatcaatca cgttgggatc 960
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cctggatggc tttgaatggc aggatgctta ctccactcgc cgaggattat tttatgtgga 1500
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gctgggatta agtaaatacg aactgggagt ttgacttttt tgaactctgt gcttgattta 4260
ttcactgtat tctaaatttt aaggaaaacc tgaatgtaaa cccattcata ccctttcttt 4320
gggttagtaa acatttaacc acccatttca 4350

<210> 414
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H23v1-69

<400> 414
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45
Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60
Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Ser Asp Tyr Tyr Gly Ser Arg Ser Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 415
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FGFR1 beta-IIIc, NP_075594.1

<400> 415
Arg Pro Ser Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
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20 25 30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
35 40 45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
50 55 60
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
65 70 75 80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
85 90 95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
100 105 110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
115 120 125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
130 135 140
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
145 150 155 160
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
165 170 175
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
180 185 190
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
195 200 205
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
210 215 220
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
245 250 255
Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
260 265 270
Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
275 280 285
Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
290 295 300
Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
305 310 315 320
Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
325 330 335
Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
340 345 350
Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
355 360 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
370 375 380
Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
385 390 395 400
Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu

405 410 415
Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
450 455 460
Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
465 470 475 480
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
485 490 495
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
500 505 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
515 520 525
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
530 535 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
580 585 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
645 650 655
Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
660 665 670
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
675 680 685
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
690 695 700
Gly Gly Leu Lys Arg Arg
705 710

<210> 416
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> mouse-FGFR1 (R22-E287) (Beta-IIIc, NP_001073378) fused to human FGFR1 (I286-R731, NP_075594)

<400> 416
Arg Pro Ala Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
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Asp Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp
20 25 30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
35 40 45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
50 55 60
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
65 70 75 80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
85 90 95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
100 105 110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
115 120 125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile

130 135 140
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
145 150 155 160
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
165 170 175
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
180 185 190
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
195 200 205
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
210 215 220
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
245 250 255
Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
260 265 270
Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
275 280 285
Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
290 295 300
Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
305 310 315 320
Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
325 330 335
Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
340 345 350
Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
355 360 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
370 375 380
Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
385 390 395 400
Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
405 410 415
Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
450 455 460
Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
465 470 475 480
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
485 490 495
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
500 505 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
515 520 525
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
530 535 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
580 585 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
645 650 655
Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
660 665 670
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro

675 680 685
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
690 695 700
Gly Gly Leu Lys Arg Arg
705 710

<210> 417
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> hamster-FGFR1 (R54-E319) (Beta-IIIc) XP_007610900.1
fused to human FGFR1 (I286-R731, NP_075594)

<400> 417
Arg Pro Ala Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
1 5 10 15
Asp Asp Asp Asp Asp Asp Asp Ser Ser Glu Glu Lys Glu Thr Asp
20 25 30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
35 40 45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
50 55 60
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
65 70 75 80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
85 90 95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
100 105 110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
115 120 125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
130 135 140
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
145 150 155 160
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
165 170 175
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
180 185 190
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
195 200 205
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
210 215 220
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
245 250 255
Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
260 265 270
Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
275 280 285
Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
290 295 300
Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
305 310 315 320
Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
325 330 335
Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
340 345 350
Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
355 360 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
370 375 380
Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
385 390 395 400
Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu

405 410 415
Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
450 455 460
Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
465 470 475 480
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
485 490 495
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
500 505 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
515 520 525
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
530 535 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
580 585 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
645 650 655
Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
660 665 670
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
675 680 685
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
690 695 700
Gly Gly Leu Lys Arg Arg
705 710

<210> 418
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> dog-FGFR1 (R22-E287) (Beta-IIIc), XP_005629909.1 fused to human FGFR1 (I286-R731, NP_075594)

<400> 418
Arg Pro Ala Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
1 5 10 15
Asp Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp
20 25 30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
35 40 45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
50 55 60
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
65 70 75 80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
85 90 95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
100 105 110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
115 120 125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile

130 135 140

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

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
165 170 175

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
180 185 190

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
195 200 205

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
210 215 220

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240

Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Ala
245 250 255

Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
260 265 270

Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
275 280 285

Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
290 295 300

Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
305 310 315 320

Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
325 330 335

Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
340 345 350

Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
355 360 365

Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
370 375 380

Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
385 390 395 400

Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
405 410 415

Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430

Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445

Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
450 455 460

Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
465 470 475 480

Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
485 490 495

Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
500 505 510

Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
515 520 525

Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
530 535 540

Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560

Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575

Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
580 585 590

Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605

Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620

Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640

Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
645 650 655

Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
660 665 670

Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro

675 680 685
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
690 695 700
Gly Gly Leu Lys Arg Arg
705 710

<210> 419
<211> 710
<212> PRT
<213> Artificial Sequence

<220>
<223> rat-FGFR1 (R22-E287) (Beta-IIIc), XP_006253387.1 fused to human FGFR1 (I286-R731, NP_075594)

<400> 419
Arg Pro Ala Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
1 5 10 15
Asp Asp Asp Asp Asp Asp Asp Ser Ser Glu Glu Lys Glu Thr Asp
20 25 30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
35 40 45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
50 55 60
Lys Cys Pro Ser Ser Gly Thr Pro Ser Pro Thr Leu Arg Trp Leu Lys
65 70 75 80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
85 90 95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
100 105 110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
115 120 125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
130 135 140
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
145 150 155 160
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
165 170 175
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
180 185 190
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
195 200 205
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
210 215 220
Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
245 250 255
Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
260 265 270
Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys
275 280 285
Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
290 295 300
Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
305 310 315 320
Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
325 330 335
Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu
340 345 350
Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
355 360 365
Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
370 375 380
Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
385 390 395 400
Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu

405 410 415
Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
420 425 430
Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
435 440 445
Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
450 455 460
Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
465 470 475 480
Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
485 490 495
Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
500 505 510
Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
515 520 525
Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
530 535 540
Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
545 550 555 560
Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
565 570 575
Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
580 585 590
Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
595 600 605
Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
610 615 620
Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
625 630 635 640
Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu Tyr Leu Asp
645 650 655
Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
660 665 670
Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
675 680 685
Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn
690 695 700
Gly Gly Leu Lys Arg Arg
705 710

<210> 420
<211> 713
<212> PRT
<213> Artificial Sequence

<220>
<223> rabbit-FGFR1 (R22-E288) (Beta-IIIc), XP_008272198.1 fused to human FGFR1 (I286-R731, NP_075594)

<400> 420
Arg Pro Ala Ala Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser
1 5 10 15
Glu Asp Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr
20 25 30
Asp Asn Thr Lys Pro Asn Arg Met Pro Val Ala Pro Tyr Trp Thr Ser
35 40 45
Pro Glu Lys Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr
50 55 60
Val Lys Phe Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg
65 70 75 80
Trp Leu Lys Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly
85 90 95
Tyr Lys Val Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val
100 105 110
Pro Ser Asp Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly
115 120 125
Ser Ile Asn His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His

130 135 140

Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu
145 150 155 160

Gly Ser Asn Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro
165 170 175

His Ile Gln Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly
180 185 190

Pro Asp Asn Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn
195 200 205

Thr Thr Asp Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe
210 215 220

Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu
225 230 235 240

Ser His His Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg
245 250 255

Pro Ala Val Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys
260 265 270

Thr Gly Ala Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr
275 280 285

Lys Met Lys Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala
290 295 300

Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val
305 310 315 320

Ser Ala Asp Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg
325 330 335

Pro Ser Arg Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser
340 345 350

Glu Tyr Glu Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg
355 360 365

Leu Val Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
370 375 380

Leu Ala Glu Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr
385 390 395 400

Lys Val Ala Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu
405 410 415

Ser Asp Leu Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
420 425 430

Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
435 440 445

Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
450 455 460

Gln Ala Arg Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His
465 470 475 480

Asn Pro Glu Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr
485 490 495

Gln Val Ala Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His
500 505 510

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met
515 520 525

Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr
530 535 540

Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
545 550 555 560

Glu Ala Leu Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser
565 570 575

Phe Gly Val Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
580 585 590

Pro Gly Val Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
595 600 605

Arg Met Asp Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met
610 615 620

Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
625 630 635 640

Leu Val Glu Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Asn Gln Glu
645 650 655

Tyr Leu Asp Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro
660 665 670

Asp Thr Arg Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser

675 680 685
His Glu Pro Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln
690 695 700
Leu Ala Asn Gly Gly Leu Lys Arg Arg
705 710

<210> 421
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK alpha-KLH VH mIgG1

<400> 421
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Gly Tyr His Met His Trp Val Arg Gln Ala Pro Gly
50 55 60
Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
65 70 75 80
Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
85 90 95
Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Ser Tyr Tyr Trp Phe
115 120 125
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr
130 135 140
Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
145 150 155 160
Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
165 170 175
Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
180 185 190
Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
195 200 205
Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
210 215 220
Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
225 230 235 240
Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
245 250 255
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
260 265 270
Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
275 280 285
Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
290 295 300
Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
305 310 315 320
Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335
Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
340 345 350
Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
355 360 365
Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
370 375 380
Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
385 390 395 400
Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
405 410 415

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
420 425 430
Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
435 440 445
Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
450 455 460
Lys
465

<210> 422
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK alpha-KLH VH mIgG2-alpha

<400> 422
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Thr Gly Tyr His Met His Trp Val Arg Gln Ala Pro Gly
50 55 60
Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
65 70 75 80
Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
85 90 95
Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Ser Tyr Tyr Trp Phe
115 120 125
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr
130 135 140
Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr
145 150 155 160
Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
165 170 175
Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
180 185 190
Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
195 200 205
Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn
210 215 220
Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro
225 230 235 240
Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
245 250 255
Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
260 265 270
Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val
275 280 285
Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn
290 295 300
Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
305 310 315 320
Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
325 330 335
Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
340 345 350
Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg
355 360 365
Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys
370 375 380
Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp

385 390 395 400
Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
405 410 415
Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
420 425 430
Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
435 440 445
Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
450 455 460
Phe Ser Arg Thr Pro Gly Lys
465 470

<210> 423
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK alpha-KLH VL mKappa

<400> 423
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35 40 45
Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60
Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
100 105 110
His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125
Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
130 135 140
Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn
145 150 155 160
Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu
165 170 175
Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp
180 185 190
Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr
195 200 205
Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr
210 215 220
Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> 424
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK-KLH-(VH)-hIgG1(E233A)(L235A)

<400> 424
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15
Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly

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        35                  40                  45
Tyr Thr Phe Thr Gly Tyr His Met His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
65                  70                  75                  80
Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
                85                  90                  95
Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Ser Tyr Tyr Trp Phe
        115                 120                 125
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
Ala Leu Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460
Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 425
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> hIgK-KLH-(VL)-hIgK

<400> 425
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1               5                  10                  15
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Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35   40   45
Gln Gly Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
            100   105   110
His Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
        115   120   125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130   135   140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145   150   155   160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165   170   175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180   185   190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195   200   205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210   215   220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235

<210> 426
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> Example of extracellular region of FGFR1c
      (beta-IIIc, NP_075594)

<400> 426
Arg Pro Ser Pro Thr Leu Pro Glu Gln Asp Ala Leu Pro Ser Ser Glu
 1   5   10   15
Asp Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp
            20   25   30
Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
        35   40   45
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
    50   55   60
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
65   70   75   80
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
                85   90   95
Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
            100   105   110
Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
        115   120   125
His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
    130   135   140
Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn
145   150   155   160
Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
                165   170   175
Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
            180   185   190
Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
        195   200   205
Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
    210   215   220

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
225 230 235 240
Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
245 250 255
Met Thr Ser Pro Leu Tyr Leu Glu
260

<210> 427
<211> 354
<212> PRT
<213> Artificial Sequence

<220>
<223> Example of extracellular region of FGFR1c
(Alpha-IIIc, NP_056934)

<400> 427
Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln Pro Trp Gly Ala Pro
1 5 10 15
Val Glu Val Glu Ser Phe Leu Val His Pro Gly Asp Leu Leu Gln Leu
20 25 30
Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile Asn Trp Leu Arg Asp
35 40 45
Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg Ile Thr Gly Glu Glu
50 55 60
Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser Gly Leu Tyr Ala Cys
65 70 75 80
Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr Tyr Phe Ser Val Asn
85 90 95
Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Asp Asp
100 105 110
Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Arg Met
115 120 125
Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys Met Glu Lys Lys Leu
130 135 140
His Ala Val Pro Ala Ala Lys Thr Val Lys Phe Lys Cys Pro Ser Ser
145 150 155 160
Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys Asn Gly Lys Glu Phe
165 170 175
Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val Arg Tyr Ala Thr Trp
180 185 190
Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr
195 200 205
Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr Gln Leu
210 215 220
Asp Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu
225 230 235 240
Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn Val Glu Phe Met Cys
245 250 255
Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln Trp Leu Lys His Ile
260 265 270
Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn Leu Pro Tyr Val Gln
275 280 285
Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp Lys Glu Met Glu Val
290 295 300
Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala Gly Glu Tyr Thr Cys
305 310 315 320
Leu Ala Gly Asn Ser Ile Gly Leu Ser His His Ser Ala Trp Leu Thr
325 330 335
Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val Met Thr Ser Pro Leu
340 345 350
Tyr Glu

<210> 428
<211> 630

<212> DNA
<213> Artificial Sequence

<220>
<223> A full length FGF21, NM_019113.2

<400> 428
atggactcgg acgagaccgg gttcgagcac tcaggactgt gggtttctgt gctggctggt 60
cttctgctgg gagcctgcca ggcacacccc atccctgact ccagtcctct cctgcaattc 120
gggggccaag tccggcagcg gtacctctac acagatgatg cccagcagac agaagcccac 180
ctggagatca gggaggatgg gacggtgggg ggcgctgctg accagagccc cgaaagtctc 240
ctgcagctga aagccttgaa gccgggagtt attcaaatct tgggagtcaa gacatccagg 300
ttcctgtgcc agcggccaga tggggccctg tatggatcgc tccactttga ccctgaggcc 360
tgcagcttcc gggagctgct tcttgaggac ggatacaatg tttaccagtc cgaagcccac 420
ggcctcccgc tgcacctgcc agggaacaag tccccacacc gggaccctgc accccgagga 480
ccagctcgct tcctgccact accaggcctg ccccccgcac tcccggagcc acccggaatc 540
ctggcccccc agccccccga tgtgggctcc tcggaccctc tgagcatggt gggaccttcc 600
cagggccgaa gccccagcta cgcttcctga   630

<210> 429
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> A full length FGF21, NP_061986.1

<400> 429
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
 1   5   10   15
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20   25   30
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35   40   45
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50   55   60
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65   70   75   80
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85   90   95
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100   105   110
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115   120   125
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130   135   140
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145   150   155   160
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu
                165   170   175
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180   185   190
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195   200   205
Ser

<210> 430
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> VH SEQ ID NO: 68 in U.S. Patent Publication 20110135657

<400> 430
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu

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 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Asn Asn Ala
            20                  25                  30
Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65                  70                  75                  80
Val Leu Ile Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95
Cys Ala Arg Ser Val Val Thr Gly Gly Tyr Tyr Tyr Asp Gly Met Asp
            100                 105                 110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 431
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> VH SEQ ID NO: 50 in U.S. Patent Publication 20110135657

<400> 431
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1               5                  10                  15
Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Glu Ser Val
            20                  25                  30
His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
        35                  40                  45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65                  70                  75                  80
Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Gly Asn Ser Asp His
                85                  90                  95
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
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