SEQUENCE LISTING

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<120> CBLB ENDONUCLEASE VARIANTS, COMPOSITIONS, AND METHODS OF USE

<130> BLBD-087/02WO 315698-2662

<150> US 62/567,417
<151> 2017-10-30

<150> US 62/511,194
<151> 2017-05-25

<160> 84

<170> PatentIn version 3.5

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35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Val Ile Ala Asn Ser Gly Asp Asn Ala Val Ser Leu Lys
65 70 75 80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Met Leu Phe Lys Gln
100 105 110

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Ala Phe Cys Val Met Glu Asn Lys Glu His Leu Lys Ile Asn Gly Ile
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Lys Glu Leu Val Arg Ile Lys Ala Lys Leu Asn Trp Gly Leu Thr Asp
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Glu Leu Lys Lys Ala Phe Pro Glu Ile Ile Ser Lys Glu Arg Ser Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

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

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

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
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225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe
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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
        35                  40                  45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50                  55                  60

Lys Val Gly Val Ile Ala Asn Ser Gly Asp Asn Ala Val Ser Leu Lys
65                  70                  75                  80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85                  90                  95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Leu Asn Trp Gly Leu Thr Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

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

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp
        195                 200                 205
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Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
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Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe
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            20                  25                  30

Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
        35                  40                  45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50                  55                  60
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Lys Val Gly Val Ile Ala Asn Ser Gly Asp Asn Ala Val Ser Leu Lys
65                  70                  75                  80


Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85                  90                  95


Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110


Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125


Lys Glu Leu Val Arg Ile Lys Ala Lys Leu Asn Trp Gly Leu Thr Asp
    130                 135                 140


Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
145                 150                 155                 160


Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175


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


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


Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
    210                 215                 220


Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225                 230                 235                 240


Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255


Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270


Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Val Ile Ala Asn Ser Gly Asp Asn Ala Val Ser Leu Lys
65 70 75 80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
100 105 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

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Lys Glu Leu Val Arg Ile Lys Ala Lys Leu Asn Trp Gly Leu Thr Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

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

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

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
    210                 215                 220

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Gly Phe Ala Asp Ala Glu Gly Ser Phe Leu Leu Arg Ile Arg Asn Asn
            20   25   30

Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
        35   40   45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50   55   60

Lys Val Gly Val Ile Ala Asn Ser Gly Asp Asn Ala Val Ser Leu Lys
65   70   75   80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85   90   95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100   105   110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115   120   125

Lys Glu Leu Val Arg Ile Lys Ala Lys Leu Asn Trp Gly Leu Thr Asp
    130   135   140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
145   150   155   160

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
                165   170   175

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


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


Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
    210                 215                 220


Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225                 230                 235                 240


Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255


Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270


Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285


Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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            20                  25                  30

Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
        35                  40                  45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50                  55                  60

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65                  70                  75                  80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85                  90                  95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

Gly Asp Gly Ser Phe Val Val Glu Leu Lys Lys Arg Arg Ser Pro Val
            180                 185                 190

Lys Val Gly Val Arg Leu Arg Phe Ser Ile Thr Gln His Ile Arg Asp
        195                 200                 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220
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Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240


Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255


Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270


Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285


Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa Xaa
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Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
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Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
        35                  40                  45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50                  55                  60

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65                  70                  75                  80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85                  90                  95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
            180                 185                 190

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
        195                 200                 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255
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Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

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Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Ser
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

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Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65                  70                  75                  80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
                85                  90                  95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
            180                 185                 190

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
        195                 200                 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Val
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Lys Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65 70 75 80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
            180                 185                 190

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
        195                 200                 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285

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20 25 30

Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Ser
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65 70 75 80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
100 105 110

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile

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        115                 120                 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
            180                 185                 190

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
        195                 200                 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa Xaa
    290                 295                 300

Xaa Xaa
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Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Val
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65 70 75 80

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
100 105 110

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160


Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175


Gly Asp Gly Ser Phe Val Val Glu Leu Lys Lys Arg Arg Ser Pro Val
            180                 185                 190


Lys Val Gly Val Arg Leu Arg Phe Gly Ile Thr Gln His Ile Arg Asp
        195                 200                 205


Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220


Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240


Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255


Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270


Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285


Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa Xaa
    290                 295                 300


Xaa Xaa
305
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<220>

<221> MOD_RES
<222> (1)..(8)
<223> Any amino acid or absent

<220>
<221> MOD_RES
<222> (302)..(306)
<223> Any amino acid or absent

<400> 12

```
Xaa Xaa Xaa Xaa Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
1               5                   10                  15


Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
            20                  25                  30


Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
        35                  40                  45


Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
    50                  55                  60


Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
65                  70                  75                  80


Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Gly His Phe Glu Lys
                85                  90                  95


Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
            100                 105                 110


Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
        115                 120                 125


Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
    130                 135                 140


Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
145                 150                 155                 160


Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
                165                 170                 175
```

```
Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
            180                 185                 190


Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
        195                 200                 205


Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
    210                 215                 220


Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
225                 230                 235                 240


Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
                245                 250                 255


Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
            260                 265                 270


Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
        275                 280                 285


Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa Xaa
    290                 295                 300


Xaa Xaa
305


<210>  13
<211>  914
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Made in Lab - synthesized megaTAL CBLB.E3 construct

<400>  13

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


Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val
            20                  25                  30
```

```
Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
        35                  40                  45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65                  70                  75                  80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
                85                  90                  95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
            100                 105                 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
        115                 120                 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
    130                 135                 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145                 150                 155                 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
```

```
               245                 250                 255

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
               405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460
```

```
Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
625                 630                 635                 640

Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
```

```
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Ser Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Val Val Glu Leu Lys Lys Arg Arg Ser Pro Val
785                 790                 795                 800

Lys Val Gly Val Arg Leu Arg Phe Ser Ile Thr Gln His Ile Arg Asp
                805                 810                 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
            820                 825                 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
        835                 840                 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
    850                 855                 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865                 870                 875                 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
                885                 890                 895
```

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
900 905 910

Gly Arg

<210> 14
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.F6 construct

<400> 14

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

```
Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145                 150                 155                 160


Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175


Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190


Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205


Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220


Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240


Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255


Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270


Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285


Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300


Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320


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


Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350


Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
```

```
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575
```

```
Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
625                 630                 635                 640

Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
```

785 790 795 800

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
805 810 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
820 825 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
835 840 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
850 855 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865 870 875 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
885 890 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
900 905 910

Gly Arg

<210> 15
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.E6 construct

<400> 15

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe

```
        35                  40                  45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65                  70                  75                  80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
                85                  90                  95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
            100                 105                 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
        115                 120                 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
    130                 135                 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145                 150                 155                 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255
```

```
Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
```

```
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
625                 630                 635                 640

Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Ser
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685
```

```
Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
785                 790                 795                 800

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
                805                 810                 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
            820                 825                 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
        835                 840                 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
    850                 855                 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865                 870                 875                 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
                885                 890                 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
```

900 905 910

Gly Arg

<210> 16
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.D2 construct

<400> 16

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn

```
145                 150                 155                 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365
```

```
Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
```

```
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile His Asn Ala
625                 630                 635                 640

Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Val
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Lys Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
785                 790                 795                 800
```

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
805 810 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
820 825 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
835 840 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
850 855 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865 870 875 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
885 890 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
900 905 910

Gly Arg

<210> 17
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.C2 construct

<400> 17

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

```
Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly
    50                  55                  60

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65                  70                  75                  80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
                85                  90                  95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
            100                 105                 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
        115                 120                 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
    130                 135                 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145                 150                 155                 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
```

```
            260                 265                 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480
```

```
Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Gly Leu Tyr Ile His Asn Ser
625                 630                 635                 640

Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Ser
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
```

```
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
785                 790                 795                 800

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
                805                 810                 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
            820                 825                 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
        835                 840                 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
    850                 855                 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865                 870                 875                 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
                885                 890                 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
            900                 905                 910
```

Gly Arg

<210> 18
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.B5 construct

<400> 18

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145 150 155 160

```
Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
```

```
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590
```

```
Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile His Asn Ala
625                 630                 635                 640

Asn Val Leu Arg Ser Gly Tyr Arg Thr Arg Leu Ser Phe Glu Ile Val
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
    690                 695                 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Val Val Glu Leu Lys Lys Arg Arg Ser Pro Val
785                 790                 795                 800

Lys Val Gly Val Arg Leu Arg Phe Gly Ile Thr Gln His Ile Arg Asp
```

805 810 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
820 825 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
835 840 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
850 855 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865 870 875 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
885 890 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
900 905 910

Gly Arg

<210> 19
<211> 914
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized megaTAL CBLB.A8 construct

<400> 19

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

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly

```
    50                  55                  60

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65                  70                  75                  80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
                85                  90                  95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
            100                 105                 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
        115                 120                 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
    130                 135                 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145                 150                 155                 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
                165                 170                 175

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
            180                 185                 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
        195                 200                 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
    210                 215                 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225                 230                 235                 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
                245                 250                 255

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
            260                 265                 270
```

```
Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
        275                 280                 285

Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu
    290                 295                 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305                 310                 315                 320

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

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
            340                 345                 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
        355                 360                 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
    370                 375                 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385                 390                 395                 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
                405                 410                 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
            420                 425                 430

Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
        435                 440                 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
    450                 455                 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465                 470                 475                 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
```

```
                485                 490                 495

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
            500                 505                 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
        515                 520                 525

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile
    530                 535                 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545                 550                 555                 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
                565                 570                 575

Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val
            580                 585                 590

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
        595                 600                 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
    610                 615                 620

Gly Phe Ala Asp Ala Glu Gly Cys Phe Arg Leu Asp Ile Arg Asn Ala
625                 630                 635                 640

Asn Asp Leu Arg Ala Gly Tyr Arg Thr Arg Leu Ala Phe Glu Ile Val
                645                 650                 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
            660                 665                 670

Lys Val Gly Thr Ile Tyr Asn Ala Gly Asp Asn Ala Val Arg Leu Gln
        675                 680                 685

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Gly His Phe Glu Lys
    690                 695                 700
```

```
Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705                 710                 715                 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
                725                 730                 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
            740                 745                 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
        755                 760                 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
    770                 775                 780

Gly Asp Gly Ser Phe Met Val Glu Leu Met Lys Asn Lys Asn Asn Val
785                 790                 795                 800

Ile Val Arg Val Arg Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
                805                 810                 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile
            820                 825                 830

Val Glu Asn Asn Lys Ser Glu His Ser Trp Leu Glu Phe Ile Val Thr
        835                 840                 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
    850                 855                 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865                 870                 875                 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
                885                 890                 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe Ser
            900                 905                 910

Gly Arg
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<210> 20
<211> 22
<212> DNA
<213> Homo sapiens

<400> 20
ctgtaagata ttcccatccc ca 22

<210> 21
<211> 13
<212> DNA
<213> Homo sapiens

<400> 21
ttgttatgag gta 13

<210> 22
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<212> DNA
<213> Homo sapiens

<400> 22
ttgttatgag gtatggtctg taagatattc ccatcccca 39

<210> 23
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<212> DNA
<213> Homo sapiens

<400> 23
ctgtaagata ttcaaccttt ta 22

<210> 24
<211> 22
<212> DNA
<213> Homo sapiens

<400> 24
tttccactta ttcccatccc ca 22

<210> 25
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<400> 25

ctgtaagata ttctacgtct gc 22

<210> 26
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<213> Homo sapiens

<400> 26
cttccaggaa ttcccatccc ca 22

<210> 27
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<212> DNA
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<400> 27
ctgtaagata ttccacaggc tc 22

<210> 28
<211> 22
<212> PRT
<213> Homo sapiens

<400> 28

Thr Gly Thr Cys Cys Ala Ala Thr Ala Ala Thr Thr Cys Cys Cys Ala
1 5 10 15

Thr Cys Cys Cys Cys Ala
20

<210> 29
<211> 22
<212> DNA
<213> Homo sapiens

<400> 29
ctgtaagata ttcaccgatt tt 22

<210> 30
<211> 7244
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - synthesized I-OnuI variant CBLB.E3 surface display plasmid

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cttaggacgg atcgcttgcc tgtaacttac acgcgcctcg tatcttttaa tgatggaata 120

atttgggaat ttactctgtg tttatttatt tttatgtttt gtatttggat tttagaaagt 180

aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa aataaacaaa ggtttaaaaa 240

atttcaacaa aaagcgtact ttacatatat atttattaga caagaaaagc agattaaata 300

gatatacatt cgattaacga taagtaaaat gtaaaatcac aggattttcg tgtgtggtct 360

tctacacaga caagatgaaa caattcggca ttaatacctg agagcaggaa gagcaagata 420

aaaggtagta tttgttggcg atccccctag agtcttttac atcttcggaa aacaaaaact 480

atttttttctt taatttcttt ttttactttc tatttttaat ttatatattt atattaaaaa 540

atttaaatta taattatttt tatagcacgt gatgaaaagg acccaggtgg cacttttcgg 600

ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 660

ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 720

attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt 780

gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg 840

ggttacatcg aactggatct caacagcggt aagatccttg agagttttcg ccccgaagaa 900

cgttttccaa tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtatt 960

gacgccgggc aagagcaact cggtcgccgc atacactatt ctcagaatga cttggttgag 1020

tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt 1080

gctgccataa ccatgagtga taacactgcg gccaacttac ttctgacaac gatcggagga 1140

ccgaaggagc taaccgcttt ttttcacaac atgggggatc atgtaactcg ccttgatcgt 1200

tgggaaccgg agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta 1260

gcaatggcaa caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg 1320

caacaattaa tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc 1380

cttccggctg gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggt 1440

atcattgcag cactggggcc agatggtaag ccctcccgta tcgtagttat ctacacgacg 1500

ggcagtcagg caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg 1560

attaagcatt ggtaactgtc agaccaagtt tactcatata tactttagat tgatttaaaa 1620

cttcattttt aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa 1680

atcccttaac gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga 1740

tcttcttgag atccttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg 1800

ctaccagcgg tggtttgttt gccggatcaa gagctaccaa ctctttttcc gaaggtaact 1860

ggcttcagca gagcgcagat accaaatact gtccttctag tgtagccgta gttaggccac 1920

cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatcct gttaccagtg 1980

gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg 2040

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gaagggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg 2220

agggagcttc cagggggaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc 2280

tgacttgagc gtcgattttt gtgatgctcg tcaggggggc cgagcctatg gaaaaacgcc 2340

agcaacgcgg cctttttacg gttcctggcc ttttgctggc cttttgctca catgttcttt 2400

cctgcgttat cccctgattc tgtggataac cgtattaccg cctttgagtg agctgatacc 2460

gctcgccgca gccgaacgac cgagcgcagc gagtcagtga gcgaggaagc ggaagagcgc 2520

ccaatacgca aaccgcctct ccccgcgcgt tggccgattc attaatgcag ctggcacgac 2580

aggtttcccg actggaaagc gggcagtgag cgcaacgcaa ttaatgtgag ttacctcact 2640

cattaggcac cccaggcttt acactttatg cttccggctc ctatgttgtg tggaattgtg 2700

agcggataac aatttcacac aggaaacagc tatgaccatg attacgccaa gctcggaatt 2760

aaccctcact aaagggaaca aaagctgggt acccgacagg ttatcagcaa caacacagtc 2820

atatccattc tcaattagct ctaccacagt gtgtgaacca atgtatccag caccacctgt 2880

aaccaaaaca attttagaag tactttcact ttgtaactga gctgtcattt atattgaatt 2940

ttcaaaaatt cttacttttt ttttggatgg acgcaaagaa gtttaataat catattacat 3000

ggcattacca ccatatacat atccatatac atatccatat ctaatcttac ttatatgttg 3060

tggaaatgta aagagcccca ttatcttagc ctaaaaaaac cttctctttg gaactttcag 3120

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acagccctcc gaaggaagac tctcctccgt gcgtcctcgt cttcaccggt cgcgttcctg 3240

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cuagagagca uuguggccca gcugagccgg ccugauccgg cguuggccgc guugaccaac 1680

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ucccaucgcg uugcgauauc uagaguggga ggaagcucgc gcagagaguc caucaaccca 1860

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gacaaaucga uucuggagaa uauccagucg acuuggaagg ucggcaaaau cuacaacgcg 2040

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auuguacgug ugcgucugag auucucaauc ucccagcaca ucagagacaa gaaccugaug 2460

aauucauuga uaacauaccu aggcuguggu cguaucguug agaauaacaa aucugagcac 2520

aguuggcucg aauucauugu aacaaaauuc agcgauauca acgacaagau cauuccggua 2580

uuccaggaaa auacucugau uggcgucaaa cucgaggacu uugaagauug gugcaagguu 2640

gccaaauuga ucgaagagaa gaaacaccug accgaauccg guuuggauga gauuaagaaa 2700

aucaagcuga acaugaacaa aggucguguc uucagcggcc gcugauaa 2748

<210> 35
<211> 2748
<212> RNA
<213> Artificial Sequence

<220>
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gaggcacugg ugggccaugg guuuacacac gcgcacaucg uugcgcucag ccaacacccg 180

gcagcguuag ggaccgucgc ugucacguau cagcacauaa ucacggcguu gccagaggcg 240

acacacgaag acaucguugg cgucggcaaa cagugguccg gcgcacgcgc ccuggaggcc 300

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gugaagauug caaaacgugg cggcgugacc gcaauggagg cagugcaugc aucgcgcaau 420

gcacugacgg gugccccccu gaacuuaaca cccgaucaag ugguagcgau agcgucaaac 480

ggcgggggua aacaggcuuu ggagacggua cagcgguuau ugccgguacu cugccaggac 540

cacggauuga caccggacca agugguggcg auugcgucca acaacggagg caagcaggca 600

cuagagacug uccaacggcu ucuucccguu cuuugucagg aucaugggcu aaccccugau 660

cagguagucg cuauagcuuc aaauggaggg ggcaagcaag cacuggagac uguucaacga 720

cuccugccag ugcucugcca agaccacgga cuuacaccag aucaaguggu ugcuauugcc 780

uccaauggug gcgggaaaca agcguuggaa acugugcaga gacuguuacc ugucuugugu 840

caagaccacg gccucacgcc agaucaggug guagccauag cgucgaacau ugggugguaag 900

caagcccuug aaacggucca gcgucuucug ccgguguugu gccaggacca cggacuaacg 960

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ggcgacaacg cagucagacu gcaagucaca cguuucgaag auuugaaagu gauuaucgac 2100

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aauucauuga uaacauaccu aggcuguggu cguaucguug agaauaacaa aucugagcac 2520

aguuggcucg aauucauugu aacaaaauuc agcgauauca acgacaagau cauuccggua 2580

uuccaggaaa auacucugau uggcgucaaa cucgaggacu uugaagauug gugcaagguu 2640

gccaaauuga ucgaagagaa gaaacaccug accgaauccg guuuggauga gauuaagaaa 2700

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<211> 2748

<212> RNA
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gaggcacugg ugggccaugg guuuacacac gcgcacaucg uugcgcucag ccaacacccg 180

gcagcguuag ggaccgucgc ugucacguau cagcacauaa ucacggcguu gccagaggcg 240

acacacgaag acaucguugg cgucggcaaa cagugguccg gcgcacgcgc ccuggaggcc 300

uugcucacgg augcggggga guugagaggu ccgccguuac aguuggacac aggccaacuu 360

gugaagauug caaaacgugg cggcgugacc gcaauggagg cagugcaugc aucgcgcaau 420

gcacugacgg gugccccccu gaacuuaaca cccgaucaag ugguagcgau agcgucaaac 480

ggcgggggua aacaggcuuu ggagacggua cagcgguuau ugccgguacu cugccaggac 540

cacggauuga caccggacca agugguggcg auugcgucca acaacggagg caagcaggca 600

cuagagacug uccaacggcu ucuucccguu cuuugucagg aucaugggcu aaccccugau 660

cagguagucg cuauagcuuc aaauggaggg ggcaagcaag cacuggagac uguucaacga 720

cuccugccag ugcucugcca agaccacgga cuuacaccag aucaaguggu ugcuauugcc 780

uccaauggug gcgggaaaca agcguuggaa acugugcaga gacuguuacc ugucuugugu 840

caagaccacg gccucacgcc agaucaggug guagccauag cgucgaacau uggugguaag 900

caagcccuug aaacggucca gcgucuucug ccgguguugu gccaggacca cggacuaacg 960

ccggaucagg ucguagccau ugcuucaaau gggggcggca aacaggcgcu agagacaguc 1020

cagcgccucu ugccuguguu augccaggau cacggcuuaa ccccagacca aguuguggcu 1080

auugcaucua acaauggugg caaacaagcc uuggagacag ugcaacgauu acugccuguc 1140

uuaugucagg aucauggccu gacgcccgau cagguagugg caaucgcauc uaacauugga 1200

gguaagcaag cacuggagac uguccagaga uuguuacccg uacuauguca agaucauggu 1260

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guagcuaucg ccagcaauaa cgguggaaaa caggcccugg aaaccguaca acgucuccuc 1440

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gguggggggga agcaggcgcu ggaaacuguu cagagacugc ugccuguacu uugucaggac 1560

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ucccaucgcg uugcgauauc uagaguggga ggaagcucgc gcagagaguc caucaaccca 1860

uggauucuga cugguuucgc ugaugccgaa ggaugcuucc gacuagacau ccgcaacgca 1920

aacgauuuaa gagccggaua cagaacuaga cuggccuucg aaaucguacu gcacaacaag 1980

gacaaaucga uucuggagaa uauccagucg acuuggaagg ucggcacaau cuacaacgcg 2040

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cacuucgaga aauauccgcu gauaacacag aaauugggcg auuacaaguu guuuaaacag 2160

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auuguacgug ugcgucugag auucucaauc ucccagcaca ucagagacaa gaaccugaug 2460

aauucauuga uaacauaccu aggcuguggu cguaucguug agaauaacaa aucugagcac 2520

aguuggcucg aauucauugu aacaaaauuc agcgauauca acgacaagau cauuccggua 2580

uuccaggaaa auacucugau uggcgucaaa cucgaggacu uugaagauug gugcaagguu 2640

gccaaauuga ucgaagagaa gaaacaccug accgaauccg guuuggauga gauuaagaaa 2700

aucaagcuga acaugaacaa aggucguguc uucagcggcc gcugauaa 2748

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<213> Mus musculus

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gagaacccag aacgggauga uucugguucc uuggugcugc cccguguucu ggacaagcuc 180

acacugugca ugugcccgga gcgccccuuu acugccaagg ccagugagau uacugguuug 240

agcagcgaaa gccugaugca cugcgggaag gcugguuuca auggcgcugu gguaaggaca 300

cugcagggcu uccuaagccg ccaggagggc cccaucugcc uuguggccca caauggcuuc 360

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gacacugucu gccuggacac acugccugca uugcggggcc uggaccgugc ucacagccac 480

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caggcugaac ccagugcugc ccauucagca gaaggugaug ugcacacccu gcuucugauc 600

uuccugcauc gugcuccuga gcugcucgcc ugggcagaug agcaggcccg cagcugggcu 660

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<210> 38
<211> 236
<212> PRT
<213> Mus musculus

<400> 38

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Ala Thr Gly Leu Pro Asn Met Asp Pro Glu Ile Ala Glu Ile Ser Leu
20 25 30

Phe Ala Val His Arg Ser Ser Leu Glu Asn Pro Glu Arg Asp Asp Ser
35 40 45

Gly Ser Leu Val Leu Pro Arg Val Leu Asp Lys Leu Thr Leu Cys Met
50 55 60

Cys Pro Glu Arg Pro Phe Thr Ala Lys Ala Ser Glu Ile Thr Gly Leu
65 70 75 80

Ser Ser Glu Ser Leu Met His Cys Gly Lys Ala Gly Phe Asn Gly Ala
85 90 95

Val Val Arg Thr Leu Gln Gly Phe Leu Ser Arg Gln Glu Gly Pro Ile
100 105 110

Cys Leu Val Ala His Asn Gly Phe Asp Tyr Asp Phe Pro Leu Leu Cys
115 120 125

Thr Glu Leu Gln Arg Leu Gly Ala His Leu Pro Gln Asp Thr Val Cys
130 135 140

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

Gly Thr Arg Ala Gln Gly Arg Lys Ser Tyr Ser Leu Ala Ser Leu Phe
165 170 175

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

Asp Val His Thr Leu Leu Leu Ile Phe Leu His Arg Ala Pro Glu Leu
195 200 205

Leu Ala Trp Ala Asp Glu Gln Ala Arg Ser Trp Ala His Ile Glu Pro
210 215 220

Met Tyr Val Pro Pro Asp Gly Pro Ser Leu Glu Ala
225 230 235

<210> 39
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<223> Exemplary linker sequence

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Gly Gly Gly
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<210> 40
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<400> 40

Asp Gly Gly Gly Ser
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<210> 41
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<400> 41

Thr Gly Glu Lys Pro
1   5

<210> 42
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<220>
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<400> 42

Gly Gly Arg Arg
1

<210> 43
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<212> PRT
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<220>
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<400> 43

Gly Gly Gly Gly Ser
1   5

<210> 44
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 44

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
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<210> 45
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 45

Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
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Leu Asp

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 46

Gly Gly Arg Arg Gly Gly Gly Ser
1   5

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 47

Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary linker sequence

<400> 48

Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1 5 10

<210> 49
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 49

Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
1 5 10 15

<210> 50
<211> 7
<212> PRT
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<220>
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<222> (2)..(3)
<223> Xaa is any amino acid

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<222> (5)..(5)
<223> Xaa is any amino acid

<220>
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<222> (7)..(7)

<223> Xaa = Gly or Ser

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<210> 51
<211> 7
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<220>
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<400> 51

Glu Asn Leu Tyr Phe Gln Gly
1   5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavage sequence by TEV protease

<400> 52

Glu Asn Leu Tyr Phe Gln Ser
1   5

<210> 53
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 53

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1   5   10   15

Glu Glu Asn Pro Gly Pro
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<210> 54
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
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<400> 54

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 55
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 55

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
1 5 10

<210> 56
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 56

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 57
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 57

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1   5   10   15

Gly Pro

<210> 58
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 58

Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
1   5   10

<210> 59
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 59

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1   5   10   15

Val Glu Ser Asn Pro Gly Pro
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<210> 60
<211> 20
<212> PRT
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<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 60

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
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<210> 61
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<220>
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<400> 61

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
1 5 10

<210> 62
<211> 25
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<220>
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<400> 62

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 63
<211> 22
<212> PRT
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<220>
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<400> 63

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
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<210> 64
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<220>
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<400> 64

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
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<210> 65
<211> 19
<212> PRT
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<220>
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<400> 65

Leu Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
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Pro Gly Pro

<210> 66
<211> 19
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<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 66

Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn
1   5   10   15

Pro Gly Pro

<210> 67
<211> 14
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<220>
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<400> 67

Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
1 5 10

<210> 68
<211> 17
<212> PRT
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<220>
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<400> 68

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
1 5 10 15

Pro

<210> 69
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<220>
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<400> 69

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Asn Pro Gly Pro
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<210> 70
<211> 24

<212> PRT
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<220>
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<400> 70

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
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Asp Val Glu Ser Asn Pro Gly Pro
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<210> 71
<211> 40
<212> PRT
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<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 71

Val Thr Glu Leu Leu Tyr Arg Met Lys Arg Ala Glu Thr Tyr Cys Pro
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Arg Pro Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys
20 25 30

Ile Val Ala Pro Val Lys Gln Thr
35 40

<210> 72
<211> 18
<212> PRT
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<220>
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<400> 72

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
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Gly Pro

<210> 73
<211> 40
<212> PRT
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<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 73

Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val
1 5 10 15

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
20 25 30

Asp Val Glu Ser Asn Pro Gly Pro
35 40

<210> 74
<211> 33
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<220>
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<400> 74

Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro Val Lys Gln Thr Leu
1 5 10 15

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
20 25 30

Pro

<210> 75
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Consensus Kozak sequence

<400> 75
gccrccatgg 10

<210> 76
<211> 22
<212> DNA
<213> Homo sapiens

<400> 76
tggggatggg aatatcttac ag 22

<210> 77
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.E3

<400> 77

Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1 5 10 15

Phe Arg Leu Asp Ile Arg Asn Ala Asn Asp Leu Arg Ala Gly Tyr Arg
20 25 30

Thr Arg Leu Ala Phe Glu Ile Val Leu His Asn Lys Asp Lys Ser Ile
35 40 45

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
50 55 60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65 70 75 80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu
85 90 95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys
100 105 110

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

```
Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
    130                 135                 140

Asn Ile Ser Lys Glu Arg Ser Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Val Val Glu
                165                 170                 175

Leu Lys Lys Arg Arg Ser Pro Val Lys Val Gly Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Thr Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
            260                 265                 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
        275                 280                 285

Met Asn Lys Gly Arg
    290
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<210> 78
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.F6

<400> 78

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Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1               5                  10                  15

Phe Arg Leu Asp Ile Arg Asn Ala Asn Asp Leu Arg Ala Gly Tyr Arg
            20                  25                  30

Thr Arg Leu Ala Phe Glu Ile Val Leu His Asn Lys Asp Lys Ser Ile
        35                  40                  45

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
    50                  55                  60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65                  70                  75                  80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu
                85                  90                  95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys
            100                 105                 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
    130                 135                 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Met Val Glu
                165                 170                 175

Leu Met Lys Asn Lys Asn Asn Val Ile Val Arg Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
```

210 215 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225 230 235 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
245 250 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
260 265 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
275 280 285

Met Asn Lys Gly Arg
290

<210> 79
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.E6

<400> 79

Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1 5 10 15

Phe Arg Leu Asp Ile Arg Asn Ala Asn Asp Leu Arg Ala Gly Tyr Arg
20 25 30

Thr Arg Leu Ser Phe Glu Ile Ser Leu His Asn Lys Asp Lys Ser Ile
35 40 45

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
50 55 60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65 70 75 80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu

```
                85                  90                  95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys
            100                 105                 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
    130                 135                 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Met Val Glu
                165                 170                 175

Leu Met Lys Asn Lys Asn Asn Val Ile Val Arg Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
            260                 265                 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
        275                 280                 285

Met Asn Lys Gly Arg
    290
```

<210> 80
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.D2

<400> 80

Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1 5 10 15

Phe Arg Leu Asp Ile His Asn Ala Asn Val Leu Arg Ser Gly Tyr Arg
20 25 30

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

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Lys Ile Tyr Asn Ala
50 55 60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65 70 75 80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu
85 90 95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys
100 105 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
130 135 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145 150 155 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Met Val Glu
165 170 175

```
Leu Met Lys Asn Lys Asn Asn Val Ile Val Arg Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
            260                 265                 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
        275                 280                 285

Met Asn Lys Gly Arg
    290


<210>  81
<211>  293
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthesized I-OnuI variant CBLB.C2

<400>  81

Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1               5                   10                  15

Phe Gly Leu Tyr Ile His Asn Ser Asn Val Leu Arg Ser Gly Tyr Arg
            20                  25                  30

Thr Arg Leu Ser Phe Glu Ile Ser Leu His Asn Lys Asp Lys Ser Ile
        35                  40                  45
```

```
Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
    50                  55                  60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65                  70                  75                  80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu
                85                  90                  95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Leu Met Glu Asn Lys
            100                 105                 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
    130                 135                 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Met Val Glu
                165                 170                 175

Leu Met Lys Asn Lys Asn Asn Val Ile Val Arg Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
```

260 265 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
275 280 285

Met Asn Lys Gly Arg
290

<210> 82
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.B5

<400> 82

Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
1 5 10 15

Phe Arg Leu Asp Ile His Asn Ala Asn Val Leu Arg Ser Gly Tyr Arg
20 25 30

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

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
50 55 60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65 70 75 80

Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys Leu
85 90 95

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Leu Met Glu Asn Lys
100 105 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu

```
    130                 135                 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Val Val Glu
                165                 170                 175

Leu Lys Lys Arg Arg Ser Pro Val Lys Val Gly Val Arg Leu Arg Phe
            180                 185                 190

Gly Ile Thr Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220

Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240

Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255

Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
            260                 265                 270

His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
        275                 280                 285

Met Asn Lys Gly Arg
    290
```

<210> 83
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized I-OnuI variant CBLB.A8

<400> 83

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Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly Cys
```

```
1               5                   10                  15

Phe Arg Leu Asp Ile Arg Asn Ala Asn Asp Leu Arg Ala Gly Tyr Arg
            20                  25                  30

Thr Arg Leu Ala Phe Glu Ile Val Leu His Asn Lys Asp Lys Ser Ile
        35                  40                  45

Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Thr Ile Tyr Asn Ala
    50                  55                  60

Gly Asp Asn Ala Val Arg Leu Gln Val Thr Arg Phe Glu Asp Leu Lys
65                  70                  75                  80

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

Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn Lys
            100                 105                 110

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

Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu
    130                 135                 140

Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn Leu
145                 150                 155                 160

Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser Phe Met Val Glu
                165                 170                 175

Leu Met Lys Asn Lys Asn Asn Val Ile Val Arg Val Arg Leu Arg Phe
            180                 185                 190

Ser Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu Ile
        195                 200                 205

Thr Tyr Leu Gly Cys Gly Arg Ile Val Glu Asn Asn Lys Ser Glu His
    210                 215                 220
```

```
Ser Trp Leu Glu Phe Ile Val Thr Lys Phe Ser Asp Ile Asn Asp Lys
225                 230                 235                 240


Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu Glu
                245                 250                 255


Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys Lys
            260                 265                 270


His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn
        275                 280                 285


Met Asn Lys Gly Arg
    290
```

<210> 84
<211> 39
<212> DNA
<213> Homo sapiens

<400> 84
tggggatggg aatatcttac agaccatacc tcataacaa 39