Fig. 1

SEQ ID NO: 1: nucleotide sequence of K3-1115 antibody heavy chain (h#32A1-H1-1)

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCGAAGTCC
AGCTTGTGGAAAGCGGAGGGGGACTCGTTCAGCCAGGAGGCTCTCTGCGCCTGTCATGCGCTGC
CAGCGGATTTAATTTCAATGATTATTTTATGAACTGGGTCAGGCAGGCTCCGGGAAAAGGGCTG
GAATGGGTCGCCCAGATCAGAAACAAGATCTATACTTACGCTACATTCTACGCCGCATCTGTAA
AGGGGAGGTTTACAATTAGTCGCGACAATGCAAAAAATAGTCTGTATCTCCAAATGAACTCCCT
CCGCGCAGAGGATACTGCTGTCTACTACTGCGCCAGGTCCTTGACTGGCGGCGACTATTTTGAT
TACTGGGGACAGGGCACCCTGGTGACGGTGAGCTCAGCCAGCACCAAGGGCCCTTCCGTGTTCC
CTCTGGCCCCTTGTAGCCGTTCCACCAGCGAGTCCACCGCCGCCCTTGGCTGTCTGGTGAAGGA
CTACTTCCCTGAGCCTGTGACCGTGAGCTGGAACTCCGGAGCCCTTACCAGCGGCGTGCACACC
TTCCCTGCCGTGCTGCAGTCCAGCGGCCTTTACTCCCTGAGCTCCGTGGTGACCGTGCCTAGCT
CCAACTTCGGCACCCAAACCTACACCTGTAACGTGGACCACAAGCCTAGCAACACCAAGGTGGA
CAAGACCGTGGAGCGTAAGTGTTGTGTGGAGTGTCCTCCTTGTCCTGCCCCTCCTGTGGCCGGA
CCTTCCGTGTTCCTTTTCCCTCCTAAGCCTAAGGACACCCTGATGATCAGCCGTACCCCTGAGG
TGACCTGTGTGGTGGTGGACGTGTCCCACGAGGACCCTGAGGTGCAGTTCAACTGGTACGTGGA
CGGCGTGGAGGTGCACAACGCCAAGACCAAGCCTCGTGAGGAGCAATTCAACAGCACCTTCCGT
GTGGTGTCCGTGCTTACCGTGGTGCACCAAGACTGGCTGAACGGCAAGGAGTACAAGTGTAAGG
TGAGCAACAAGGGACTTCCTGCCCCTATCGAGAAGACCATCTCCAAGACCAAGGGCCAACCTCG
TGAGCCTCAAGTGTACACCCTTCCTCCTAGCCGTGAGGAGATGACCAAGAACCAAGTGTCCCTT
ACCTGTCTGGTGAAGGGCTTCTACCCTAGCGACATCGCCGTGGAGTGGGAGTCCAACGGACAAC
CTGAGAACAACTACAAGACCACCCCTCCTATGCTTGACAGCGACGGCTCCTTCTTCCTGTACAG
CAAGCTGACCGTGGACAAGTCCCGTTGGCAACAAGGCAACGTGTTCAGCTGTTCCGTGATGCAC
GAGGCCCTGCACAACCACTACACCCAAAAGAGCCTTTCCCTGAGCCCTGGAAAG

signal sequence (1-57), variable region (58-420), constant region (421-1398)

SEQ ID NO: 2: amino acid sequence of K3-1115 antibody heavy chain (h#32A1-H1-1)

MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGGSLRLSCAASGFNFNDYFMNWVRQAPGKGL
EWVAQIRNKIYTYATFYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARSLTGGDYFD
YWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR

VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

signal sequence (1-19), variable region (20-140), constant region (141-466)

Fig. 2

SEQ ID NO: 3: nucleotide sequence of K3-1115 antibody light chain (h#32A1-L2-15)

ATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCATATGGCGAAA
TTCTGATGACGCAGAGTCCTGCAACTCTTAGTCTGTCACCTGGCGAGAGAGCCACACTCAGCTG
CCGAGCGTCCCAGTCCGTGACCATTAGCGGCTATTCTTTTATTCATTGGTATCAGCAAAAGCCT
GGACAGGCGCCAAGGCTGCTCATTTACAGAGCAAGCAACCTTGCCTCTGGCATTCCAGCAAGAT
TCAGCGGGAGCGGATCAGGGACAGATTTCACCTTGACCATCTCCTCCCTGGAGCCGGAGGATTT
CGCGTTGTATTATTGTCAGCAATCTAGGAAGAGTCCATGGACATTTGGCCAGGGCACCAAAGTG
GAGATCAAGCGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGA
AGTCCGGCACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCA
GTGGAAGGTGGACAACGCCCTGCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGC
AAGGACAGCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAAGCCGACTACGAGAAGCACA
AGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAG
GGGGGAGTGT

signal sequence (1-60), variable region (61-399), constant region (400-714)

SEQ ID NO: 4: amino acid sequence of K3-1115 antibody light chain (h#32A1-L2-15)

MVLQTQVFISLLLWISGAYGEILMTQSPATLSLSPGERATLSCRASQSVTISGYSFIHWYQQKP
GQAPRLLIYRASNLASGIPARFSGSGSGTDFTLTISSLEPEDFALYYCQQSRKSPWTFGQGTKV
EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence (1-20), variable region (21-133), constant region (134-238)

Fig. 3

SEQ ID NO: 5: nucleotide sequence of K3-1115/T103E antibody heavy chain

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcga
agtccagcttgtggaaagcggaggggactcgttcagccaggaggctctctgcgcctgt
catgcgctgccagcggatttaatttcaatgattattttatgaactgggtcaggcaggct
ccgggaaaagggctggaatgggtcgcccagatcagaaacaagatctatacttacgctac
attctacgccgcatctgtaaaggggaggtttacaattagtcgcgacaatgcaaaaaata
gtctgtatctccaaatgaactccctccgcgcagaggatactgctgtctactactgcgcc
aggtccttggagggcggcgactattttgattactggggacagggcaccctggtgacggt
gagctcagccagcaccaagggcccttccgtgttccctctggccccttgtagccgttcca
ccagcgagtccaccgccgcccttggctgtctggtgaaggactacttccctgagcctgtg
accgtgagctggaactccggagcccttaccagcggcgtgcacaccttccctgccgtgct
gcagtccagcggcctttactccctgagctccgtggtgaccgtgcctagctccaacttcg
gcacccaaacctacacctgtaacgtggaccacaagcctagcaacaccaaggtggacaag
accgtggagcgtaagtgttgtgtggagtgtcctccttgtcctgcccctcctgtggccgg
accttccgtgttccttttccctcctaagcctaaggacaccctgatgatcagccgtaccc
ctgaggtgacctgtgtggtggtggacgtgtcccacgaggaccctgaggtgcagttcaac
tggtacgtggacggcgtggaggtgcacaacgccaagaccaagcctcgtgaggagcaatt
caacagcaccttccgtgtggtgtccgtgcttaccgtggtgcaccaagactggctgaacg
gcaaggagtacaagtgtaaggtgagcaacaagggacttcctgcccctatcgagaagacc
atctccaagaccaagggccaacctcgtgagcctcaagtgtacacccttcctcctagccg
tgaggagatgaccaagaaccaagtgtcccttacctgtctggtgaagggcttctacccta
gcgacatcgccgtggagtgggagtccaacggacaacctgagaacaactacaagaccacc
cctcctatgcttgacagcgacggctccttcttcctgtacagcaagctgaccgtggacaa
gtcccgttggcaacaaggcaacgtgttcagctgttccgtgatgcacgaggccctgcaca
accactacacccaaaagagcctttccctgagccctggaaag

signal sequence (1-57), variable region (58-420), constant region (421-1398)

SEQ ID NO: 6: amino acid sequence of K3-1115/T103E antibody heavy chain

MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGGSLRLSCAASGFNFNDYFMNWVRQA
PGKGLEWVAQIRNKIYTYATFYAASVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCA
RSLEGGDYFDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV

TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK
TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFN
WYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT
ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

signal sequence (1-19), variable region (20-140), constant region (141-466)

Fig. 4

Amino acid sequences of respective CDRs of #32A1 antibody and K3-1115/T103E antibody

SEQ ID NO: 7: CDRH1 of #32A1 antibody
(DYFMN)

SEQ ID NO: 8: CDRH2 of #32A1 antibody
(QIRNKIYTYATFYAESLEG)

SEQ ID NO: 9: CDRH2 of #32A1 antibody
(QIRNKIYTYATFYA)

SEQ ID NO: 10: CDRH3 of #32A1 antibody
(SLTGGDYFDY)

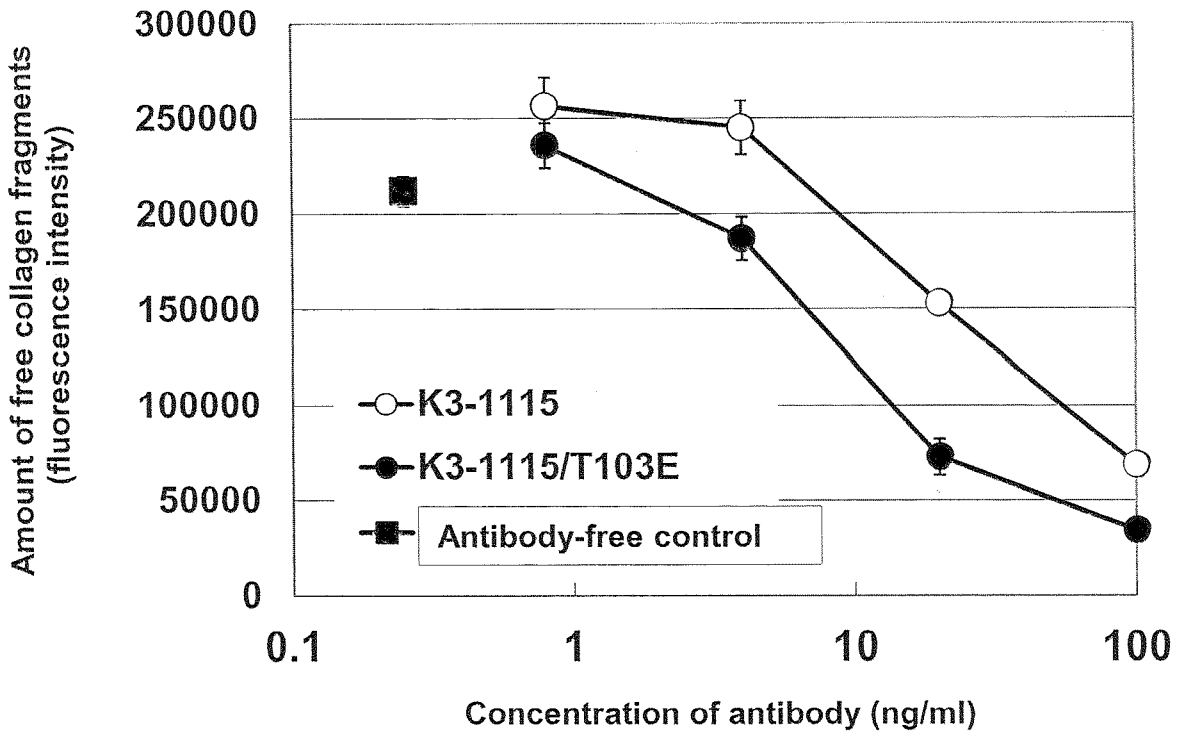
SEQ ID NO: 11: CDRH3 of K3-1115/T103E antibody
(SLEGGDYFDY)

SEQ ID NO: 12: CDRL1 of #32A1 antibody
(RASQSVTISGYSFIH)

SEQ ID NO: 13: CDRL2 of #32A1 antibody
(RASNLAS)

SEQ ID NO: 14: CDRL3 of #32A1 antibody
(QQSRKSPWT)

Fig. 5 Inhibition of bone resorption activity of normal osteoclast precursor cells by addition of K3-1115/T103E antibody



SEQUENCE LISTING

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> CDR modified anti-Siglec-15 antibody

<130> FP1310

<150> JP2012-078842
<151> 2012-03-30

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of K3-1115

<220>
<221> CDS
<222> (1)..(1398)

<400> 1

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc gaa gtc cag ctt gtg gaa agc gga ggg gga ctc gtt cag          96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

cca gga ggc tct ctg cgc ctg tca tgc gct gcc agc gga ttt aat ttc         144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
        35                  40                  45

aat gat tat ttt atg aac tgg gtc agg cag gct ccg gga aaa ggg ctg         192
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gaa tgg gtc gcc cag atc aga aac aag atc tat act tac gct aca ttc         240
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65                  70                  75                  80

tac gcc gca tct gta aag ggg agg ttt aca att agt cgc gac aat gca         288
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

aaa aat agt ctg tat ctc caa atg aac tcc ctc cgc gca gag gat act         336
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

gct gtc tac tac tgc gcc agg tcc ttg act ggc ggc gac tat ttt gat         384
Ala Val Tyr Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
        115                 120                 125

tac tgg gga cag ggc acc ctg gtg acg gtg agc tca gcc agc acc aag         432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

ggc cct tcc gtg ttc cct ctg gcc cct tgt agc cgt tcc acc agc gag         480
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145                 150                 155                 160
```

```
tcc acc gcc gcc ctt ggc tgt ctg gtg aag gac tac ttc cct gag cct          528
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tcc gga gcc ctt acc agc ggc gtg cac acc          576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

ttc cct gcc gtg ctg cag tcc agc ggc ctt tac tcc ctg agc tcc gtg          624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg cct agc tcc aac ttc ggc acc caa acc tac acc tgt aac          672
Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
    210                 215                 220

gtg gac cac aag cct agc aac acc aag gtg gac aag acc gtg gag cgt          720
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225                 230                 235                 240

aag tgt tgt gtg gag tgt cct cct tgt cct gcc cct cct gtg gcc gga          768
Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
                245                 250                 255

cct tcc gtg ttc ctt ttc cct cct aag cct aag gac acc ctg atg atc          816
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

agc cgt acc cct gag gtg acc tgt gtg gtg gtg gac gtg tcc cac gag          864
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

gac cct gag gtg cag ttc aac tgg tac gtg gac ggc gtg gag gtg cac          912
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

aac gcc aag acc aag cct cgt gag gag caa ttc aac agc acc ttc cgt          960
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305                 310                 315                 320

gtg gtg tcc gtg ctt acc gtg gtg cac caa gac tgg ctg aac ggc aag         1008
Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

gag tac aag tgt aag gtg agc aac aag gga ctt cct gcc cct atc gag         1056
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
            340                 345                 350

aag acc atc tcc aag acc aag ggc caa cct cgt gag cct caa gtg tac         1104
Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

acc ctt cct cct agc cgt gag gag atg acc aag aac caa gtg tcc ctt         1152
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

acc tgt ctg gtg aag ggc ttc tac cct agc gac atc gcc gtg gag tgg         1200
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

gag tcc aac gga caa cct gag aac aac tac aag acc acc cct cct atg         1248
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
                405                 410                 415

ctt gac agc gac ggc tcc ttc ttc ctg tac agc aag ctg acc gtg gac         1296
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430
```

```
aag tcc cgt tgg caa caa ggc aac gtg ttc agc tgt tcc gtg atg cac      1344
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

gag gcc ctg cac aac cac tac acc caa aag agc ctt tcc ctg agc cct      1392
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

gga aag                                                              1398
Gly Lys
465
```

<210> 2
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
        35                  40                  45

Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65                  70                  75                  80

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Ser Leu Thr Gly Gly Asp Tyr Phe Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145                 150                 155                 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
```

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

```
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

Gly Lys
465
```

<210> 3
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of K3-1115

<220>
<221> CDS
<222> (1)..(714)

<400> 3

```
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc          48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggc gca tat ggc gaa att ctg atg acg cag agt cct gca act ctt agt          96
Gly Ala Tyr Gly Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

ctg tca cct ggc gag aga gcc aca ctc agc tgc cga gcg tcc cag tcc         144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

gtg acc att agc ggc tat tct ttt att cat tgg tat cag caa aag cct         192
Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro
    50                  55                  60

gga cag gcg cca agg ctg ctc att tac aga gca agc aac ctt gcc tct         240
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
65                  70                  75                  80

ggc att cca gca aga ttc agc ggg agc gga tca ggg aca gat ttc acc         288
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95

ttg acc atc tcc tcc ctg gag ccg gag gat ttc gcg ttg tat tat tgt         336
Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys
            100                 105                 110

cag caa tct agg aag agt cca tgg aca ttt ggc cag ggc acc aaa gtg         384
Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
        115                 120                 125

gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc         432
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140

tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg         480
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160

aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac         528
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175

gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc         576
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
```

```
            180                 185                 190

aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc      624
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205

gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc      672
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    210                 215                 220

ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt               714
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  4
<211>  238
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  4

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

Gly Ala Tyr Gly Glu Ile Leu Met Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
        35                  40                  45

Val Thr Ile Ser Gly Tyr Ser Phe Ile His Trp Tyr Gln Gln Lys Pro
    50                  55                  60

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Arg Ala Ser Asn Leu Ala Ser
65                  70                  75                  80

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95

Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys
            100                 105                 110

Gln Gln Ser Arg Lys Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
        115                 120                 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
    130                 135                 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145                 150                 155                 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                165                 170                 175
```

```
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
            180                 185                 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
        195                 200                 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
    210                 215                 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 5
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of K3-1115/T103E

<220>
<221> CDS
<222> (1)..(1398)

<400> 5

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc gaa gtc cag ctt gtg gaa agc gga ggg gga ctc gtt cag          96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

cca gga ggc tct ctg cgc ctg tca tgc gct gcc agc gga ttt aat ttc         144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
        35                  40                  45

aat gat tat ttt atg aac tgg gtc agg cag gct ccg gga aaa ggg ctg         192
Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gaa tgg gtc gcc cag atc aga aac aag atc tat act tac gct aca ttc         240
Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65                  70                  75                  80

tac gcc gca tct gta aag ggg agg ttt aca att agt cgc gac aat gca         288
Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

aaa aat agt ctg tat ctc caa atg aac tcc ctc cgc gca gag gat act         336
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

gct gtc tac tac tgc gcc agg tcc ttg gag ggc ggc gac tat ttt gat         384
Ala Val Tyr Tyr Cys Ala Arg Ser Leu Glu Gly Gly Asp Tyr Phe Asp
        115                 120                 125

tac tgg gga cag ggc acc ctg gtg acg gtg agc tca gcc agc acc aag         432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

ggc cct tcc gtg ttc cct ctg gcc cct tgt agc cgt tcc acc agc gag         480
```

```
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145                 150                 155                 160

tcc acc gcc gcc ctt ggc tgt ctg gtg aag gac tac ttc cct gag cct   528
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tcc gga gcc ctt acc agc ggc gtg cac acc   576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

ttc cct gcc gtg ctg cag tcc agc ggc ctt tac tcc ctg agc tcc gtg   624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg cct agc tcc aac ttc ggc acc caa acc tac acc tgt aac   672
Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
    210                 215                 220

gtg gac cac aag cct agc aac acc aag gtg gac aag acc gtg gag cgt   720
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225                 230                 235                 240

aag tgt tgt gtg gag tgt cct cct tgt cct gcc cct cct gtg gcc gga   768
Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
                245                 250                 255

cct tcc gtg ttc ctt ttc cct cct aag cct aag gac acc ctg atg atc   816
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

agc cgt acc cct gag gtg acc tgt gtg gtg gtg gac gtg tcc cac gag   864
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        275                 280                 285

gac cct gag gtg cag ttc aac tgg tac gtg gac ggc gtg gag gtg cac   912
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    290                 295                 300

aac gcc aag acc aag cct cgt gag gag caa ttc aac agc acc ttc cgt   960
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305                 310                 315                 320

gtg gtg tcc gtg ctt acc gtg gtg cac caa gac tgg ctg aac ggc aag  1008
Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
                325                 330                 335

gag tac aag tgt aag gtg agc aac aag gga ctt cct gcc cct atc gag  1056
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
            340                 345                 350

aag acc atc tcc aag acc aag ggc caa cct cgt gag cct caa gtg tac  1104
Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        355                 360                 365

acc ctt cct cct agc cgt gag gag atg acc aag aac caa gtg tcc ctt  1152
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    370                 375                 380

acc tgt ctg gtg aag ggc ttc tac cct agc gac atc gcc gtg gag tgg  1200
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385                 390                 395                 400

gag tcc aac gga caa cct gag aac aac tac aag acc acc cct cct atg  1248
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
                405                 410                 415

ctt gac agc gac ggc tcc ttc ttc ctg tac agc aag ctg acc gtg gac  1296
```

```
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            420                 425                 430

aag tcc cgt tgg caa caa ggc aac gtg ttc agc tgt tcc gtg atg cac      1344
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        435                 440                 445

gag gcc ctg cac aac cac tac acc caa aag agc ctt tcc ctg agc cct      1392
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    450                 455                 460

gga aag                                                              1398
Gly Lys
465
```

<210> 6
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
        35                  40                  45

Asn Asp Tyr Phe Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe
65                  70                  75                  80

Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
                85                  90                  95

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
            100                 105                 110

Ala Val Tyr Tyr Cys Ala Arg Ser Leu Glu Gly Gly Asp Tyr Phe Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145                 150                 155                 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
```

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 7
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 7

Asp Tyr Phe Met Asn
1 5

<210> 8
<211> 19
<212> PRT
<213> Rattus norvegicus

<400> 8

Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala Glu Ser
1 5 10 15

Leu Glu Gly

<210> 9
<211> 14
<212> PRT
<213> Rattus norvegicus

<400> 9

Gln Ile Arg Asn Lys Ile Tyr Thr Tyr Ala Thr Phe Tyr Ala
1 5 10

<210> 10
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 10

Ser Leu Thr Gly Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 of K3-1115/T103E

<400> 11

Ser Leu Glu Gly Gly Asp Tyr Phe Asp Tyr
1 5 10

<210> 12
<211> 15
<212> PRT
<213> Rattus norvegicus

<400> 12

Arg Ala Ser Gln Ser Val Thr Ile Ser Gly Tyr Ser Phe Ile His
1 5 10 15

<210> 13
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 13

Arg Ala Ser Asn Leu Ala Ser
1 5

<210> 14
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 14

Gln Gln Ser Arg Lys Ser Pro Trp Thr
1 5

<210> 15
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer 32A1_HT103EFw

<400> 15
ctactactgc gccaggtcct tggagggcgg cgac 34

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer 32A1_HT103ERv

<400> 16
gtcgccgccc tccaaggacc tggcgcagta gtag 34