Fig. 1

SEQ ID NO: 4: AMINO ACID SEQUENCE OF No.76 LIGHT CHAIN VARIABLE REGION

MESQTLVFISILLWLYGADGNIVMTQSPKSMSMSVGERVTLSCKASENVGTSVSWYQEKPEQSPKLL
IFGASNRYTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQSYSYPYTFGGRTKLEIKRA

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129)

SEQ ID NO: 5: AMINO ACID SEQUENCE OF No.76 LIGHT CHAIN CDR1

KASENVGTSVS

SEQ ID NO: 6: AMINO ACID SEQUENCE OF No.76 LIGHT CHAIN CDR2

GASNRYT

SEQ ID NO: 7: AMINO ACID SEQUENCE OF No.76 LIGHT CHAIN CDR3

GQSYSYPYT

SEQ ID NO: 8: AMINO ACID SEQUENCE OF No.76 HEAVY CHAIN VARIABLE REGION

MGWSCIILFLVAAATGVHSQVQLQQPGAELVKPGASVNLSCKSSGYTFTNYWINWVKQRPGQGLEWI
GDIYPGTSTTNYNEKFKNKATLTVDTSSSTAYMQLSSLTSDDSAVYYCTRIYYDYDGYYFDYWGQGT
TLTVSS

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140)

SEQ ID NO: 9: AMINO ACID SEQUENCE OF No.76 HEAVY CHAIN CDR1

NYWIN

SEQ ID NO: 10: AMINO ACID SEQUENCE OF No.76 HEAVY CHAIN CDR2

DIYPGTSTTNYNEKFKN

SEQ ID NO: 11: AMINO ACID SEQUENCE OF No.76 HEAVY CHAIN CDR13

IYYDYDGYYFDY

Fig. 2

SEQ ID NO: 12: AMINO ACID SEQUENCE OF #1G5 LIGHT CHAIN VARIABLE REGION

MESQTLVFISILLWLYGSDGNIVMTQSPKSMSMSVGERVTLSCKASENVGNSVSWYQQKAEQSPKPL
IYGASNRYTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQSYSYPYTFGGGTKLEIKRA

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129)

SEQ ID NO: 13: AMINO ACID SEQUENCE OF #1G5 LIGHT CHAIN CDR1

KASENVGNSVS

SEQ ID NO: 14: AMINO ACID SEQUENCE OF #1G5 LIGHT CHAIN CDR2

GASNRYT

SEQ ID NO: 15: AMINO ACID SEQUENCE OF #1G5 LIGHT CHAIN CDR3

GQSYSYPYT

SEQ ID NO: 16: AMINO ACID SEQUENCE OF #1G5 HEAVY CHAIN VARIABLE REGION

MGWSCIILFLVAAATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWI
GNIYPGSSSINYNEKFKSKATLTVDTSSSTAYMQLSSLTSDDSAVYYCSRTIYNYGSSGYNYAMDYW
GQGTSVIVSS

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144)

SEQ ID NO: 17: AMINO ACID SEQUENCE OF #1G5 HEAVY CHAIN CDR1

SYWIN

SEQ ID NO: 18: AMINO ACID SEQUENCE OF #1G5 HEAVY CHAIN CDR2

NIYPGSSSINYNEKFKS

SEQ ID NO: 19: AMINO ACID SEQUENCE OF #1G5 HEAVY CHAIN CDR3

TIYNYGSSGYNYAMDY

Fig. 3

SEQ ID NO: 20: AMINO ACID SEQUENCE OF #4C12 LIGHT CHAIN VARIABLE REGION

MESQTLVFISILLWLYGADGNIVMTQSPKSMSMSVGERVTLSCKASENVGVSVSWYQQKPEQSPKLL
IYGASNRCTGVPDRFTGSRSATDFTLTVSNVQAEDLADYHCGQSYSYPYTFGGGTRLEIKRA

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129)

SEQ ID NO: 21: AMINO ACID SEQUENCE OF #4C12 LIGHT CHAIN CDR1

KASENVGVSVS

SEQ ID NO: 22: AMINO ACID SEQUENCE OF #4C12 LIGHT CHAIN CDR2

GASNRCT

SEQ ID NO: 23: AMINO ACID SEQUENCE OF #4C12 LIGHT CHAIN CDR3

GQSYSYPYT

SEQ ID NO: 24: AMINO ACID SEQUENCE OF #4C12 HEAVY CHAIN VARIABLE REGION

MGWSCIILFLVAAATGVQSQVQLQQPGAELVKPGASVKLSCKASGYTFTTYWINWMQQRPGQGLEWI
GNIYPGTRSSNYNEKFKNKATLTVDTSSSTAYMQLNSLTSDDSAVYYCTRVYYDHVGYYFDYWGQGT
TLTVSS

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140)

SEQ ID NO: 25: AMINO ACID SEQUENCE OF #4C12 HEAVY CHAIN CDR1

TYWIN

SEQ ID NO: 26: AMINO ACID SEQUENCE OF #4C12 HEAVY CHAIN CDR2

NIYPGTRSSNYNEKFKN

SEQ ID NO: 27: AMINO ACID SEQUENCE OF #4C12 HEAVY CHAIN CDR3

VYYDHVGYYFDY

Fig. 4

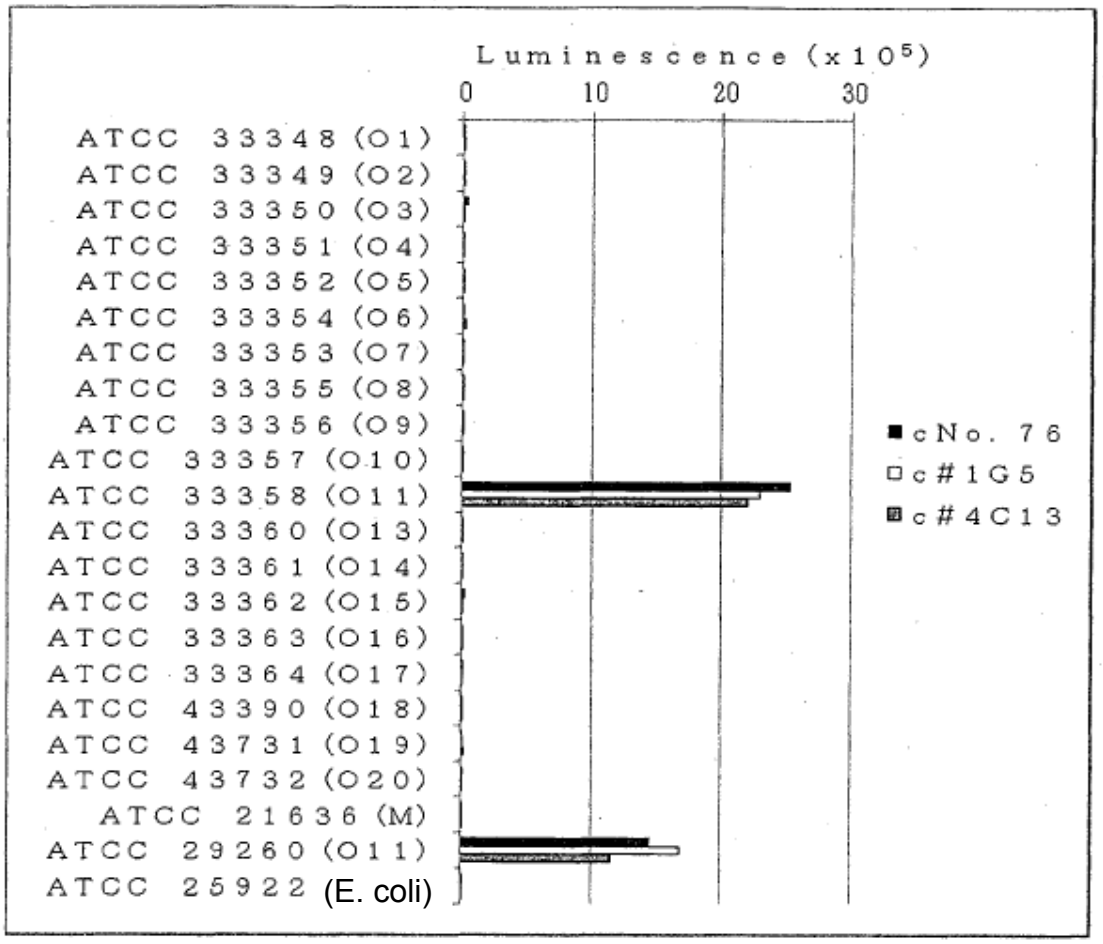

Luminescence (x10⁵)
0
10
20
30
ATCC 33348 (O1)
ATCC 33349 (O2)
ATCC 33350 (O3)
ATCC 33351 (O4)
ATCC 33352 (O5)
ATCC 33354 (O6)
ATCC 33353 (O7)
ATCC 33355 (O8)
ATCC 33356 (O9)
ATCC 33357 (O10)
ATCC 33358 (O11)
ATCC 33360 (O13)
ATCC 33361 (O14)
ATCC 33362 (O15)
ATCC 33363 (O16)
ATCC 33364 (O17)
ATCC 43390 (O18)
ATCC 43731 (O19)
ATCC 43732 (O20)
ATCC 21636 (M)
ATCC 29260 (O11)
ATCC 25922 (E. coli)
cNo. 76
c#1G5
c#4C13

Fig. 5

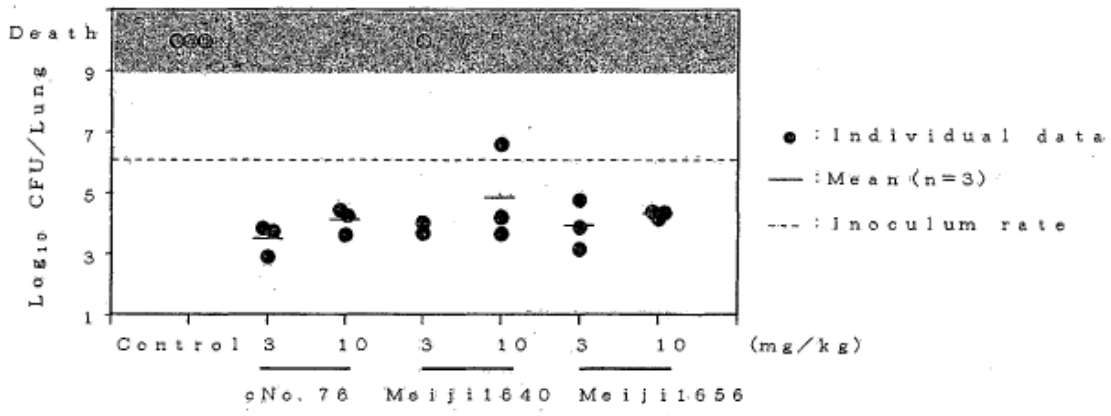

Death
Log10 CFU/Lung
9
7
5
3
1
Control
3
10
3
10
3
10
(mg/kg)
cNo. 76
Meiji1640
Meiji1656
: Individual data
: Mean (n=3)
: Inoculum rate

Fig. 6

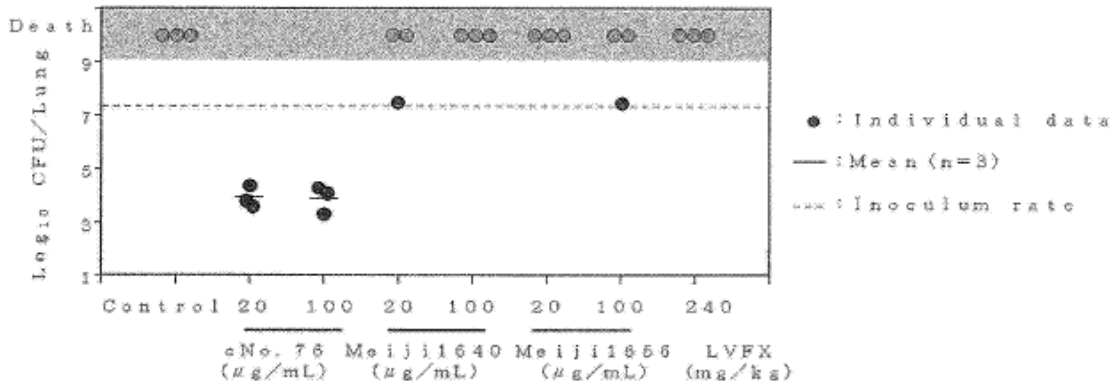


Fig. 7

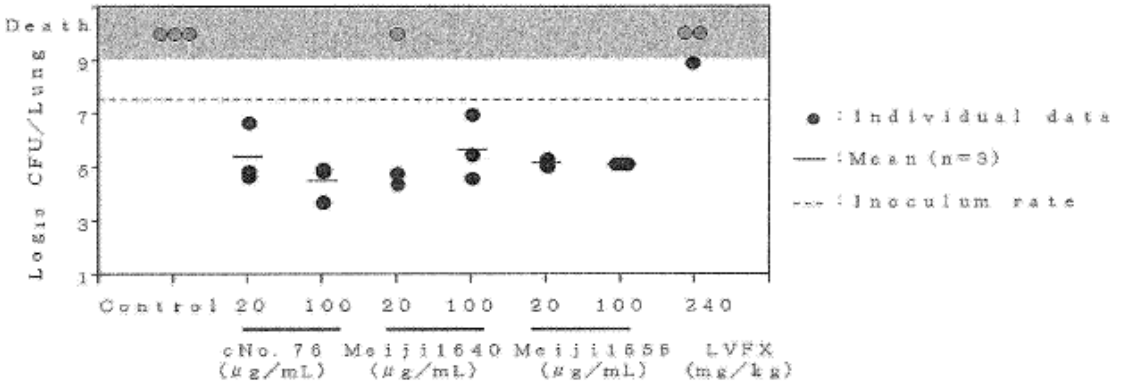


Fig. 8

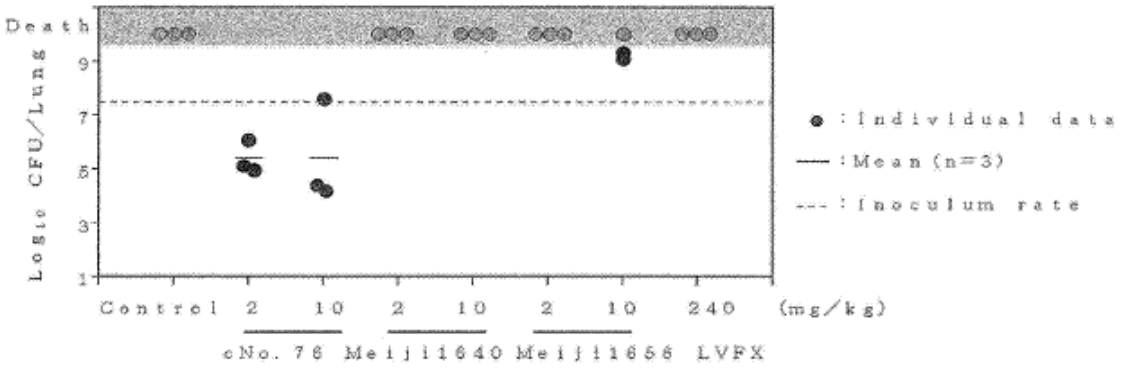


Fig. 9

SEQ ID NO: 56: NUCLEOTIDE SEQUENCE OF h#1G5-H1

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctggtgcagtctggcgccgaagtgaagaaaccaggcgccagcgtgaaggtgtcctgcaaggc
cagcggctacacctttaccagctactggatcaactgggtgcgccaggcccctggacagggcctg
gaatggatgggcaacatctaccccggcagcagcagcatcaactacaacgagaagttcaagagcc
gcgtgaccatcaccgccgacaccagcacaagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgcccggaccatctacaactacggcagctccggctacaat
tacgccatggactactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcc
caagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctg
cctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagc
ggcgtgcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtga
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gagcagtacaacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctga
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cgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaac
gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccc
tgtctcccggcaaa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-432), CONSTANT REGION (433-1422)

SEQ ID NO: 57: AMINO ACID SEQUENCE OF h#1G5-H1

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGL
EWMGNIYPGSSSINYNEKFKSRVTITADTSTSTAYMELSSLRSEDTAVYYCARTIYNYGSSGYN
YAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144), CONSTANT REGION (145-474)

Fig. 10

SEQ ID NO: 58: NUCLEOTIDE SEQUENCE OF h#1G5-H2

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctggtgcagtctggcgccgaagtgaagaaaccaggcgccagcgtgaaggtgtcctgcaaggc
cagcggctacacctttaccagctactggatcaactgggtgcgccaggcccctggacagggcctg
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gcgtgaccctgaccgtggacaccagcacaagcaccgcctacatggaactgagcagcctgcggag
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tacgccatggactactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcc
caagcgtcttcccccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctg
cctggtcaaggactacttccccgaacccgtgaccgtgagctggaactcaggcgccctgaccagc
ggcgtgcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtga
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atgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccg
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tgtctcccggcaaa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-432), CONSTANT REGION (433-1422)

SEQ ID NO: 59: AMINO ACID SEQUENCE OF h#1G5-H2

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGL
EWMGNIYPGSSSINYNEKFKSRVTLTVDTSTSTAYMELSSLRSEDTAVYYCSRTIYNYGSSGYN
YAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144), CONSTANT REGION (145-474)

Fig. 11

SEQ ID NO: 60: NUCLEOTIDE SEQUENCE OF h#1G5-H3

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctgcagcagcctggcgccgaagtgaaaaagccaggcgccagcgtgaaggtgtcctgcaaggc
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gtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccc
tgtctcccggcaaa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-432), CONSTANT REGION (433-1422)

SEQ ID NO: 61: AMINO ACID SEQUENCE OF h#1G5-H3

MKHLWFFLLLVAAPRWVLSQVQLQQPGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGL
EWMGNIYPGSSSINYNEKFKSRATLTVDTSTSTAYMELSSLTSEDTAVYYCSRTIYNYGSSGYN
YAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144), CONSTANT REGION (145-474)

Fig. 12

SEQ ID NO: 62: NUCLEOTIDE SEQUENCE OF h#1G5-H4

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctgcagcagcctggcgccgagctgaaaaaacctggcgcctccgtgaaggtgtcctgcaaggc
cagcggctacacctttaccagctactggatcaactgggtgcgccaggcccctggacagggcctg
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ccagcacctgaactcctgggggggaccctcagtcttcctcttcccccaaaacccaaggacaccc
tcatgatctcccggaccccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctga
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SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-432), CONSTANT REGION (433-1422)

SEQ ID NO: 63: AMINO ACID SEQUENCE OF h#1G5-H4

MKHLWFFLLLVAAPRWVLSQVQLQQPGAELKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGL
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VFSCSVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144), CONSTANT REGION (145-474)

Fig. 13

SEQ ID NO: 64: NUCLEOTIDE SEQUENCE OF h#1G5-H5

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
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tgtctcccggcaaa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-432), CONSTANT REGION (433-1422)

SEQ ID NO: 65: AMINO ACID SEQUENCE OF h#1G5-H5

MKHLWFFLLLVAAPRWVLSQVQLQQPGAELKKPGASVKVSCKASGYTFTSYWINWVKQRPGQGL
EWIGNIYPGSSSINYNEKFKSKATLTVDTSSSTAYMQLSSLTSDDSAVYYCSRTIYNYGSSGYN
YAMDYWGQGTSVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-144), CONSTANT REGION (145-474)

Fig. 14

SEQ ID NO: 66: NUCLEOTIDE SEQUENCE OF h#1G5-L1

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcgaca
tcgtgatgacccagagccctgacagcctggccgtgtctctgggagagagagccaccatcaactg
caaggccagcgagaacgtgggcaacagcgtgtcctggtatcagcagaagcccggccagcccccc
aagctgctgatctacggcgccagcaacagatacaccggcgtgcccgatagattcagcggcagcg
gctctggcaccgacttcaccctgacaatcagctccctgcaggccgaggacgtggccgtgtacta
ctgtggccagagctacagctacccctacaccttcggccagggcaccaaggtggaaatcaagcgt
acggtggccgcccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccg
cctccgtggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtgga
caacgccctgcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacc
tacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

SIGNAL SEQUENCE (1-60), VARIABLE REGION (61-387), CONSTANT REGION (388-702)

SEQ ID NO: 67: AMINO ACID SEQUENCE OF h#1G5-L1

MVLQTQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKASENVGNSVSWYQQKPGQPP
KLLIYGASNRYTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCGQSYSYPYTFGQGTKVEIKR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129), CONSTANT REGION (130-234)

Fig. 15

SEQ ID NO: 68: NUCLEOTIDE SEQUENCE OF h#1G5-L2

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcaaca
tcgtgatgacccagagccccgacagcctggccgtgtctctgggagagagagccaccatcagctg
caaggccagcgagaacgtgggcaacagcgtgtcctggtatcagcagaagcccggccagagccct
aagcccctgatctacggcgccagcaacagatacaccggcgtgcccgatagattcagcggcagcg
gctctgccaccgacttcaccctgacaatcagctccctgcaggccgaggacgtggccgtgtatca
ctgtggccagagctacagctacccctacaccttcggcggaggcaccaaggtggaaatcaagcgt
acggtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccg
cctccgtggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtgga
caacgccctgcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacc
tacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

SIGNAL SEQUENCE (1-60), VARIABLE REGION (61-387), CONSTANT REGION (388-702)

SEQ ID NO: 69: AMINO ACID SEQUENCE OF h#1G5-L2

MVLQTQVFISLLLWISGAYGNIVMTQSPDSLAVSLGERATISCKASENVGNSVSWYQQKPGQSP
KPLIYGASNRYTGVPDRFSGSGSATDFTLTISSLQAEDVAVYHCGQSYSYPYTFGGGTKVEIKR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129), CONSTANT REGION (130-234)

Fig. 16

SEQ ID NO: 70: NUCLEOTIDE SEQUENCE OF h#1G5-L3

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcaaca
tcgtgatgacccagagccccgacagcctggccgtgtctctgggagagagagccaccatcagctg
caaggccagcgagaacgtgggcaacagcgtgtcctggtatcagcagaagcccggccagagccct
aagcccctgatctacggcgccagcaacagatacaccggcgtgcccgatagattcagcggcagcg
gctctgccaccgacttcaccctgacaatcagctccctgcaggccgaggacgtggccgattatca
ctgcggccagtcctacagctacccctacacctttggcggaggcaccaaggtggaaatcaagcgt
acggtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccg
cctccgtggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtgga
caacgccctgcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacc
tacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

SIGNAL SEQUENCE (1-60), VARIABLE REGION (61-387), CONSTANT REGION (388-702)

SEQ ID NO: 71: AMINO ACID SEQUENCE OF h#1G5-L3

MVLQTQVFISLLLWISGAYGNIVMTQSPDSLAVSLGERATISCKASENVGNSVSWYQQKPGQSP
KPLIYGASNRYTGVPDRFSGSGSATDFTLTISSLQAEDVADYHCGQSYSYPYTFGGGTKVEIKR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129), CONSTANT REGION (130-234)

Fig. 17

SEQ ID NO: 72: NUCLEOTIDE SEQUENCE OF h#1G5-L4

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcaaca
tcgtgatgacccagagccccgacagcatgagcatgagcgtgggcgagagagccaccctgagctg
caaggcctctgagaacgtgggcaacagcgtgtcctggtatcagcagaaggccgagcagagcccc
aagcccctgatctacggcgccagcaacagatacaccggcgtgcccgatagattcaccggcagcg
gcagcgccaccgacttcaccctgacaatcagctccctgcaggccgaggacctggccgattatca
ctgcggccagagctacagctacccctacacctttggcggaggcaccaagctggaaatcaagcgt
acggtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccg
cctccgtggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtgga
caacgccctgcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacc
tacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

SIGNAL SEQUENCE (1-60), VARIABLE REGION (61-387), CONSTANT REGION (388-702)

SEQ ID NO: 73: AMINO ACID SEQUENCE OF h#1G5-L4

MVLQTQVFISLLLWISGAYGNIVMTQSPDSMSMSVGERATLSCKASENVGNSVSWYQQKAEQSP
KPLIYGASNRYTGVPDRFTGSGSATDFTLTISSLQAEDLADYHCGQSYSYPYTFGGGTKLEIKR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129), CONSTANT REGION (130-234)

Fig. 18

SEQ ID NO: 74: NUCLEOTIDE SEQUENCE OF h#1G5-L5

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcaaca
tcgtgatgacccagagccccgacagcatgagcatgagcgtgggcgagagagtgaccctgagctg
caaggccagcgagaacgtgggcaacagcgtgtcctggtatcagcagaaggccgagcagagcccc
aagcccctgatctacggcgccagcaacagatacaccggcgtgcccgatagattcaccggcagcg
gcagcgccaccgacttcaccctgacaatcagctccctgcaggccgaggacctggccgattatca
ctgcggccagagctacagctacccctacaccttttggcggaggcaccaagctggaaatcaagcgt
acggtggccgccccctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccg
cctccgtggtgtgcctgctgaataacttctaccccagagaggccaaggtgcagtggaaggtgga
caacgccctgcagtccgggaactcccaggagagcgtgaccgagcaggacagcaaggacagcacc
tacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

SIGNAL SEQUENCE (1-60), VARIABLE REGION (61-387), CONSTANT REGION (388-702)

SEQ ID NO: 75: AMINO ACID SEQUENCE OF h#1G5-L5

MVLQTQVFISLLLWISGAYGNIVMTQSPDSMSMSVGERVTLSCKASENVGNSVSWYQQKAEQSP
KPLIYGASNRYTGVPDRFTGSGSATDFTLTISSLQAEDLADYHCGQSYSYPYTFGGGTKLEIKR
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SIGNAL SEQUENCE (1-20), VARIABLE REGION (21-129), CONSTANT REGION (130-234)

Fig. 19

SEQ ID NO: 76: NUCLEOTIDE SEQUENCE OF h#4C13K-H1

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctggtgcagtctggcgccgaagtgaagaaaccaggcgccagcgtgaaggtgtcctgcaaggc
cagcggctacacctttaccacctactggatcaactgggtgcgccaggcccctggacagggcctg
gaatggatgggcaacatctaccccggcaccagaagcagcaactacaacgagaagttcaagaacc
gcgtgaccatcaccgccgacaccagcaccagcacagcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccagagtgtactacgaccacgtgggctactacttcgac
tactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcccaagcgtcttcc
ccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctgcctggtcaagga
ctacttccccgaacccgtgaccgtgagctggaactcaggcgccctgaccagcggcgtgcacacc
ttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctcca
gcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtgga
caagagagttgagcccaaatcttgtgacaaaactcacacatgcccaccctgcccagcacctgaa
ctcctggggggaccctcagtcttcctcttcccccaaaacccaaggacaccctcatgatctccc
ggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaa
ctggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaac
agcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagt
acaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaa
aggccagccccgggaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaac
caggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggaga
gcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctcctt
cttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgc
tccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctcccggca
aa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-420), CONSTANT REGION (421-1410)

SEQ ID NO: 77: AMINO ACID SEQUENCE OF h#4C13K-H1

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWINWVRQAPGQGL
EWMGNIYPGTRSSNYNEKFKNRVTITADTSTSTAYMELSSLRSEDTAVYYCARVYYDHVGYYFD
YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140), CONSTANT REGION (141-470)

Fig. 20

SEQ ID NO: 78: NUCLEOTIDE SEQUENCE OF h#4C13K-H2

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctggtgcagtctggcgccgaagtgaagaaaccaggcgccagcgtgaaggtgtcctgcaaggc
cagcggctacacctttaccacctactggatcaactgggtgcgccaggcccctggacagggcctg
gaatggatgggcaacatctaccccggcaccagaagcagcaactacaacgagaagttcaagaacc
gcgtgaccctgaccgtggacaccagcaccagcacagcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgtacccgggtgtactacgaccacgtgggctactacttcgac
tactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcccaagcgtcttcc
ccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctgcctggtcaagga
ctacttccccgaaccctgaccgtgagctggaactcaggcgccctgaccagcggcgtgcacacc
ttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctcca
gcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtgga
caagagagttgagcccaaatcttgtgacaaaactcacacatgcccaccctgcccagcacctgaa
ctcctgggggacctcagtcttcctcttcccccaaaacccaaggacaccctcatgatctccc
ggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaa
ctggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaac
agcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagt
acaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaa
aggccagccccgggaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaac
caggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggaga
gcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctcctt
cttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgc
tccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctcccggca
aa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-420), CONSTANT REGION (421-1410)

SEQ ID NO: 79: AMINO ACID SEQUENCE OF h#4C13K-H2

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTTYWINWVRQAPGQGL
EWMGNIYPGTRSSNYNEKFKNRVTLTVDTSTSTAYMELSSLRSEDTAVYYCTRVYYDHVGYYFD
YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140), CONSTANT REGION (141-470)

Fig. 21

SEQ ID NO: 80: NUCLEOTIDE SEQUENCE OF h#4C13K-H3

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctgcagcagcctggcgccgaagtgaaaaagccaggcgccagcgtgaaggtgtcctgcaaggc
cagcggctacacctttaccacctactggatcaactggatgcagcagcggccaggccagggcctg
gaatggatgggcaatatctaccccggcaccagaagcagcaactacaacgagaagttcaagaacc
gggccaccctgaccgtggacaccagcacaagcaccgcctacatggaactgagcagcctgaccag
cgaggacaccgccgtgtactactgcaccagagtgtactacgaccacgtgggctactacttcgac
tactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcccaagcgtcttcc
ccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctgcctggtcaagga
ctacttccccgaaccctgaccgtgagctggaactcaggcgccctgaccagcggcgtgcacacc
ttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctcca
gcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtgga
caagagagttgagcccaaatcttgtgacaaaactcacacatgcccaccctgcccagcacctgaa
ctcctggggggaccctcagtcttcctcttcccccaaaacccaaggacaccctcatgatctccc
ggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaa
ctggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaac
agcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagt
acaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaa
aggccagccccgggaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaac
caggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggaga
gcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctcctt
cttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgc
tccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctcccggca
aa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-420), CONSTANT REGION (421-1410)

SEQ ID NO: 81: AMINO ACID SEQUENCE OF h#4C13K-H3

MKHLWFFLLLVAAPRWVLSQVQLQQPGAEVKKPGASVKVSCKASGYTFTTYWINWMQQRPGQGL
EWMGNIYPGTRSSNYNEKFKNRATLTVDTSTSTAYMELSSLTSEDTAVYYCTRVYYDHVGYYFD
YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140), CONSTANT REGION (141-470)

Fig. 22

SEQ ID NO: 82: NUCLEOTIDE SEQUENCE OF h#4C13K-H4

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
agctgcagcagcctggcgccgagctgaaaaaacctggcgcctccgtgaaggtgtcctgcaaggc
cagcggctacacctttaccacctactggatcaactggatgcagcagcggccaggccagggcctg
gaatggatcggcaatatctaccccggcaccagaagcagcaactacaacgagaagttcaagaaca
aggccaccctgaccgtggacaccagcagctccaccgcctacatggaactgagcagcctgaccag
cgacgacagcgccgtgtactactgcaccagagtgtactacgaccacgtgggctactacttcgac
tactggggccagggcaccctcgtgaccgtgagctcagcctccaccaagggcccaagcgtcttcc
ccctggcaccctcctccaagagcacctctggcggcacagccgccctgggctgcctggtcaagga
ctacttccccgaaccccgtgaccgtgagctggaactcaggcgccctgaccagcggcgtgcacacc
ttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctcca
gcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtgga
caagagagttgagcccaaatcttgtgacaaaactcacacatgcccaccctgcccagcacctgaa
ctcctgggggacccctcagtcttcctcttcccccaaaacccaaggacaccctcatgatctccc
ggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaa
ctggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaac
agcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagt
acaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaaccatctccaaagccaa
aggccagccccgggaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaac
caggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggaga
gcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctcctt
cttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgc
tccgtgatgcatgaggctctgcacaaccactacacccagaagagcctctccctgtctcccggca
aa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-420), CONSTANT REGION (421-1410)

SEQ ID NO: 83: AMINO ACID SEQUENCE OF h#4C13K-H4

MKHLWFFLLLVAAPRWVLSQVQLQQPGAELKKPGASVKVSCKASGYTFTTYWINWMQQRPGQGL
EWIGNIYPGTRSSNYNEKFKNKATLTVDTSSSTAYMELSSLTSDDSAVYYCTRVYYDHVGYYFD
YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140), CONSTANT REGION (141-470)

Fig. 23

SEQ ID NO: 84: NUCLEOTIDE SEQUENCE OF h#4C13K-H5

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgc
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aa

SIGNAL SEQUENCE (1-57), VARIABLE REGION (58-420), CONSTANT REGION (421-1410)

SEQ ID NO: 85: AMINO ACID SEQUENCE OF h#4C13K-H5

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QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SIGNAL SEQUENCE (1-19), VARIABLE REGION (20-140), CONSTANT REGION (141-470)

Fig. 24

SEQ ID NO: 123: AMINO ACID SEQUENCE OF #4C13 LIGHT CHAIN CDR1

KASENVGVSVS

SEQ ID NO: 124: AMINO ACID SEQUENCE OF #4C13 LIGHT CHAIN CDR2

GASNRYT

SEQ ID NO: 125: AMINO ACID SEQUENCE OF #4C13 LIGHT CHAIN CDR3

GQSYSYPYT

SEQ ID NO: 86: AMINO ACID SEQUENCE OF #4C13 HEAVY CHAIN CDR1

TYWIN

SEQ ID NO: 87: AMINO ACID SEQUENCE OF #4C13 HEAVY CHAIN CDR2

NIYPGTRSSNYNEKFKN

SEQ ID NO: 88: AMINO ACID SEQUENCE OF #4C13 HEAVY CHAIN CDR3

VYYDHVGYYFDY

Fig. 25

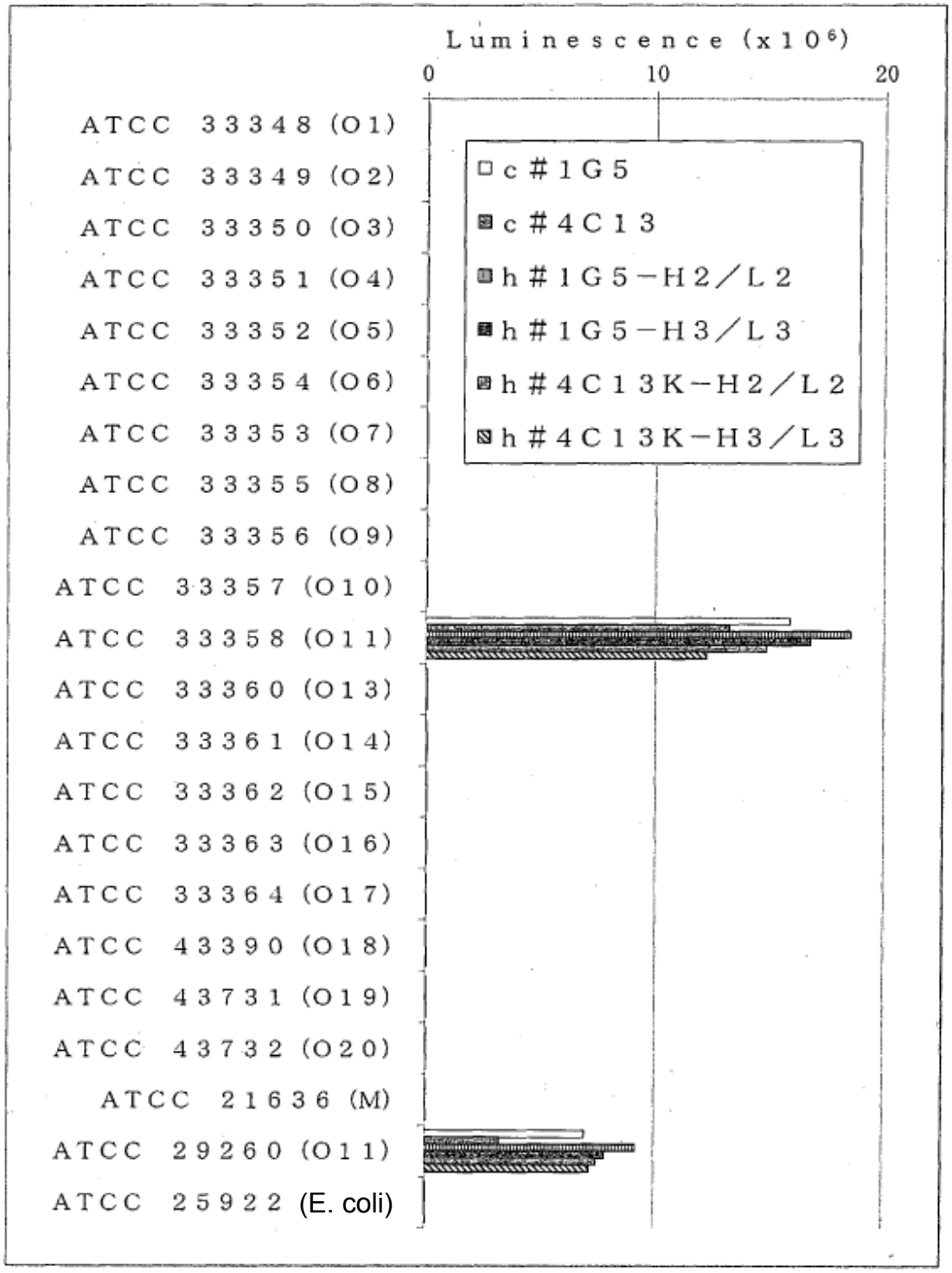

Luminescence (x10⁶)
0
10
20
c#1G5
c#4C13
h#1G5-H2/L2
h#1G5-H3/L3
h#4C13K-H2/L2
h#4C13K-H3/L3
ATCC 33348 (O1)
ATCC 33349 (O2)
ATCC 33350 (O3)
ATCC 33351 (O4)
ATCC 33352 (O5)
ATCC 33354 (O6)
ATCC 33353 (O7)
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ATCC 33360 (O13)
ATCC 33361 (O14)
ATCC 33362 (O15)
ATCC 33363 (O16)
ATCC 33364 (O17)
ATCC 43390 (O18)
ATCC 43731 (O19)
ATCC 43732 (O20)
ATCC 21636 (M)
ATCC 29260 (O11)
ATCC 25922 (E. coli)

Fig. 26

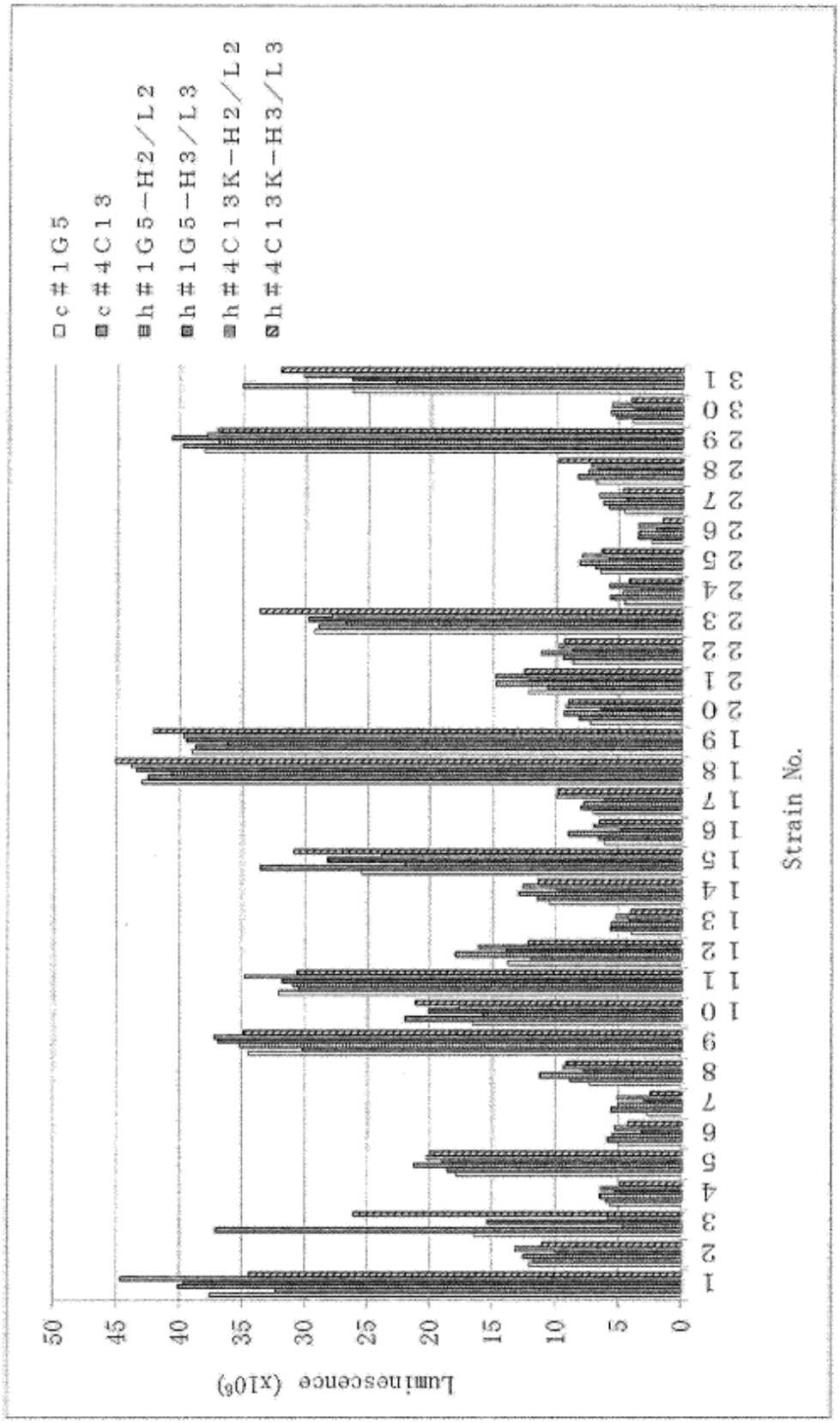

□c#1G5
■c#4C13
■h#1G5−H2/L2
■h#1G5−H3/L3
■h#4C13K−H2/L2
■h#4C13K−H3/L3
Luminescence (x10⁶)
0
5
10
15
20
25
30
35
40
45
50
Strain No.
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Fig. 27

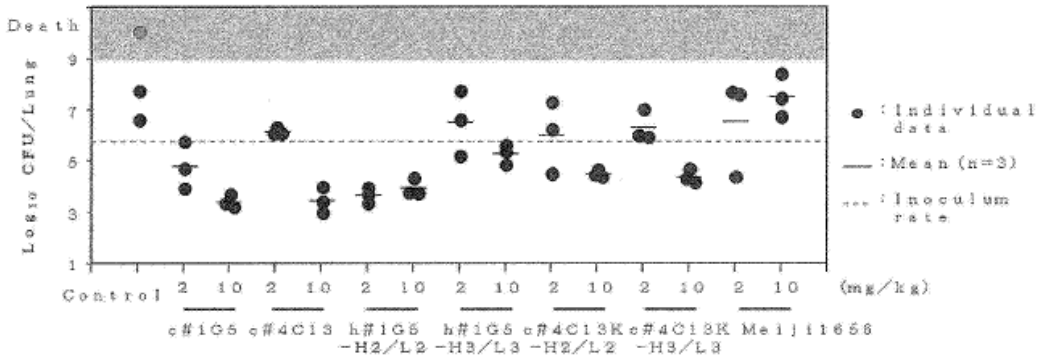
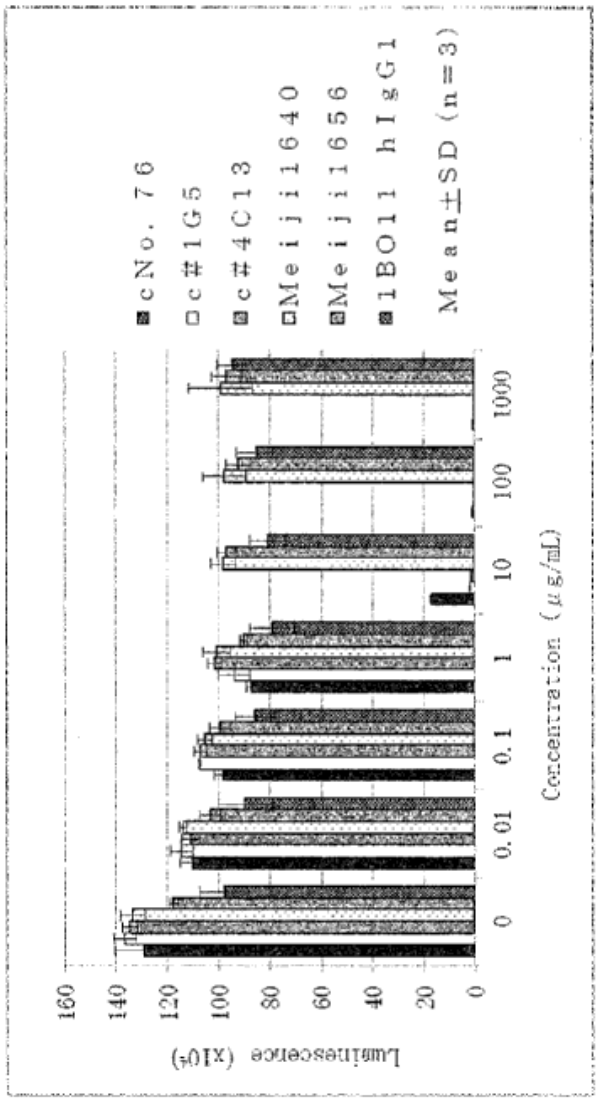

Death
Log10 CFU/Lung
9
7
5
3
1
Control
2
10
2
10
2
10
2
10
2
10
2
10
2
10
(mg/kg)
c#1G5
c#4C13
h#1G5 -H2/L2
h#1G5 -H3/L3
c#4C13K -H2/L2
c#4C13K -H3/L3
Meiji1656
: Individual data
: Mean (n=3)
: Inoculum rate

Fig. 28


cNo. 76
c#1G5
c#4C13
Meiji1640
Meiji1656
1BO11 hIgG1
Mean±SD (n=3)
Concentration (μg/mL)
0
0.01
0.1
1
10
100
1000
Luminescence (x10⁴)
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140
120
100
80
60
40
20
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SEQUENCE LISTING

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tgcagtcgac ggtaccgcgg gcccgggatc ccccccccc ccgatgggac gtccacatat 660

acctgccgtt cactattatt tagtgaaatg agatattatg atattttctg aattgtgatt 720

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acagatagat tttttagttc tttaggcccg tagtctgcaa atccttttat gattttctat 840

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gaaaagtaaa tcgcgcgggt ttgttactga taaagcaggc aagacctaaa atgtgtaaag 960

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aactaacttg ccatcttcaa acaggagggc tggaagaagc agaccgctaa cacagtacat 1080

aaaaaaggag acatgaacga tgaacatcaa aaagtttgca aaacaagcaa cagtattaac 1140

ctttactacc gcactgctgg caggaggcgc aactcaagcg tttgcgaaag aaacgaacca 1200

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Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
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Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Thr Ser Val Ser Trp Tyr Gln Glu Lys Pro Glu Gln Ser Pro
50 55 60

Lys Leu Leu Ile Phe Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65 70 75 80

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

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Ala

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<400> 5

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Gly Ala Ser Asn Arg Tyr Thr
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Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr
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<400> 8

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
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Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Asn Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Asp Ile Tyr Pro Gly Thr Ser Thr Thr Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser

85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Ile Tyr Tyr Asp Tyr Asp Gly Tyr Tyr Phe Asp
115 120 125

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

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Asn Tyr Trp Ile Asn
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<400> 10

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

Asn

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Ile Tyr Tyr Asp Tyr Asp Gly Tyr Tyr Phe Asp Tyr
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<400> 12

Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile Leu Leu Trp Leu Tyr
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Gly Ser Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
20 25 30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
50 55 60

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

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

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Ala

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Lys Ala Ser Glu Asn Val Gly Asn Ser Val Ser
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Gly Ala Ser Asn Arg Tyr Thr
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<400> 15

Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr
1 5

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<400> 16

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

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
115 120 125

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
130 135 140

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<400> 17

Ser Tyr Trp Ile Asn
1 5

<210> 18
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<400> 18

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

Ser

<210> 19
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<400> 19

Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn Tyr Ala Met Asp Tyr
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<210> 20
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<400> 20

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Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
20 25 30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Val Ser Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Cys Thr Gly Val Pro Asp
65 70 75 80

Arg Phe Thr Gly Ser Arg Ser Ala Thr Asp Phe Thr Leu Thr Val Ser

85 90 95

Asn Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Ala

<210> 21
<211> 11
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<400> 21

Lys Ala Ser Glu Asn Val Gly Val Ser Val Ser
1 5 10

<210> 22
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<220>
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<400> 22

Gly Ala Ser Asn Arg Cys Thr
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<400> 23

Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr
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<400> 24

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly

1 5 10 15

Val Gln Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65 70 75 80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
115 120 125

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

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Thr Tyr Trp Ile Asn
1 5

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<400> 26

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

Asn

<210> 27

<211> 12
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<400> 27

Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp Tyr
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<223> Nuc of signal and constant of light chain

<400> 28
gcctccggac tctagagcca ccatggtgct gcagacccag gtgttcatct ccctgctgct 60

gtggatctcc ggcgcgtacg gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120

cgtgttcatc ttcccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg 180

cctgctgaat aacttctacc ccagagaggc caaggtgcag tggaaggtgg acaacgccct 240

gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300

cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360

cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420

ttaggggccc gtttaaacgg gggaggcta 449

<210> 29
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Nuc of signal and constant of IgG1 chain

<400> 29
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120

ggcccaagcg tcttcccccct ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 240

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 540

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 780

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 840

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1080

tccctgtctc ccggcaaatg agatatcggg cccgtttaaa cgggggaggc ta 1132

<210> 30
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of chimeric No.76

<220>
<221> CDS
<222> (1)..(702)

<400> 30
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 gcg tac ggc aac att gta atg acc caa tct ccc aaa tcc atg tcc 96
Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
20 25 30

atg tca gta gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat 144
Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

gtg ggt act tct gta tcc tgg tat caa gag aaa cca gag cag tct cct 192
Val Gly Thr Ser Val Ser Trp Tyr Gln Glu Lys Pro Glu Gln Ser Pro
50 55 60

aaa ctg ctg ata ttc ggg gca tcc aac cgc tac act ggg gtc ccc gat 240
Lys Leu Leu Ile Phe Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65 70 75 80

cgc ttc aca ggc agt gga tct gca aca gat ttc act ctg acc atc agc 288
Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

agt gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag agt tac 336
Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

agt tat ccg tac acg ttc gga ggg agg acc aag ctg gaa ata aaa cgg 384
Ser Tyr Pro Tyr Thr Phe Gly Gly Arg Thr Lys Leu Glu Ile Lys Arg
115 120 125

gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag 432
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

```
ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 31
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
            20                  25                  30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

Val Gly Thr Ser Val Ser Trp Tyr Gln Glu Lys Pro Glu Gln Ser Pro
    50                  55                  60

Lys Leu Leu Ile Phe Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

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

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

Ser Tyr Pro Tyr Thr Phe Gly Gly Arg Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125
```

```
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  32
<211>  1410
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding heavy chain of chimeric No.76


<220>
<221>  CDS
<222>  (1)..(1410)

<400>  32
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 cag gtc caa ctg cag cag cct ggt gct gag ctt gtg aag          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggg gcc tca gtg aat ctg tcc tgc aag tct tct ggc tac act ttc         144
Pro Gly Ala Ser Val Asn Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe
        35                  40                  45

acc aac tac tgg ata aac tgg gtg aag cag agg cct gga caa ggc ctt         192
Thr Asn Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gag tgg att gga gat att tat cct ggt act agt act act aac tac aat         240
Glu Trp Ile Gly Asp Ile Tyr Pro Gly Thr Ser Thr Thr Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac aag gcc aca ctg act gta gac aca tcc tcc agc         288
Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctc agc agc ctg aca tct gac gac tct gcg gtc         336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
```

```
            100                 105                 110

tat tat tgt aca aga atc tac tat gat tac gac ggg tac tac ttt gac        384
Tyr Tyr Cys Thr Arg Ile Tyr Tyr Asp Tyr Asp Gly Tyr Tyr Phe Asp
        115                 120                 125

tac tgg ggc caa ggc acc act ctc aca gtc agc tca gcc tcc acc aag        432
Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc        480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc        528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg        624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac        672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc        720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa        768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac        816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac        864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
```

```
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                               1410
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 33
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33

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

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Val Asn Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Asn Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Asp Ile Tyr Pro Gly Thr Ser Thr Thr Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Ile Tyr Tyr Asp Tyr Asp Gly Tyr Tyr Phe Asp
        115                 120                 125
```

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

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

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

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

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
```

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 34
<211> 752
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of chimeric #1G5

<220>
<221> CDS
<222> (26)..(727)

<400> 34
ccagcctccg gactctagag ccacc atg gtg ctg cag acc cag gtg ttc atc 52
Met Val Leu Gln Thr Gln Val Phe Ile
1 5

agc ctg ctg ctg tgg atc agc ggc gcc tac ggc aac atc gtg atg acc 100
Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asn Ile Val Met Thr
10 15 20 25

cag agc ccc aag agc atg agc atg tcc gtg ggc gag aga gtg acc ctg 148
Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu
30 35 40

agc tgc aag gcc agc gag aac gtg ggc aac agc gtg tcc tgg tat cag 196
Ser Cys Lys Ala Ser Glu Asn Val Gly Asn Ser Val Ser Trp Tyr Gln
45 50 55

cag aag gcc gag cag tcc ccc aag ccc ctg atc tac ggc gcc agc aac 244
Gln Lys Ala Glu Gln Ser Pro Lys Pro Leu Ile Tyr Gly Ala Ser Asn
60 65 70

aga tac acc ggc gtg ccc gat aga ttc acc ggc agc ggc agc gcc acc 292
Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr
75 80 85

gac ttc acc ctg aca atc agc agc gtg cag gcc gag gac ctg gcc gat 340
Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp
90 95 100 105

tat cac tgc ggc cag agc tac agc tac ccc tac acc ttt ggc gga ggc 388
Tyr His Cys Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly
110 115 120

acc aag ctg gaa atc aag cgg gct gtg gcc gct ccc tcc gtg ttc atc 436

```
Thr Lys Leu Glu Ile Lys Arg Ala Val Ala Ala Pro Ser Val Phe Ile
            125                 130                 135

ttt cca ccc agc gac gag cag ctg aag tcc ggc aca gct agc gtc gtg        484
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
        140                 145                 150

tgc ctg ctg aac aac ttc tac ccc cgc gag gcc aag gtg cag tgg aag        532
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
    155                 160                 165

gtg gac aat gcc ctg cag agc ggc aac tcc cag gaa agc gtg acc gag        580
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
170                 175                 180                 185

cag gac agc aag gac tcc acc tac agc ctg agc agc acc ctg acc ctg        628
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
                190                 195                 200

tcc aag gcc gac tac gag aag cac aag gtg tac gcc tgc gaa gtg acc        676
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
            205                 210                 215

cac cag ggc ctg tct agc ccc gtg acc aag agc ttc aac cgg ggc gag        724
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
        220                 225                 230

tgt tgagtttaaa cgggggaggc taact                                       752
Cys
```

<210> 35
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
            20                  25                  30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
    50                  55                  60

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

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

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110
```

```
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  36
<211>  1422
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding heavy chain of chimeric #1G5


<220>
<221>  CDS
<222>  (1)..(1422)

<400>  36
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 cag gtg cag ctg cag cag cct ggc gcc gaa ctc gtg aaa          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggc gcc tct gtg aag ctg agc tgc aag gcc agc ggc tac acc ttc         144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atc aac tgg gtc aag cag cgg cca ggc cag ggc ctg         192
Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atc ggc aat atc tac ccc ggc agc agc agc atc aac tac aac         240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80
```

```
gag aag ttc aag agc aag gcc acc ctg acc gtg gac acc agc agc tcc        288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctg tcc agc ctg acc agc gac gac agc gcc gtg        336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc agc cgg acc atc tac aac tac ggc agc tcc ggc tac aat        384
Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc agc gtg atc gtc agc tca        432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag        480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac        528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc        576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc        624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc        672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag        720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc        768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca        816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350
```

```
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                              1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 37
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 37

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

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
```

```
          100                 105                 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
    130                 135                 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
```

370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 38
<211> 752
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of chimeric #4C13

<220>
<221> CDS
<222> (26)..(727)

<400> 38
ccagcctccg gactctagag ccacc atg gtg ctg cag acc cag gtg ttc atc 52
Met Val Leu Gln Thr Gln Val Phe Ile
1 5

agc ctg ctg ctg tgg atc agc ggc gcc tac ggc aac atc gtg atg acc 100
Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asn Ile Val Met Thr
10 15 20 25

cag agc ccc aag agc atg agc atg tcc gtg ggc gag aga gtg acc ctg 148
Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu
30 35 40

agc tgc aag gcc agc gag aac gtg ggc gtg tcc gtg tcc tgg tat cag 196
Ser Cys Lys Ala Ser Glu Asn Val Gly Val Ser Val Ser Trp Tyr Gln
45 50 55

cag aag ccc gag cag tcc ccc aag ctg ctg atc tac ggc gcc agc aac 244
Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn
60 65 70

aga tac acc ggc gtg ccc gat cgg ttc acc ggc tct aga agc gcc acc 292
Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Arg Ser Ala Thr
75 80 85

gac ttc acc ctg acc gtg tcc aat gtg cag gcc gag gac ctg gcc gat 340
Asp Phe Thr Leu Thr Val Ser Asn Val Gln Ala Glu Asp Leu Ala Asp
90 95 100 105

```
tac cac tgt ggc cag agc tac agc tac ccc tac acc ttc ggc gga ggc        388
Tyr His Cys Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly
                110                 115                 120

acc cgg ctg gaa atc aag aga gct gtg gcc gct ccc tcc gtg ttc atc        436
Thr Arg Leu Glu Ile Lys Arg Ala Val Ala Ala Pro Ser Val Phe Ile
            125                 130                 135

ttc cca cct agc gac gag cag ctg aag tcc ggc aca gcc tct gtc gtg        484
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
        140                 145                 150

tgc ctg ctg aac aac ttc tac ccc cgc gag gcc aag gtg cag tgg aag        532
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
    155                 160                 165

gtg gac aat gcc ctg cag agc ggc aac agc cag gaa agc gtg acc gag        580
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
170                 175                 180                 185

cag gac agc aag gac tcc acc tac agc ctg agc agc acc ctg aca ctg        628
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
                190                 195                 200

agc aag gcc gac tac gag aag cac aag gtg tac gcc tgc gaa gtg acc        676
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
            205                 210                 215

cac cag ggc ctg tct agc ccc gtg acc aag agc ttc aac cgg ggc gag        724
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
        220                 225                 230

tgt tgagtttaaa cgggggaggc taact                                       752
Cys
```

<210> 39
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
            20                  25                  30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

Val Gly Val Ser Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80
```

```
Arg Phe Thr Gly Ser Arg Ser Ala Thr Asp Phe Thr Leu Thr Val Ser
                85                  90                  95

Asn Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

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

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

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

<210> 40
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding heavy chain of chimeric #4C13

<220>
<221> CDS
<222> (1)..(1410)

<400> 40

```
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 cag gtg cag ctg cag cag cct ggc gcc gaa ctc gtg aaa          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggc gcc tct gtg aag ctg agc tgc aag gcc agc ggc tac acc ttc         144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg atg cag cag cgg cca ggc cag ggc ctg         192
Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
```

```
    50                  55                  60

gaa tgg atc ggc aat atc tac ccc ggc acc aga agc agc aac tac aac        240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac aag gcc acc ctg acc gtg gac acc agc agc tcc        288
Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctg aac tcc ctg acc agc gac gac agc gcc gtg        336
Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc acc aga gtg tac tac gac cac gtg ggc tac tac ttc gac        384
Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc        480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc        528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg        624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac        672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc        720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa        768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac        816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac        864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
```

```
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                              1410
Ser Leu Ser Pro Gly Lys
465                 470


<210>  41
<211>  470
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  41

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


Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30


Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45


Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60


Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80
```

```
Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

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

```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365


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


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


Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415


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


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445


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


Ser Leu Ser Pro Gly Lys
465                 470


<210>  42
<211>  708
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding light chain of Meiji1640


<220>
<221>  CDS
<222>  (1)..(708)

<400>  42
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 gcg tac ggc gac atc cag atg acc cag agc ccc agc agc ctg agc         96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30

gcc agc gtg ggc gac aga gtg acc atc acc tgt cgg gcc agc cag agc        144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
        35                  40                  45

atc ggc aag tac ctg aac tgg tat cag cag aag ccc ggc aag gcc ccc        192
Ile Gly Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

aag ctg ctg atc tac gcc gcc agc aac ctg cag agc ggc gtg ccc agc        240
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser
65                  70                  75                  80

aga ttt ggc ggc agc ggc tcc ggc acc gac ttc acc ctg acc atc agc        288
```

```
Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

agc ctg cag ccc gag gac tgc gcc acc tac tac tgc cag cag agc ttc        336
Ser Leu Gln Pro Glu Asp Cys Ala Thr Tyr Tyr Cys Gln Gln Ser Phe
            100                 105                 110

acc gcc cct cag aag tac acc ttc ggc cag ggc acc aag ctg gaa atc        384
Thr Ala Pro Gln Lys Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
        115                 120                 125

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

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

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

cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac        576
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

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

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

tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt                       708
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  43
<211>  236
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  43

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


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


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


Ile Gly Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60


Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser
65                  70                  75                  80
```

Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

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

Thr Ala Pro Gln Lys Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
115 120 125

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

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

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

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

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

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

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

<210> 44
<211> 1431
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding heavy chain of Meiji1640

<220>
<221> CDS
<222> (1)..(1431)

<400> 44
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 gag gtg cag ctg gtg gaa agc ggc gga gga ctg gtg cag 96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

cct ggc ggc agc ctg aga ctg tct tgc gcc gcc agc ggc ttc acc atc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile
35 40 45

```
ccc ttc aga aag tac tgg ctg cac tgg gtc cgc cag gcc cct ggc aag        192
Pro Phe Arg Lys Tyr Trp Leu His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60

gga ctc gtg tgg gtg tcc ctg atc atc ggc gac ggc agc agc acc aac        240
Gly Leu Val Trp Val Ser Leu Ile Ile Gly Asp Gly Ser Ser Thr Asn
65                  70                  75                  80

tac gcc gac agc gtg aag ggc cgg ttc acc atc agc cgg gac aac gac        288
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp
                85                  90                  95

aag aac acc ctg tac ctg cag atg aac agc ctg cgg gtg gaa gat acc        336
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr
            100                 105                 110

gcc gtg tac tac tgc gcc agg gac ctg ggc gag cgg acc ggc gat aat        384
Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Glu Arg Thr Gly Asp Asn
        115                 120                 125

tgg cac agc ctg ggc ccc gac tac tgg ggc cag ggc aca ctg gtc acc        432
Trp His Ser Leu Gly Pro Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

gtc agc tca gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc        480
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160

tcc tcc aag agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc        528
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

aag gac tac ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc        576
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

ctg acc agc ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga        624
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc        672
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
    210                 215                 220

acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag        720
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240

gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc        768
Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

cca ccc tgc cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc        816
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag        864
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285

gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag        912
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag        960
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320
```

```
ccc cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc       1008
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag       1056
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350

gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa       1104
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
        355                 360                 365

gcc aaa ggc cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc       1152
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa       1200
Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag       1248
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415

ccc gag aac aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc       1296
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430

tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag       1344
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445

cag ggc aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac       1392
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460

cac tac acc cag aag agc ctc tcc ctg tct ccc ggc aaa                   1431
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475


<210>  45
<211>  477
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  45

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 Thr Ile
        35                  40                  45


Pro Phe Arg Lys Tyr Trp Leu His Trp Val Arg Gln Ala Pro Gly Lys
    50                  55                  60


Gly Leu Val Trp Val Ser Leu Ile Ile Gly Asp Gly Ser Ser Thr Asn
```

```
65                  70                  75                  80

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

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

Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Glu Arg Thr Gly Asp Asn
        115                 120                 125

Trp His Ser Leu Gly Pro Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
    210                 215                 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
```

340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 46
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of Meiji1656

<220>
<221> CDS
<222> (1)..(702)

<400> 46
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 gcg tac ggc gac atc cag ctg acc cag agc ccc agc ttc ctg agc 96
Gly Ala Tyr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
20 25 30

acc agc gtg ggc gac aga gtg acc atc acc tgt cgg gcc agc cag ggc 144
Thr Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
35 40 45

atc agc aac tac ctg gcc tgg tat cag cag aag ccc ggc acc gcc ccc 192
Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro
50 55 60

aag ctg ctg atc tac agc gcc agc acc ctg cag agc ggc gtg ccc agc 240
Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

```
aga ttt tct ggc agc ggc agc ggc acc gag ttc acc ctg acc atc agc        288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
                85                  90                  95

agc ctg cag ccc gag gac ttc gcc acc tac tac tgc cag cac ctg aaa        336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Lys
            100                 105                 110

acc agc ctg gtc acc ttc ggc cag ggc acc cgg ctg gaa atg aag cgt        384
Thr Ser Leu Val Thr Phe Gly Gln Gly Thr Arg Leu Glu Met Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 47
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47

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

Gly Ala Tyr Gly Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser
            20                  25                  30

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

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

```
Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Gln Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Lys
            100                 105                 110

Thr Ser Leu Val Thr Phe Gly Gln Gly Thr Arg Leu Glu Met Lys Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  48
<211>  1440
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding heavy chain of Meiji1656


<220>
<221>  CDS
<222>  (1)..(1440)

<400>  48
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 gag gtg cag ctg gtg gaa agc ggc gga gga ctg gtg cag         96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

cct ggc ggc agc ctg aga ctg agc tgc agc gcc agc ggc ttc acc gac        144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Asp
```

```
        35                  40                  45

agc cgg ttc acc ttc cgg aac tac tgg atg cac tgg gtc cga cag gct        192
Ser Arg Phe Thr Phe Arg Asn Tyr Trp Met His Trp Val Arg Gln Ala
    50                  55                  60

cca ggc aag ggc ctc gtg tgg gtg tcc aga atc aac ggc gac ggc gga        240
Pro Gly Lys Gly Leu Val Trp Val Ser Arg Ile Asn Gly Asp Gly Gly
65                  70                  75                  80

ggc acc gtg tac agc gac agc gtg aag ggc aga ttc acc atc agc cgg        288
Gly Thr Val Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
                85                  90                  95

gac aac gcc cgg aac atc gtg tac ctg cag atg gac agc ctg cgg gcc        336
Asp Asn Ala Arg Asn Ile Val Tyr Leu Gln Met Asp Ser Leu Arg Ala
            100                 105                 110

gag gac acc gcc gtg tac tac tgc gtg cgc gag ttc ggc ctg ttc gac        384
Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg Glu Phe Gly Leu Phe Asp
        115                 120                 125

agc ggc aca tgg tac agc ggc ggc ttc gac tac tgg ggc cag ggc acc        432
Ser Gly Thr Trp Tyr Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
    130                 135                 140

ctg gtc acc gtc agc tca gcc tcc acc aag ggc cca agc gtc ttc ccc        480
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
145                 150                 155                 160

ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc gcc ctg ggc        528
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
                165                 170                 175

tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg agc tgg aac        576
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
            180                 185                 190

tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct gtc ctg cag        624
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
        195                 200                 205

tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc        672
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
    210                 215                 220

agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc        720
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
225                 230                 235                 240

aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa act        768
Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
                245                 250                 255

cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg gga ccc tca        816
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
            260                 265                 270

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg        864
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        275                 280                 285

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct        912
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    290                 295                 300

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc        960
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
```

```
305                 310                 315                 320

aag aca aag ccc cgg gag gag cag tac aac agc acg tac cgg gtg gtc       1008
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                325                 330                 335

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac       1056
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            340                 345                 350

aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc       1104
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        355                 360                 365

atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg tac acc ctg       1152
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    370                 375                 380

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc       1200
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
385                 390                 395                 400

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc       1248
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                405                 410                 415

aat ggc cag ccc gag aac aac tac aag acc acc cct ccc gtg ctg gac       1296
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            420                 425                 430

tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc       1344
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        435                 440                 445

agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg cat gag gct       1392
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    450                 455                 460

ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct ccc ggc aaa       1440
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470                 475                 480


<210>  49
<211>  480
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  49

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 Ser Ala Ser Gly Phe Thr Asp
        35                  40                  45


Ser Arg Phe Thr Phe Arg Asn Tyr Trp Met His Trp Val Arg Gln Ala
    50                  55                  60
```

```
Pro Gly Lys Gly Leu Val Trp Val Ser Arg Ile Asn Gly Asp Gly Gly
65                  70                  75                  80

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

Asp Asn Ala Arg Asn Ile Val Tyr Leu Gln Met Asp Ser Leu Arg Ala
            100                 105                 110

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

Ser Gly Thr Trp Tyr Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
    130                 135                 140

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
145                 150                 155                 160

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
                165                 170                 175

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
            180                 185                 190

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
        195                 200                 205

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
    210                 215                 220

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
225                 230                 235                 240

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
                245                 250                 255

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
            260                 265                 270

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        275                 280                 285

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    290                 295                 300

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
305                 310                 315                 320

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                325                 330                 335
```

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
340 345 350

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
355 360 365

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
370 375 380

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
385 390 395 400

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
405 410 415

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
420 425 430

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
435 440 445

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
450 455 460

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475 480

<210> 50
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of mouse IgG2b type chimeric 1BO11

<400> 50
atgagcgtgc tgacccaggt gcttgccctg cttctgcttt ggctgaccgg cgctcggtgt 60

gacgtggtga tgacccagag ccctctgtcc cttcctgtga ccctgggcca gcctgccagc 120

atctcctgtc ggagctccca gagccttgtg tactccgacg gcaacaccta cctgaactgg 180

ttccagcaga gacctggcca gagccctcgg agacttatct acaaggtgtc caaccgggac 240

agcggagtgc ctgacagatt ctccggcagc ggatccggca ccgacttcac cctgaagatc 300

agccgggtgg aggctgagga cgtgggagtg tactactgta tgcagggcac ccactggcct 360

cttaccttcg gcggaggcac caaggtggag atcaagagag ccgacgctgc ccctaccgtg 420

tccatcttcc ctcctagctc cgagcagctt accagcggcg gcgcctccgt ggtgtgtttc 480

ctgaacaact tctaccctaa ggacatcaac gtgctttgga agatcgacgg cagcgagaga 540

caaaacggcg tgctgaactc ctggaccgac caggacagca aggactccac ctacagcatg 600

tccagcaccc ttaccctgac caaggacgag tacgagcggc acaactccta cacctgtgag 660

gctacccaca agaccagcac ctcccctatc gtgaagagct tcaacagaaa cgagtgt 717

<210> 51
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of human IgG1 type 1BO11

<220>
<221> CDS
<222> (1)..(717)

<400> 51
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 gcg tac ggc gac gtg gtg atg acc cag agc cct ctg tcc ctt cct 96
Gly Ala Tyr Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
20 25 30

gtg acc ctg ggc cag cct gcc agc atc tcc tgt cgg agc tcc cag agc 144
Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
35 40 45

ctt gtg tac tcc gac ggc aac acc tac ctg aac tgg ttc cag cag aga 192
Leu Val Tyr Ser Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg
50 55 60

cct ggc cag agc cct cgg aga ctt atc tac aag gtg tcc aac cgg gac 240
Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp
65 70 75 80

agc gga gtg cct gac aga ttc tcc ggc agc gga tcc ggc acc gac ttc 288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

acc ctg aag atc agc cgg gtg gag gct gag gac gtg gga gtg tac tac 336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

tgt atg cag ggc acc cac tgg cct ctt acc ttc ggc gga ggc acc aag 384
Cys Met Gln Gly Thr His Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys
115 120 125

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

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

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

aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac 576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

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

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

ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt          717
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 52
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52

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

Gly Ala Tyr Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
            20                  25                  30

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

Leu Val Tyr Ser Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg
    50                  55                  60

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

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                85                  90                  95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
            100                 105                 110

Cys Met Gln Gly Thr His Trp Pro Leu Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125

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

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

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

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

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

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

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

<210> 53
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding heavy chain of mouse IgG2b type chimeric 1BO11

<400> 53
atggccgtgc tgggccttct gttctgtctt gtgaccttcc cttcctgtgt gctgagcgag 60

gagcaagtgg tggagagcgg cggcggattc gtgcagcctg gcggctccct gcggctttcc 120

tgtgccgctt ccggattcac cttcagccct tactggatgc actgggtgag acaagccct 180

ggcaagggcc tggtgtgggt gtcccggatc aacagcgacg gatccaccta ctacgctgac 240

agcgtgaagg gccggttcac catctccaga gacaacgccc ggaacaccct ttacctgcag 300

atgaacagcc ttagagctga ggacaccgcc gtgtactact gtgctcggga cagatactac 360

ggccctgaga tgtggggaca aggcaccatg gtgaccgtga gctcagccaa gaccaccct 420

cctagcgtgt accctctggc tcctggctgt ggcgacacca ccggctccag cgtgaccctt 480

ggctgtctgg tgaagggcta cttccctgag tccgtgaccg tgacctggaa cagcggctcc 540

cttagctcca gcgtgcacac cttccctgcc ctgcttcagt ccggcctgta caccatgagc 600

tccagcgtga ccgtgccttc cagcacctgg ccttcccaga ccgtgacctg tagcgtggct 660

caccctgcct ccagcaccac cgtggacaag aagcttgagc cttccggccc tatcagcacc 720

atcaaccctt gtcctccttg taaggagtgt cacaagtgtc ctgctcctaa cctggagggc 780

ggcccttccg tgttcatctt ccctcctaac atcaaggacg tgcttatgat cagcctgacc 840

cctaaggtga cctgtgtggt ggtggacgtg tccgaggacg accctgacgt gcagatcagc 900

tggttcgtga acaacgtgga ggtgcacacc gcccagaccc agacccaccg ggaggactac 960

aactccacca tcagagtggt gagcaccctt cctatccagc accaggactg gatgtccggc 1020

aaggagttca agtgtaaggt gaacaacaag gacctgccta gccctatcga gcggaccatc 1080

tccaagatca agggccttgt gcgggctcct caggtgtaca tcctgcctcc tcctgccgag 1140

cagctttcca gaaaggacgt gtccctgacc tgtcttgtgg tgggcttcaa ccctggcgac 1200

atcagcgtgg agtggacctc caacggccac accgaggaga actacaagga caccgctcct 1260

gtgctggaca gcgacggctc ctacttcatc tacagcaagc ttaacatgaa gacctccaag 1320

tgggagaaga ccgacagctt ctcctgtaac gtgcggcacg agggcctgaa gaactactac 1380

cttaagaaga ccatcagcag atcccctggc aag 1413

<210> 54
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding heavy chain of human IgG1 type 1BO11

<220>
<221> CDS
<222> (1)..(1395)

<400> 54

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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 gag gag caa gtg gtg gag agc ggc ggc gga ttc gtg cag          96
Val Leu Ser Glu Glu Gln Val Val Glu Ser Gly Gly Gly Phe Val Gln
            20                  25                  30

cct ggc ggc tcc ctg cgg ctt tcc tgt gcc gct tcc gga ttc acc ttc         144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc cct tac tgg atg cac tgg gtg aga caa gcc cct ggc aag ggc ctg         192
Ser Pro Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gtg tgg gtg tcc cgg atc aac agc gac gga tcc acc tac tac gct gac         240
Val Trp Val Ser Arg Ile Asn Ser Asp Gly Ser Thr Tyr Tyr Ala Asp
65                  70                  75                  80

agc gtg aag ggc cgg ttc acc atc tcc aga gac aac gcc cgg aac acc         288
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr
                85                  90                  95

ctt tac ctg cag atg aac agc ctt aga gct gag gac acc gcc gtg tac         336
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
            100                 105                 110

tac tgt gct cgg gac aga tac tac ggc cct gag atg tgg gga caa ggc         384
Tyr Cys Ala Arg Asp Arg Tyr Tyr Gly Pro Glu Met Trp Gly Gln Gly
        115                 120                 125

acc atg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc gtc ttc         432
Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
    130                 135                 140

ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc gcc ctg         480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
145                 150                 155                 160

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg agc tgg         528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                165                 170                 175

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct gtc ctg         576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
            180                 185                 190

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc         624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
        195                 200                 205
```

```
agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc        672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
    210                 215                 220

agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa        720
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
225                 230                 235                 240

act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg gga ccc        768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                245                 250                 255

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc        816
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            260                 265                 270

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac        864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
        275                 280                 285

cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat        912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
    290                 295                 300

gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac cgg gtg        960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
305                 310                 315                 320

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag       1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                325                 330                 335

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa       1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            340                 345                 350

acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg tac acc       1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
        355                 360                 365

ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc       1152
Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
    370                 375                 380

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag       1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
385                 390                 395                 400

agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc gtg ctg       1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
                405                 410                 415

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

agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg cat gag       1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
        435                 440                 445

gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct ccc ggc       1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
    450                 455                 460

aaa                                                                  1395
Lys
465
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<210> 55
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55

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

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

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

Ser Pro Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Val Trp Val Ser Arg Ile Asn Ser Asp Gly Ser Thr Tyr Tyr Ala Asp
65 70 75 80

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

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

Tyr Cys Ala Arg Asp Arg Tyr Tyr Gly Pro Glu Met Trp Gly Gln Gly
115 120 125

Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
130 135 140

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
145 150 155 160

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
195 200 205

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
210 215 220

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys

225 230 235 240

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys
465

<210> 56
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-H1

<220>
<221> CDS
<222> (1)..(1422)

<400> 56
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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 cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg         192
Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aac atc tac ccc ggc agc agc agc atc aac tac aac         240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag agc cgc gtg acc atc acc gcc gac acc agc aca agc         288
Glu Lys Phe Lys Ser Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc cgg acc atc tac aac tac ggc agc tcc ggc tac aat         384
Tyr Tyr Cys Ala Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc ctc gtg acc gtg agc tca         432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag         480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac         528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc         576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc         624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc         672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag         720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240
```

```
aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc        768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca        816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                              1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 57
<211> 474
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 57

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Ser Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255
```

```
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  58
<211>  1422
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#1G5-H2


<220>
<221>  CDS
<222>  (1)..(1422)
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<400> 58

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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 cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg         192
Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aac atc tac ccc ggc agc agc agc atc aac tac aac         240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag agc cgc gtg acc ctg acc gtg gac acc agc aca agc         288
Glu Lys Phe Lys Ser Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc agc cgg acc atc tac aac tac ggc agc tcc ggc tac aat         384
Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc ctc gtg acc gtg agc tca         432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag         480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac         528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc         576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc         624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc         672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag         720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc         768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca         816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
```

```
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                              1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  59
<211>  474
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  59

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Ser Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285
```

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
340 345 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 60
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-H3

<220>
<221> CDS
<222> (1)..(1422)

<400> 60
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 cag gtg cag ctg cag cag cct ggc gcc gaa gtg aaa aag 96

```
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt        144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg        192
Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aac atc tac ccc ggc agc agc agc atc aac tac aac        240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag agc cgg gcc acc ctg acc gtg gac acc agc aca agc        288
Glu Lys Phe Lys Ser Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg acc agc gag gac acc gcc gtg        336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc agc cgg acc atc tac aac tac ggc agc tcc ggc tac aat        384
Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc ctc gtg acc gtg agc tca        432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag        480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac        528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc        576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc        624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc        672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag        720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc        768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca        816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
```

```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                              1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  61
<211>  474
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  61

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


Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Val Lys Lys
            20                  25                  30


Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
```

```
Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Ser Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320
```

```
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 62
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-H4

<220>
<221> CDS
<222> (1)..(1422)

<400> 62

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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 cag gtg cag ctg cag cag cct ggc gcc gag ctg aaa aaa         96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30

cct ggc gcc tcc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt        144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
```

```
acc agc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg        192
Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atc ggc aac atc tac ccc ggc agc agc agc atc aac tac aac        240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag agc aag gcc acc ctg acc gtg gac acc agc agc tcc        288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctg tcc agc ctg acc agc gac gac agc gcc gtg        336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc agc cgg acc atc tac aac tac ggc agc tcc ggc tac aat        384
Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc ctc gtg acc gtg agc tca        432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag        480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac        528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc        576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc        624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc        672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag        720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc        768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca        816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320
```

```
gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                               1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 63
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63

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

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
```

65 70 75 80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
115 120 125

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

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145 150 155 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
180 185 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
210 215 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225 230 235 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
245 250 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
260 265 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
275 280 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
290 295 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305 310 315 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
325 330 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn

340 345 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
355 360 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
370 375 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385 390 395 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
405 410 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
435 440 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
450 455 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 64
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-H5

<220>
<221> CDS
<222> (1)..(1422)

<400> 64
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 cag gtg cag ctg cag cag cct ggc gcc gag ctg aaa aaa 96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
20 25 30

cct ggc gcc tcc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

acc agc tac tgg atc aac tgg gtc aag cag cgg cca ggc cag ggc ctg 192
Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

gaa tgg atc ggc aat atc tac ccc ggc agc agc agc atc aac tac aac 240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65 70 75 80

```
gag aag ttc aag agc aag gcc acc ctg acc gtg gac acc agc agc tcc        288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctg tcc agc ctg acc agc gac gac agc gcc gtg        336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc agc cgg acc atc tac aac tac ggc agc tcc ggc tac aat        384
Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

tac gcc atg gac tac tgg ggc cag ggc acc agc gtg atc gtg agc tca        432
Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
    130                 135                 140

gcc tcc acc aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag        480
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

agc acc tct ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac        528
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

ttc ccc gaa ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc        576
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

ggc gtg cac acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc        624
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc        672
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag        720
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

aga gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc        768
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

cca gca cct gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca        816
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc        864
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg        912
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag        960
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

gag cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg       1008
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac       1056
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350
```

```
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc       1104
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

cag ccc cgg gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag       1152
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat       1200
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

ccc agc gac atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac       1248
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

aac tac aag acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc       1296
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac       1344
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc       1392
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

cag aag agc ctc tcc ctg tct ccc ggc aaa                              1422
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 65
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

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

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Ser Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Ser Ser Ser Ile Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95
```

```
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ser Arg Thr Ile Tyr Asn Tyr Gly Ser Ser Gly Tyr Asn
        115                 120                 125

Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser
    130                 135                 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365
```

```
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470


<210>  66
<211>  702
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#1G5-L1


<220>
<221>  CDS
<222>  (1)..(702)

<400>  66
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 gcg tac ggc gac atc gtg atg acc cag agc cct gac agc ctg gcc          96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
            20                  25                  30

gtg tct ctg gga gag aga gcc acc atc aac tgc aag gcc agc gag aac         144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Glu Asn
        35                  40                  45

gtg ggc aac agc gtg tcc tgg tat cag cag aag ccc ggc cag ccc ccc         192
Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
    50                  55                  60

aag ctg ctg atc tac ggc gcc agc aac aga tac acc ggc gtg ccc gat         240
Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

aga ttc agc ggc agc ggc tct ggc acc gac ttc acc ctg aca atc agc         288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

tcc ctg cag gcc gag gac gtg gcc gtg tac tac tgt ggc cag agc tac         336
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gly Gln Ser Tyr
```

```
            100                 105                 110

agc tac ccc tac acc ttc ggc cag ggc acc aag gtg gaa atc aag cgt        384
Ser Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  67
<211>  234
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  67

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


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


Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Glu Asn
        35                  40                  45


Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
    50                  55                  60


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


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95
```

```
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gly Gln Ser Tyr
            100                 105                 110


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


Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190


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


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  68
<211>  702
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#1G5-L2


<220>
<221>  CDS
<222>  (1)..(702)

<400>  68
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 gcg tac ggc aac atc gtg atg acc cag agc ccc gac agc ctg gcc         96
Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
            20                  25                  30

gtg tct ctg gga gag aga gcc acc atc agc tgc aag gcc agc gag aac        144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

gtg ggc aac agc gtg tcc tgg tat cag cag aag ccc ggc cag agc cct        192
Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    50                  55                  60

aag ccc ctg atc tac ggc gcc agc aac aga tac acc ggc gtg ccc gat        240
```

```
Lys Pro Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

aga ttc agc ggc agc ggc tct gcc acc gac ttc acc ctg aca atc agc        288
Arg Phe Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

tcc ctg cag gcc gag gac gtg gcc gtg tat cac tgt ggc cag agc tac        336
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

agc tac ccc tac acc ttc ggc gga ggc acc aag gtg gaa atc aag cgt        384
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  69
<211>  234
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  69

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


Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
            20                  25                  30


Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45


Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    50                  55                  60
```

```
Lys Pro Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  70
<211>  702
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#1G5-L3


<220>
<221>  CDS
<222>  (1)..(702)

<400>  70
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 gcg tac ggc aac atc gtg atg acc cag agc ccc gac agc ctg gcc         96
Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
            20                  25                  30
```

```
gtg tct ctg gga gag aga gcc acc atc agc tgc aag gcc agc gag aac        144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

gtg ggc aac agc gtg tcc tgg tat cag cag aag ccc ggc cag agc cct        192
Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    50                  55                  60

aag ccc ctg atc tac ggc gcc agc aac aga tac acc ggc gtg ccc gat        240
Lys Pro Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

aga ttc agc ggc agc ggc tct gcc acc gac ttc acc ctg aca atc agc        288
Arg Phe Ser Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

tcc ctg cag gcc gag gac gtg gcc gat tat cac tgc ggc cag tcc tac        336
Ser Leu Gln Ala Glu Asp Val Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

agc tac ccc tac acc ttt ggc gga ggc acc aag gtg gaa atc aag cgt        384
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 71
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71

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

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

20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

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

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

Ser Leu Gln Ala Glu Asp Val Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 72
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-L4

<220>
<221> CDS
<222> (1)..(702)

<400> 72

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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 gcg tac ggc aac atc gtg atg acc cag agc ccc gac agc atg agc         96
Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Met Ser
            20                  25                  30

atg agc gtg ggc gag aga gcc acc ctg agc tgc aag gcc tct gag aac        144
Met Ser Val Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

gtg ggc aac agc gtg tcc tgg tat cag cag aag gcc gag cag agc ccc        192
Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
    50                  55                  60

aag ccc ctg atc tac ggc gcc agc aac aga tac acc ggc gtg ccc gat        240
Lys Pro Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

aga ttc acc ggc agc ggc agc gcc acc gac ttc acc ctg aca atc agc        288
Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

tcc ctg cag gcc gag gac ctg gcc gat tat cac tgc ggc cag agc tac        336
Ser Leu Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

agc tac ccc tac acc ttt ggc gga ggc acc aag ctg gaa atc aag cgt        384
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 73
<211> 234
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 73

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Met Ser
20 25 30

Met Ser Val Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
50 55 60

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

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

Ser Leu Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 74
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#1G5-L5

<220>
<221> CDS
<222> (1)..(702)

<400> 74

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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 gcg tac ggc aac atc gtg atg acc cag agc ccc gac agc atg agc          96
Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Met Ser
            20                  25                  30

atg agc gtg ggc gag aga gtg acc ctg agc tgc aag gcc agc gag aac         144
Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

gtg ggc aac agc gtg tcc tgg tat cag cag aag gcc gag cag agc ccc         192
Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
    50                  55                  60

aag ccc ctg atc tac ggc gcc agc aac aga tac acc ggc gtg ccc gat         240
Lys Pro Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
65                  70                  75                  80

aga ttc acc ggc agc ggc agc gcc acc gac ttc acc ctg aca atc agc         288
Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

tcc ctg cag gcc gag gac ctg gcc gat tat cac tgc ggc cag agc tac         336
Ser Leu Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
            100                 105                 110

agc tac ccc tac acc ttt ggc gga ggc acc aag ctg gaa atc aag cgt         384
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag         432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac         480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc         528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc         576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc         672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                 702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
```

225 230

<210> 75
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 75

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Asp Ser Met Ser
20 25 30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
35 40 45

Val Gly Asn Ser Val Ser Trp Tyr Gln Gln Lys Ala Glu Gln Ser Pro
50 55 60

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

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

Ser Leu Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

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


<210>  76
<211>  1410
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#4C13K-H1


<220>
<221>  CDS
<222>  (1)..(1410)

<400>  76
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 cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg         192
Thr Thr Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aac atc tac ccc ggc acc aga agc agc aac tac aac         240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac cgc gtg acc atc acc gcc gac acc agc acc agc         288
Glu Lys Phe Lys Asn Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
                85                  90                  95

aca gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc aga gtg tac tac gac cac gtg ggc tac tac ttc gac         384
Tyr Tyr Cys Ala Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc         480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc         528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg         624
```

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

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac  672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc  720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa  768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac  816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac  864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc  912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac  960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa 1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac 1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc 1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc 1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag 1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc 1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc 1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                         1410
```

Ser Leu Ser Pro Gly Lys
465 470

<210> 77
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Thr Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65 70 75 80

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

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Val Tyr Tyr Asp His Val Gly Tyr 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 Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

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

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

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

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

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

Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 78
<211> 1410

<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#4C13K-H2

<220>
<221> CDS
<222> (1)..(1410)

<400> 78

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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 cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg gtg cgc cag gcc cct gga cag ggc ctg         192
Thr Thr Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aac atc tac ccc ggc acc aga agc agc aac tac aac         240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac cgc gtg acc ctg acc gtg gac acc agc acc agc         288
Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

aca gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgt acc cgg gtg tac tac gac cac gtg ggc tac tac ttc gac         384
Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc         480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc         528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg         624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac         672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
```

```
gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc        720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa        768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac        816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac        864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                              1410
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 79
<211> 470
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 79

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

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

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Thr Tyr Trp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Arg Val Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr 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 Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
```

245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

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

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

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

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 80
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#4C13K-H3

<220>
<221> CDS
<222> (1)..(1410)

<400> 80

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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 cag gtg cag ctg cag cag cct ggc gcc gaa gtg aaa aag          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Val Lys Lys
            20                  25                  30

cca ggc gcc agc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg atg cag cag cgg cca ggc cag ggc ctg         192
Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc aat atc tac ccc ggc acc aga agc agc aac tac aac         240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac cgg gcc acc ctg acc gtg gac acc agc aca agc         288
Glu Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg acc agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc acc aga gtg tac tac gac cac gtg ggc tac tac ttc gac         384
Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc         480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc         528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg         624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac         672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc         720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa         768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
```

```
ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac        816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac        864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                              1410
Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 81
<211> 470
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81

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

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr 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 Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
```

```
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

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

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

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

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

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

Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 82
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding of h#4C13K-H4

<220>
<221> CDS
<222> (1)..(1410)

<400> 82

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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 cag gtg cag ctg cag cag cct ggc gcc gag ctg aaa aaa          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30

cct ggc gcc tcc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg atg cag cag cgg cca ggc cag ggc ctg         192
Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atc ggc aat atc tac ccc ggc acc aga agc agc aac tac aac         240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac aag gcc acc ctg acc gtg gac acc agc agc tcc         288
Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg acc agc gac gac agc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc acc aga gtg tac tac gac cac gtg ggc tac tac ttc gac         384
Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc         480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc         528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg         624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac         672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc         720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa         768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac         816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac         864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
```

```
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                              1410
Ser Leu Ser Pro Gly Lys
465                 470


<210>  83
<211>  470
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  83

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


Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30
```

```
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr 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 Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300
```

```
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

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

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

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

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

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

Ser Leu Ser Pro Gly Lys
465                 470


<210>  84
<211>  1410
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleotide coding of h#4C13K-H5


<220>
<221>  CDS
<222>  (1)..(1410)

<400>  84
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 cag gtg cag ctg cag cag cct ggc gcc gag ctg aaa aaa          96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30

cct ggc gcc tcc gtg aag gtg tcc tgc aag gcc agc ggc tac acc ttt         144
```

```
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc acc tac tgg atc aac tgg atg cag cag cgg cca ggc cag ggc ctg        192
Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atc ggc aat atc tac ccc ggc acc aga agc agc aac tac aac        240
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag aac aag gcc acc ctg acc gtg gac acc agc agc tcc        288
Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

aca gcc tac atg cag ctg aac tcc ctg acc agc gac gac agc gcc gtg        336
Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

tac tac tgc acc aga gtg tac tac gac cac gtg ggc tac tac ttc gac        384
Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp
        115                 120                 125

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

ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc        480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc        528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

gtg acc gtg agc tgg aac tca ggc gcc ctg 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 ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg        624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac        672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc        720
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
225                 230                 235                 240

aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa        768
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac        816
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac        864
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc        912
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac        960
```

```
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg       1008
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca       1056
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa       1104
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac       1152
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc       1200
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc       1248
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag       1296
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc       1344
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc       1392
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

tcc ctg tct ccc ggc aaa                                              1410
Ser Leu Ser Pro Gly Lys
465                 470


<210>  85
<211>  470
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  85

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


Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Lys Lys
            20                  25                  30


Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45


Thr Thr Tyr Trp Ile Asn Trp Met Gln Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60
```

```
Glu Trp Ile Gly Asn Ile Tyr Pro Gly Thr Arg Ser Ser Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Val Tyr Tyr Asp His Val Gly Tyr 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 Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly 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 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

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

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

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

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
```

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

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

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

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

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

Ser Leu Ser Pro Gly Lys
465 470

<210> 86
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH1 of #4C13

<400> 86

Thr Tyr Trp Ile Asn
1 5

<210> 87
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH2 of #4C13

<400> 87

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

Asn

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3 of #4C13

<400> 88

Val Tyr Tyr Asp His Val Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 89
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> AP3dC-S

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<400> 89
cggtaccgcg ggcccgggat ccccccccccc cccdn 35

<210> 90
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> mIggamma RT1 1111-AS

<400> 90
accytgcatt tgaactcctt gcc 23

<210> 91
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgkappa 1st 589-AS

<400> 91
actgccatca atcttccact tgaca 25

<210> 92
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> MCS-AP3-S

<400> 92
cttcgaattc tgcagtcgac ggtaccgcgg gcccggga 38

<210> 93
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> mIggamma 3rd 656T-AS

<400> 93
ctggacaggg atccagagtt cca 23

<210> 94
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgkappa 3rd 525-AS

<400> 94
actgaggcac ctccagatgt taact 25

<210> 95
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgG joint PCR-S

<400> 95
gcctggtcaa gggctatttc cctgag 26

<210> 96
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> polyG-AS

<400> 96
ggggggggggg gggggggatc ccgg 24

<210> 97
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgkappa joint PCR-S

<400> 97
ctgtatccat cttcccacca tccagt 26

<210> 98
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> miniCMV f1-S

<400> 98
agagaaaccg tctatcaggg cgatggc 27

<210> 99
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> miniCMV f1-AS

<400> 99
agagaccctt tgacgttgga gtccacg 27

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgG sequence

<400> 100
acaccgctgg acagggatcc agag 24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> mIgkappa sequence

<400> 101
gtagaagttg ttcaagaagc acac 24

<210> 102
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3.3-F1

<400> 102
tataccgtcg acctctagct agagcttggc 30

<210> 103
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3.3-R1

<400> 103
gctatggcag ggcctgccgc cccgacgttg 30

<210> 104
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> 76L-F

<400> 104
atctccggcg cgtacggcaa cattgtaatg acccaatctc ccaaatc 47

<210> 105
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> 76L-R

<400> 105
ggaggggcg gccacagccc gttttatttc cagcttggtc ctccc 45

<210> 106
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> 76H-F

<400> 106
ccagatgggt gctgagccag gtccaactgc agcagcctgg tgctgag 47

<210> 107
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> 76H-R

<400> 107
cttggtggag gctgagctga ctgtgagagt ggtgccttgg ccccag 46

<210> 108
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> CM-inf-F

<400> 108
ccagcctccg gactctagag ccacc 25

<210> 109
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> CM-inf-R

<400> 109
agttagcctc ccccgtttaa actc 24

<210> 110
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> EG-Inf-F

<400> 110
agctcccaga tgggtgctga gc 22

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> EG1-Inf-R

<400> 111
gggcccttgg tggaggctga gc 22

<210> 112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> CM-LKF

<400> 112
ctgtggatct ccggcgcgta cggc 24

<210> 113
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> KCL-Inf-R

<400> 113
ggaggggcg gccaccgtac g 21

<210> 114
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> h1BO-LF

<400> 114
atctccggcg cgtacggcga cgtggtgatg acccagagcc ctctgtcc 48

<210> 115
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

<223> h1BO-LR

<400> 115
gggcggccac cgtacgcttg atctccacct tggtgcctcc gccg 44

<210> 116
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> h1BO-HF

<400> 116
ccagatgggt gctgagcgag gagcaagtgg tggagagcgg 40

<210> 117
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> h1BO-HR

<400> 117
cttggtggag gctgagctca cggtcaccat ggtgccttgt c 41

<210> 118
<211> 752
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding light chain of No.76 mIgG2a

<220>
<221> CDS
<222> (26)..(727)

<400> 118
ccagcctccg gactctagag ccacc atg gtg ctg cag acc cag gtg ttc atc 52
Met Val Leu Gln Thr Gln Val Phe Ile
1 5

agc ctg ctg ctg tgg atc agc ggc gcc tac ggc aac atc gtg atg acc 100
Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asn Ile Val Met Thr
10 15 20 25

cag agc ccc aag agc atg agc atg tcc gtg ggc gag aga gtg acc ctg 148
Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu
30 35 40

agc tgc aag gcc agc gag aac gtg ggc aca agc gtg tcc tgg tat cag 196
Ser Cys Lys Ala Ser Glu Asn Val Gly Thr Ser Val Ser Trp Tyr Gln
45 50 55

gaa aag ccc gag cag tcc ccc aag ctg ctg atc ttc ggc gcc agc aac 244
Glu Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile Phe Gly Ala Ser Asn
60 65 70

aga tac acc ggc gtg ccc gat aga ttc acc ggc agc ggc agc gcc acc 292
Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr
75 80 85

```
gac ttc acc ctg aca atc agc agc gtg cag gcc gag gac ctg gcc gat        340
Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp
90                  95                  100                 105

tat cac tgc ggc cag agc tac agc tac ccc tac acc ttt ggc ggc agg        388
Tyr His Cys Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Arg
                110                 115                 120

acc aag ctg gaa atc aag cgg gcc gat gcc gcc cct acc gtg tcc atc        436
Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile
            125                 130                 135

ttt cca ccc agc agc gag cag ctg aca agc ggc gga gct agc gtc gtg        484
Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val
        140                 145                 150

tgc ttc ctg aac aac ttc tac ccc aag gac atc aac gtg aag tgg aag        532
Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys
    155                 160                 165

atc gac ggc agc gag cgg cag aac ggc gtg ctg aat agc tgg acc gac        580
Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp
170                 175                 180                 185

cag gac agc aag gac tcc acc tac agc atg tcc agc acc ctg acc ctg        628
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu
                190                 195                 200

acc aag gac gag tac gag cgg cac aac agc tac aca tgc gag gcc acc        676
Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr
            205                 210                 215

cac aag acc agc acc agc ccc atc gtg aag tcc ttc aac cgg aac gag        724
His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu
        220                 225                 230

tgc tgagtttaaa cgggggaggc taact                                       752
Cys
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<210> 119
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 119

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

Gly Ala Tyr Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser
            20                  25                  30

Met Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn
        35                  40                  45

Val Gly Thr Ser Val Ser Trp Tyr Gln Glu Lys Pro Glu Gln Ser Pro
    50                  55                  60

Lys Leu Leu Ile Phe Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp
```

65 70 75 80

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

Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr
100 105 110

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

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

<210> 120
<211> 1460
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide coding heavy chain of No.76 mIgG2a

<220>
<221> CDS
<222> (26)..(1435)

<400> 120
ccagcctccg gactctagag ccacc atg aag cac ctg tgg ttc ttt ctg ctg 52
Met Lys His Leu Trp Phe Phe Leu Leu
1 5

ctg gtg gcc gct ccc aga tgg gtg ctg tct cag gtg cag ctg cag cag 100
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln
10 15 20 25

cct ggc gcc gag ctc gtg aaa cct ggc gcc tct gtg aac ctg agc tgc 148
Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Asn Leu Ser Cys
30 35 40

```
aag agc agc ggc tac acc ttc acc aac tac tgg atc aac tgg gtc aag        196
Lys Ser Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Ile Asn Trp Val Lys
            45                  50                  55

cag cgg cca ggc cag ggc ctg gaa tgg atc ggc gat atc tac ccc ggc        244
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro Gly
        60                  65                  70

acc agc acc acc aat tac aac gag aag ttc aag aac aag gcc acc ctg        292
Thr Ser Thr Thr Asn Tyr Asn Glu Lys Phe Lys Asn Lys Ala Thr Leu
    75                  80                  85

acc gtg gac acc agc tcc agc aca gcc tac atg cag ctg tcc agc ctg        340
Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
90                  95                  100                 105

acc agc gac gac agc gcc gtg tac tac tgc acc cgg atc tac tac gac        388
Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys Thr Arg Ile Tyr Tyr Asp
                110                 115                 120

tac gac ggc tac tac ttc gac tac tgg ggc cag ggc aca acc ctg aca        436
Tyr Asp Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
            125                 130                 135

gtg tcc agc gcc aag acc acc gcc cct agc gtg tac cct ctg gct cct        484
Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
        140                 145                 150

gtg tgt ggc gat acc acc ggc agc tct gtg aca ctg ggc tgc ctc gtg        532
Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val
    155                 160                 165

aag ggc tac ttc ccc gag cct gtg acc ctg aca tgg aac agc ggc agc        580
Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser
170                 175                 180                 185

ctg tct agc ggc gtg cac acc ttt cca gcc gtg ctg cag agc gac ctg        628
Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
                190                 195                 200

tac acc ctg agc agc agc gtg acc gtg acc tcc agc acc tgg ccc agc        676
Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser
            205                 210                 215

cag agc atc acc tgt aac gtg gcc cac cct gcc agc agc acc aag gtg        724
Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val
        220                 225                 230

gac aag aag atc gag ccc aga ggc ccc acc atc aag cct tgc ccc cct        772
Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro
    235                 240                 245

tgc aaa tgc cct gcc ccc aat ctg ctg ggc gga ccc agc gtg ttc atc        820
Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile
250                 255                 260                 265

ttc cca ccc aag atc aag gac gtg ctg atg atc agc ctg agc ccc atc        868
Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile
                270                 275                 280

gtg acc tgc gtg gtg gtg gac gtg tcc gag gac gac ccc gat gtg cag        916
Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln
            285                 290                 295

atc agt tgg ttc gtg aac aac gtg gaa gtg cac acc gcc cag acc cag        964
Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln
        300                 305                 310
```

```
aca cac aga gag gac tac aac agc acc ctg aga gtg gtg tcc gcc ctg       1012
Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu
    315                 320                 325

ccc atc cag cac cag gat tgg atg agc ggc aaa gaa ttc aag tgc aaa       1060
Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys
330                 335                 340                 345

gtg aac aac aag gac ctg cca gcc ccc atc gag cgg acc atc tct aag       1108
Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys
                350                 355                 360

cct aag ggc agc gtg cgg gct ccc cag gtg tac gtg ctg cct cct cca       1156
Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro
            365                 370                 375

gag gaa gag atg acc aag aaa caa gtg aca ctg acc tgt atg gtc acc       1204
Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr
        380                 385                 390

gac ttc atg ccc gag gac atc tac gtg gaa tgg acc aac aac ggc aag       1252
Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys
    395                 400                 405

acc gag ctg aac tac aag aac acc gag ccc gtg ctg gac tcc gat ggc       1300
Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly
410                 415                 420                 425

agc tac ttc atg tac agc aag ctg cgg gtg gaa aag aaa aac tgg gtg       1348
Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val
                430                 435                 440

gaa cgg aac agc tac agc tgc tcc gtg gtg cac gag ggc ctg cac aat       1396
Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn
            445                 450                 455

cac cac acc aca aag agc ttc agc cgg acc ccc ggc aaa tgagtttaaa       1445
His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
        460                 465                 470

cgggggaggc taact                                                    1460


<210>  121
<211>  470
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  121

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


Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30


Pro Gly Ala Ser Val Asn Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe
        35                  40                  45


Thr Asn Tyr Trp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60
```

```
Glu Trp Ile Gly Asp Ile Tyr Pro Gly Thr Ser Thr Thr Asn Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Thr Arg Ile Tyr Tyr Asp Tyr Asp Gly Tyr Tyr Phe Asp
        115                 120                 125

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

Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly
145                 150                 155                 160

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

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

Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
        195                 200                 205

Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val
    210                 215                 220

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

Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
            260                 265                 270

Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
    290                 295                 300

Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
305                 310                 315                 320

Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
                325                 330                 335
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Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
340 345 350

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

Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
370 375 380

Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
385 390 395 400

Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
405 410 415

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

Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
435 440 445

Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
450 455 460

Ser Arg Thr Pro Gly Lys
465 470

<210> 122
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> H-R

<400> 122
cttggtggag gctgagctca cggtcacgag ggtgccctgg cc 42

<210> 123
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL1 of #4C13

<400> 123

Lys Ala Ser Glu Asn Val Gly Val Ser Val Ser
1 5 10

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL2 of #4C13

<400> 124

Gly Ala Ser Asn Arg Tyr Thr
1 5

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRL3 of #4C13

<400> 125

Gly Gln Ser Tyr Ser Tyr Pro Tyr Thr
1 5