FIG. 1

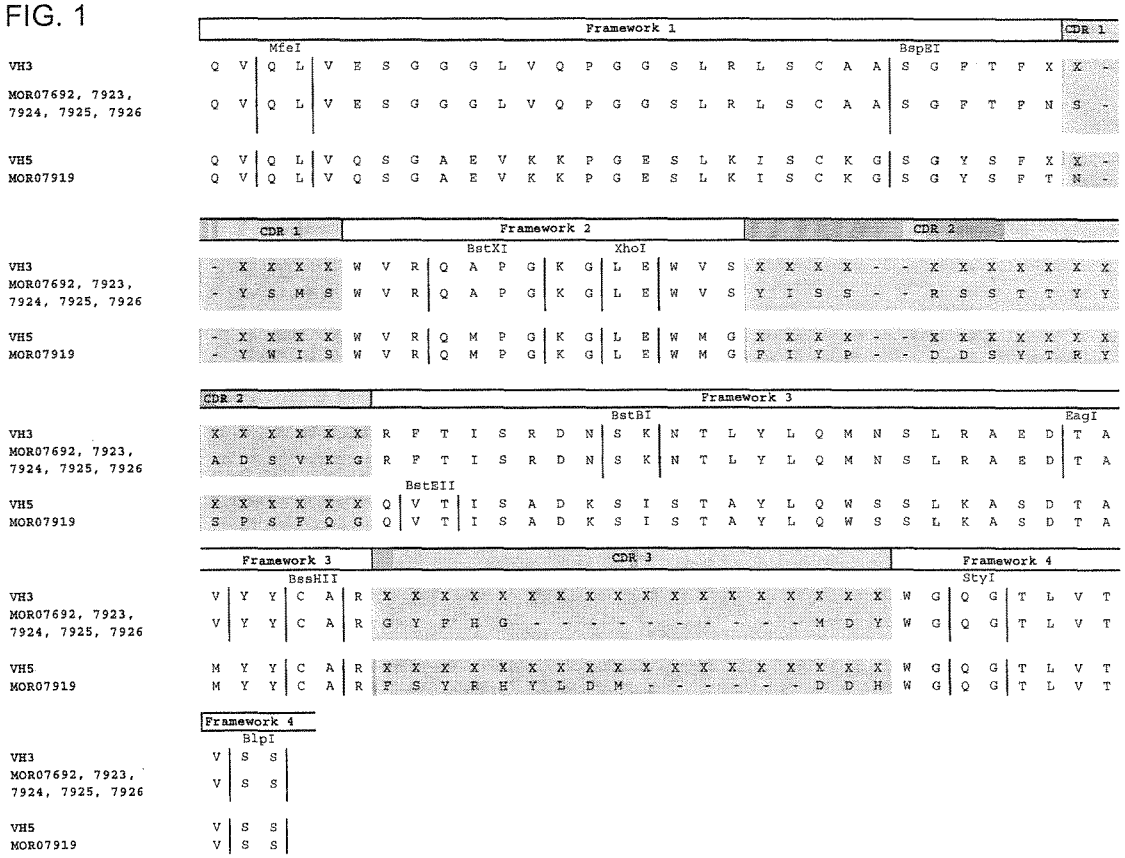

Framework 1
CDR 1
MfeI
BspEI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
CDR 1
Framework 2
CDR 2
BstXI
XhoI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
CDR 2
Framework 3
BstBI
EagI
BstEII
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
Framework 3
CDR 3
Framework 4
BssHII
StyI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919
Framework 4
BlpI
VH3
MOR07692, 7923, 7924, 7925, 7926
VH5
MOR07919

FIG. 2A

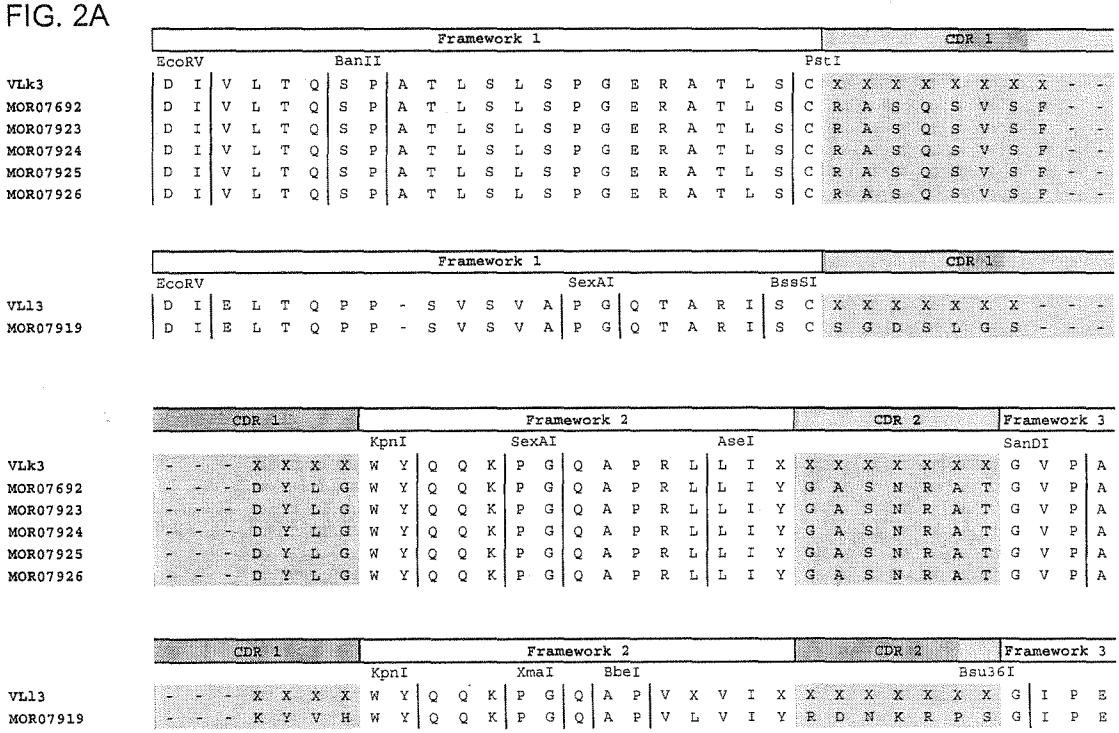
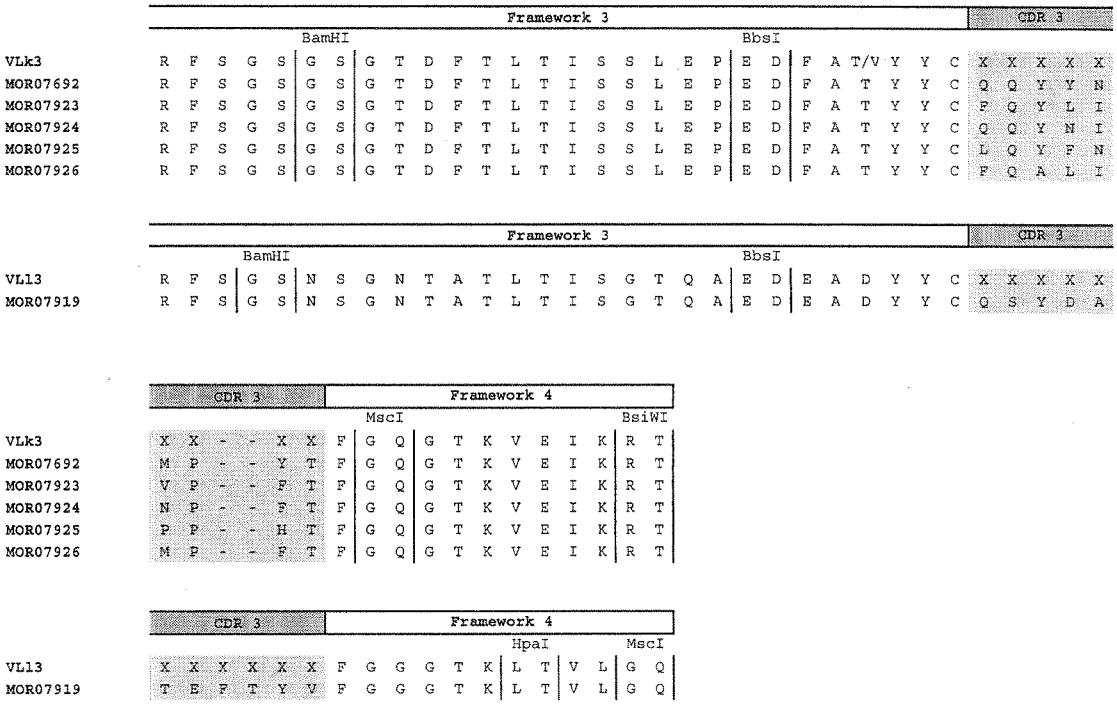
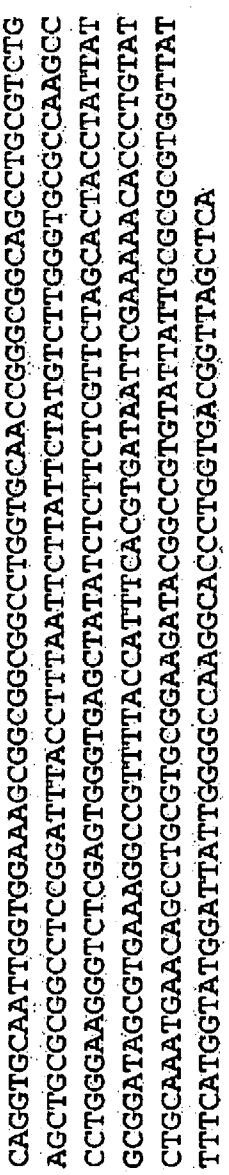

Framework 1
CDR 1
EcoRV
BanII
PstI
VLk3 D I V L T Q S P A T L S L S P G E R A T L S C X X X X X X X X - -
MOR07692 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F - -
MOR07923 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F - -
MOR07924 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F - -
MOR07925 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F - -
MOR07926 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F - -
Framework 1
CDR 1
EcoRV
SexAI
BssSI
VLl3 D I E L T Q P P - S V S V A P G Q T A R I S C X X X X X X X - - -
MOR07919 D I E L T Q P P - S V S V A P G Q T A R I S C S G D S L G S - - -
CDR 1
Framework 2
CDR 2
Framework 3
KpnI
SexAI
AseI
SanDI
VLk3 - - - X X X X W Y Q Q K P G Q A P R L L I X X X X X X X G V P A
MOR07692 - - - D Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A
MOR07923 - - - D Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A
MOR07924 - - - D Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A
MOR07925 - - - D Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A
MOR07926 - - - D Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A
CDR 1
Framework 2
CDR 2
Framework 3
KpnI
XmaI
BbeI
Bsu36I
VLl3 - - - X X X X W Y Q Q K P G Q A P V X V I X X X X X X X X G I P E
MOR07919 - - - K Y V H W Y Q Q K P G Q A P V L V I Y R D N K R P S G I P E

FIG. 2B


Framework 3
CDR 3
BamHI
BbsI
VLk3 R F S G S G S G T D F T L T I S S L E P E D F A T/V Y Y C X X X X X
MOR07692 R F S G S G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y Y N
MOR07923 R F S G S G S G T D F T L T I S S L E P E D F A T Y Y C F Q Y L I
MOR07924 R F S G S G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y N I
MOR07925 R F S G S G S G T D F T L T I S S L E P E D F A T Y Y C L Q Y F N
MOR07926 R F S G S G S G T D F T L T I S S L E P E D F A T Y Y C F Q A L I
Framework 3
CDR 3
BamHI
BbsI
VL13 R F S G S N S G N T A T L T I S G T Q A E D E A D Y Y C X X X X X
MOR07919 R F S G S N S G N T A T L T I S G T Q A E D E A D Y Y C Q S Y D A
CDR 3
Framework 4
MscI
BsiWI
VLk3 X X - - X X F G Q G T K V E I K R T
MOR07692 M P - - Y T F G Q G T K V E I K R T
MOR07923 V P - - F T F G Q G T K V E I K R T
MOR07924 N P - - F T F G Q G T K V E I K R T
MOR07925 P P - - H T F G Q G T K V E I K R T
MOR07926 M P - - F T F G Q G T K V E I K R T
CDR 3
Framework 4
HpaI
MscI
VL13 X X X X X X F G G G T K L T V L G Q
MOR07919 T E F T Y V F G G G T K L T V L G Q

[Fig. 3A]

FIG. 3A

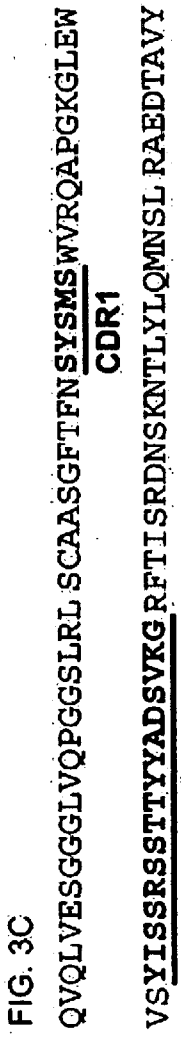

CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTG
AGCTGCCGCCGGCCTCCGGATTTACCTTTAATTCTTATTCTATGTCTTGGGTGCGCCAAGCC
CCTGGGAAGGGTCTCGAGTGGGTGAGCTATATCTCTTCTCGTTCTAGCACTACCTATTAT
GCGGATAGCGTGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTAT
CTGCAAATGAACAGCCTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTAT
TTTCATGGTATGGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

[Fig. 3B]

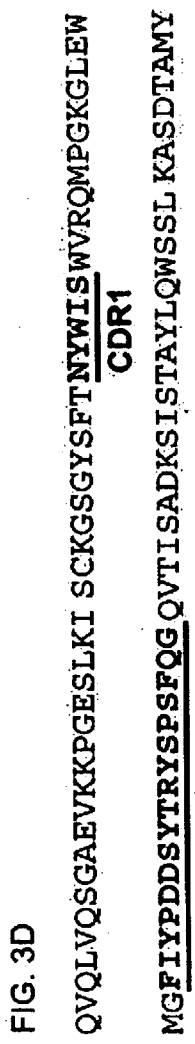
FIG. 3B

CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATT
AGCTGCAAAGGTTCCGGATATTCCTTTACTAATTATTGGATTTCTTGGGTGCGCCAGATG
CCTGGGAAGGGTCTCGAGTGGATGGGCTTTATCTATCCGGATGATAGCTATACCCGTTAT
TCTCCGAGCTTTCAGGGCCAGGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTAT
CTTCAATGGAGCAGCCTGAAAGCGATACGGCCATGTATTATTGCGCGCGTTTTTCT
TATCGTCATTATCTTGATATGGATGATCATTGGGGCCAAGGCACCCTGGTGACGGTTAGC
TCA

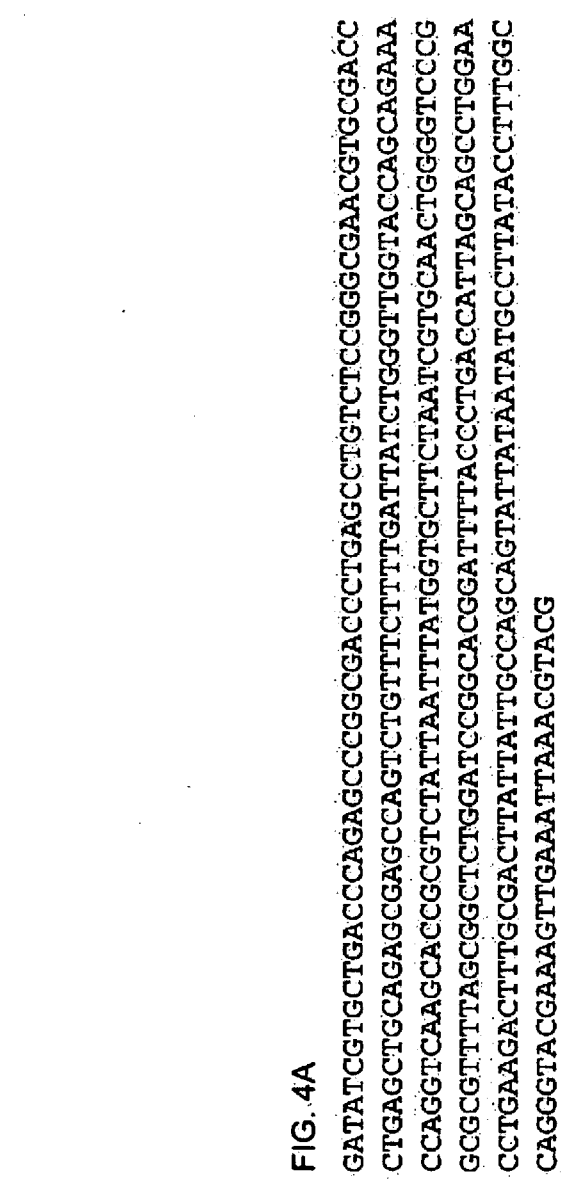
[Fig. 3C]


FIG. 3C
QVQLVESGGGLVQPGGSLRLSCAASGFTFNSYSMSWVRQAPGKGLEW
CDR1
VSYISSRSSTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY
CDR2
YCARGYFHGMDYWGQGTLVTVSS
CDR3

[Fig. 3D]


FIG. 3D
QVQLVQSGAEVKKPGESLKI SCKGSGYSFTNYWIS WVRQMPGKGLEW
CDR1
MGFIYPDDSYTRYSPSFQG QVTISADKSISTAYLQWSSL KASDTAMY
CDR2
YCARFSYRHYLDMDDH WGQGTLVTVSS
CDR3

[Fig. 4A]

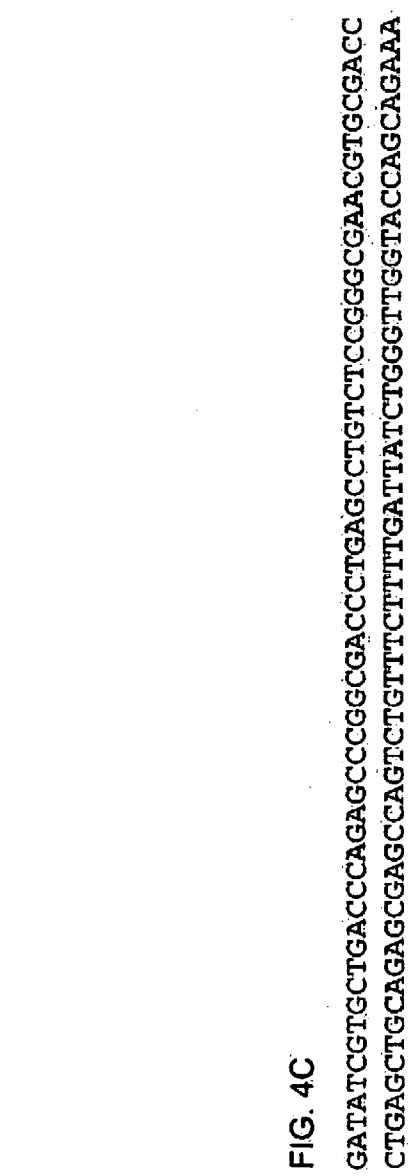

FIG. 4A
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACC
CTGAGCTGCAGAGCGAGCCAGTCTGTTTCTTTTGATTATCTGGGTTGGTACCAGCAGAAA
CCAGGTCAAGCACCGCGTCTATTTAATTTATGGTGCTTCTAATCGTGCAACTGGGGTCCCG
GCGCGTTTTAGCGGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAA
CCTGAAGACTTTGCGACTTATTATTGCCAGCAGTATTATAATATGCCTTATACCTTTGGC
CAGGGTACCGAAAGTTGAAATTAAACGTACG

[Fig. 4B]

FIG. 4B

GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATC
TCGTGTAGCGGCGATTCTCTTGGTTCTAAGTATGTTCATTGGTACCAGCAGAAACCCGGG
CAGGCGCCAGTTCTTGTGATTTATCGTGATAATAAGCGTCCCTCAGGCATCCCGGAACGC
TTTAGCGGATCCAACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAA
GACGAAGCGGATTATTATTGCCAGTCTTATGATGCTACTGAGTTTACTTATGTGTTTGGC
GGCGGCACGAAGTTAACCGTTCTTGGCCAG

[Fig. 4C]

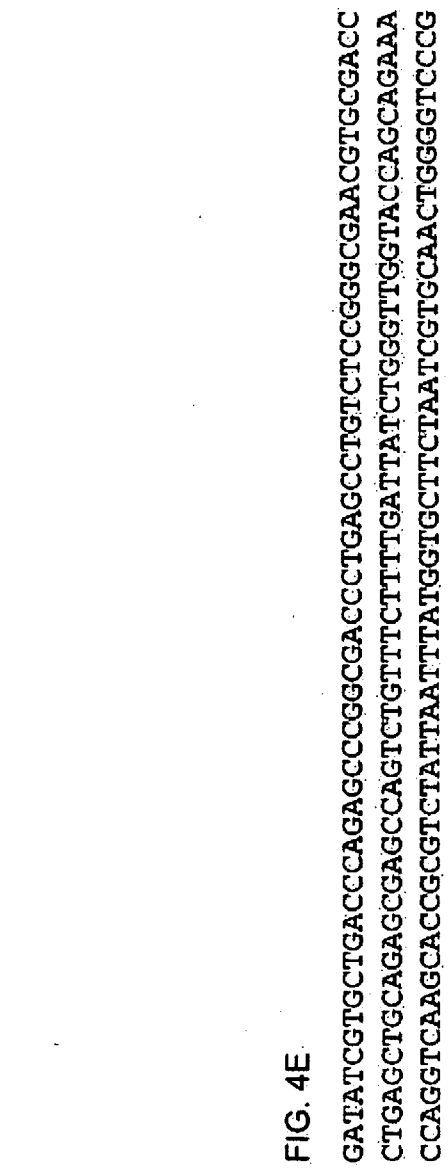

FIG. 4C
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACC
CTGAGCTGCAGAGCGAGCCAGTCTGTTTCTTTTGATTATCTGGGTTGGTACCAGCAGAAA
CCAGGTCAAGCACCGCGTCTATTTAATTTATGGTGCTTCTAATCGTGCAACTGGGGTCCCG
GCGCGTTTTAGCGGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAA
CCTGAAGACTTTGCGACCTATTATTGCTTTCAGTATCTTATTGTTCCTTTTACCTTTGGC
CAGGGTACGAAAGTTGAAATTAAACGTACG

[Fig. 4D]

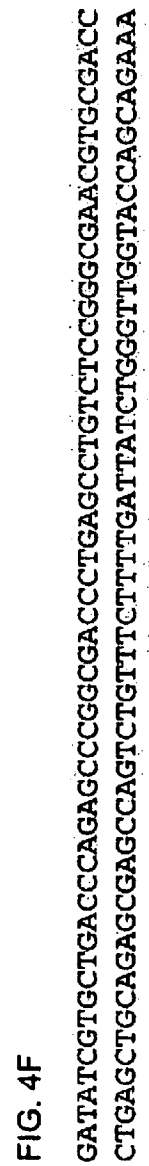
FIG. 4D

GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACC
CTGAGCTGCAGAGCGAGCCAGTCTGTTTCTTTGATTATCTGGGTTGGTACCAGCAGAAA
CCAGGTCAAGCACCGCGTCTATTAATTTATGGTGCTTCTAATCGTGCAACTGGGGTCCCG
GCGCGTTTTAGCGGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAA
CCTGAAGACTTTGCGACCTATTATTGCCAGCAGTATAATATTAATCCTTTTACCTTTGGC
CAGGGTACGAAAGTTGAAATTAAACGTACG

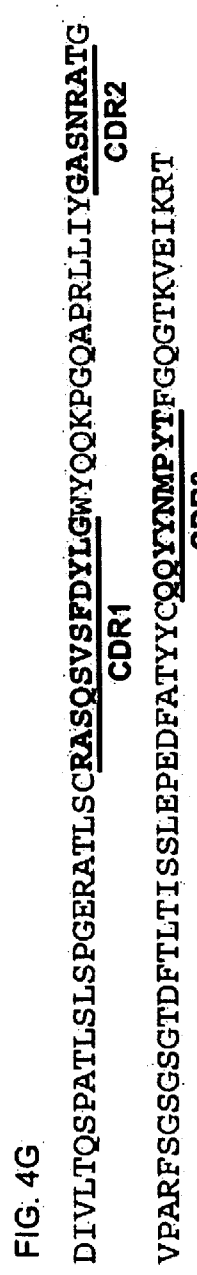
[Fig. 4E]


FIG. 4E
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACC
CTGAGCTGCAGAGCCAGTCTGTTTCTTTTGATTATCTGGGTTGGTACCAGCAGAAA
CCAGGTCAAGCACCGCGTCTATTAATTTATGGTGCTTCTAATCGTGCAACTGGGGTCCCG
GCGCGTTTTAGCGGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAA
CCTGAAGACTTTGCGACCTATTATTGCCTTCAGTATTTTAATCCTCCTCATACCTTTGGC
CAGGGTACGAAAGTTGAAATTAAACGTACG

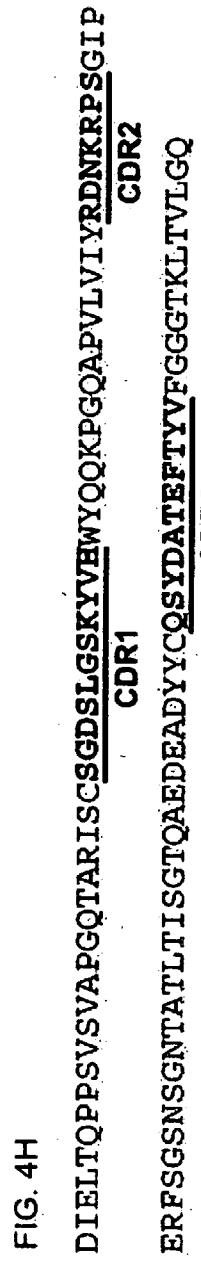
[Fig. 4F]


FIG. 4F
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACC
CTGAGCTGCAGAGCGAGCCAGTCTGTTTCTTTTGATTATCTGGGTTGGTACCAGCAGAAA
CCAGGTCAAGCACCGCGTCTATTAATTTATGGTGCTTCTAATCGTGCAACTGGGGTCCCG
GCGCGTTTTAGCGGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAA
CCTGAAGACTTTGCGACCTATTATTGCTTTCAGGCTCTTATTATGCCTTTTACCTTTGGC
CAGGGTACGAAAGTTGAAATTAAACGTACG

[Fig. 4G]

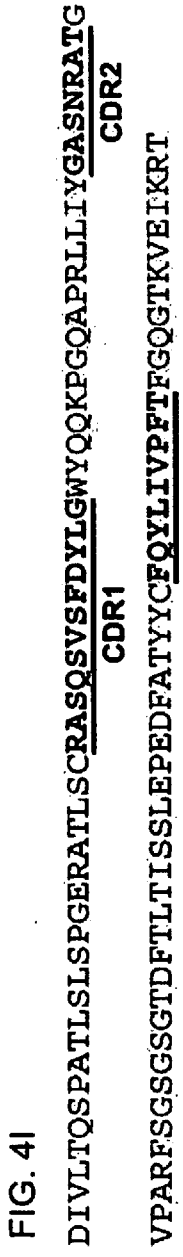

FIG. 4G
DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATG
CDR1
CDR2
VPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYYNMPYTFGQGTKVEIKRT
CDR3

[Fig. 4H]

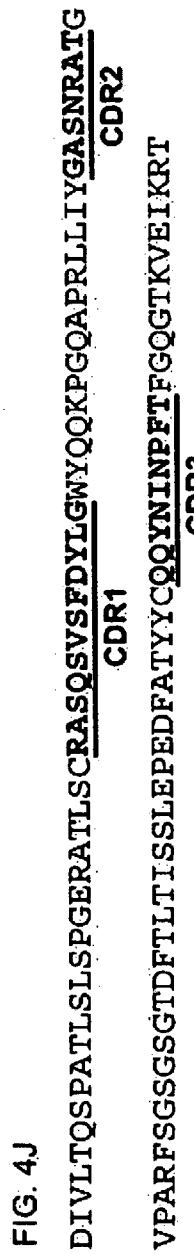

FIG. 4H
DIELTQPPSVSVAPGQTARISCSGDSLGSKYVHWYQQKPGQAPVLVIYRDNKRPSGIP
CDR1
CDR2
ERFSGSNSGNTATLTISGTQAEDEADYYCQSYDATEFTYVFGGGTKLTVLGQ
CDR3

[Fig. 4I]

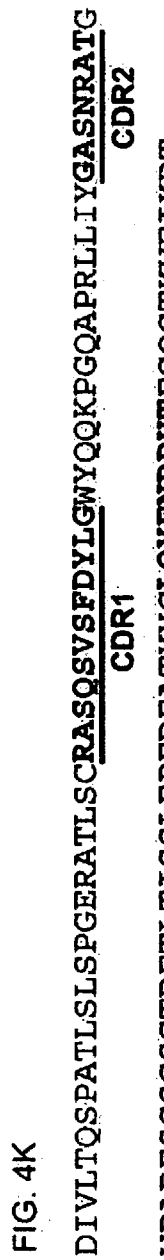
FIG. 4I


DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATG
CDR1
CDR2
VPARFSGSGSGTDFTLTISSLEPEDFATYYCFQYLIVPFTFGQGTKVEIKRT
CDR3

[Fig. 4J]


FIG. 4J
DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATG
CDR1
CDR2
VPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNINPFTFGQGTKVEIKRT
CDR3

[Fig. 4K]


FIG. 4K
DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATG
CDR1
CDR2
VPARFSGSGSGTDFTLTISSLEPEDFATYYCLQYFNPPHTFGQGTKVEIKRT
CDR3

[Fig. 4L]

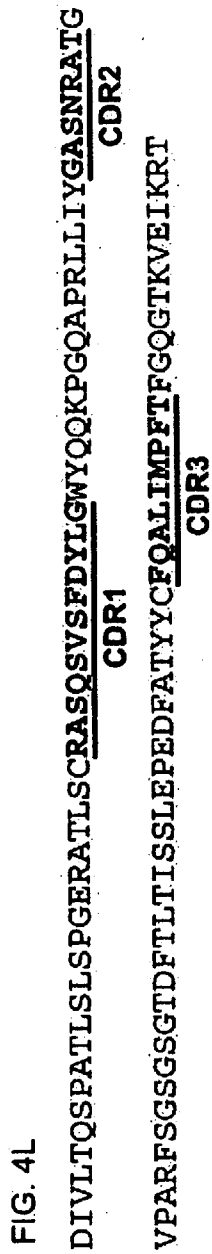

FIG. 4L
DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATG
CDR1
CDR2
VPARFSGSGSGTDFTLTISSLEPEDFATYYCFQALIMPFTFGQGTKVEIKRT
CDR3

FIG. 5

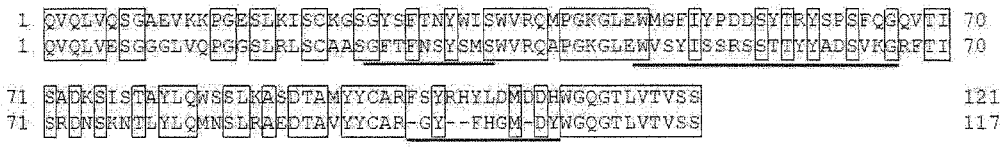

1 QVQLVQSGAEVKKPGESLKISCKGSGYSFTNYWISWVRQMPGKGLEWMGFIYPDDSYTRYSPSFQGQVTI 70
1 QVQLVESGGGLVQPGGSLRLSCAASGFTFNSYSMSWVRQAPGKGLEWVSYISSRSSTIYYADSVKGRFTI 70
71 SADKSISTAYLQWSSLKASDTAMYYCARFSYRHYLDMDDHWGQGTLVTVSS 121
71 SRDNSKNTLYLQMNSLRAEDTAVYYCAR-GY--FHGM-DYWGQGTLVTVSS 117

FIG. 6


1 DIELTQ-PPSVSVAPGQTARISC-SGDSLGSKYVHWYQQKPGQAPVLVIYRDNKRPSGIPERFSGSNSGN
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
1 DIVLTQSPATLSLSPGERATLSCRASQSVSFDYLGWYQQKPGQAPRLLIYGASNRATGVPARFSGSGSGT
69 TATLTISGTQAEDEADYYCQSYDATEFTYVFGGGTKLTVLGQ
71 DFTLTISSLEPEDFATYYCQQYYNMPYT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCFQYLIVPFT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCQQYNINPFT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCLQYFNPPHT--FGQGTKVEIKRT
71 DFTLTISSLEPEDFATYYCFQALIMPFT--FGQGTKVEIKRT

FIG 7A

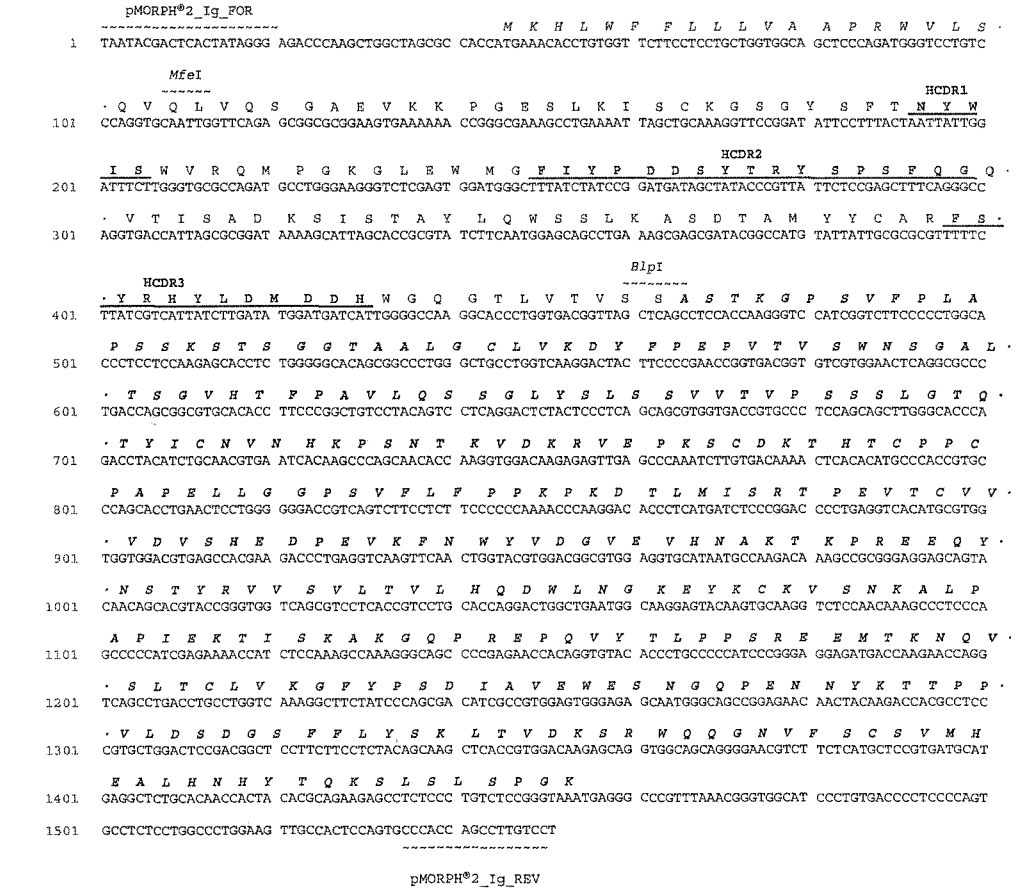


FIG. 7B

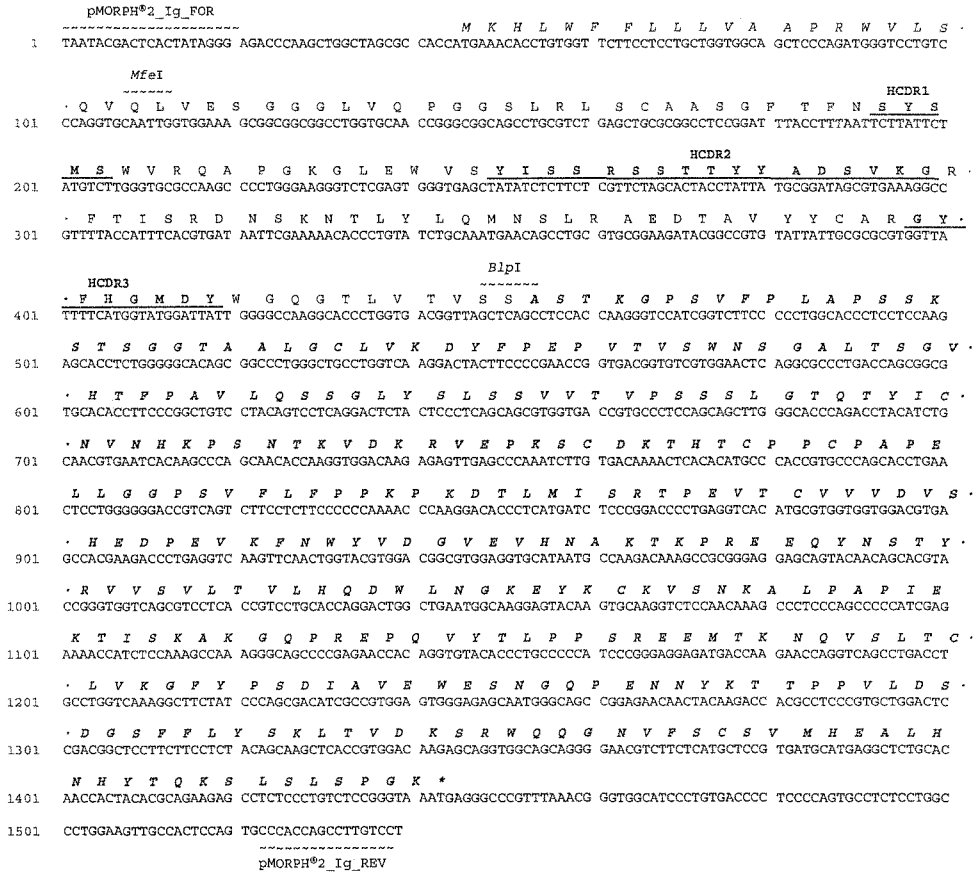


FIG. 8

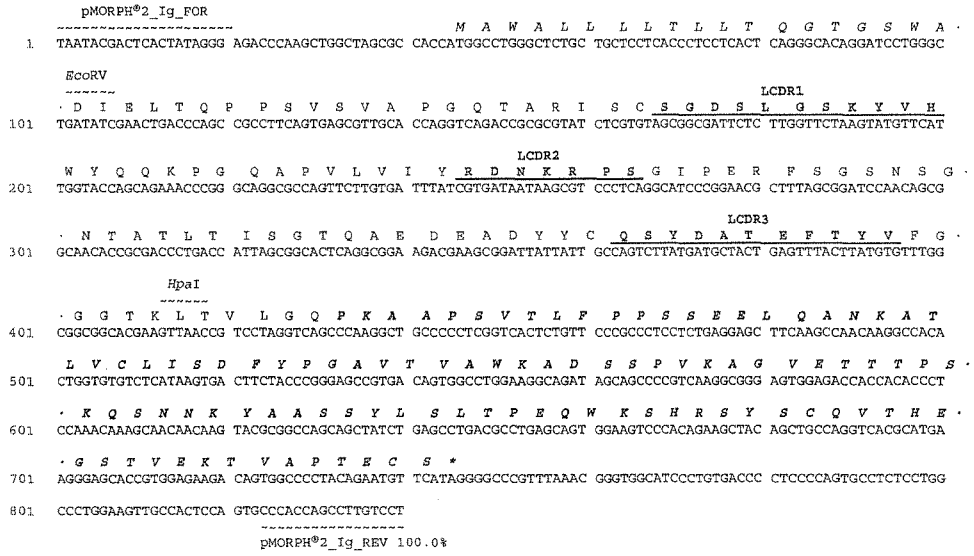

pMORPH®2_Ig_FOR
EcoRV
LCDR1
LCDR2
LCDR3
HpaI
pMORPH®2_Ig_REV 100.0%

FIG. 9A

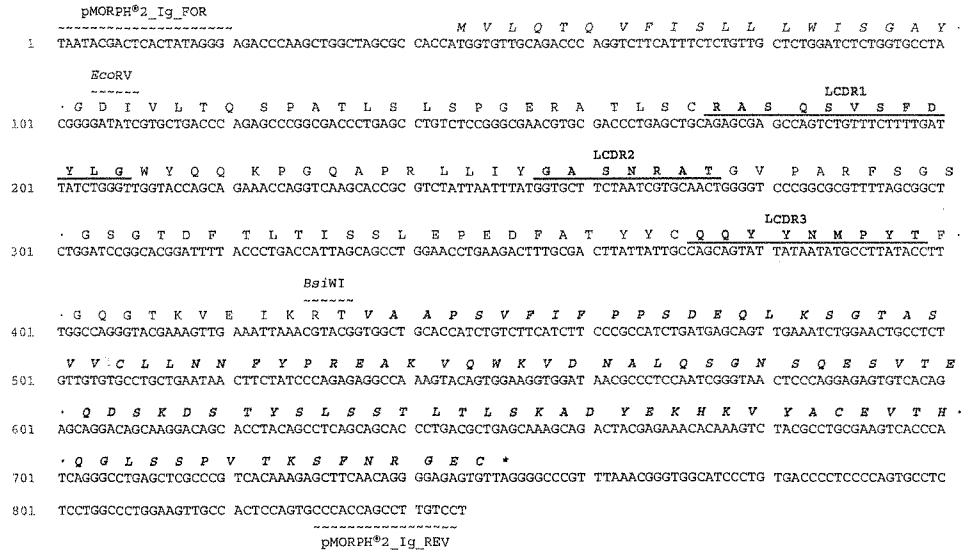

pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y Y N M P Y T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CTTATTATTGCCAGCAGTAT TATAATATGCCTTATACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

FIG. 9B

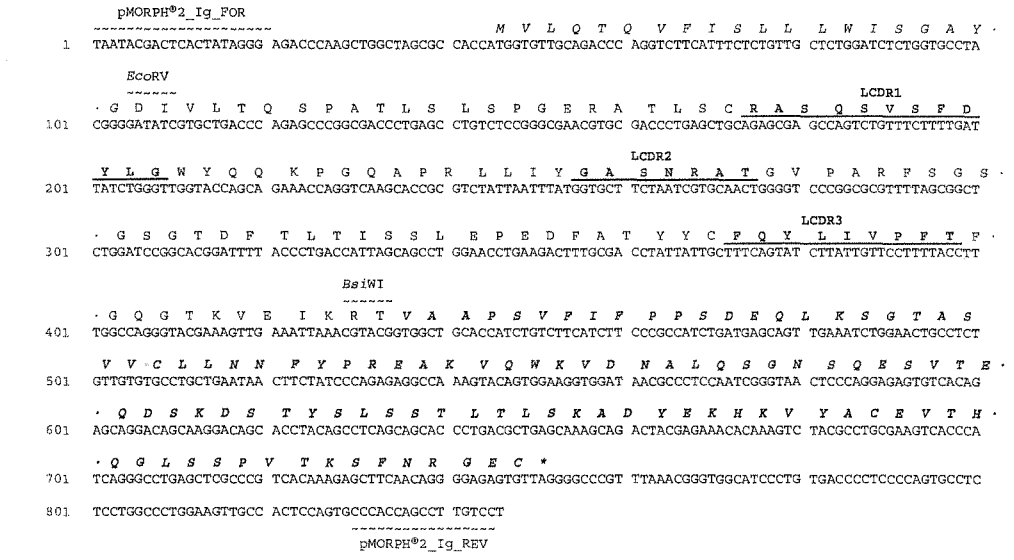

pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C F Q Y L I V P F T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCTTTCAGTAT CTTATTGTTCCTTTTACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

FIG. 9C


pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C Q Q Y N I N P F T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCCAGCAGTAT AATATTAATCCTTTTACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

FIG. 9D

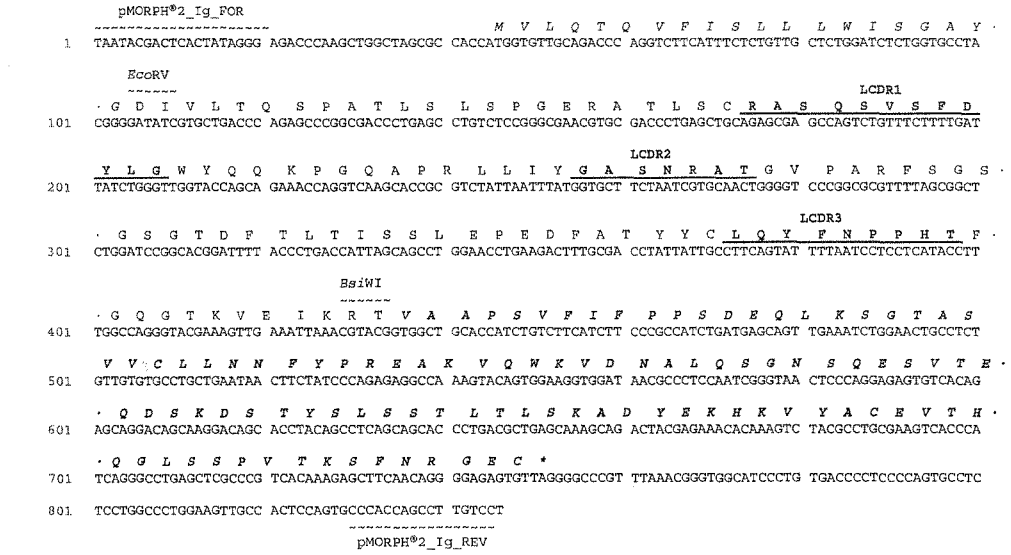
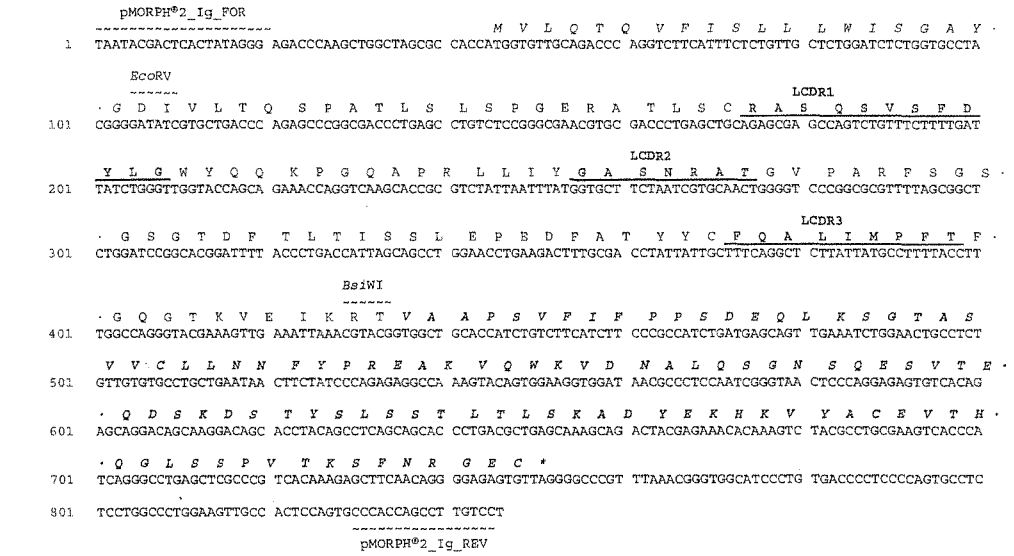

pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y ·
1 TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
· G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
101 CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S ·
201 TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
· G S G T D F T L T I S S L E P E D F A T Y Y C L Q Y F N P P H T F ·
301 CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCCTTCAGTAT TTTAATCCTCCTCATACCTT
BsiWI
· G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
401 TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E ·
501 GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
· Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H ·
601 AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
· Q G L S S P V T K S F N R G E C *
701 TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
801 TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

FIG. 9E


pMORPH®2_Ig_FOR
M V L Q T Q V F I S L L L W I S G A Y
TAATACGACTCACTATAGGG AGACCCAAGCTGGCTAGCGC CACCATGGTGTTGCAGACCC AGGTCTTCATTTCTCTGTTG CTCTGGATCTCTGGTGCCTA
EcoRV
LCDR1
G D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S V S F D
CGGGGATATCGTGCTGACCC AGAGCCCGGCGACCCTGAGC CTGTCTCCGGGCGAACGTGC GACCCTGAGCTGCAGAGCGA GCCAGTCTGTTTCTTTTGAT
LCDR2
Y L G W Y Q Q K P G Q A P R L L I Y G A S N R A T G V P A R F S G S
TATCTGGGTTGGTACCAGCA GAAACCAGGTCAAGCACCGC GTCTATTAATTTATGGTGCT TCTAATCGTGCAACTGGGGT CCCGGCGCGTTTTAGCGGCT
LCDR3
G S G T D F T L T I S S L E P E D F A T Y Y C F Q A L I M P F T F
CTGGATCCGGCACGGATTTT ACCCTGACCATTAGCAGCCT GGAACCTGAAGACTTTGCGA CCTATTATTGCTTTCAGGCT CTTATTATGCCTTTTACCTT
BsiWI
G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
TGGCCAGGGTACGAAAGTTG AAATTAAACGTACGGTGGCT GCACCATCTGTCTTCATCTT CCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E
GTTGTGTGCCTGCTGAATAA CTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGAT AACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTCACAG
Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H
AGCAGGACAGCAAGGACAGC ACCTACAGCCTCAGCAGCAC CCTGACGCTGAGCAAAGCAG ACTACGAGAAACACAAAGTC TACGCCTGCGAAGTCACCCA
Q G L S S P V T K S F N R G E C *
TCAGGGCCTGAGCTCGCCCG TCACAAAGAGCTTCAACAGG GGAGAGTGTTAGGGGCCCGT TTAAACGGGTGGCATCCCTG TGACCCCTCCCCAGTGCCTC
TCCTGGCCCTGGAAGTTGCC ACTCCAGTGCCCACCAGCCT TGTCCT
pMORPH®2_Ig_REV

[Fig. 10]

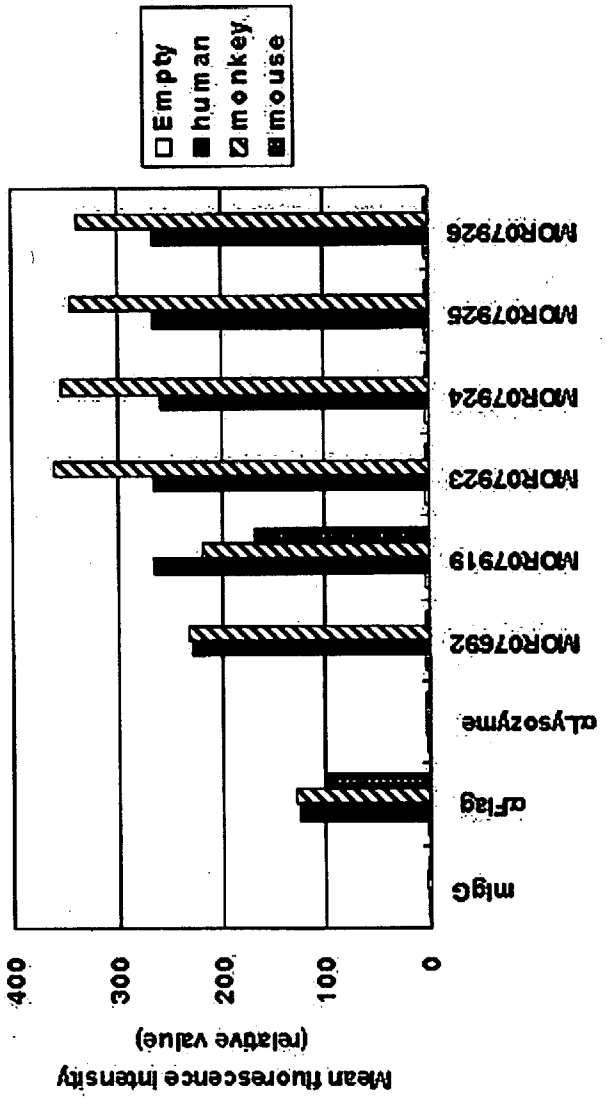
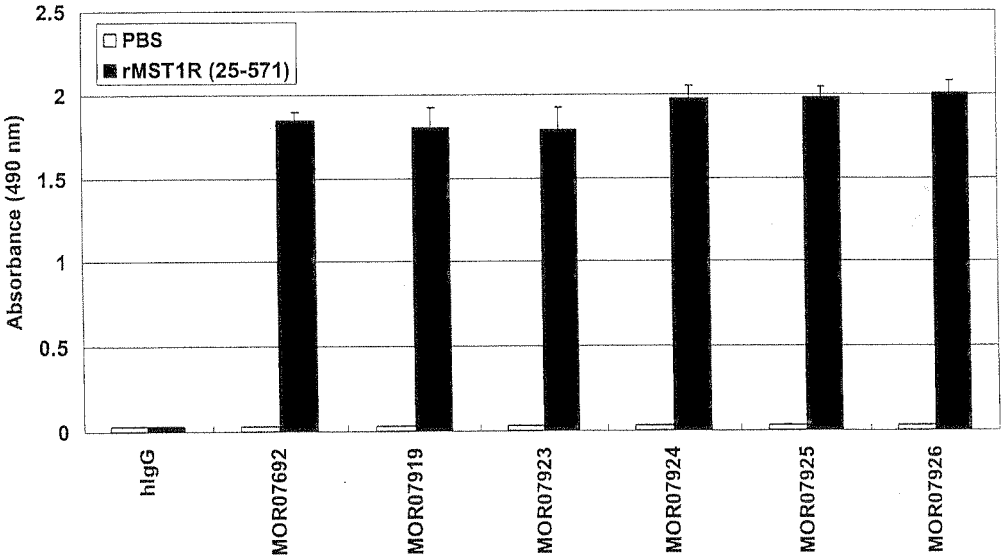

Empty
human
monkey
mouse
mIgG
αFlag
αLysozyme
MOR07692
MOR07919
MOR07923
MOR07924
MOR07925
MOR07926
0
100
200
300
400
Mean fluorescence intensity
(relative value)

FIG. 10

FIG. 11


2.5
2
1.5
1
0.5
0
Absorbance (490 nm)
PBS
rMST1R (25-571)
hIgG
MOR07692
MOR07919
MOR07923
MOR07924
MOR07925
MOR07926

[Fig. 12]

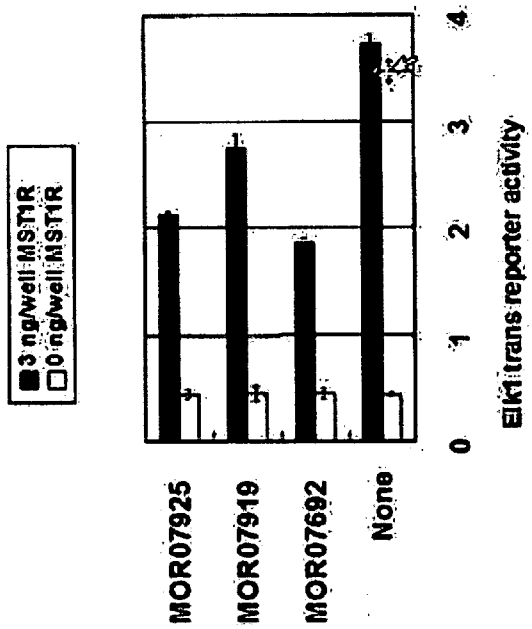

3 ng/well MST1R
0 ng/well MST1R
MOR07925
MOR07919
MOR07692
None
0
1
2
3
4
Elk1 trans reporter activity

FIG. 12

[Fig. 13]

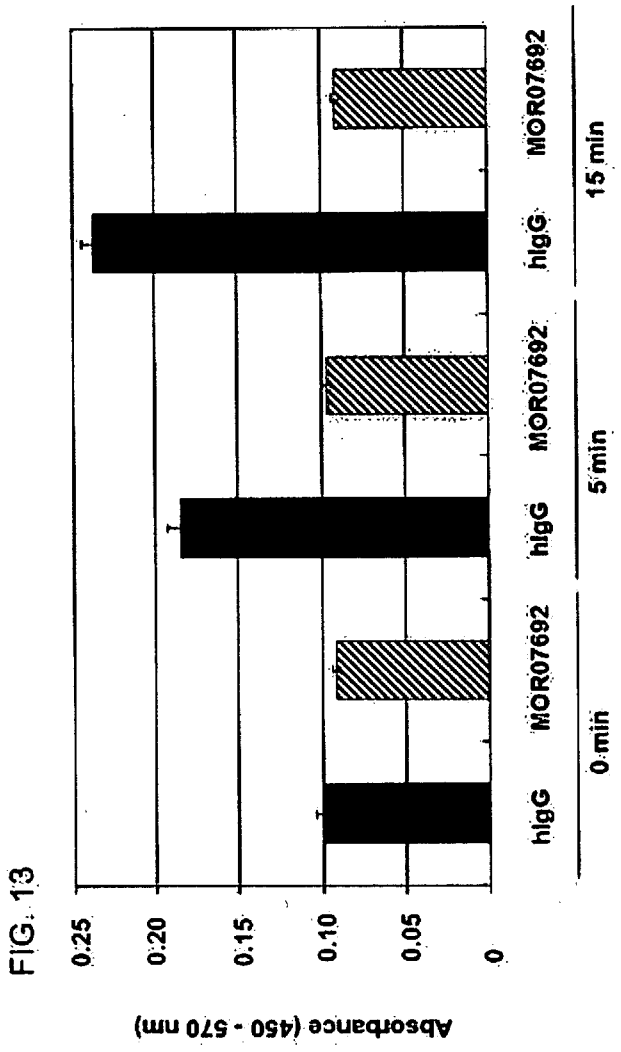
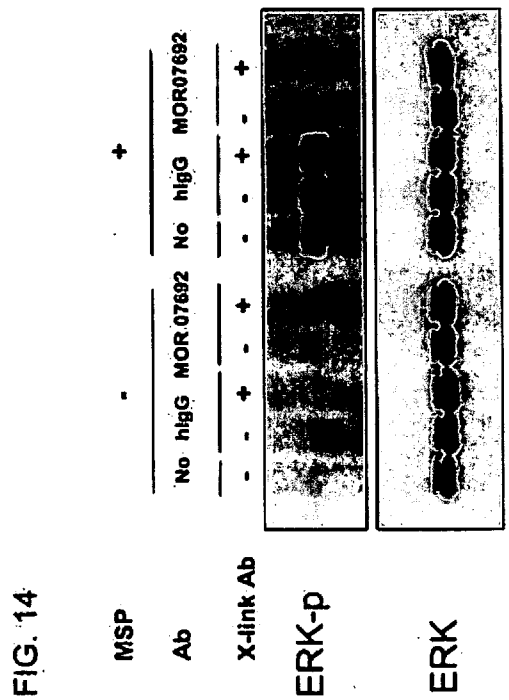

Absorbance (450 - 570 nm)
0.25
0.20
0.15
0.10
0.05
0
hIgG
MOR07692
hIgG
MOR07692
hIgG
MOR07692
0 min
5 min
15 min

FIG. 13

[Fig. 14]


FIG. 14
MSP
Ab
X-link Ab
ERK-p
ERK
No higG MOR07692 No higG MOR07692
- - + - + - - + - +

[Fig. 15]

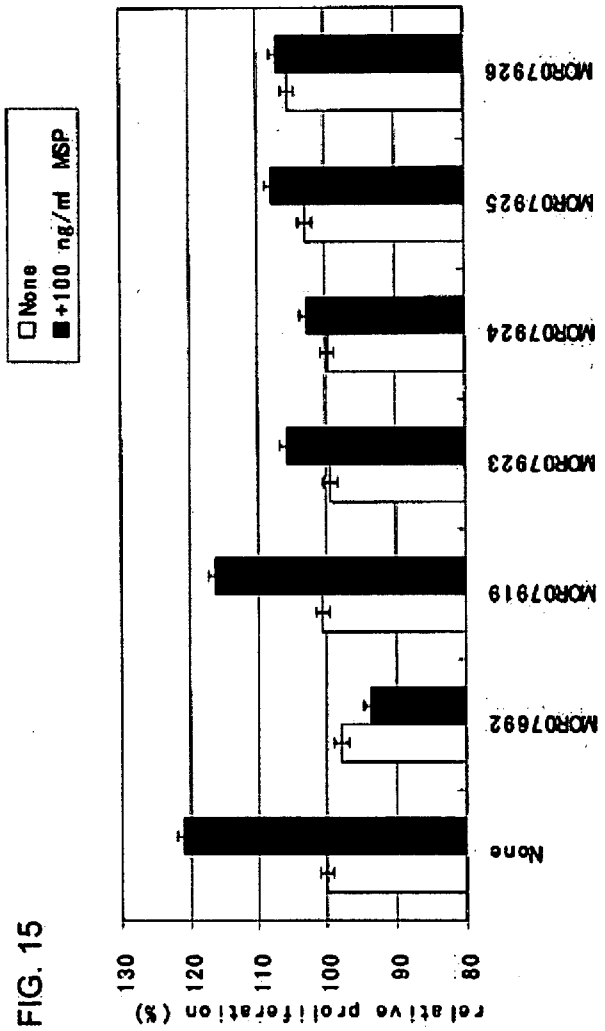

None
MOR07692
MOR07919
MOR07923
MOR07924
MOR07925
MOR07926
relative proliferation (%)
80
90
100
110
120
130
None
+100 ng/ml MSP

FIG. 15

[Fig. 16]

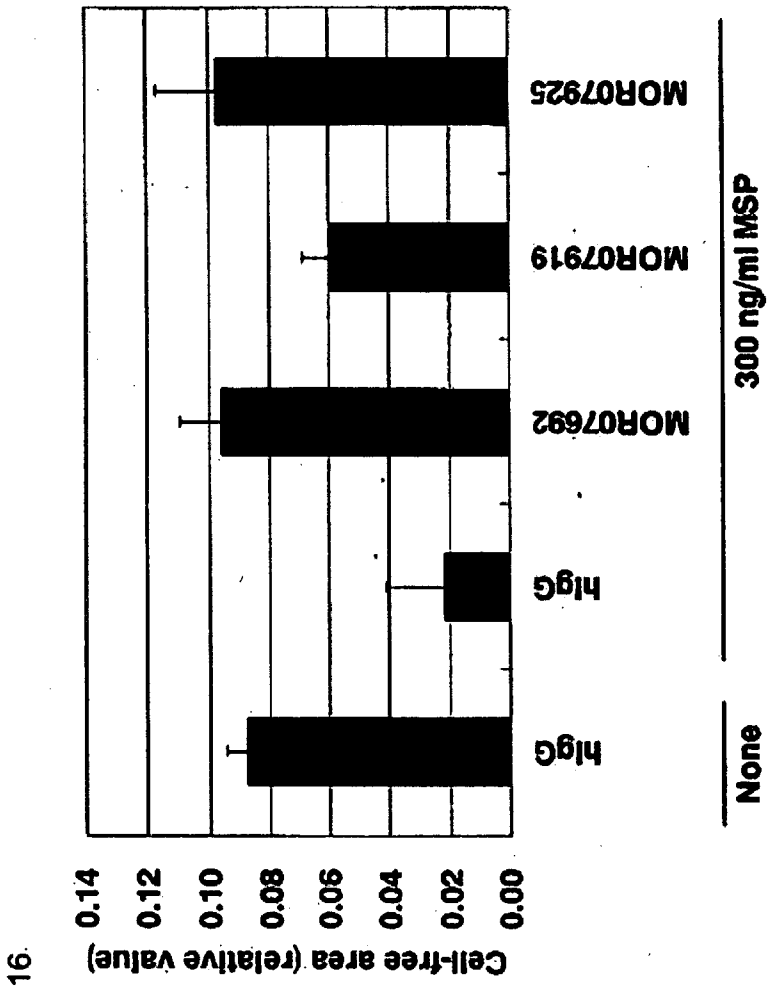

Cell-free area (relative value)
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
None
300 ng/ml MSP
hIgG
hIgG
MOR07692
MOR07919
MOR07925

FIG. 16

[Fig. 17]

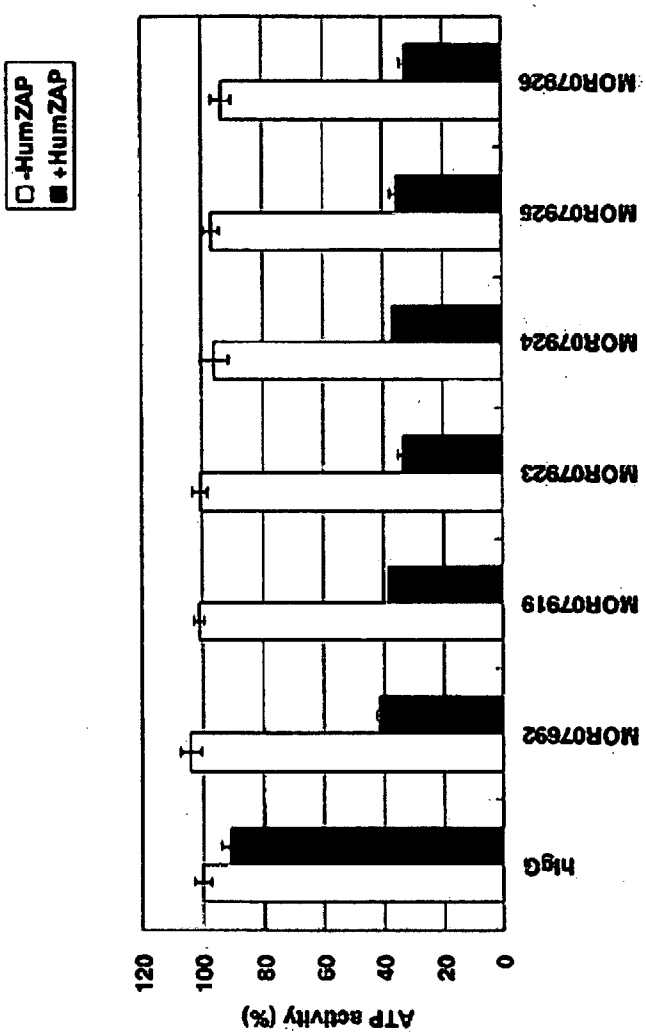

-HumZAP
+HumZAP
ATP activity (%)
120
100
80
60
40
20
0
hIgG
MOR07692
MOR07919
MOR07923
MOR07924
MOR07925
MOR07926

FIG. 17