```
   1 CCAACTGCAC CTCGGTTCTA TCGATAGGAG GCTGGAAGAA AGGACAGAAG TAGCTCTGGC TGTGATGGGG ATCTTACTGG GCCTGCTACT CCTGGGGCAC
     GGTTGACGTG GAGCCAAGAT AGCTATCCTC CGACCTTCTT TCCTGTCTTC ATCGAGACCG ACACTACCCC TAGAATGACC CGGACGATGA GGACCCCGTC
   1                                                                                 M  G  I  L  L  G  L  L  L  L  G  H
                                                                                     ^MET

 101 CTAACAGTGG ACACTTATGG CCGTCCCATC CTGGAAGTGC CAGAGAGTGT AACAGGACCT TGGAAAGGGG ATGTGAATCT TCCCTGCACC TATGACCCCC
     GATTGTCACC TGTGAATACC GGCAGGGTAG GACCTTCACG GTCTCTCACA TTGTCCTGGA ACCTTTCCCC TACACTTAGA AGGGACGTGG ATACTGGGGG
  13 L  T  V  D  T  Y  G  R  P  I  L  E  V  P  E  S  V  T  G  P  W  K  G  D  V  N  L  P  C  T  Y  D  P  L

 201 TGCAAGGCTA CACCCAAGTC TTGGTGAAGT GGCTGGTACA ACGTGGCTCA GACCCTGTCA CCATCTTTCT ACGTGACTCT TCTGGAGACC ATATCCAGCA
     ACGTTCCGAT GTGGGTTCAG AACCACTTCA CCGACCATGT TGCACCGAGT CTGGGACAGT GGTAGAAAGA TGCACTGAGA AGACCTCTGG TATAGGTCGT
  47   Q  G  Y  T  Q  V  L  V  K  W  L  V  Q  R  G  S  D  P  V  T  I  F  L  R  D  S  S  G  D  H  I  Q  Q

 301 GGCAAAGTAC CAGGGCCGCC TGCATGTGAG CCACAAGGTT CCAGGAGATG TATCCCTCCA ATTGAGCACC CTGGAGATGG ATGACCGGAG CCACTACACG
     CCGTTTCATG GTCCCGGCGG ACGTACACTC GGTGTTCCAA GGTCCTCTAC ATAGGGAGGT TAACTCGTGG GACCTCTACC TACTGGCCTC GGTGATGTGC
  80 A  K  Y  Q  G  R  L  H  V  S  H  K  V  P  G  D  V  S  L  Q  L  S  T  L  E  M  D  D  R  S  H  Y  T

 401 TGTGAAGTCA CCTGGCAGAC TCCTGATGGC AACCAAGTCG TGAGAGATAA GATTACTGAG CTCCGTGTCC AGAAACTCTC TGTCTCCAAG CCCACAGTGA
     ACACTTCAGT GGACCGTCTG AGGACTACCG TTGGTTCAGC ACTCTCTATT CTAATGACTC GAGGCACAGG TCTTTGAGAG ACAGAGGTTC GGGTGTCACT
 113 C  E  V  T  W  Q  T  P  D  G  N  Q  V  V  R  D  K  I  T  E  L  R  V  Q  K  L  S  V  S  K  P  T  V  T

 501 CAACTGGCAG CGGTTATGGC TTCACGGTGC CCCAGGGAAT GAGGATTAGC CTTCAATGCC AGGCTCGGGG TTCTCCTCCC ATCAGTTATA TTTGGTATAA
     GTTGACCGTC GCCAATACCG AAGTGCCACG GGGTCCCTTA CTCCTAATCG GAAGTTACGG TCCGAGCCCC AAGAGGAGGG TAGTCAATAT AAACCATATT
 147   T  G  S  G  Y  G  F  T  V  P  Q  G  M  R  I  S  L  Q  C  Q  A  R  G  S  P  P  I  S  Y  I  W  Y  K
```

FIG. 1A

```
601 GCAACAGACT AATAACCAGG AACCCATCAA AGTAGCAACC CTAAGTACCT TACTCTTCAA GCCTGCGGTG ATAGCCGACT CAGGCTCCTA TTTCTGCACT
    CGTTGTCTGA TTATTGGTCC TTGGGTAGTT TCATCGTTGG GATTCATGGA ATGAGAAGTT CGGACGCCAC TATCGGCTGA GTCCGAGGAT AAAGACGTGA
180  Q  Q  T  N  N  Q  E  P  I  K  V  A  T  L  S  T  L  L  F  K  P  A  V  I  A  D  S  G  S  Y  F  C  T

701 GCCAAGGGCC AGGTTGGCTC TGAGCAGCAC AGCGACATTG TGAAGTTTGT GGTCAAAGAC TCCTCAAAGC TACTCAAGAC CAAGACTGAG GCACCTACAA
    CGGTTCCCGG TCCAACCGAG ACTCGTCGTG TCGCTGTAAC ACTTCAAACA CCAGTTTCTG AGGAGTTTCG ATGAGTTCTG GTTCTGACTC CGTGGATGTT
213 A  K  G  Q  V  G  S  E  Q  H  S  D  I  V  K  F  V  V  K  D  S  S  K  L  L  K  T  K  T  E  A  P  T  T

801 CCATGACATA CCCCTTGAAA GCAACATCTA CAGTGAAGCA GTCCTGGGAC TGGACCACTG ACATGGATGG CTACCTTGGA GAGACCAGTG CTGGGCCAGG
    GGTACTGTAT GGGGAACTTT CGTTGTAGAT GTCACTTCGT CAGGACCCTG ACCTGGTGAC TGTACCTACC GATGGAACCT CTCTGGTCAC GACCCGGTCC
247  M  T  Y  P  L  K  A  T  S  T  V  K  Q  S  W  D  W  T  T  D  M  D  G  Y  L  G  E  T  S  A  G  P  G

901 AAAGAGCCTG CCTGTCTTTG CCATCATCCT CATCATCTCC TTGTGCTGTA TGGTGGTTTT TACCATGGCC TATATCATGC TCTGTCGGAA GACATCCCAA
    TTTCTCGGAC GGACAGAAAC GGTAGTAGGA GTAGTAGAGG AACACGACAT ACCACCAAAA ATGGTACCGG ATATAGTACG AGACAGCCTT CTGTAGGGTT
280  K  S  L  P  V  F  A  I  I  L  I  I  S  L  C  C  M  V  V  F  T  M  A  Y  I  M  L  C  R  K  T  S  Q

1001 CAAGAGCATG TCTACGAAGC AGCCAGGGCA CATGCCAGAG AGGCCAACGA CTCTGGAGAA ACCATGAGGG TGGCCATCTT CGCAAGTGGC TGCTCCAGTG
     GTTCTCGTAC AGATGCTTCG TCGGTCCCGT GTACGGTCTC TCCGGTTGCT GAGACCTCTT TGGTACTCCC ACCGGTAGAA GCGTTCACCG ACGAGGTCAC
313  Q  E  H  V  Y  E  A  A  R  A  H  A  R  E  A  N  D  S  G  E  T  M  R  V  A  I  F  A  S  G  C  S  S  D

1101 ATGAGCCAAC TTCCCAGAAT CTGGGCAACA ACTACTCTGA TGAGCCCTGC ATAGGACAGG AGTACCAGAT CATCGCCCAG ATCAATGGCA ACTACGCCCG
     TACTCGGTTG AAGGGTCTTA GACCCGTTGT TGATGAGACT ACTCGGGACG TATCCTGTCC TCATGGTCTA GTAGCGGGTC TAGTTACCGT TGATGCGGGC
347   E  P  T  S  Q  N  L  G  N  N  Y  S  D  E  P  C  I  G  Q  E  Y  Q  I  I  A  Q  I  N  G  N  Y  A  R

1201 CCTGCTGGAC ACAGTTCCTC TGGATTATGA GTTTCTGGCC ACTGAGGGCA AAAGTGTCTG TTAAAAATGC CCCATTAGGC CAGGATCTGC TGACATAATC
     GGACGACCTG TGTCAAGGAG ACCTAATACT CAAAGACCGG TGACTCCCGT TTTCACAGAC AATTTTTACG GGGTAATCCG GTCCTAGACG ACTGTATTAG
380  L  L  D  T  V  P  L  D  Y  E  F  L  A  T  E  G  K  S  V  C  O

1301 TAGAGTCGAC CTGCAGAAGC TTGGCCGCCA TGGCCCAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT AA
     ATCTCAGCTG GACGTCTTCG AACCGGCGGT ACCGGGTTGA ACAAATAACG TCGAATATTA CCAATGTTTA TT
```

FIG. 1B


1 GTCCAACTGC ACCTCGGTTC TATCGATAGG AGGCTGGAAG AAAGGACAGA AGTAGCTCTG GCTGTGATGG GGATCTTACT GGGCCTGCTA CTCCTGGGGC
CAGGTTGACG TGGAGCCAAG ATAGCTATCC TCCGACCTTC TTTCCTGTCT TCATCGAGAC CGACACTACC CCTAGAATGA CCCGGACGAT GAGGACCCCG
1 M G I L L G L L L L G H
^insert begins here
101 ACCTAACAGT GGACACTTAT GGCCGTCCCA TCCTGGAAGT GCCAGAGAGT GTAACAGGAC CTTGGAAAGG GGATGTGAAT CTTCCCTGCA CCTATGACCC
TGGATTGTCA CCTGTGAATA CCGGCAGGGT AGGACCTTCA CGGTCTCTCA CATTGTCCTG GAACCTTTCC CCTACACTTA GAAGGGACGT GGATACTGGG
13 L T V D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y D P
201 CCTGCAAGGC TACACCCAAG TCTTGGTGAA GTGGCTGGTA CAACGTGGCT CAGACCCTGT CACCATCTTT CTACGTGACT CTTCTGGAGA CCATATCCAG
GGACGTTCCG ATGTGGGTTC AGAACCACTT CACCGACCAT GTTGCACCGA GTCTGGGACA GTGGTAGAAA GATGCACTGA GAAGACCTCT GGTATAGGTC
46 L Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q
301 CAGGCAAAGT ACCAGGGCCG CCTGCATGTG AGCCACAAGG TTCCAGGAGA TGTATCCCTC CAATTGAGCA CCCTGGAGAT GGATGACCGG AGCCACTACA
GTCCGTTTCA TGGTCCCGGC GGACGTACAC TCGGTGTTCC AAGGTCCTCT ACATAGGGAG GTTAACTCGT GGGACCTCTA CCTACTGGCC TCGGTGATGT
79 Q A K Y Q G R L H V S H K V P G D V S L Q L S T L E M D D R S H Y T
401 CGTGTGAAGT CACCTGGCAG ACTCCTGATG GCAACCAAGT CGTGAGAGAT AAGATTACTG AGCTCCGTGT CCAGAAACAC TCCTCAAAGC TACTCAAGAC
GCACACTTCA GTGGACCGTC TGAGGACTAC CGTTGGTTCA GCACTCTCTA TTCTAATGAC TCGAGGCACA GGTCTTTGTG AGGAGTTTCG ATGAGTTCTG
113 C E V T W Q T P D G N Q V V R D K I T E L R V Q K H S S K L L K T
501 CAAGACTGAG GCACCTACAA CCATGACATA CCCCTTGAAA GCAACATCTA CAGTGAAGCA GTCCTGGGAC TGGACCACTG ACATGGATGG CTACCTTGGA
GTTCTGACTC CGTGGATGTT GGTACTGTAT GGGGAACTTT CGTTGTAGAT GTCACTTCGT CAGGACCCTG ACCTGGTGAC TGTACCTACC GATGGAACCT
146 K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G

FIG. 2A

```
601 GAGACCAGTG CTGGGCCAGG AAAGAGCCTG CCTGTCTTTG CCATCATCCT CATCATCTCC TTGTGCTGTA TGGTGGTTTT TACCATGGCC TATATCATGC
    CTCTGGTCAC GACCCGGTCC TTTCTCGGAC GGACAGAAAC GGTAGTAGGA GTAGTAGAGG AACACGACAT ACCACCAAAA ATGGTACCGG ATATAGTACG
179 E T S A G P G K S L P V F A I I L I I S L C C M V V F T M A Y I M L

701 TCTGTCGGAA GACATCCCAA CAAGAGCATG TCTACGAAGC AGCCAGGGCA CATGCCAGAG AGGCCAACGA CTCTGGAGAA ACCATGAGGG TGGCCATCTT
    AGACAGCCTT CTGTAGGGTT GTTCTCGTAC AGATGCTTCG TCGGTCCCGT GTACGGTCTC TCCGGTTGCT GAGACCTCTT TGGTACTCCC ACCGGTAGAA
213   C R K T S Q Q E H V Y E A A R A H A R E A N D S G E T M R V A I F

801 CGCAAGTGGC TGCTCCAGTG ATGAGCCAAC TTCCCAGAAT CTGGGCAACA ACTACTCTGA TGAGCCCTGC ATAGGACAGG AGTACCAGAT CATCGCCCAG
    GCGTTCACCG ACGAGGTCAC TACTCGGTTG AAGGGTCTTA GACCCGTTGT TGATGAGACT ACTCGGGACG TATCCTGTCC TCATGGTCTA GTAGCGGGTC
246 A S G C S S D E P T S Q N L G N N Y S D E P C I G Q E Y Q I I A Q

901 ATCAATGGCA ACTACGCCCG CCTGCTGGAC ACAGTTCCTC TGGATTATGA GTTTCTGGCC ACTGAGGGCA AAAGTGTCTG TTAAAAATGC CCCATTAGGC
    TAGTTACCGT TGATGCGGGC GGACGACCTG TGTCAAGGAG ACCTAATACT CAAAGACCGG TGACTCCCGT TTTCACAGAC AATTTTTACG GGGTAATCCG
279 I N G N Y A R L L D T V P L D Y E F L A T E G K S V C O

1001 CAGGATCTGC TGACATAATC TAGAGTCGAC CTGCAGAAGC TTGGCCGCCA TGGCCCAACT TGTTTATTGC AGCTTATAAT GGTTACAATA
     GTCCTAGACG ACTGTATTAG ATCTCAGCTG GACGTCTTCG AACCGGCGGT ACCGGGTTGA ACAAATAACG TCGAATATTA CCAATGTTAT
         ^insert ends here
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FIG. 2B

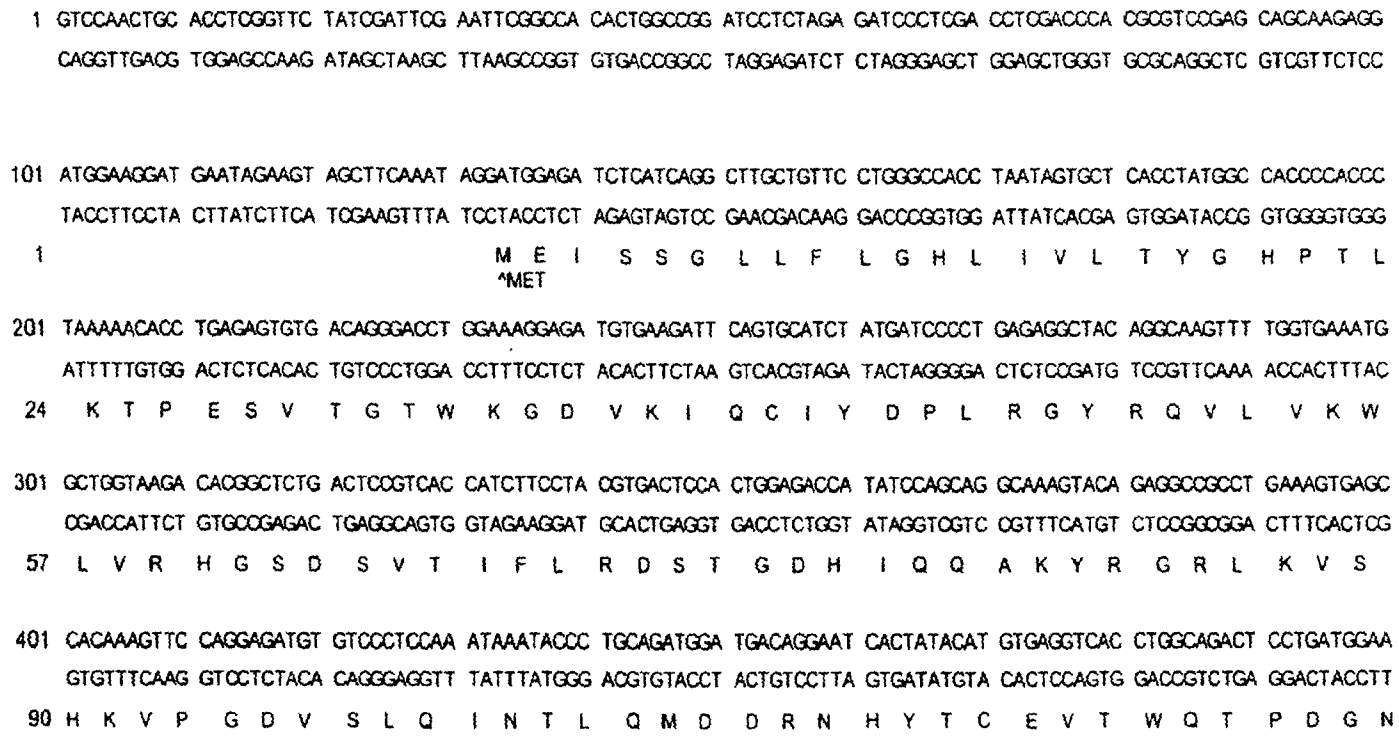
1 GTCCAACTGC ACCTCGGTTC TATCGATTCG AATTCGGCCA CACTGGCCGG ATCCTCTAGA GATCCCTCGA CCTCGACCCA CGCGTCCGAG CAGCAAGAGG
CAGGTTGACG TGGAGCCAAG ATAGCTAAGC TTAAGCCGGT GTGACCGGCC TAGGAGATCT CTAGGGAGCT GGAGCTGGGT GCGCAGGCTC GTCGTTCTCC
101 ATGGAAGGAT GAATAGAAGT AGCTTCAAAT AGGATGGAGA TCTCATCAGG CTTGCTGTTC CTGGGCCACC TAATAGTGCT CACCTATGGC CACCCCACCC
TACCTTCCTA CTTATCTTCA TCGAAGTTTA TCCTACCTCT AGAGTAGTCC GAACGACAAG GACCCGGTGG ATTATCACGA GTGGATACCG GTGGGGTGGG
1 M E I S S G L L F L G H L I V L T Y G H P T L
^MET
201 TAAAAACACC TGAGAGTGTG ACAGGGACCT GGAAAGGAGA TGTGAAGATT CAGTGCATCT ATGATCCCCT GAGAGGCTAC AGGCAAGTTT TGGTGAAATG
ATTTTTGTGG ACTCTCACAC TGTCCCTGGA CCTTTCCTCT ACACTTCTAA GTCACGTAGA TACTAGGGGA CTCTCCGATG TCCGTTCAAA ACCACTTTAC
24 K T P E S V T G T W K G D V K I Q C I Y D P L R G Y R Q V L V K W
301 GCTGGTAAGA CACGGCTCTG ACTCCGTCAC CATCTTCCTA CGTGACTCCA CTGGAGACCA TATCCAGCAG GCAAAGTACA GAGGCCGCCT GAAAGTGAGC
CGACCATTCT GTGCCGAGAC TGAGGCAGTG GTAGAAGGAT GCACTGAGGT GACCTCTGGT ATAGGTCGTC CGTTTCATGT CTCCGGCGGA CTTTCACTCG
57 L V R H G S D S V T I F L R D S T G D H I Q Q A K Y R G R L K V S
401 CACAAAGTTC CAGGAGATGT GTCCCTCCAA ATAAATACCC TGCAGATGGA TGACAGGAAT CACTATACAT GTGAGGTCAC CTGGCAGACT CCTGATGGAA
GTGTTTCAAG GTCCTCTACA CAGGGAGGTT TATTTATGGG ACGTGTACCT ACTGTCCTTA GTGATATGTA CACTCCAGTG GACCGTCTGA GGACTACCTT
90 H K V P G D V S L Q I N T L Q M D D R N H Y T C E V T W Q T P D G N

FIG. 3A

```
501 ACCAAGTAAT AAGAGATAAG ATCATTGAGC TCCGTGTTCG GAAATATAAT CCACCTAGAA TCAATACTGA AGCACCTACA ACCCTGCACT CCTCTTTGGA
    TGGTTCATTA TTCTCTATTC TAGTAACTCG AGGCACAAGC CTTTATATTA GGTGGATCTT AGTTATGACT TCGTGGATGT TGGGACGTGA GGAGAAACCT
124   Q  V  I  R  D  K  I  I  E  L  R  V  R  K  Y  N  P  P  R  I  N  T  E  A  P  T  T  L  H  S  S  L  E

601 AGCAACAACT ATAATGAGTT CAACCTCTGA CTTGACCACT AATGGGACTG GAAAACTTGA GGAGACCATT GCTGGTTCAG GGAGGAACCT GCCAATCTTT
    TCGTTGTTGA TATTACTCAA GTTGGAGACT GAACTGGTGA TTACCCTGAC CTTTTGAACT CCTCTGGTAA CGACCAAGTC CCTCCTTGGA CGGTTAGAAA
157 A  T  T  I  M  S  S  T  S  D  L  T  T  N  G  T  G  K  L  E  E  T  I  A  G  S  G  R  N  L  P  I  F

701 GCCATAATCT TCATCATCTC CCTTTGCTGC ATAGTAGCTG TCACCATACC TTATATCTTG TTCCGCTGCA GGACATTCCA ACAAGAGTAT GTCTATGGAG
    CGGTATTAGA AGTAGTAGAG GGAAACGACG TATCATCGAC AGTGGTATGG AATATAGAAC AAGGCGACGT CCTGTAAGGT TGTTCTCATA CAGATACCTC
190 A  I  I  F  I  I  S  L  C  C  I  V  A  V  T  I  P  Y  I  L  F  R  C  R  T  F  Q  Q  E  Y  V  Y  G  V

801 TGAGCAGGGT GTTTGCCAGG AAGACAAGCA ACTCTGAAGA AACCACAAGG GTGACTACCA TCGCAACTGA TGAACCAGAT TCCCAGGCTC TGATTAGTGA
    ACTCGTCCCA CAAACGGTCC TTCTGTTCGT TGAGACTTCT TTGGTGTTCC CACTGATGGT AGCGTTGACT ACTTGGTCTA AGGGTCCGAG ACTAATCACT
224   S  R  V  F  A  R  K  T  S  N  S  E  E  T  T  R  V  T  T  I  A  T  D  E  P  D  S  Q  A  L  I  S  D

901 CTACTCTGAT GATCCTTGCC TCAGCCAGGA GTACCAAATA ACCATCAGAT CAACAATGTC TATTCCTGCC TGCTGAACAC AGTTTCCAGA AACTAAGAAG
    GATGAGACTA CTAGGAACGG AGTCGGTCCT CATGGTTTAT TGGTAGTCTA GTTGTTACAG ATAAGGACGG ACGACTTGTG TCAAAGGTCT TTGATTCTTC
257 Y  S  D  D  P  C  L  S  Q  E  Y  Q  I  T  I  R  S  T  M  S  I  P  A  C  O

1001 TTCTTGCTAC TGAAGAAAAT AACATCTGCT AAAATGCCCC TACTAAGTCA AGGTCTACTG GCGTAATTAC CTGTTACTTA TTTACTACTT GCCTTCAACA
     AAGAACGATG ACTTCTTTTA TTGTAGACGA TTTTACGGGG ATGATTCAGT TCCAGATGAC CGCATTAATG GACAATGAAT AAATGATGAA CGGAAGTTGT
```

FIG. 3B

1101 TAGCTTTCTC CCTGGCTTCC TTTCTTCTTA GACAACCTAA AGTATCTATC TAGTCTGCCA ATTCTGGGGC CATTGAGAAA TCCTGGGTTT GGCTAAGAAT
ATCGAAAGAG GGACCGAAGG AAAGAAGAAT CTGTTGGATT TCATAGATAG ATCAGACGGT TAAGACCCCG GTAACTCTTT AGGACCCAAA CCGATTCTTA

1201 ATACTACATG CACCTCAAGA AATCTAGCTT CTGGGCTTCA CCCAGAACAA TTTTCTTCCT AGGGCCTTCA CAACTCTTCT CCAAACAGCA GAGAAATTCC
TATGATGTAC GTGGAGTTCT TTAGATCGAA GACCCGAAGT GGGTCTTGTT AAAAGAAGGA TCCCGGAAGT GTTGAGAAGA GGTTTGTCGT CTCTTTAAGG

1301 ATAGCAGTAG AGGTTCTTTA TCATGCCTCC AGACAGCGTG AGTCTCAGTC CTACAAACTC AGACAAGCAC ATGGGTCTAG GATTACTCCT CTTTCTCTAG
TATCGTCATC TCCAAGAAAT AGTACGGAGG TCTGTCGCAC TCAGAGTCAG GATGTTTGAG TCTGTTCGTG TACCCAGATC CTAATGAGGA GAAAGAGATC

1401 GGCCAGATGA CTTTTAATTG ATATTACTAT TGCTACATTA TGAATCTAAT GCACATGTAT TCTTTTGTTG TTAATAAATG TTTAATCATG ACATCAAAAA
CCGGTCTACT GAAAATTAAC TATAATGATA ACGATGTAAT ACTTAGATTA CGTGTACATA AGAAAACAAC AATTATTTAC AAATTAGTAC TGTAGTTTTT

1501 AAAAAAAAAA AAGGGCGGCC GCGACTCTAG AGTCGACCTG CAGTAGGGAT AACAGGGTAA TAAGCTTGGC CGCCATGGCC CAACTTGTTT
TTTTTTTTTT TTCCCGCCGG CGCTGAGATC TCAGCTGGAC GTCATCCCTA TTGTCCCATT ATTCGAACCG GCGGTACCGG GTTGAACAAA
^pRK5 continues here

FIG. 3C

Evaluation of antibodies that block murine STIgMA binding to iC3b

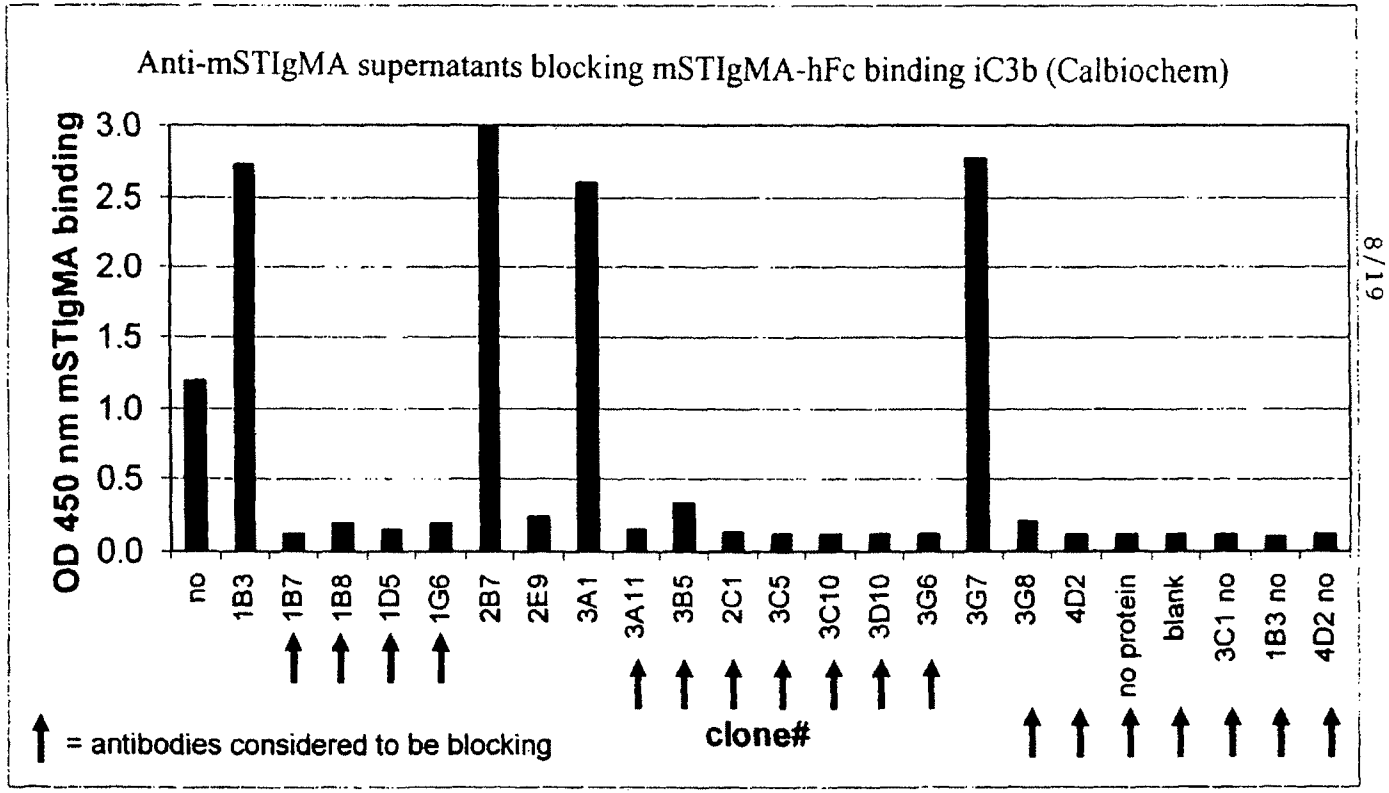

FIG. 4

Evaluation of antibodies that block human STIgMA binding to iC3b

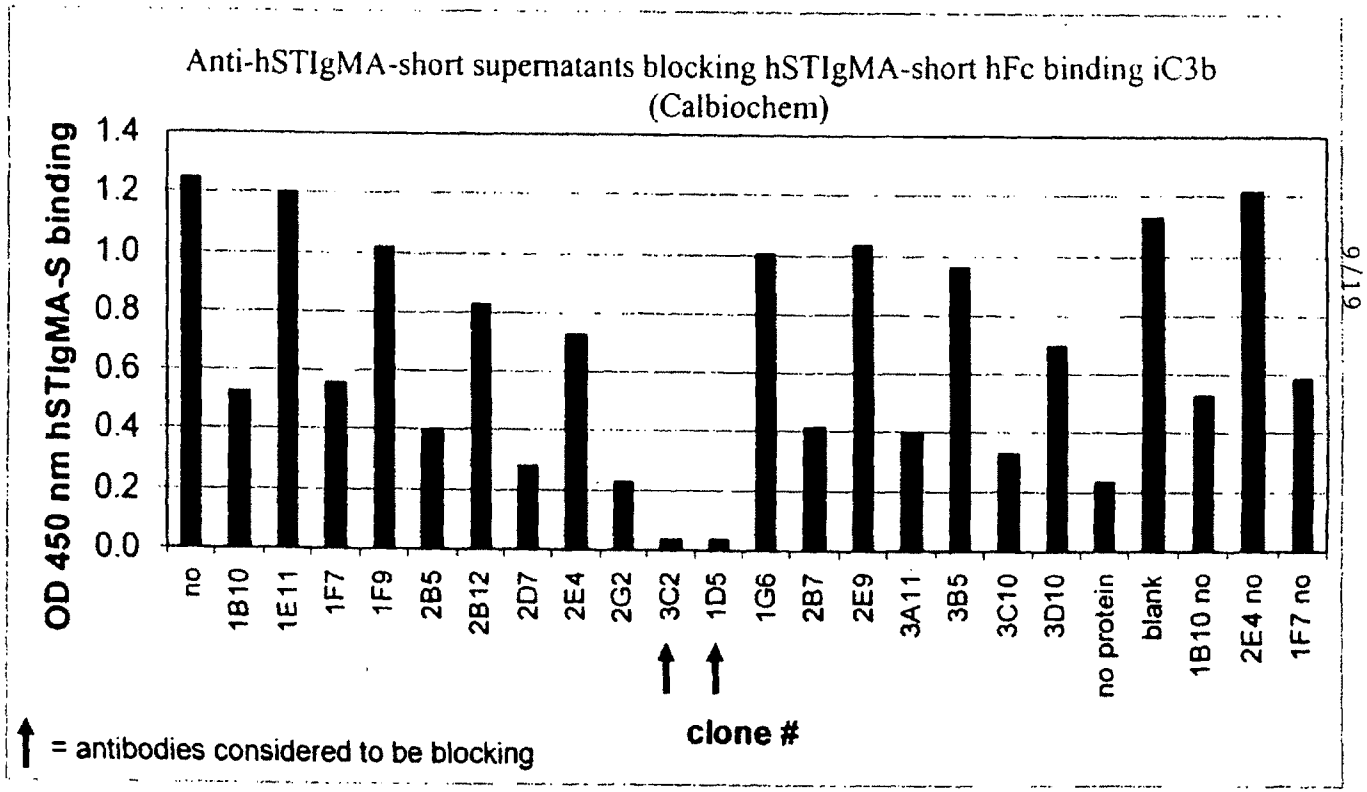

FIG. 5

mAb blocking of iC3b binding to muCRIg-expressing CHO cells

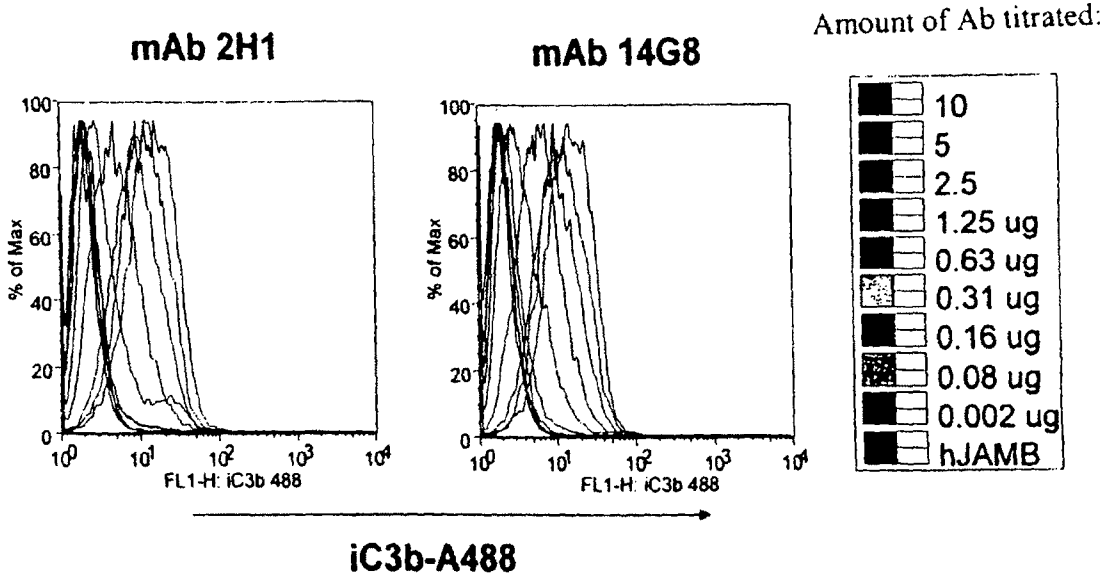

FIG. 6

Antibody 2H1 blocks binding of iC3b to CRIg+ peritoneal macrophages

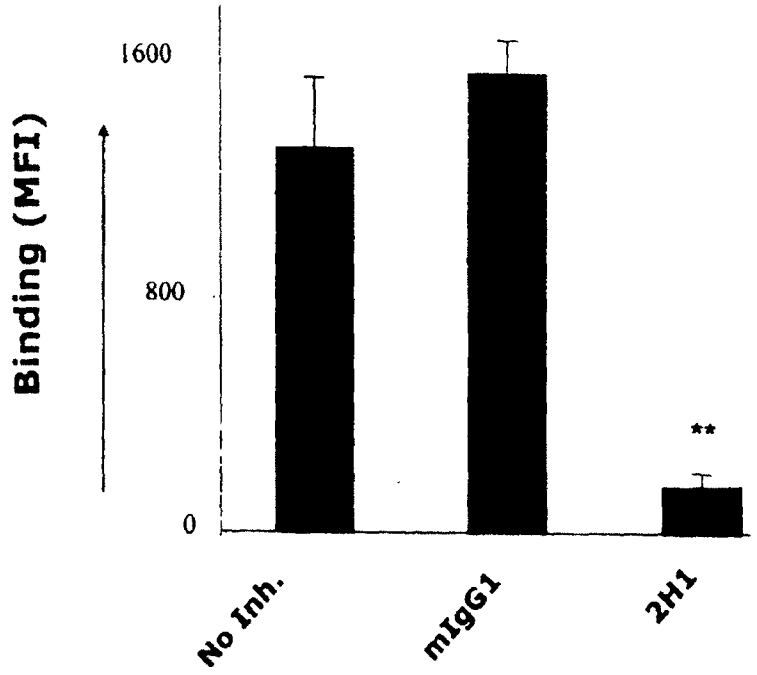

FIG. 7

** p < 0.001

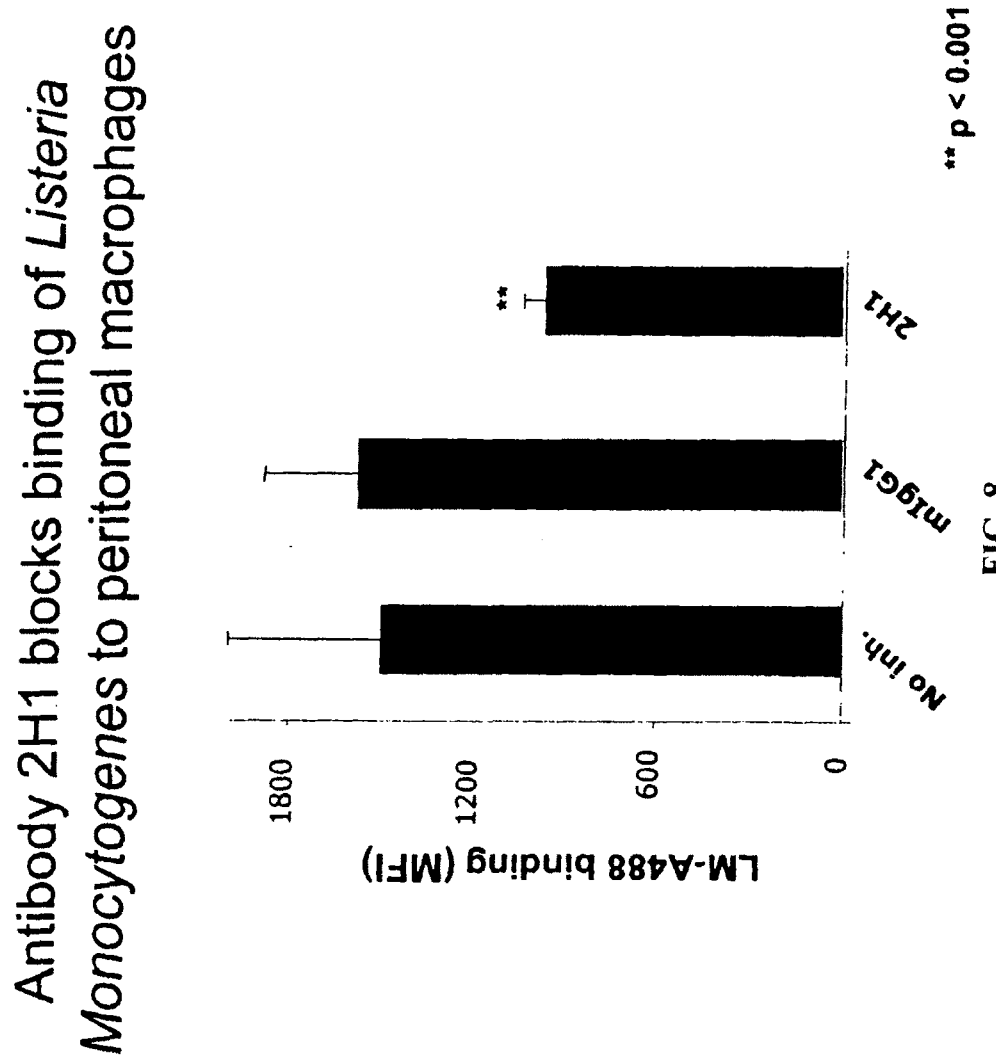
Antibody 2H1 blocks binding of *Listeria Monocytogenes* to peritoneal macrophages
LM-A488 binding (MFI)
1800
1200
600
0
No inh.
mIgG1
2H1
**
** p < 0.001

FIG. 8

Antibody 14G8 blocks uptake of *Listeria M.* from the circulation

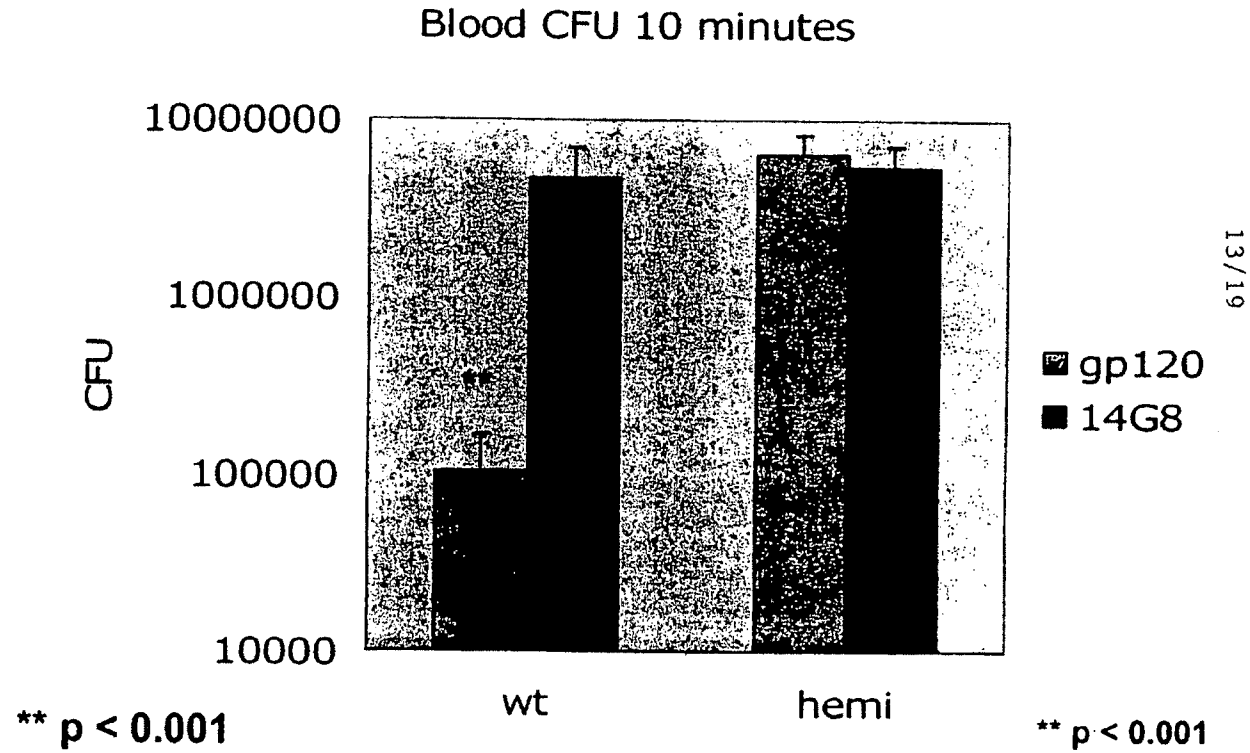

FIG. 9

Antibody 14G8 blocks uptake of *Staphylococcus Aureus* strain M from the circulation

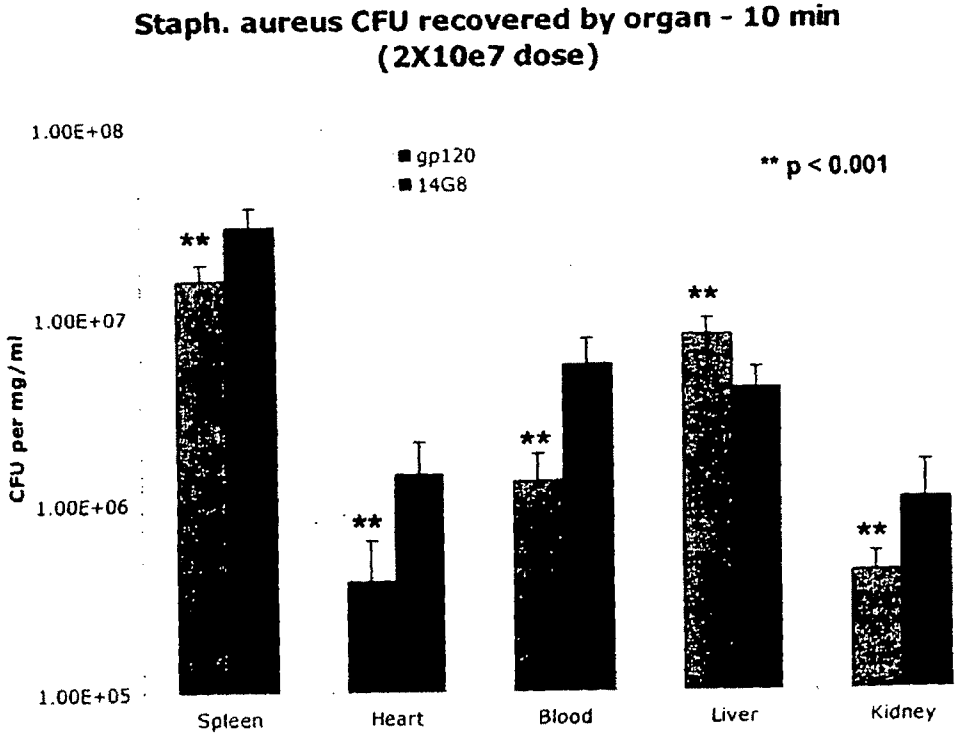

FIG. 10

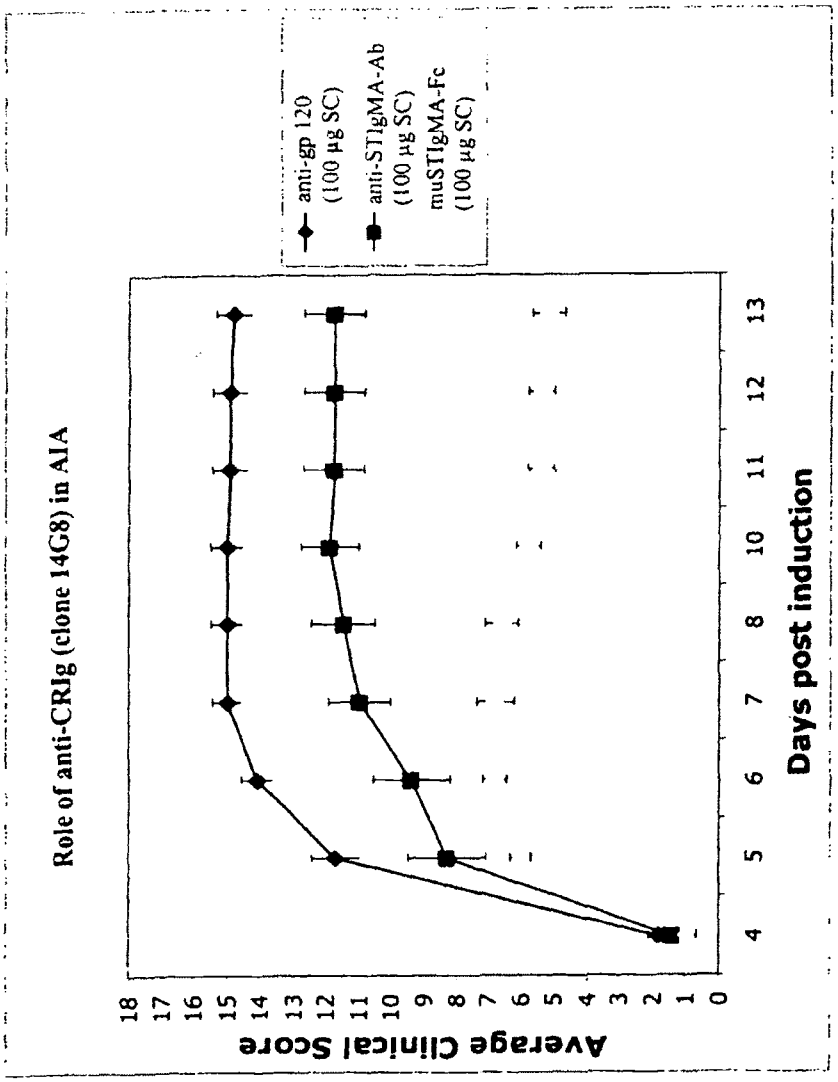
Role of anti-CRIg (clone 14G8) in AIA
Average Clinical Score
Days post induction
anti-gp 120 (100 µg SC)
anti-STIgMA-Ab (100 µg SC)
muSTIgMA-Fc (100 µg SC)

FIG. 11A

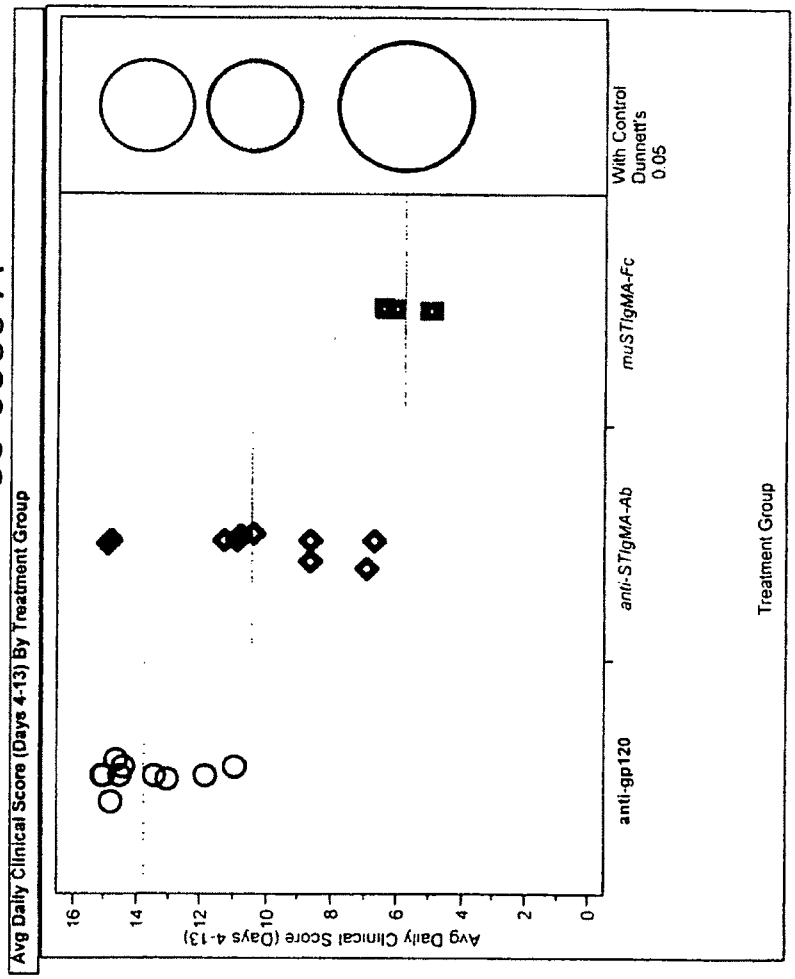
06-0385 A
Avg Daily Clinical Score (Days 4-13) By Treatment Group
Avg Daily Clinical Score (Days 4-13)
16
14
12
10
8
6
4
2
0
anti-gp120
anti-STIgMA-Ab
muSTIgMA-Fc
Treatment Group
With Control
Dunnett's
0.05
Means and Std Deviations
Level Number Mean Std Dev Lower 95% Upper 95%
anti-gp120 10 13.8 1.4 12.7 14.8
anti-STIgMA-Ab 10 10.4 2.8 8.4 12.5
muSTIgMA-Fc 5 5.8 0.732 4.9 6.7

FIG. 11B

3D10 binding to CRIg-expressing cells

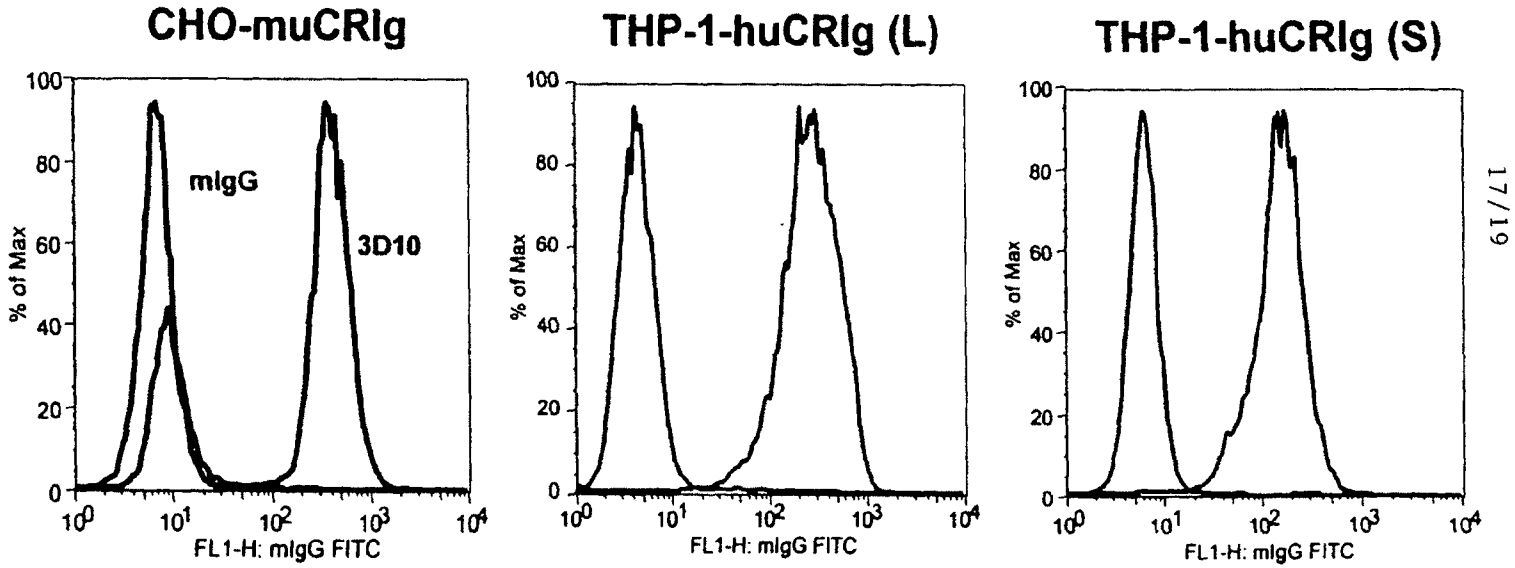

FIG. 12

mAb 3D10 blocks iC3b binding to cells expressing human and murine CRIg

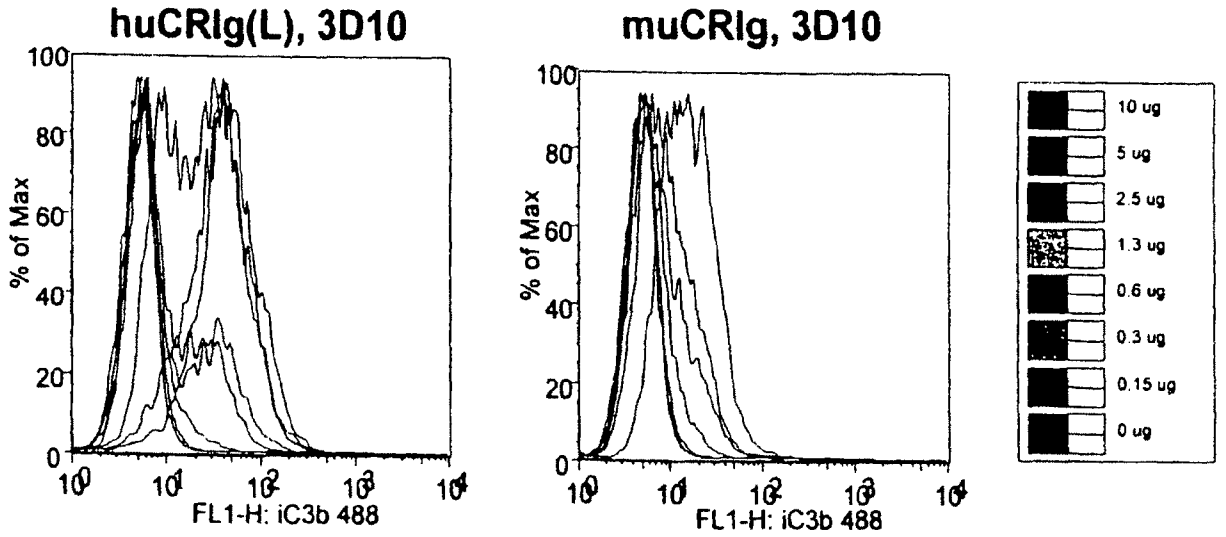

FIG. 13

Summary of antibody characteristics

purified clone	isotype	FACS mCRIg CHO	FACS hCRIg(S) THP-1	FACS hCRIg(L) THP-1	Block iC3b mCRIg CHO	Block iC3b hCRIg(S) THP-1	Block IC3b hCRIg(L) THP-1
3D10	mIgG1	++	++	++	+	+	+
2H1	mIgG1	++	-	-	+	-	-
14G8	mIgG1	++	-	-	+	-	-

Table 1