

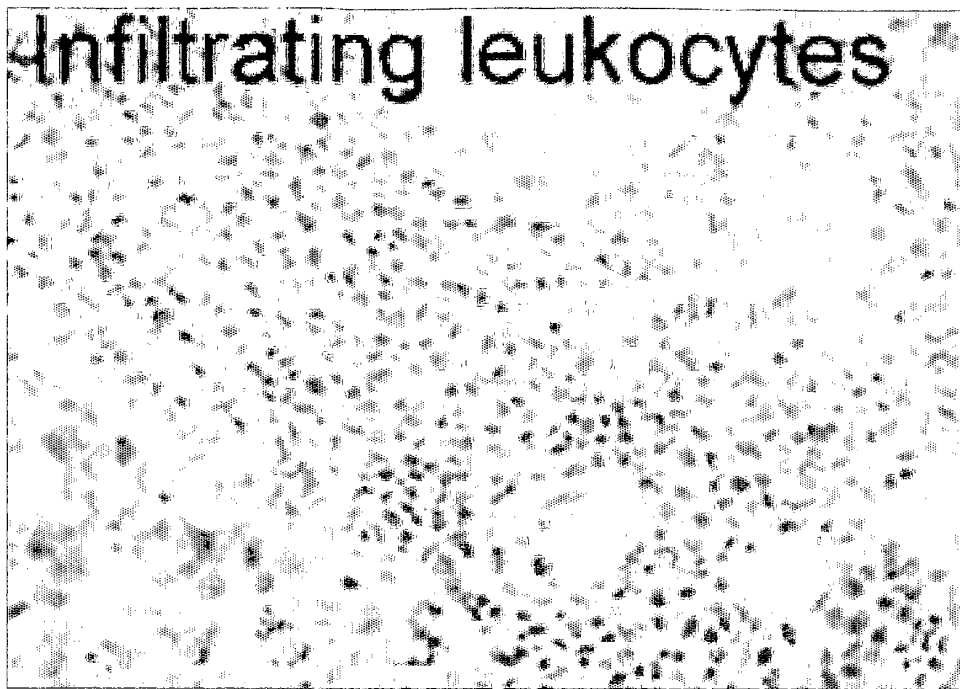


FIG. 1

FIG. 2C

3G4 IgG2a Heavy Chain (SEQ ID NO:10)

```

1      /-----Leader-----\-----
      MGWTWIFILI LSVTTGVHSE VQLQQSGPEL EKPASVKLS CKASGYSFTG YNMNWVKQSH GKSLEWIGHI

      -----3G4 VH-----\
71     DPYYGDTSYN QKFRGKATLT VDKSSSTAYM QLKSLTSEDS AVYYCVKGGY YGHWYFDVWG AGTTVTVSSA

      -----mouse IgG2a CH1 domain-----
141    KTTAPSVYPL APVCGDTTGS SVTLGCLVKG YFPEPVTLTW NSGSLSSGVH TFPVLQSDL YTLSSSVTVT

      -----\-----hinge-----\-----
211    SSTWPSQSIT CNVAHPASST KVDKKEPRGP TIKPCPPCKC PAPNLLGGPS VFIFPPKIKD VLMISLSPIV

      -----mouse IgG2a CH2 domain-----
281    TCVVVDVSED DPDFQISWFV NNVEVHTAQT QTHREDYNST LRVVSALPIQ HQDWMSGKEF KCKVNNKDLF

      -----\-----mouse IgG2a CH3 domain-----
351    APIERTISKP KGSVRAPQVY VLPPPEEEMT KKQVTLTCMV TDFMPEDIYV EWTNNGKTEL NYKNTEPVLD

      -----\
421    SDGSYFMYSK LRVEKKNWVE RNSYSCSVVH EGLHNHHTTK SFSRTPGK

```

FIG. 2D

3G4 Light Chain (C_κ) (SEQ ID NO:11)

```

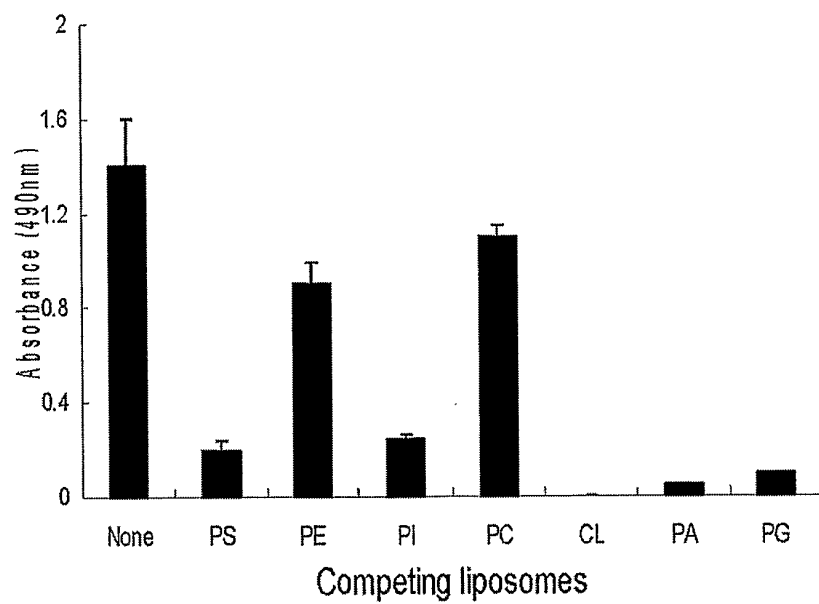
1      /-----Leader-----\-----
      MDMRAPAQIL GFLLLFPPT RCDIQMTQSP SLSASLGER VSLTCRASQD IGSSLNWLQQ GPDGTIKRLI

      -----3G4 VL-----\-----
71     YATSSLDSGV PKRFGSGSRG SDYSLTISSL ESEDFVDYYC LQYVSSPPTF GAGTKLELKR ADAAPTVSIF

      -----mouse C-kappa-----
141    PPSSEQLTSG GASVVCFLNN FYPKDINVKW KIDGSRQNG VLNSWTDQDS KDSTYSMSST LTLTKEDEYR

      -----\
211    HNSYTCEATH KTSTSPIVKS FNRNEC

```

**FIG. 3**

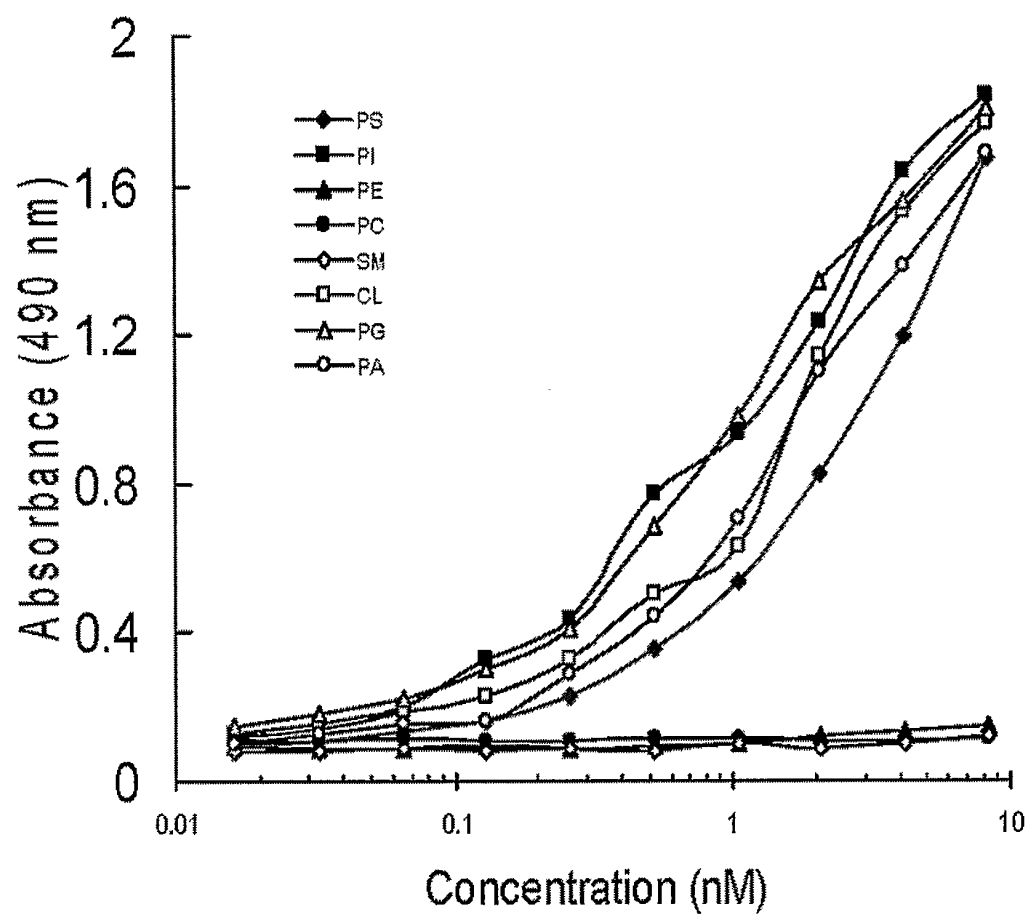
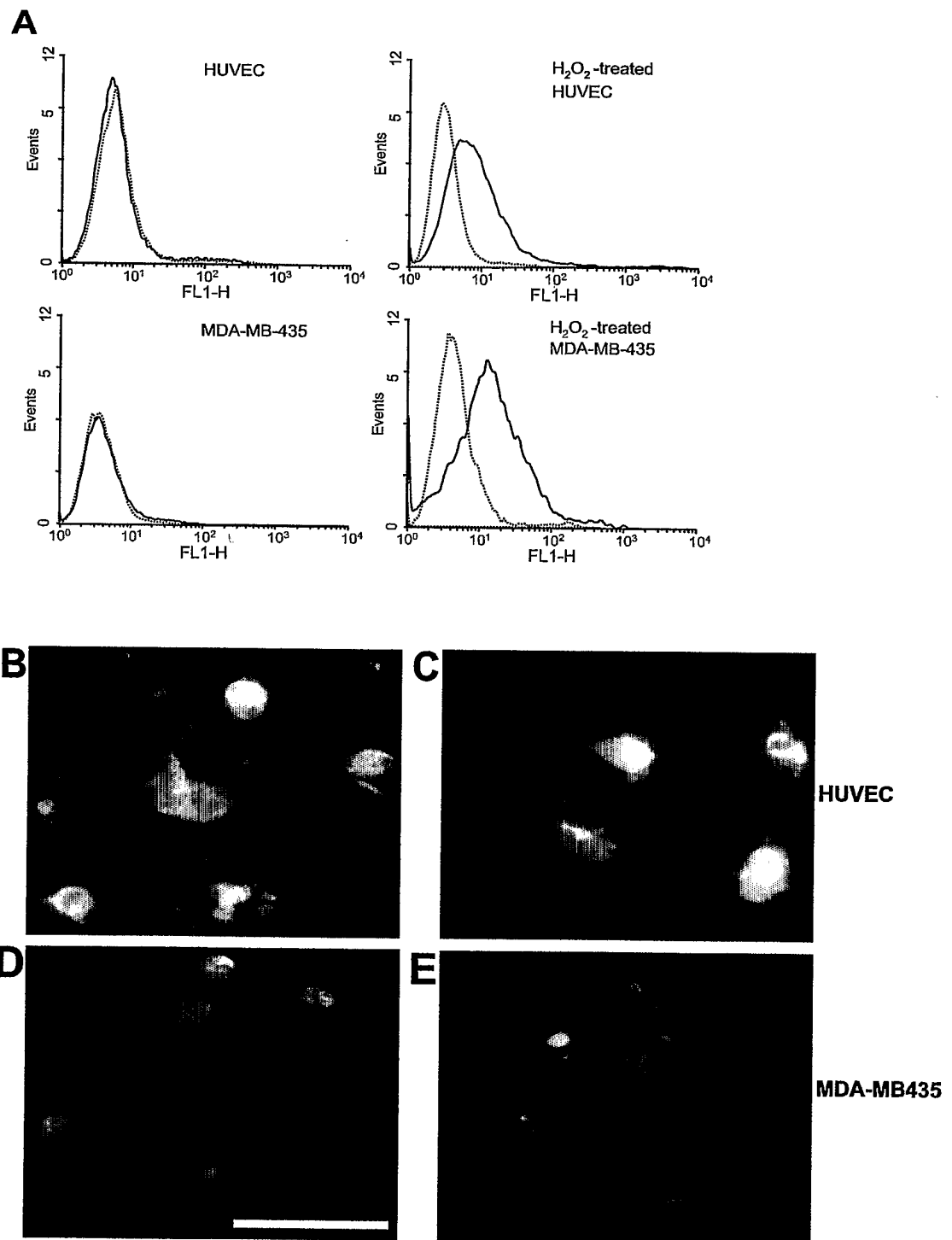


FIG. 4

FIG. 5

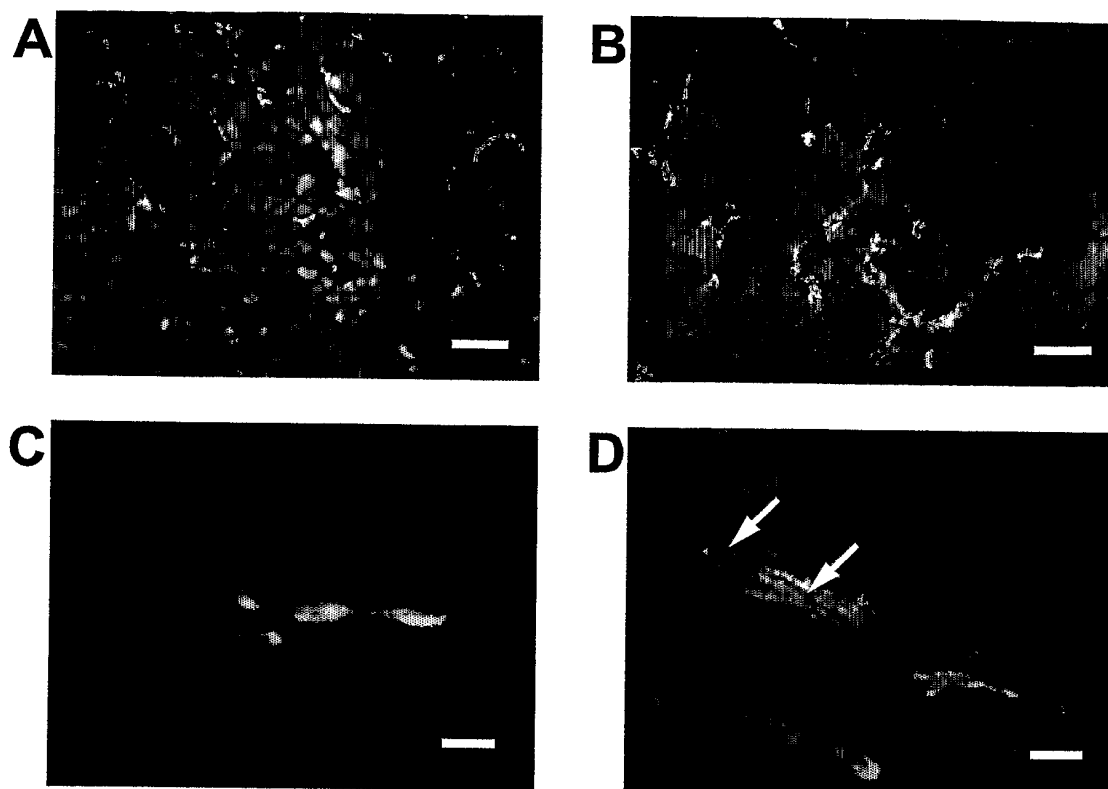


FIG. 6

THE TWO FACES OF PHAGOCYTOSIS

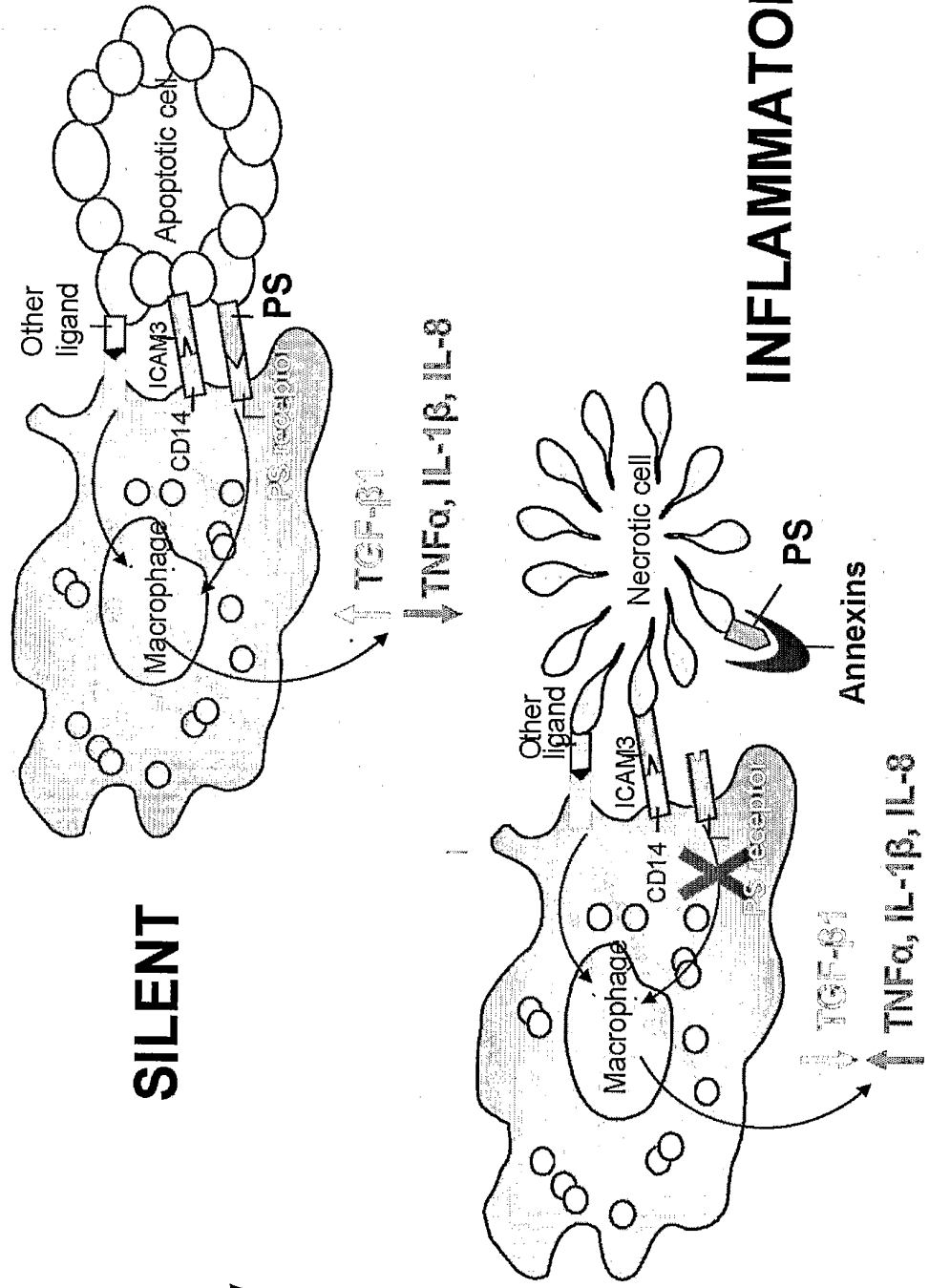


FIG. 7

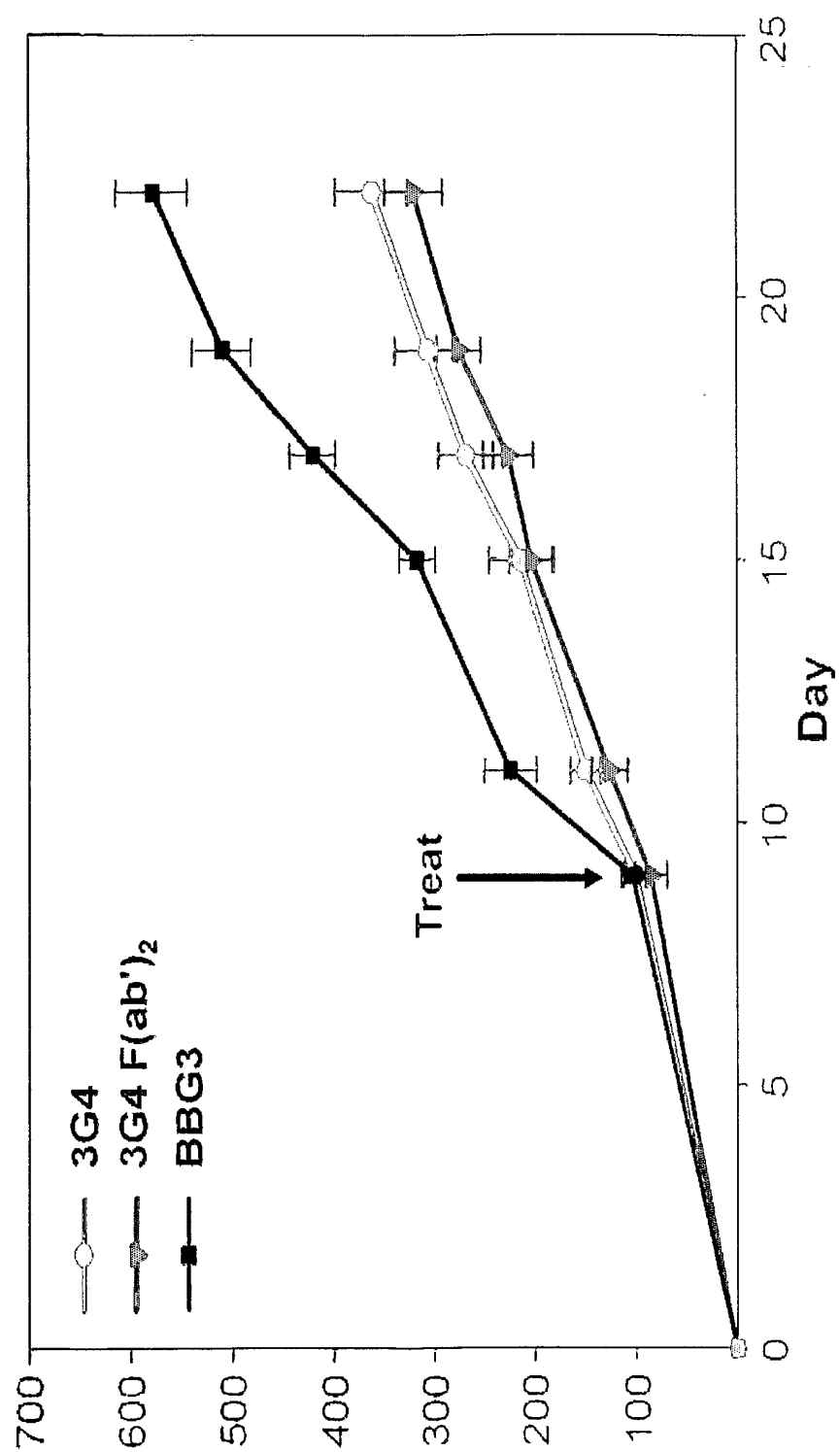


FIG. 8

FIG. 9

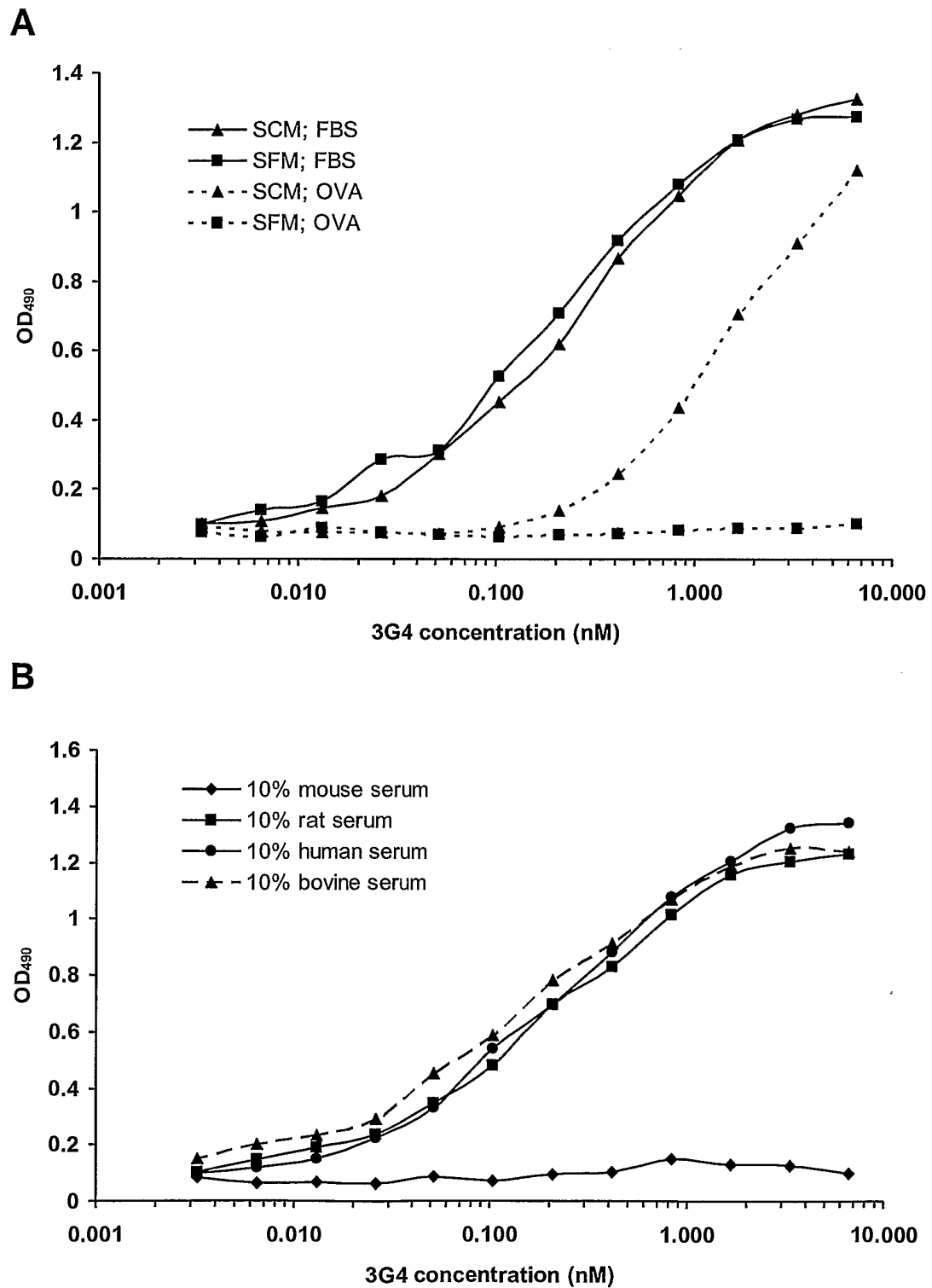
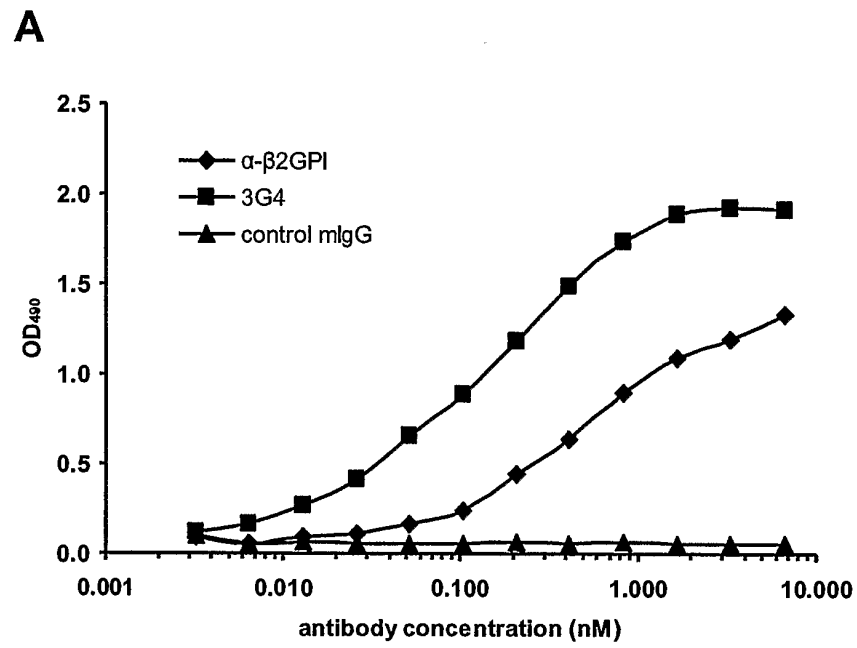


FIG. 10

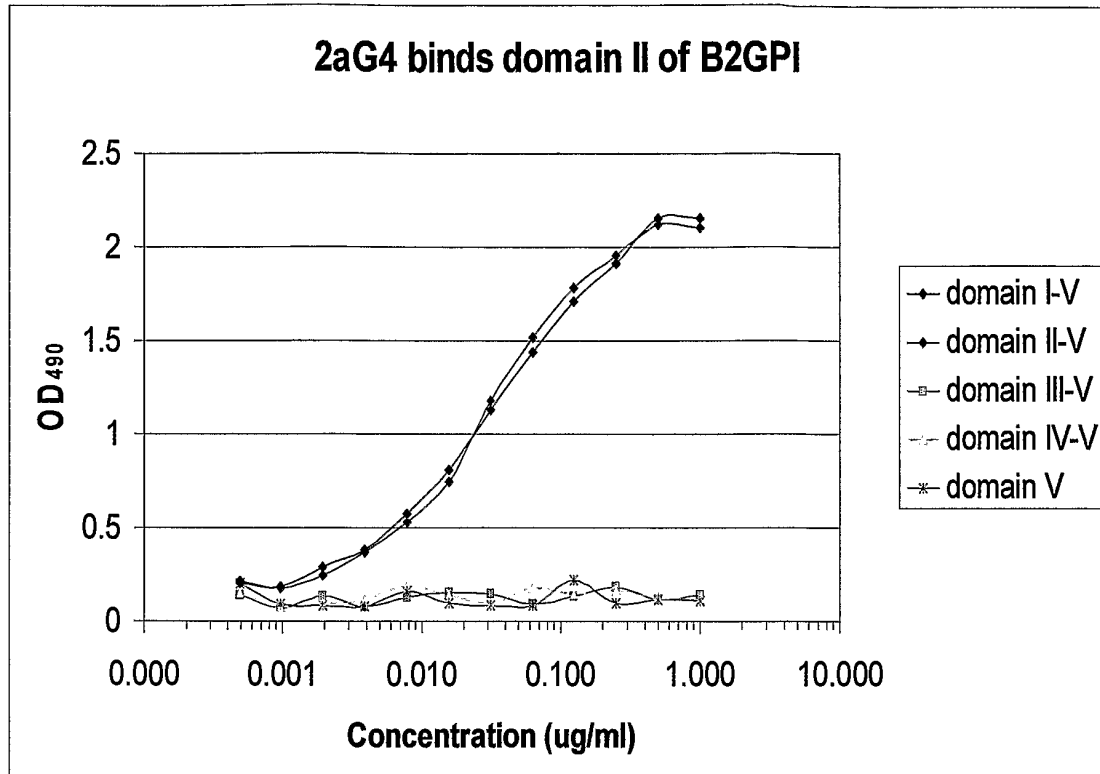
**FIG. 10B**

FIG. 11

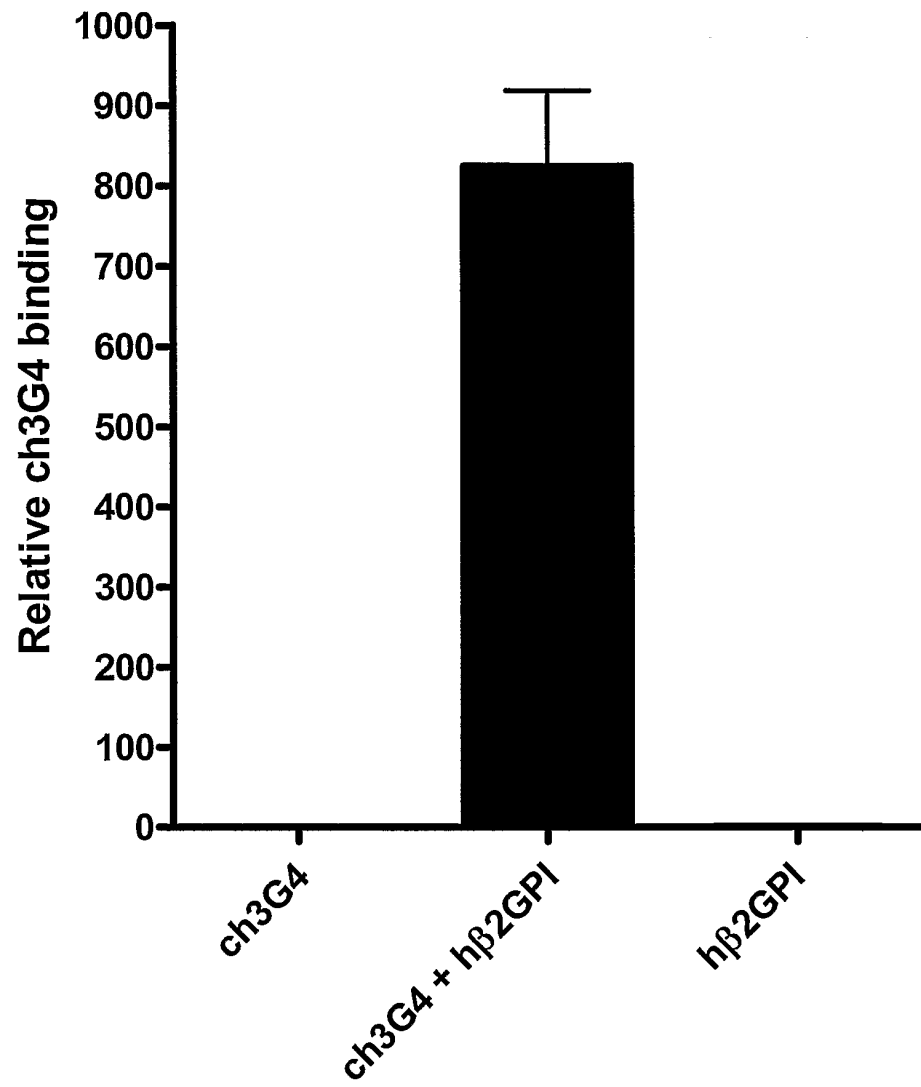
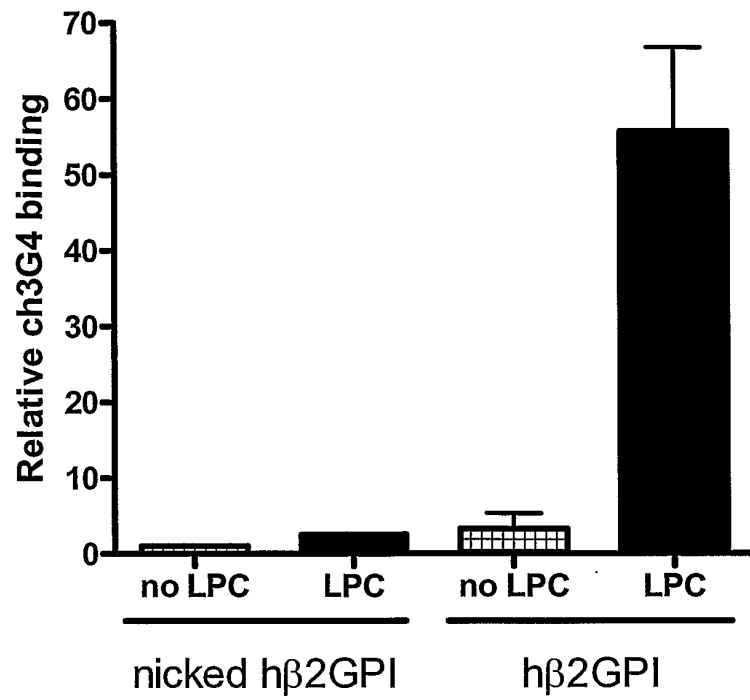


FIG. 12

A



B

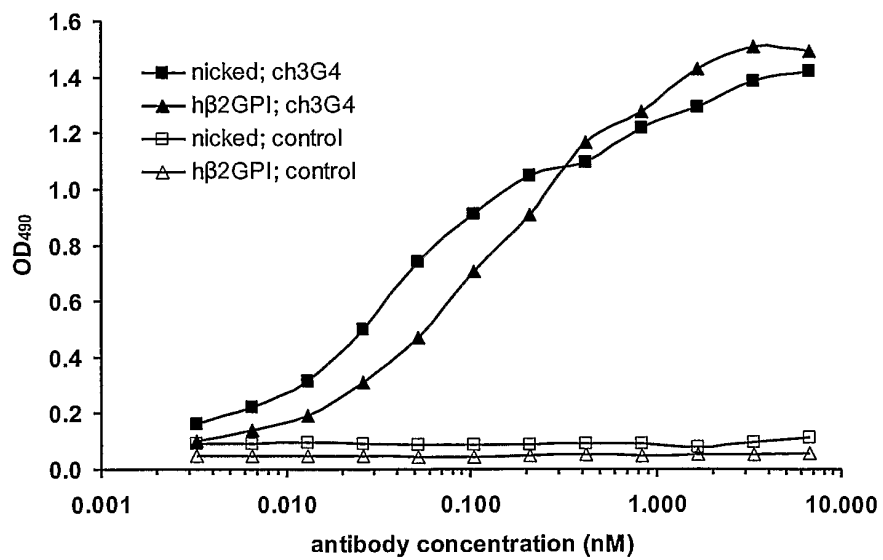


FIG. 13

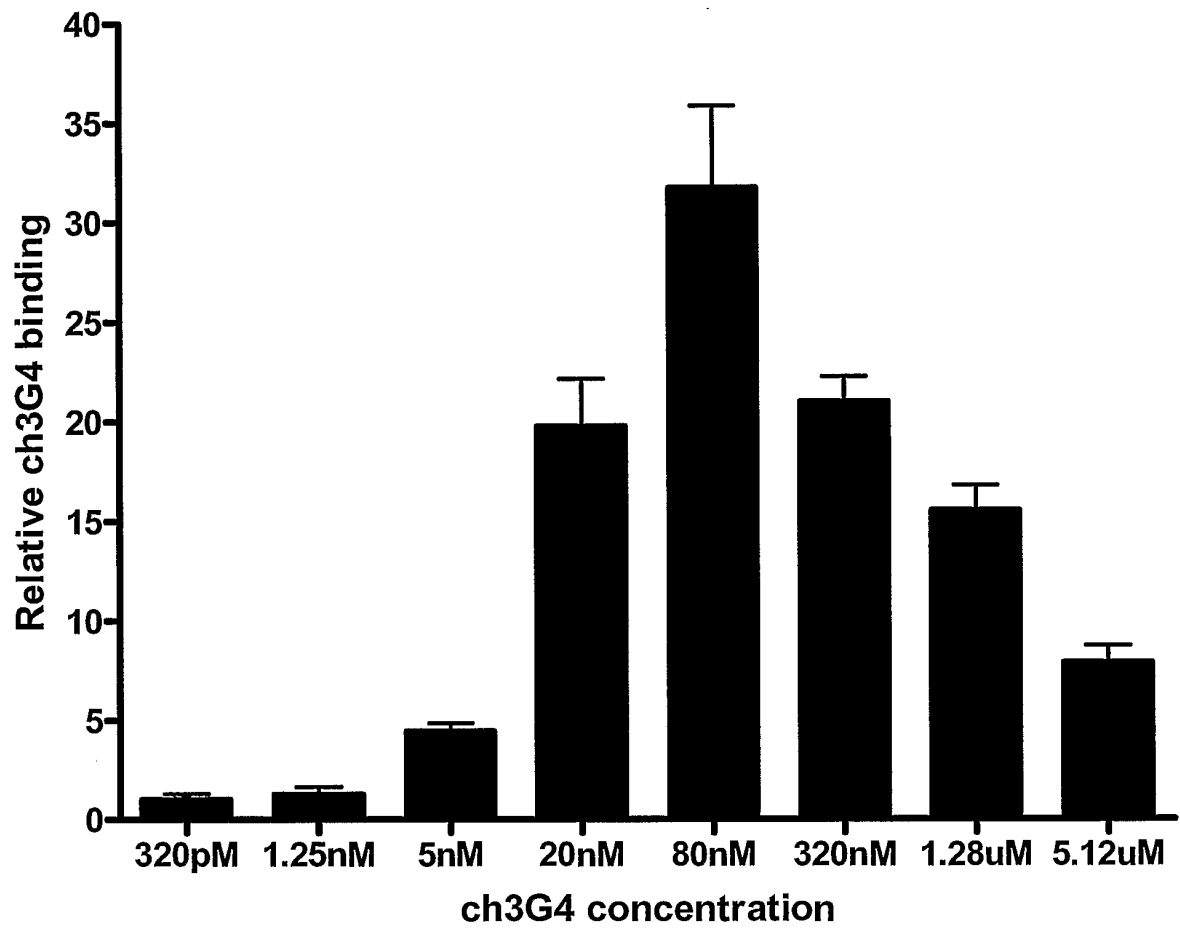
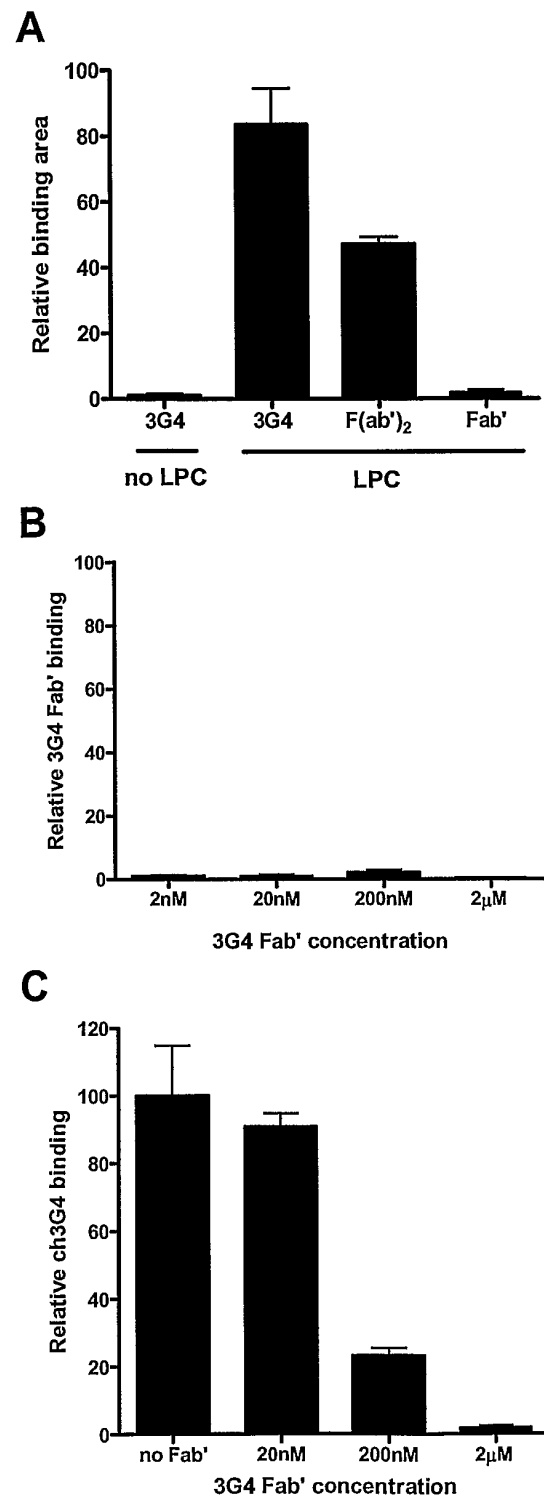


FIG. 14



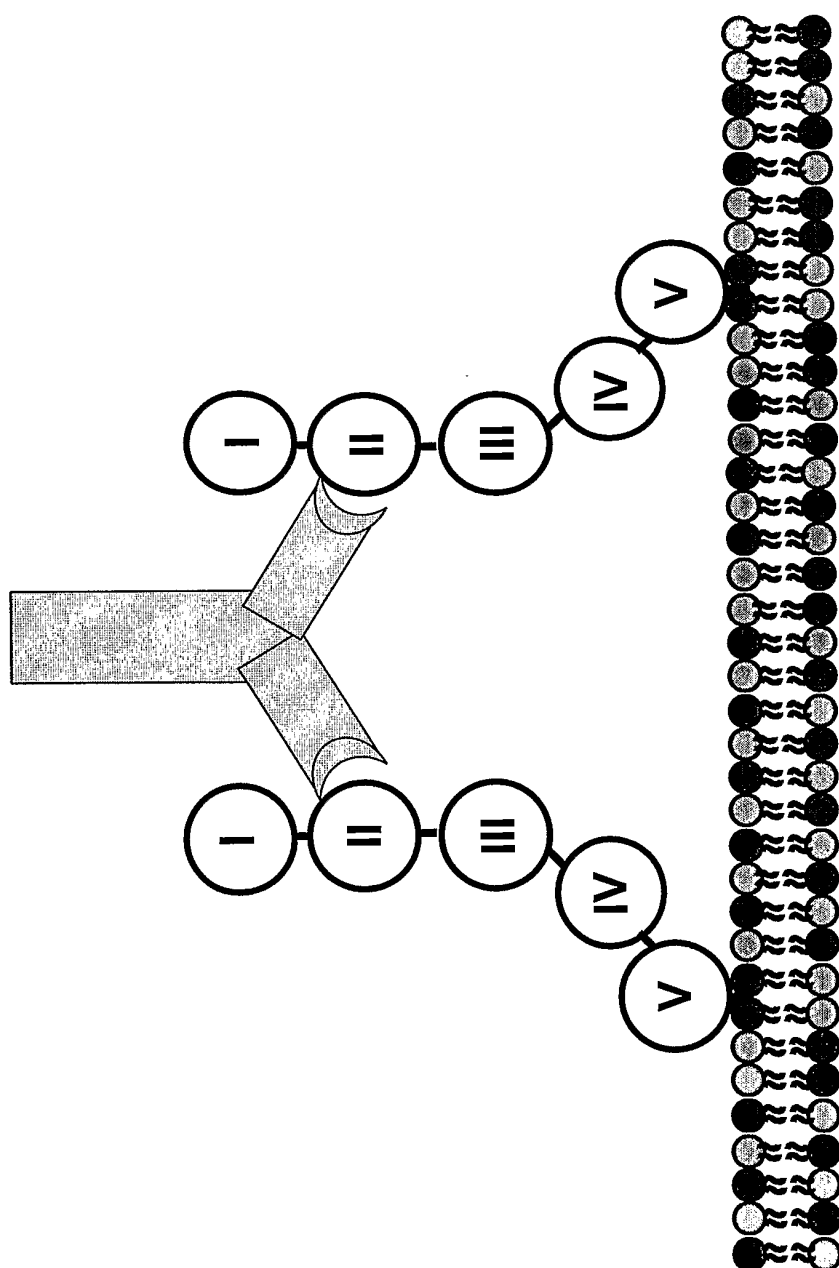


FIG. 15

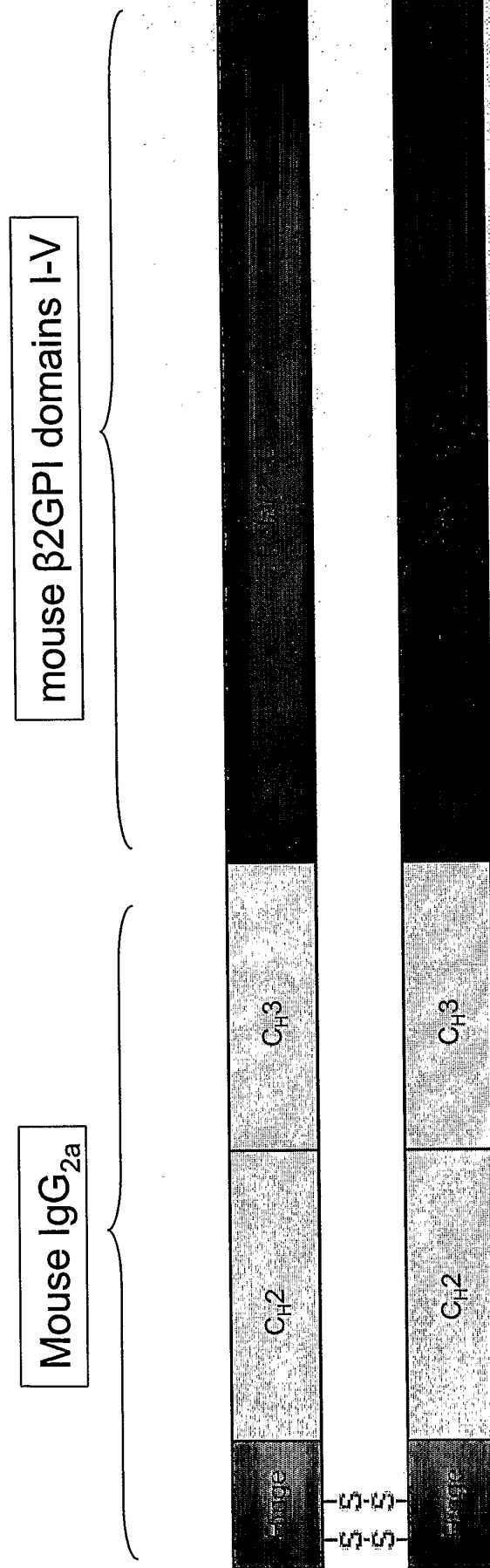


FIG. 16

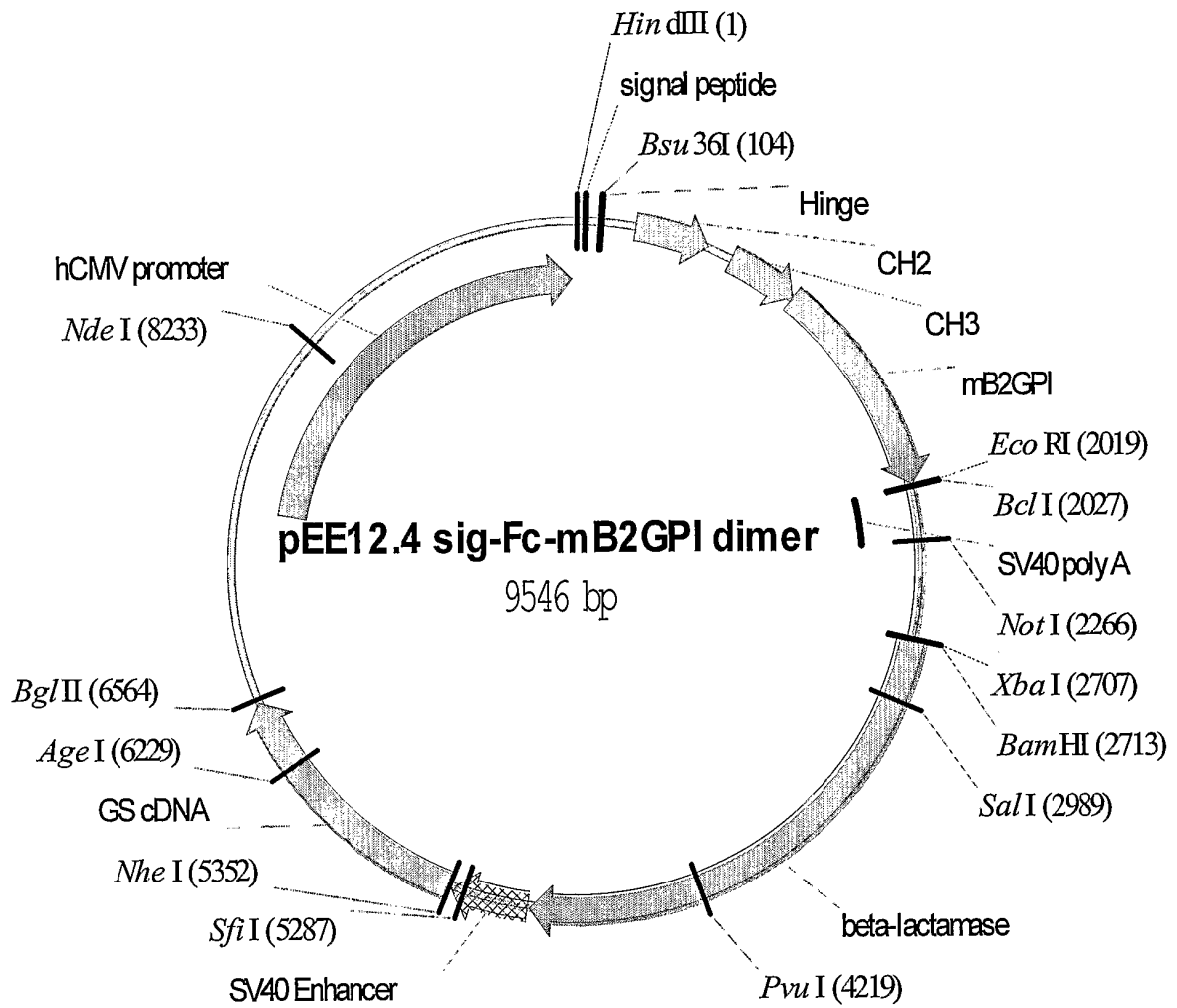


FIG. 17

FIG. 18A

Fc-mβ2GPI protein sequence:

```

1
/---mIgGk signal seq---\ /---hinge---\ /-----
-24 MDMRAPAQIL GFLLLLPFGT RCLREPRGPT IKPCPPCKCP APNLLGGPSV FIFPPKIKDV LMISLSPIVT CVVVDVSEDD

-----mouse IgG2a CH2 domain-----\ /-----
56 PDVQLSWFVN NVEVHTAQTQ THREDYNSTL RVVSALPIQH QDWMGSGKEFK CKVNNKDLPA PIERTISKPK GSVRAPQVYV

-----mouse IgG2a CH3 domain-----
136 LPPPEEEMTK KQVTLTCMVT DFMPEDIYVE WTNNGKTELN YKNTEPVLDS DGSYFMYSKL RVEKKNWVER NSYSCSVVHE

-----\ /-----
216 GLHNHHTTKS FSRTPGTKGG RICPKPDDL P FATVVPKTS YDPGEQIVYS CKPGYVSRGG MRRFTCPLTG MWPINTLRCV
[-----Domain I-----]

-----
296 PRVCFFAGIL ENGIVRYTSF EYPKNISFAC NPGFFLNGTS SSKCTEEGKW SPDIPACARI TCPPPPVPKF ALLKDYRPSA
[-----Domain II-----] [-----]

-----mouse β2GPI-----
376 GNNSLYQDTV VFKCLPLHFAM IGNDIVMCTE QGNWTRLPEC LEVKCFPPPR PENGYVNYP A KPVLLYKDKA TFGCHETYKL
---Domain III---] [-----Domain IV-----]

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200
456 DGPEEAECTK TRTWSFLPTC RESCKLPVKK ATVLYQGMRV KIQEQFKNGM MHGDKIHFYC KNKEKKCSYT VEAHC RDGTI
-----] [-----Domain V-----]

-----\
536 EIPSCFKEHS SLAFWKTDAS ELTPC
-----]

```

FIG. 18B

Human IgG₁ heavy chain constant region protein sequence:

```

/-----CH1 region-----
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT
-----\-----hinge-----\-----
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCCVVVDVS HEDPEVKFNW

-----CH2 region-----\-----
YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLNQDWLNGK EYCKVSNKA LPAPIEKTIS KAKGPREPQ VYTLPPSRDE

-----CH3 region-----
LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LSDSGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT

-----\
QKSLSLSPG

```

Human β 2GPI protein sequence:

```

/-----Domain I-----\-----
1  GRTCPKPD1DL PFSTVVPLKT FYEPGEEITY SCKPGYVSRG GMRKFIC1PLT GLWPINTLK1C TPRVC1PFAGI LENGAVRYTT

-----Domain II-----\-----Domain III-----
81  FEYPNTISFS CNTGFYLN1GA DSAKCTEEGK WSP1ELPV1CAP IIC1PPPSIPT FATLRVYKPS AGNNSLYRDT AVFECLPQHA

-----\-----Domain IV-----
161 MFGNDTIT1CT THGNWTKLPE CREVK1CFFPS RPDNGFVNYP AKPTLYYKDK ATFGCHDGYS LDGP1EEIE1CT KLG1NWSAMPS

-----\-----Domain V-----
241 CKASCKLPVK KATVVYQGER VKIQEFKNG MLHGDKVSFF CKNKEK1CSY TEDAQ1CIDGT IEVPK1CFKEH SSLAFWK1TDA

-----\
321 SDVKPC1

```

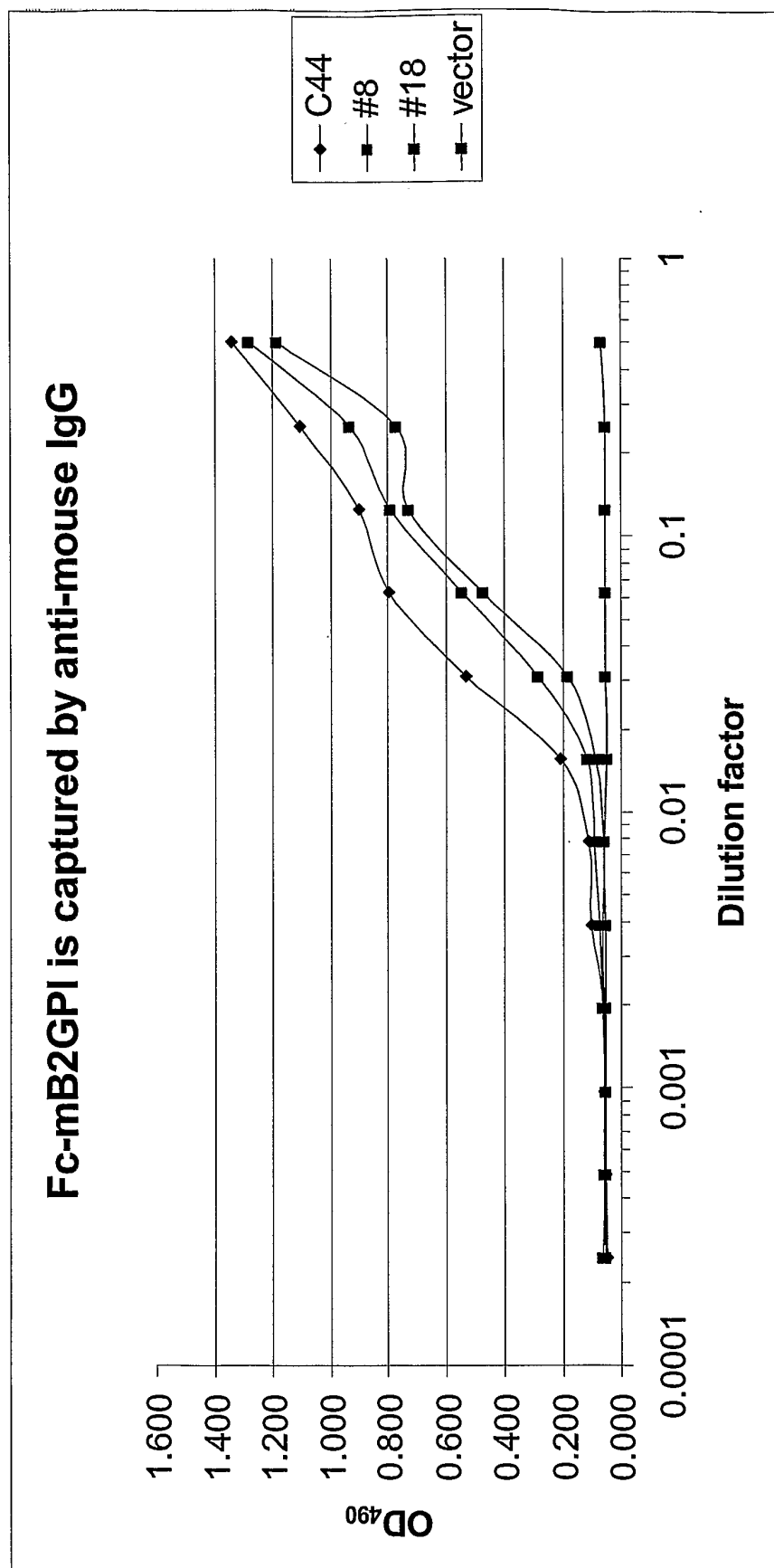


FIG. 19

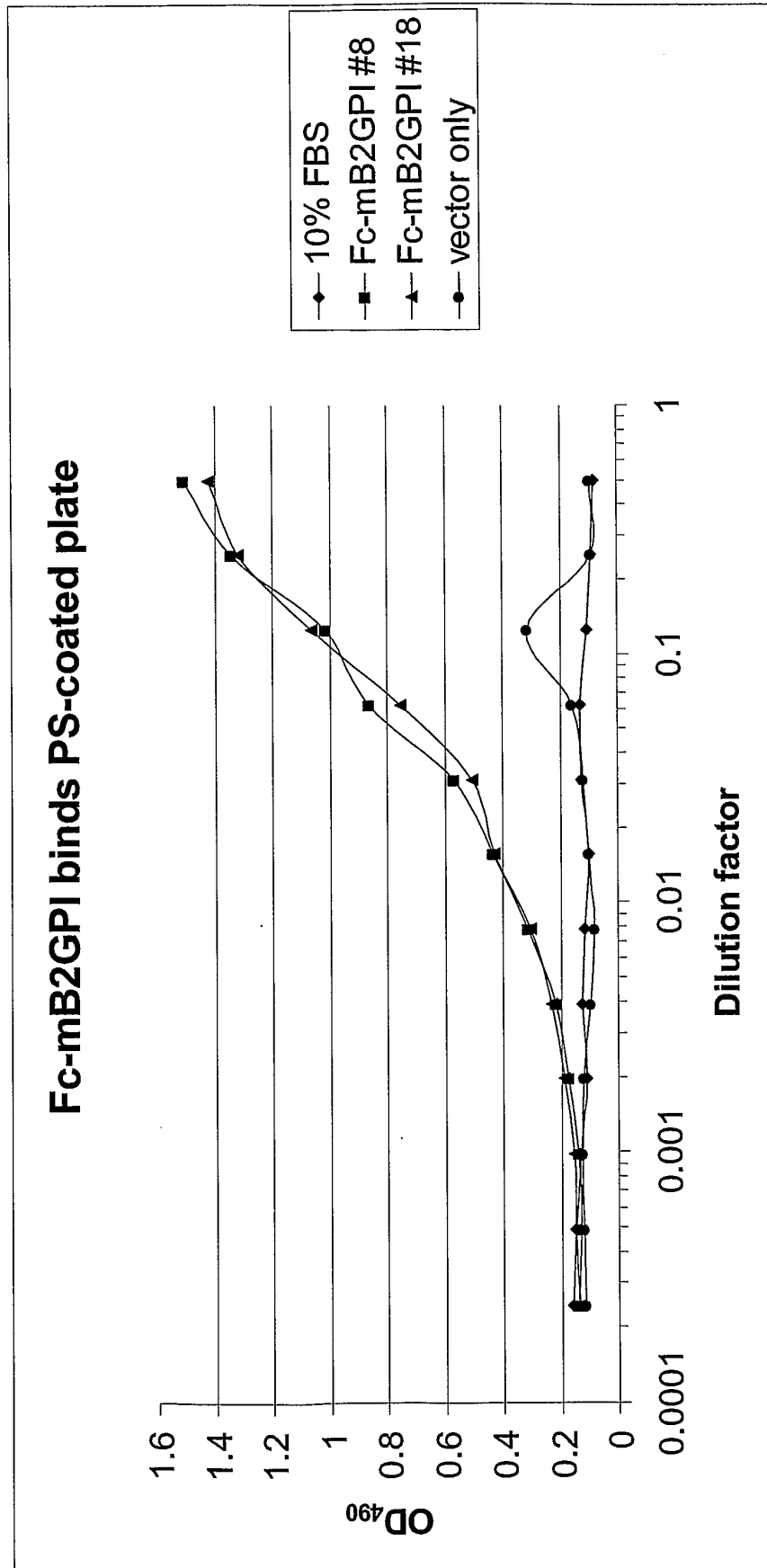


FIG. 20

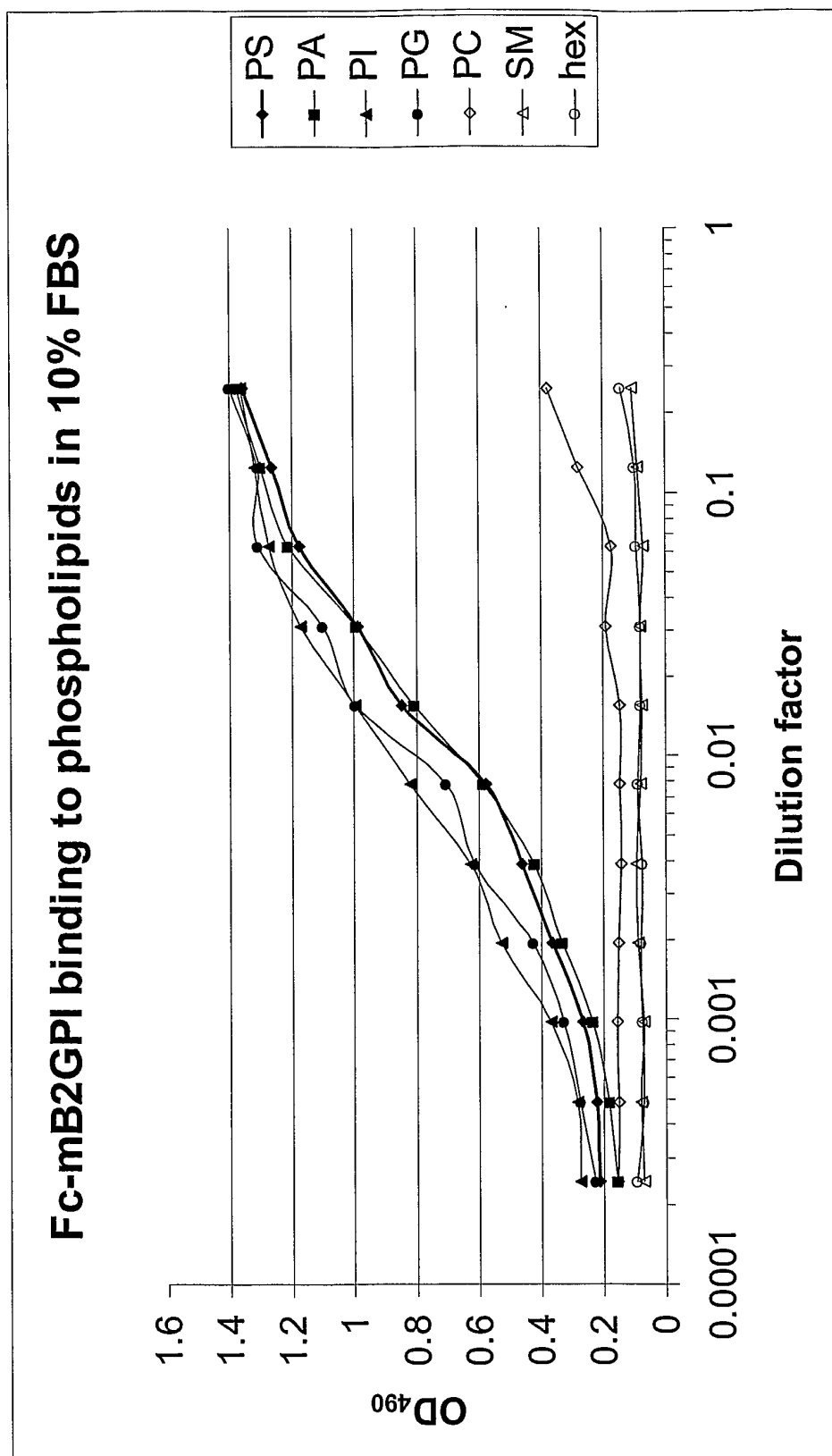


FIG. 21

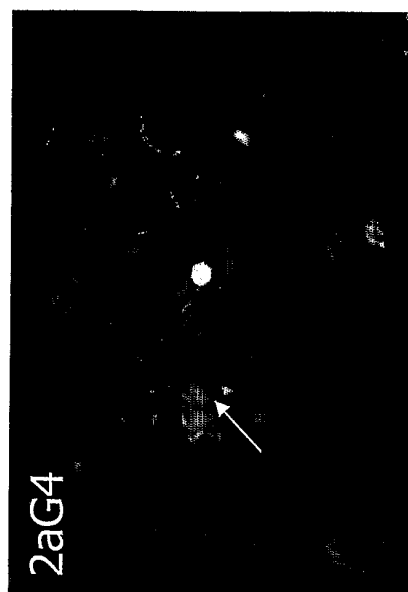


FIG. 22A

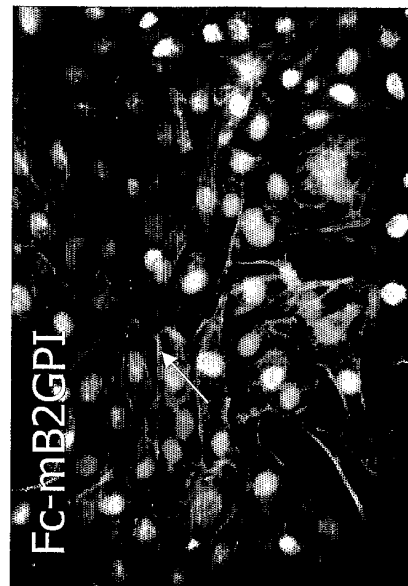


FIG. 22B

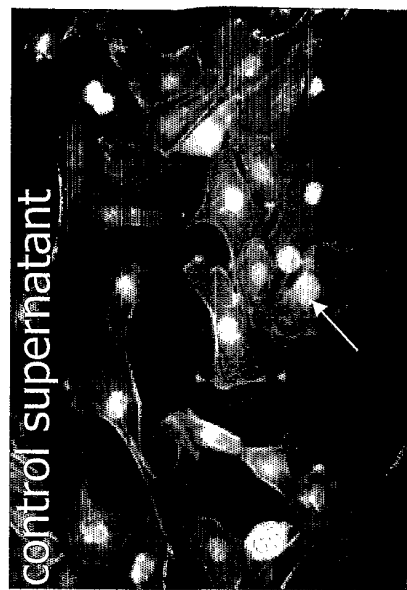


FIG. 22C



FIG. 23B

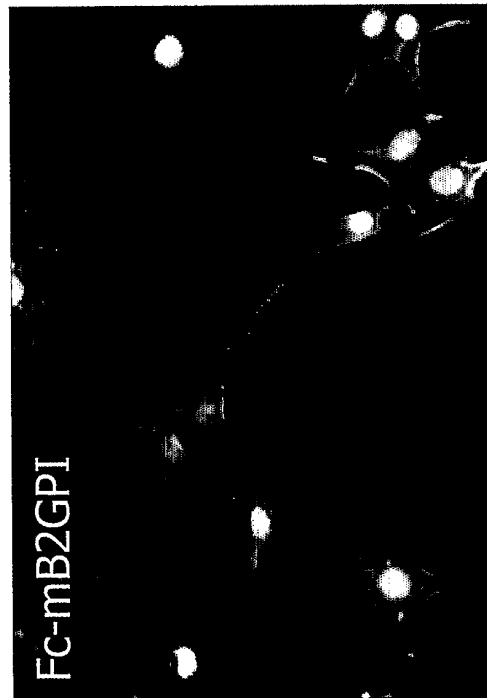


FIG. 23A

FIG. 24