

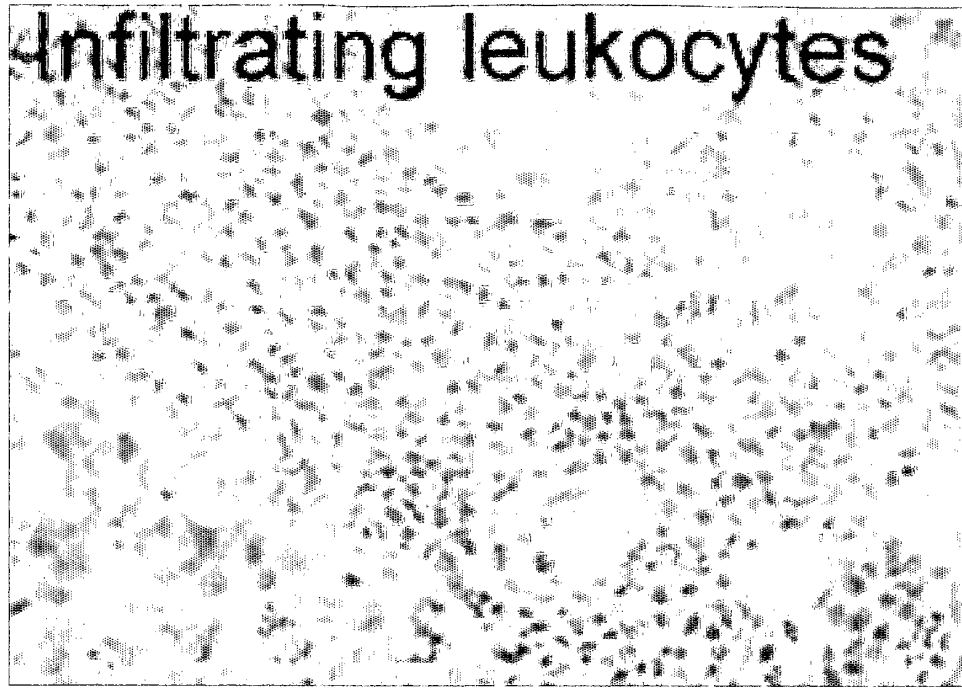


FIG. 1

121									M	G	W	T	W	I	F	I	L	I	L	S	V
									ATG	GGA	TGG	ACC	TGG	ATC	TTT	ATT	TTA	ATC	CTG	TCA	GTA
									TAC	CCT	ACC	TGG	ACC	TAG	AAA	TAA	AAT	TAG	GAC	AGT	CAT
									PvuII												
									~~~~~												
181		T	T	G	V	H	S	E	V	Q	L	Q	Q	S	G	P	E	L	E	K	P
		ACT	ACA	GGT	GTC	CAC	TCT	GAG	GTC	CAG	CTG	CAG	CAG	TCT	GGA	CCT	GAG	CTG	GAG	AAG	CCT
		TGA	TGT	CCA	GAG	GTG	AGA	CTC	CAG	GTC	GAC	GTC	GTC	AGA	CCT	GGA	CTC	GAC	CTC	TTT	GCA
		G	A	S	V	K	L	S	C	K	A	S	G	Y	S	F	T	G	Y	N	M
241		GGC	GCT	TCA	GTG	AAG	CTA	TCC	TGC	AAG	GCT	TCT	GGT	TAC	TCA	TTC	ACT	GGC	TAC	AAC	ATG
		CCG	CGA	AGT	CAC	TTT	GAT	AGG	ACG	TTT	CGA	AGA	CCA	ATG	AGT	AAG	TGA	CCG	ATG	TTG	TAC
		N	W	V	K	Q	S	H	G	K	S	L	E	W	I	G	H	I	D	P	Y
301		AAC	TGG	GTG	AAA	CAG	AGC	CAT	GGA	AAG	AGC	CTT	GAA	TGG	ATT	GGA	CAT	ATT	GAT	CTT	TAC
		TTG	ACC	CAC	TTT	GTC	TCG	GTA	CCT	TTC	TCG	GAA	CTT	ACC	TAA	CCT	GTA	TAA	CTA	GGA	ATG
		Y	G	D	T	S	Y	N	Q	K	F	R	G	K	A	T	L	T	V	D	K
361		TAT	GGT	GAT	ACT	TCC	TAC	AAC	CAG	AAG	TTC	AGG	GGC	AAG	GCC	ACA	TTG	ACT	GTA	GAC	AAA
		ATA	CCA	CTA	TGA	AGG	ATG	TTG	GTC	TTC	AAG	TCC	CCG	TTC	CGG	TGT	AAC	TGA	CAT	CTG	TTT
		S	S	S	T	A	Y	M	Q	L	K	S	L	T	S	E	D	S	A	V	Y
421		TCC	TCC	AGC	ACA	GCC	TAC	ATG	CAG	CTC	AAG	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCA	GTC	TAT
		AGG	AGG	TCG	GCT	CGG	ATG	TAC	CTC	GAG	TTC	TCG	GAC	TGT	AGA	TCT	CTG	AGA	CGT	CAG	ATA
		Y	C	V	K	G	G	Y	Y	G	H	W	Y	F	D	V	W	G	A	G	T
481		TAC	TGT	GTA	AAG	GGG	GGT	TAC	TAC	GGG	CAC	TGG	TAC	TTC	GAT	GTC	TGG	GGC	GCA	GGG	ACC
		ATG	ACA	CAT	TTC	CCC	CCA	ATG	ATG	CCC	GTG	ACC	ATG	AAG	CTA	CAG	ACC	CCG	CGT	CCC	TGG
		BstEII																			
		~~~~~																			
541		T	V	T	V	S	S	A	T	T	T	A	P	S	V	Y	P	L	V	P	
		ACG	GTC	ACC	GTC	TCC	TCA	GCT	ACA	ACA	ACA	GCC	CCA	TCT	GTC	TAT	CCC	TTG	GTC	CCG	GGC
		TGC	CAG	TGG	CAG	AGG	AGT	CGA	TGT	TGT	TGT	CGG	GGT	AGA	CAG	ATA	GGG	AAC	CAG	CCG	CCG
		BamHI																			

	Mouse Leader		↓mature protein		
1	MGWTWIFILI	LSVTTGVHSE	VQLQQSGPEL	EKPGASVKLS	CKASGYSFTG
51	YNMNWVKQSH	GKSLEWIGHI	DPYYGDTSYN	QKFRGKATLT	VDKSSSTAYM
				↓BstEII graft site	
101	QLKSLTSEDS	AVYYCVKGGY	YGHWYFDVWG	AGTTVTVSS	ASTKGPSVFPL
151	APSSKSTSG				↑human γ 1CH1

FIG. 2B

3G4-2BVL original sequence:

																		M	D	M	R	A
61																		ATG	GAC	ATG	AGG	GCT
																		TAC	CTG	TAC	TCC	CGA
	P	A	Q	I	L	G	F	L	L	L	L	F	P	G	T			R	C	D	I	Q
121	CCT	GCA	CAG	ATT	TTG	GGC	TTC	TTG	TTG	CTC	TTG	TTT	CCA	GGT	ACC	AGA	TGT	GAC	ATC	CAG		
	GGA	CGT	GTC	TAA	AAC	CCG	AAG	AAL	AAC	GAG	AAC	AAA	GGT	CCA	TGG	TCT	ACA	CTG	TAG	GTC		
	M	T	Q	S	P	S	S	L	S	A	S	L	G	E	R	V	S	L	T	C		
181	ATT	ACC	CAG	TCT	CCA	TCC	TCC	TTA	TCT	GCC	TCT	CTG	GGA	GAA	GAC	GTC	AGT	CTC	ACT	TGT		
	TAC	TGG	GTC	AGA	GGT	AGG	AGG	AAT	AGA	CGG	AGA	GAC	CCT	CTT	TCT	CAG	TCA	GAG	TGA	ACA		
	R	A	S	Q	D	I	G	S	S	L	N	W	L	Q	Q	G	P	D	G	T		
241	CGG	GCA	AGT	CAG	GAC	GAC	ATA	GGT	AGT	AGC	TTA	AAC	TGG	GTT	CAG	CAG	GGA	CCA	GAT	ACT		
	GCC	CGT	TCA	GTC	CTG	TAA	CCA	TCA	TCG	AAT	TTG	ACC	GAA	GTC	GTC	CCT	GGT	CTA	CCT	TGA		
	I	K	R	L	I	Y	A	T	S	S	L	D	S	G	V	P	K	R	F	S		
301	ATT	AAA	CGC	CTG	ATC	TAC	GCC	ACA	TCC	AGT	TTA	GAT	TCT	GGT	GTC	CCC	AAA	AGG	TTT	AGT		
	TAA	TTT	GCg	GAC	TAg	ATG	CGG	TGY	AGG	TCA	AAT	CTA	AGA	CCA	CAG	GGG	TTT	TCC	AAG	TCA		
	G	S	R	S	G	S	D	Y	S	L	T	I	S	S	L	E	S	E	D	F		
361	GGC	AGT	AGG	TCT	GGG	TCA	GAT	TAT	ACT	CTC	ACC	TAG	AGC	AGC	CTT	GAG	TCT	GAA	GAT	TTT		
	CCG	TCA	TCC	AGA	CCC	AGT	CTA	ATA	AGA	GAG	TSG	TAG	TCG	TCG	GAA	CTC	AGA	CTT	CTA	AAA		
	V	D	Y	Y	C	L	Q	Y	V	S	S	P	P	T	F	G	A	G	T	K		
421	GTA	GAC	TAT	TAC	TGT	CTA	CAA	TAT	GTT	AGT	TCT	CCT	CCC	ACG	TTC	GGT	GCT	GGG	ACC	AAG		
	CAT	CTG	ATA	ATG	ACA	GAT	GTT	ATA	CAA	TCA	AGA	GBaI	GGG	TGC	AAG	CCA	CGA	CCC	TGG	TTC		
												BbsI					BamHI					
												~~~~~					~~~~~					
	L	E	L	K	R	A	D	A	A	P	A	T	V	F	I	F	G	R	I	P		
481	CTG	GAC	CTG	AAA	CGG	GCT	GAT	GCT	GCA	CGA	CTT	GTC	TTC	ATC	TTC	GGC	CGG	ATC	CCC	CGG		
	GAC	CTG	GAC	TTT	GCC	CGA	CTA	CGA	CGT	GGT	TGA	GAC	AAG	TAG	AAG	CCC	GCC	TAG	GGG	GCC		

The RACE product 3G4-2BVL is grafted to human  $\kappa$  constant region at the BbsI site. Thus, it contains the mouse leader sequence and its VL is joined withIN the human CL1 sequence in the following way: leader/3G4-VL/TVF-IFP...

	<b>Mouse Leader</b>		↓ <b>mature protein</b>		
1	MDMRAPAQIL	GFLLLLFP	RCDIQMTQSP	SSLSASLGER	VSLTCRASQD
51	IGSSLNWLQQ	GPDGTIKRLI	YATSSLD	PKRFSGSRSG	SDYSLTISSL
			FR4↓		↓ <b>BbsI graft site</b>
101	ESEDFVDYYC	LQYVSSPPTF	GAGTKLELKR	ADAAPTVE	IFPPSDEQLKSGTAS
					↑ <b>human kappa constant</b>

FIG. 2C

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

```

1      /-----Leader-----\-----
      MGWTWIFILI LSVTTGVHSE VQLQQSGPEL EKPGASVKLS CKASGYSFTG YNMNWKQSH GKSLEWIGHI
71     -----3G4 VH-----\
      DPYYGDTSYN QKFRGKATLT VDKSSSTAYM QLKSLTSEDS AVYYCVKGGY YGHWFYFDVWG AGTTVTVSSA
141    -----mouse IgG2a CH1 domain-----
      KTTAPSVYPL APVCGD TTGS SVTLGCLVKG YFPEPVTLTW NSGSLSSGVH TFPVAVLQSDL YTLSSSVTVT
211    -----\-----hinge-----\-----
      SSTWPSQSIT CNVAHPASST KVDKKEPRGP TIKPCPPCKC PAPNLLGGPS VFIFPPKIKD VLMISLSPIV
281    -----mouse IgG2a CH2 domain-----
      TCVVVDVSED DPDVQISWFV NNVEVHTAQT QTHREDYNST LRVVSALPIQ HQDWMSGKEF KCKVNNKDLP
351    -----\-----mouse IgG2a CH3 domain-----
      APIERTISKP KGSVRAPQVY VLPPPEEEMT KKQVTLTCMV TDFMPEDIYV EWTNNGKTEL NYKNTEPVLD
421    -----\
      SDGSYFMYSK LRVEKKNWVE RNSYSCSVVH EGLHNHHTTK SFSRTPGK

```

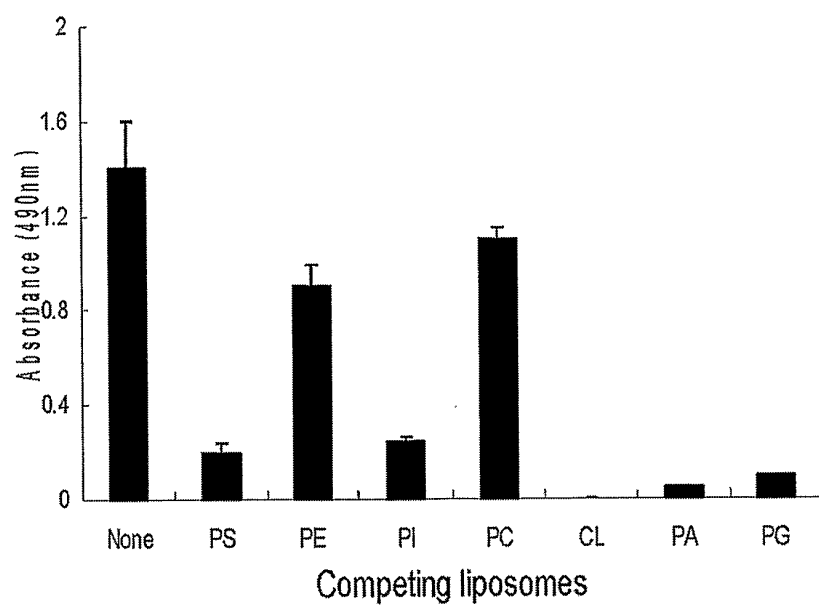
FIG. 2D

**3G4 Light Chain (C_κ) (SEQ ID NO:11)**

```

1      /-----Leader-----\-----
      MDMRAPAQIL GFLLLFP GT RCDIQMTQSP SSLASLGER VSLTCRASQD IGSSLNWLQQ GPDGTIKRLI
71     -----3G4 VL-----\-----
      YATSSLDSGV PKRFGSRSG SDYSLTISSL ESEDFVDYYC LQYVSSPPTF GAGTKLELKR ADAAPTVSIF
141    -----mouse C-kappa-----
      PPSSEQLTSG GASVVCFLNN FYPKDINVKW KIDGSRQNG VLNSWTDQDS KDSTYSMSST LTITKDEYER
211    -----\
      HNSYTCEATH KTSTSPIVKS FNRNEC

```

**FIG. 3**

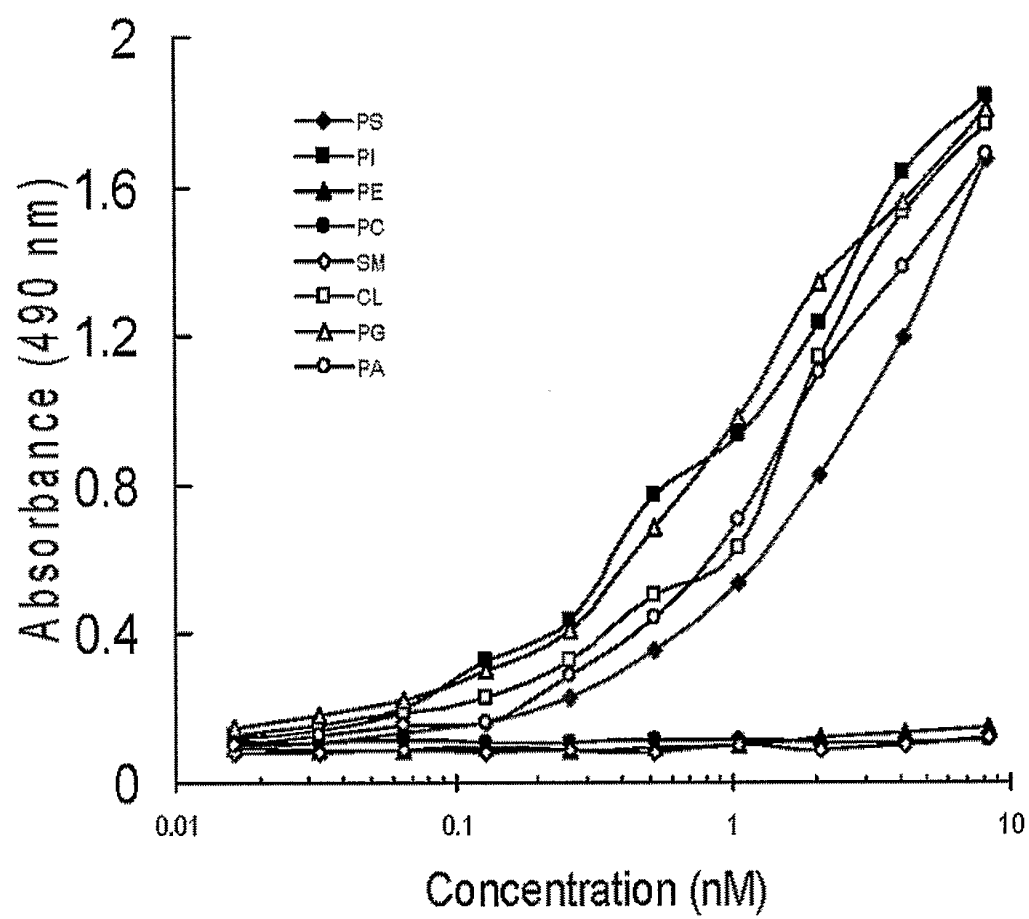
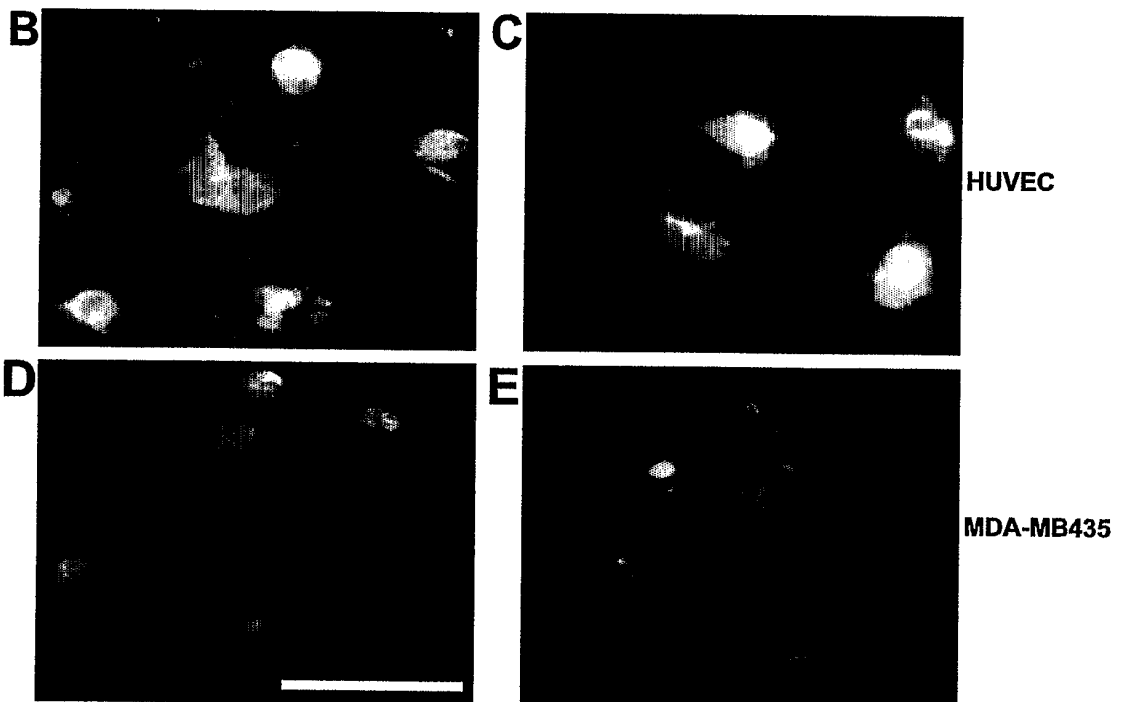
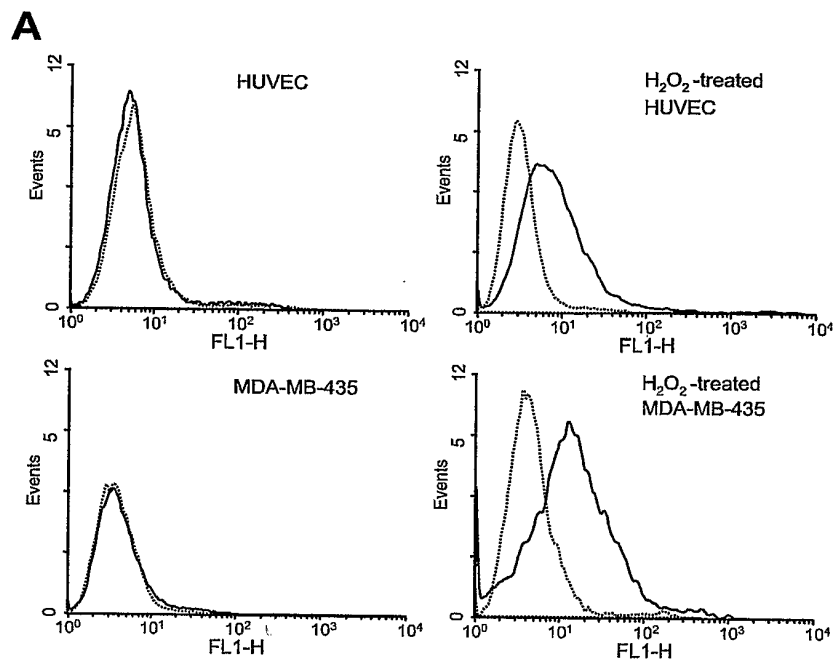
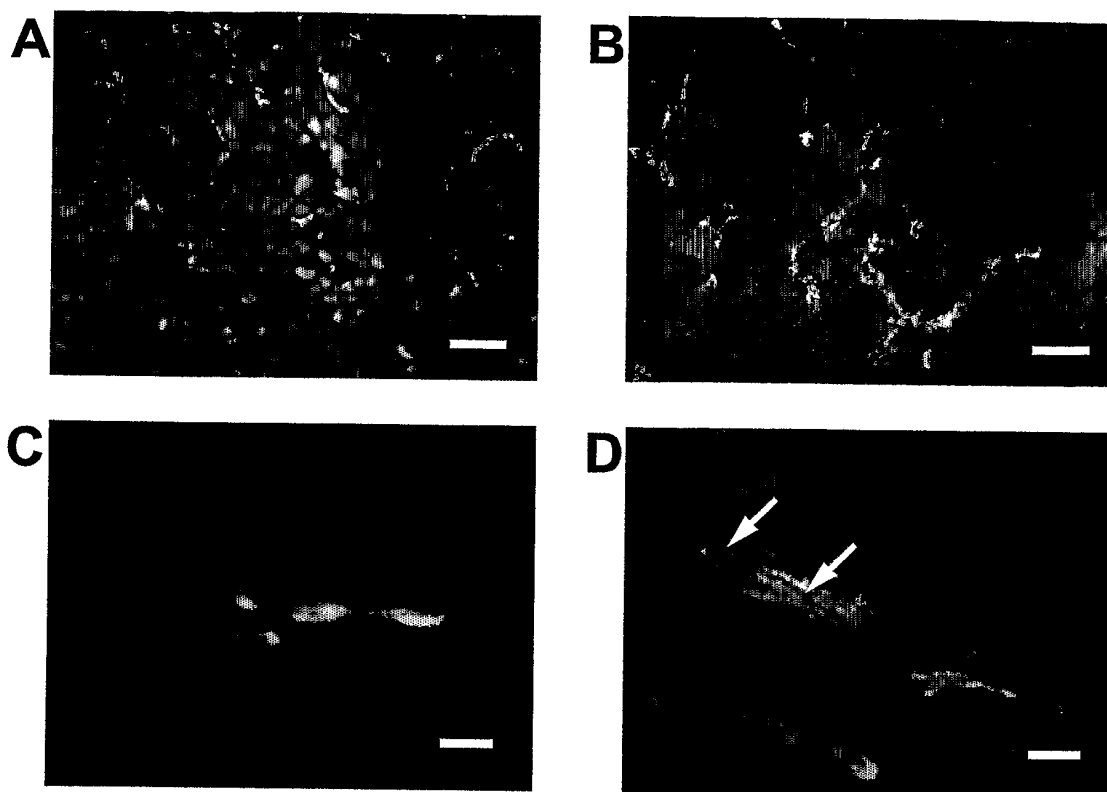


FIG. 4

**FIG. 5**



**FIG. 6**

# THE TWO FACES OF PHAGOCYTOSIS

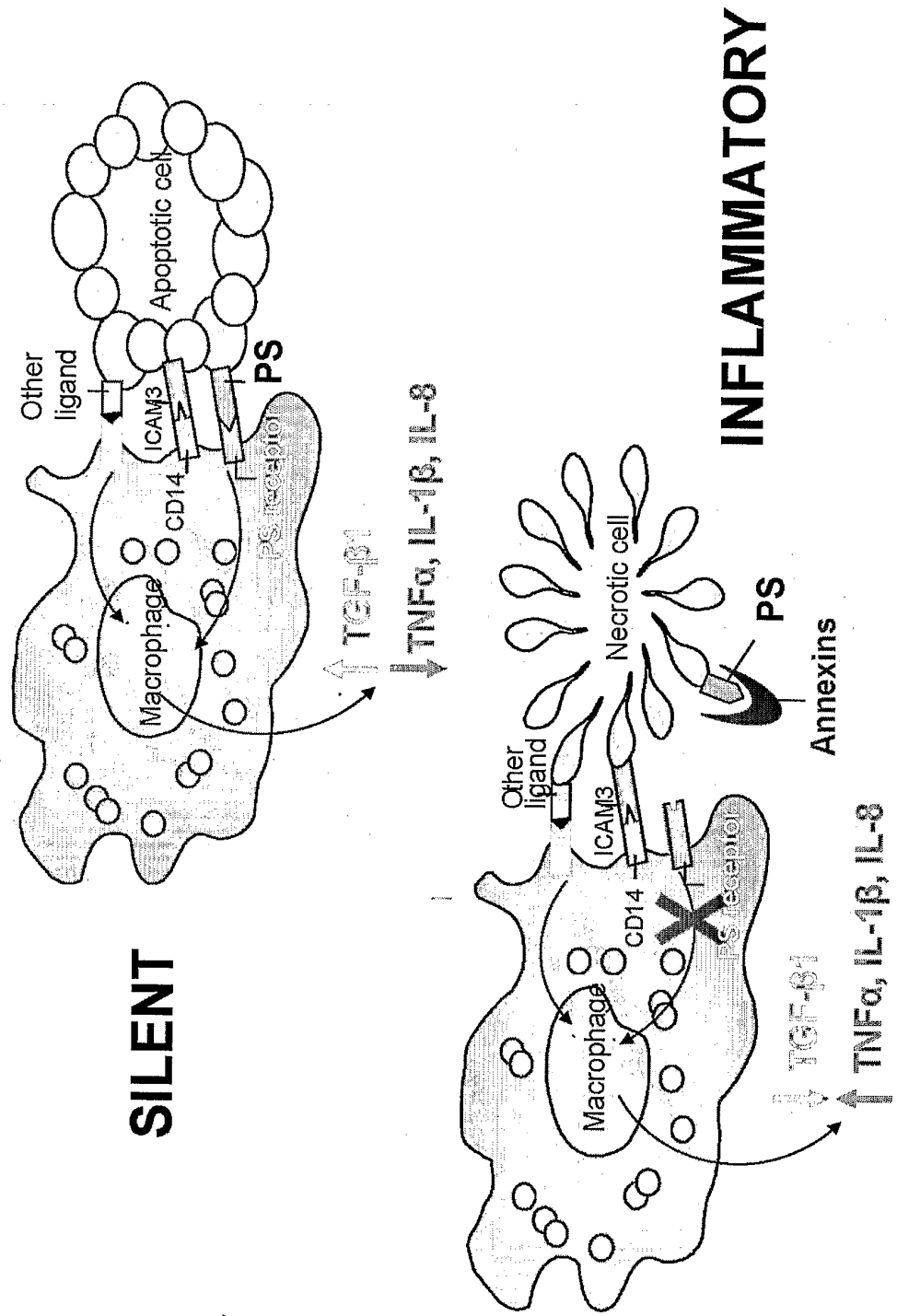


FIG. 7

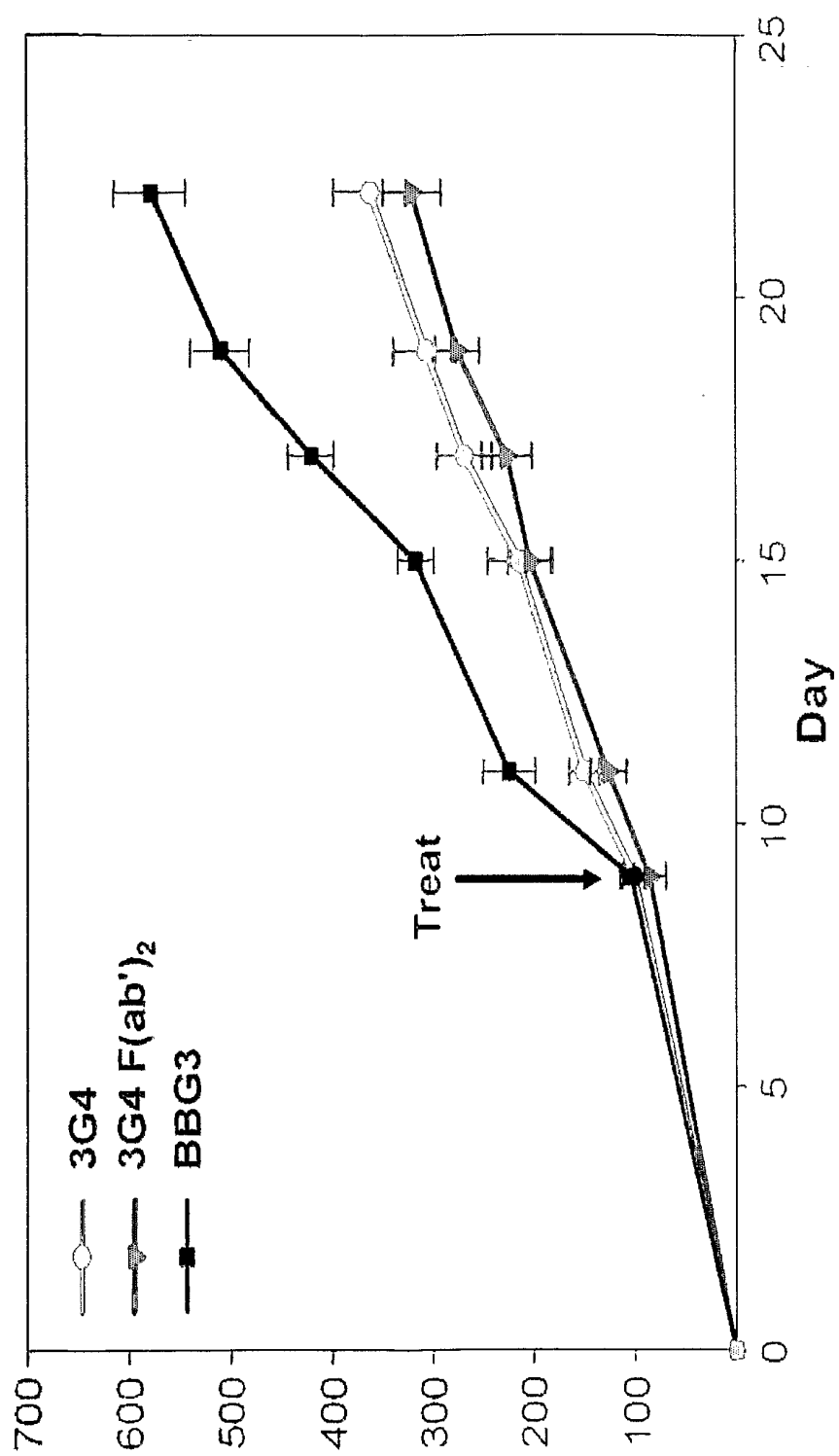
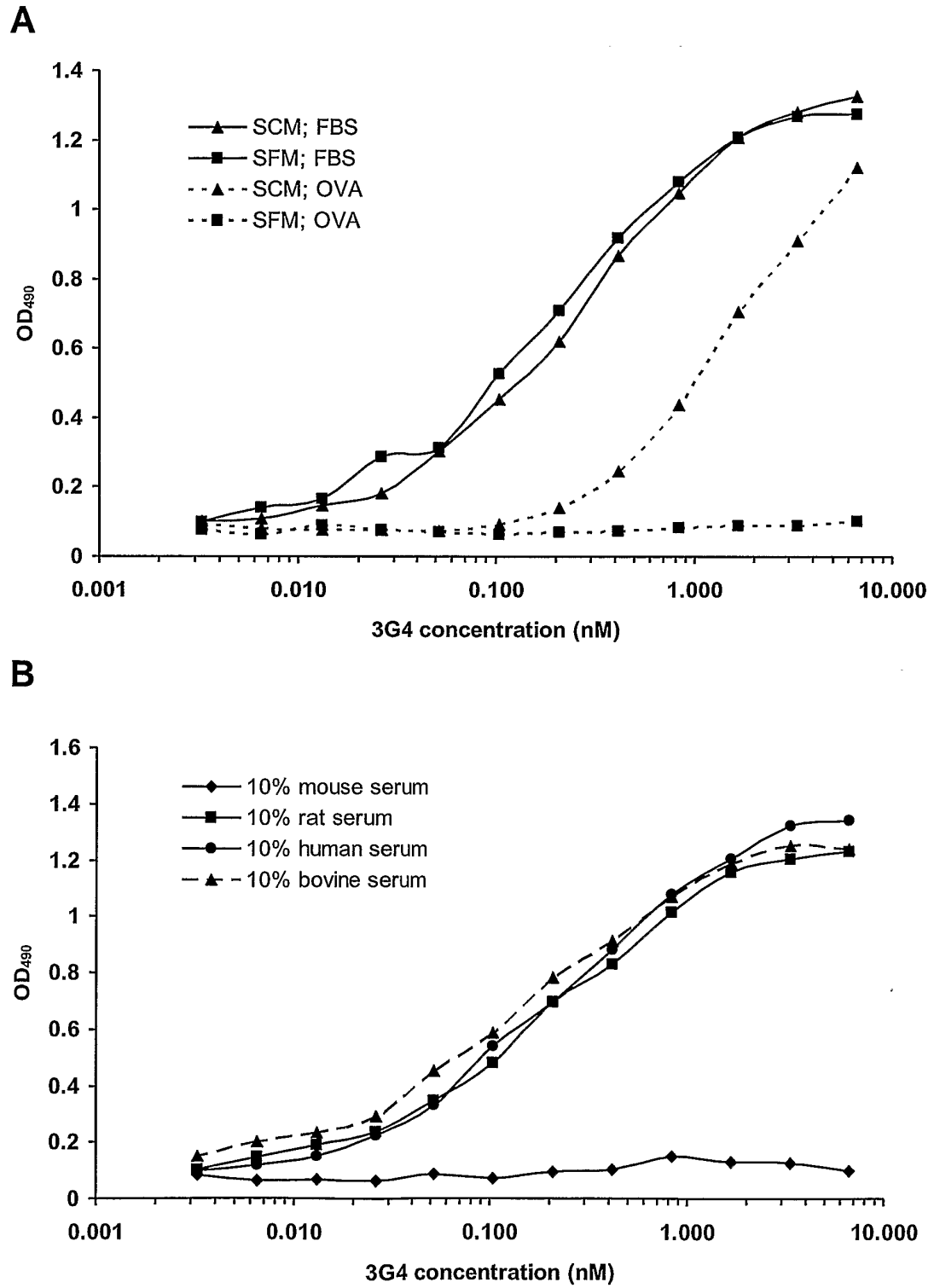
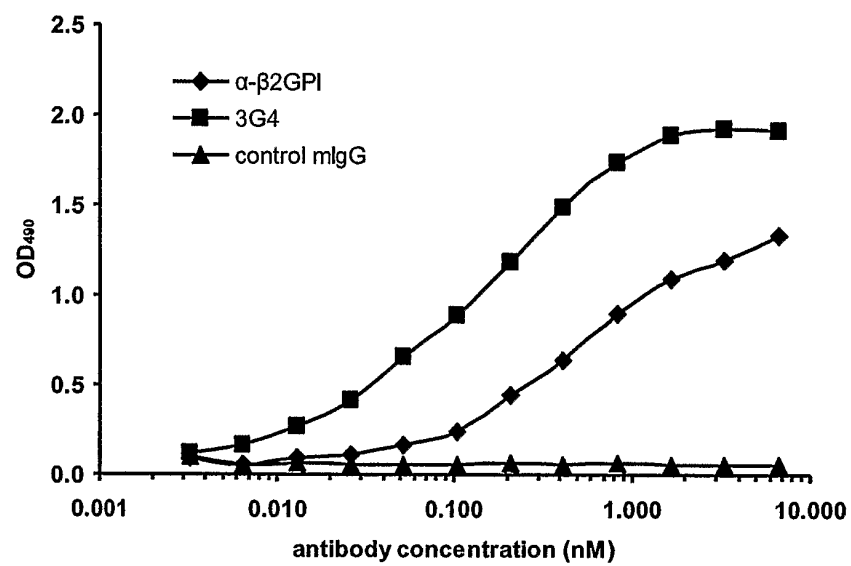


FIG. 8

FIG. 9



**FIG. 10****A**

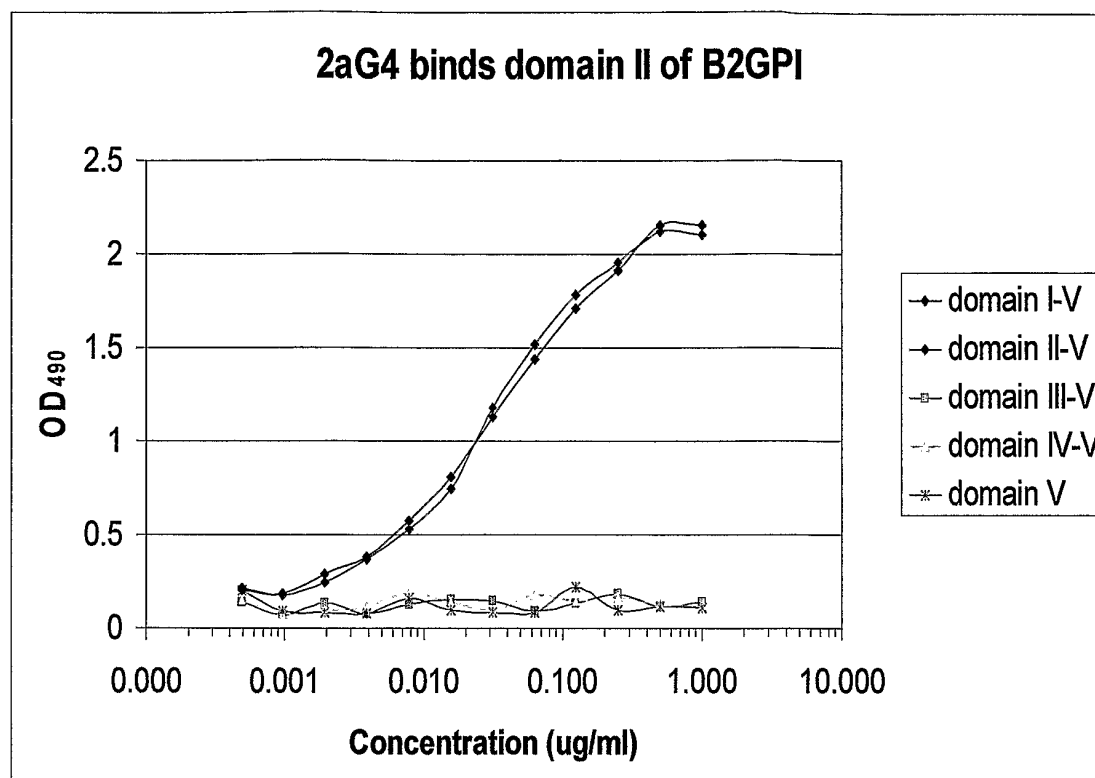
**FIG. 10B**

FIG. 11

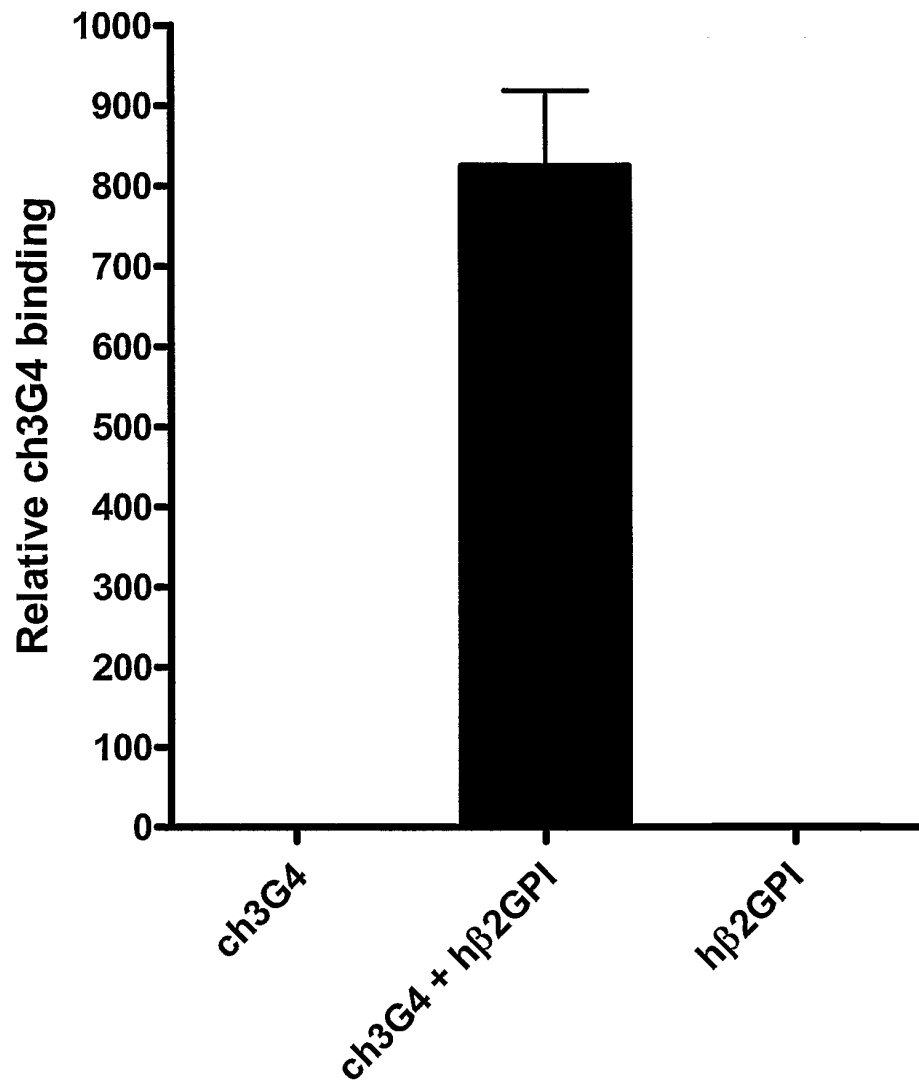


FIG. 12

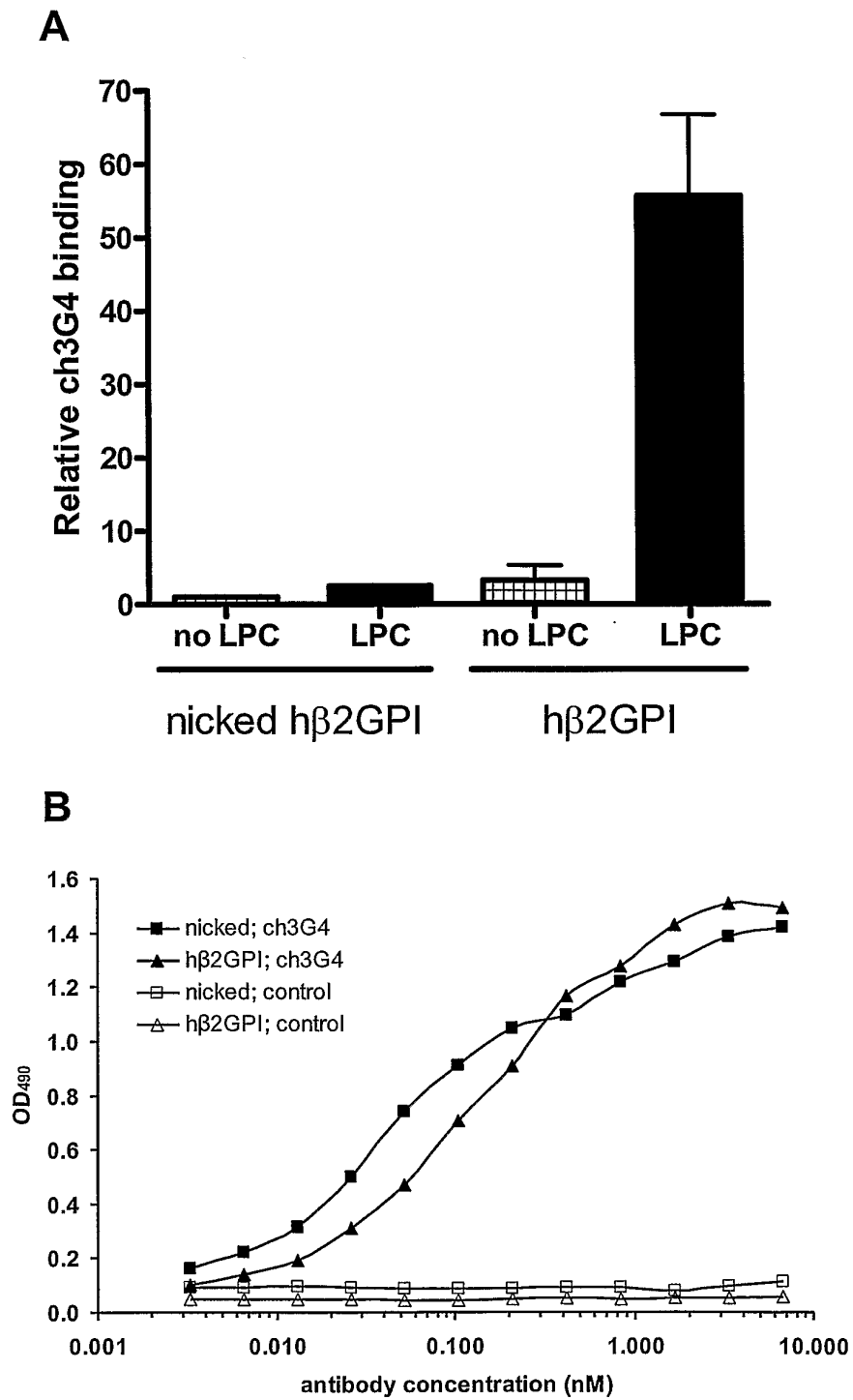


FIG. 13

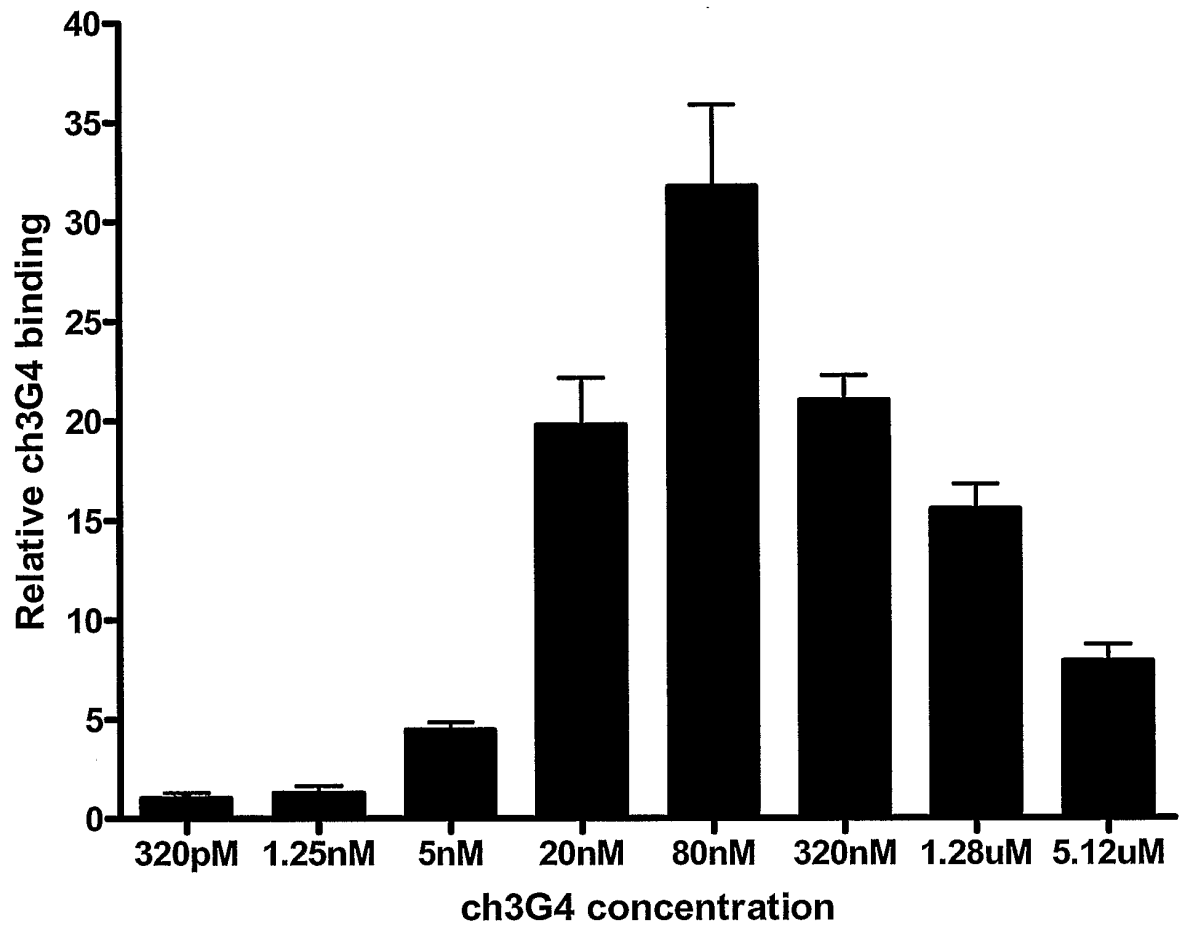
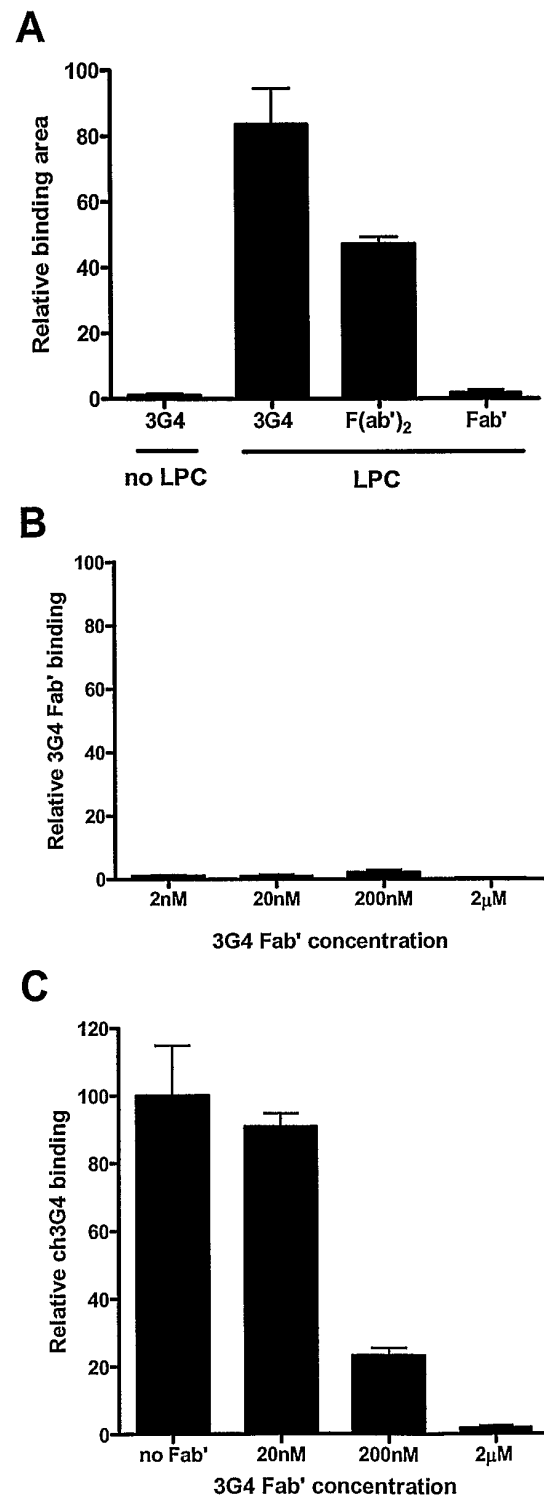


FIG. 14



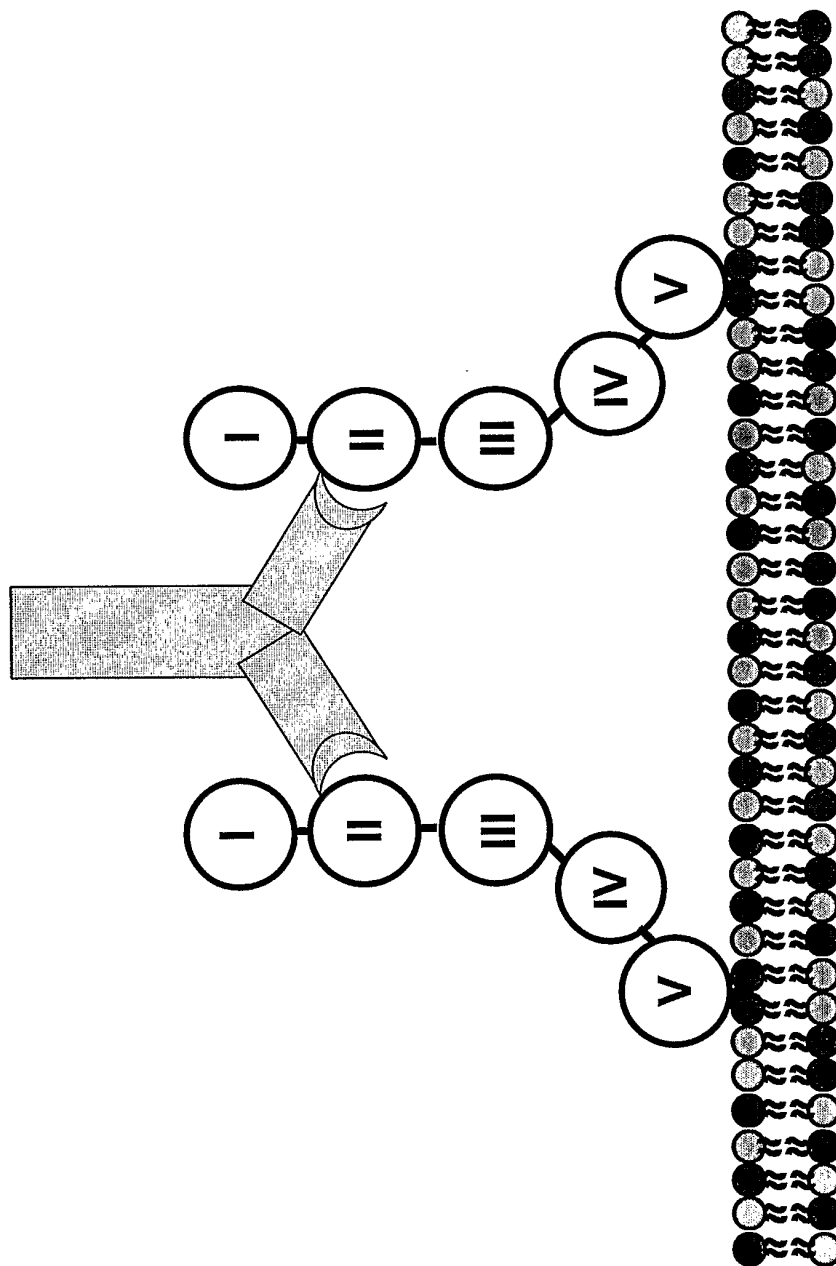


FIG. 15

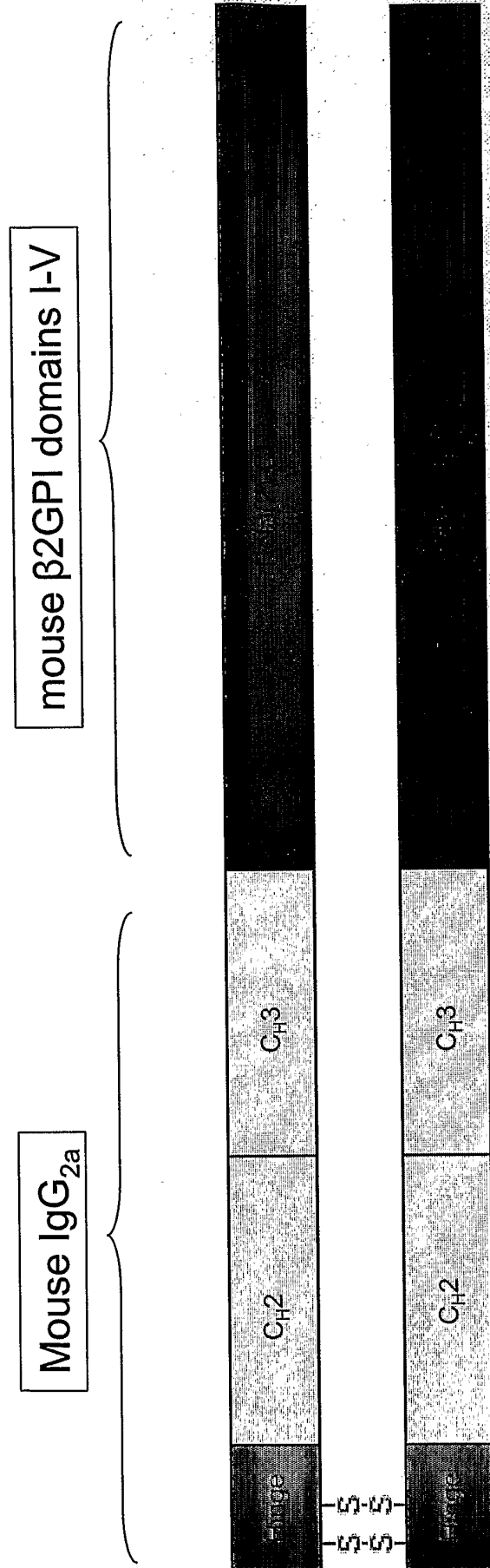


FIG. 16

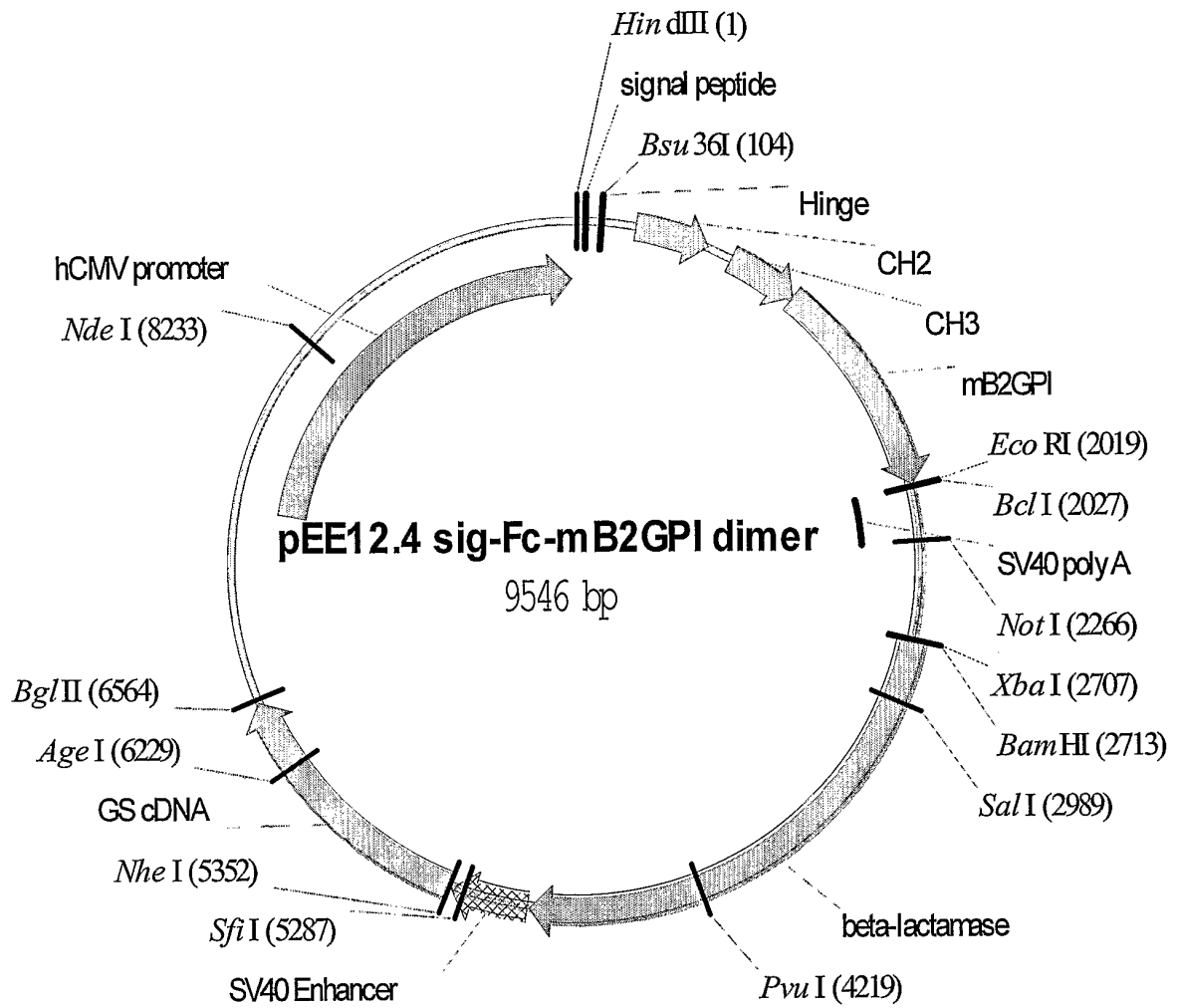
**FIG. 17**

FIG. 18A

**Fc-mβ2GPI protein sequence:**

```

1
/---mIgGκ signal seq-----\ /---hinge-----\ /-----
-24  MDMRAPAQIL GFLLLLFPGT RCLREPRGPT IKPCPPCKCP APNLLGGPSV FIFPPKIKDV LMISLSPIVT CVVVDVSEDD

-----mouse IgG2a CH2 domain-----\ /-----
56  PDVQISWFEVN NVEVHTAQIQ THREDYNSTL RVVSALFIQH QDWMSGKEFK CKVNNKDLPV PIERTISKPK GSVRAPQVYV

-----mouse IgG2a CH3 domain-----
136  LPPPEEEMTK KQVTILTCMVT DFMPEDIYVE WTNNGKTELN YKNTPEVLDS DGSYFMYSKL RVEKKNWVER NSYSCSVVHE

-----\ /-----
216  GLHNHHTTKS FSRTPGKTGG RICPKPDDL P FAVVPLKTS YDPGEQIVYS CKPGYVSRGG MRRFTCP L TG MWPINTLR CV
      [-----Domain I-----]

-----
296  PRVCPFAGIL ENGIVRYTSF EYPKNISFAC NPGFFLNGTS SSRCTEEGKW SPDIPACARI TCPPPPVPKF ALLKDYRPSA
      [-----Domain II-----]

-----mouse β2GPI-----
376  GNNSLYQDTV VFKCLPHFAM IGNDTVMCTE QGNWTRLPEC LEVKCPFPPR PENGYVNYPV KPVLLYKDKA TFGCHETYKL
      [-----Domain III-----] [-----Domain IV-----]

-----
456  DGPEEAEC TK TRTWSFLPTC RESCKLPVKK ATVLYQGM RV KIQEQFKNGM MHGDKIHFYC KNKEKKCSYT VEAHC RDGTI
      [-----Domain V-----]

-----\
536  EIPSCFKEHS SLAFWKT DAS 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 EVTCVVVDVS HEDPEVKFNW

-----CH2 region-----\-----
YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLNQDNLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE

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

-----\
QKSLSLSPG

```

**Human  $\beta$ 2GPI protein sequence:**

```

/-----Domain I-----\-----
1  GRTCPKPDDL PFSTVVPLKT FYEPGEEITY SCKPGYVSRG GMRKFICPLT GLWPINTLKC TPRVCPFAGI LENGAVRYTT
-----Domain II-----\-----Domain III-----
81  FEYPNTISFS CNTGFYLNKA DSAKCTEEGK WSPFLPVCAP IICPPPSIPT FATLRVYKPS AGNNSLYRDT AVFECLPQHA
-----\-----Domain IV-----
161  MFGNDTITCT THGNWTKLPE CREVKCPFPS RPDNGFVNYP AKPTLYYKDK ATFGCHDGYS LDGPEEIECT KLGNWSAMPS
-----\-----Domain V-----
241  CKASCKLPVK KATVVYQGER VKIQEKFKNG MLHGDKVSFF CKNKEKKCSY TEDAQCIDGT IEVPKCFKEH SSLAFWKTDA
-----\
321  SDVKPPC

```

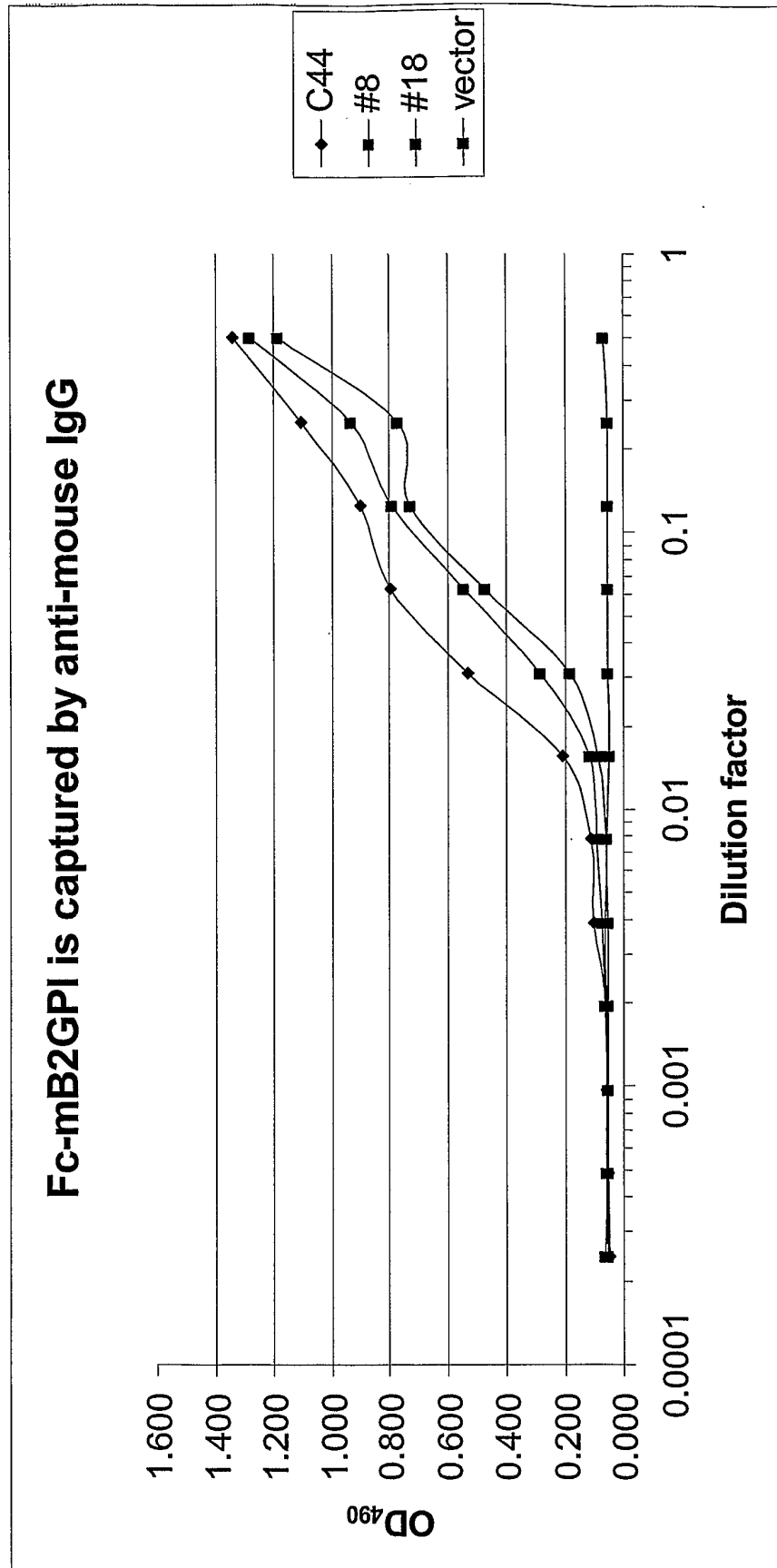


FIG. 19

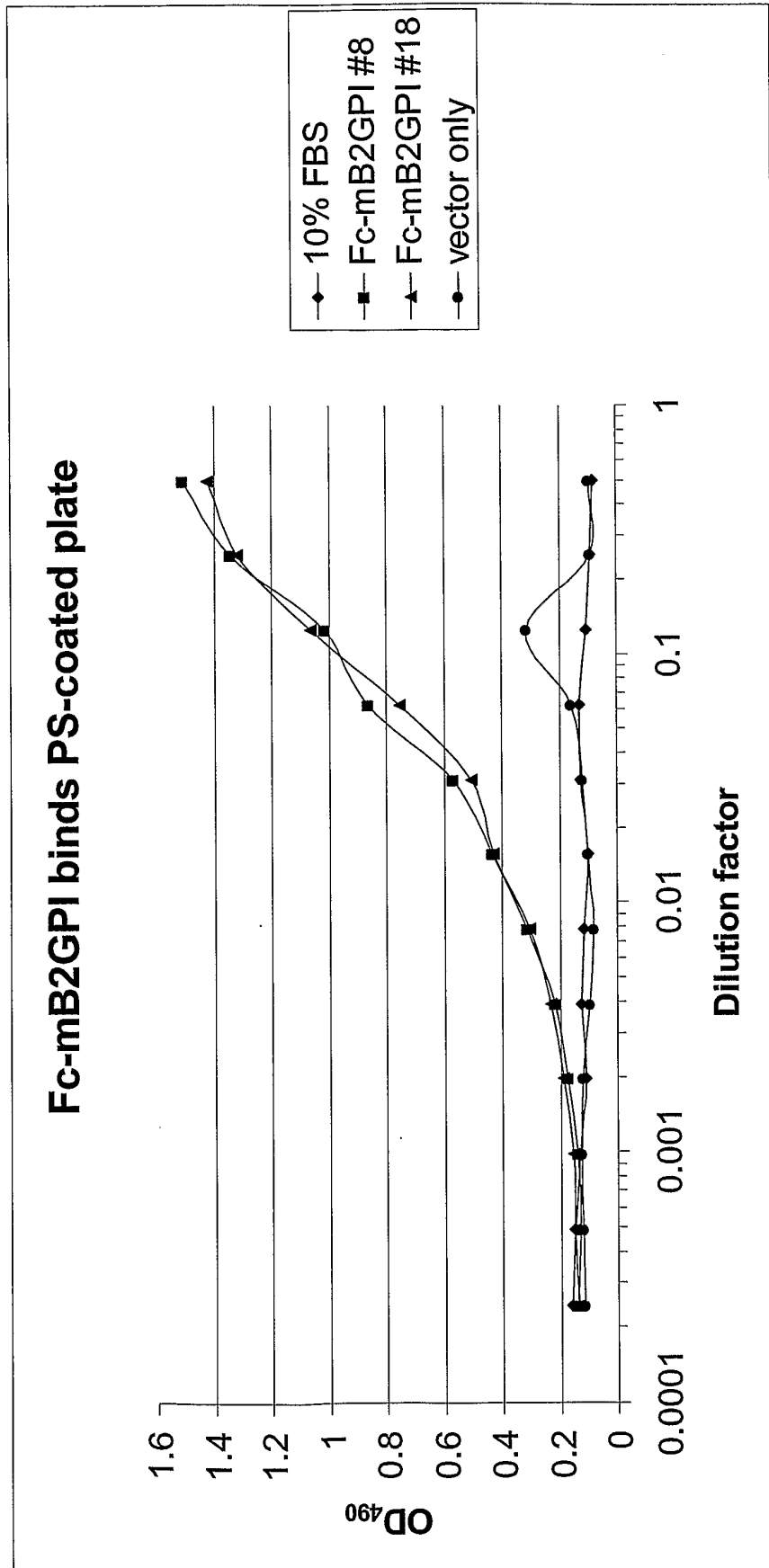


FIG. 20

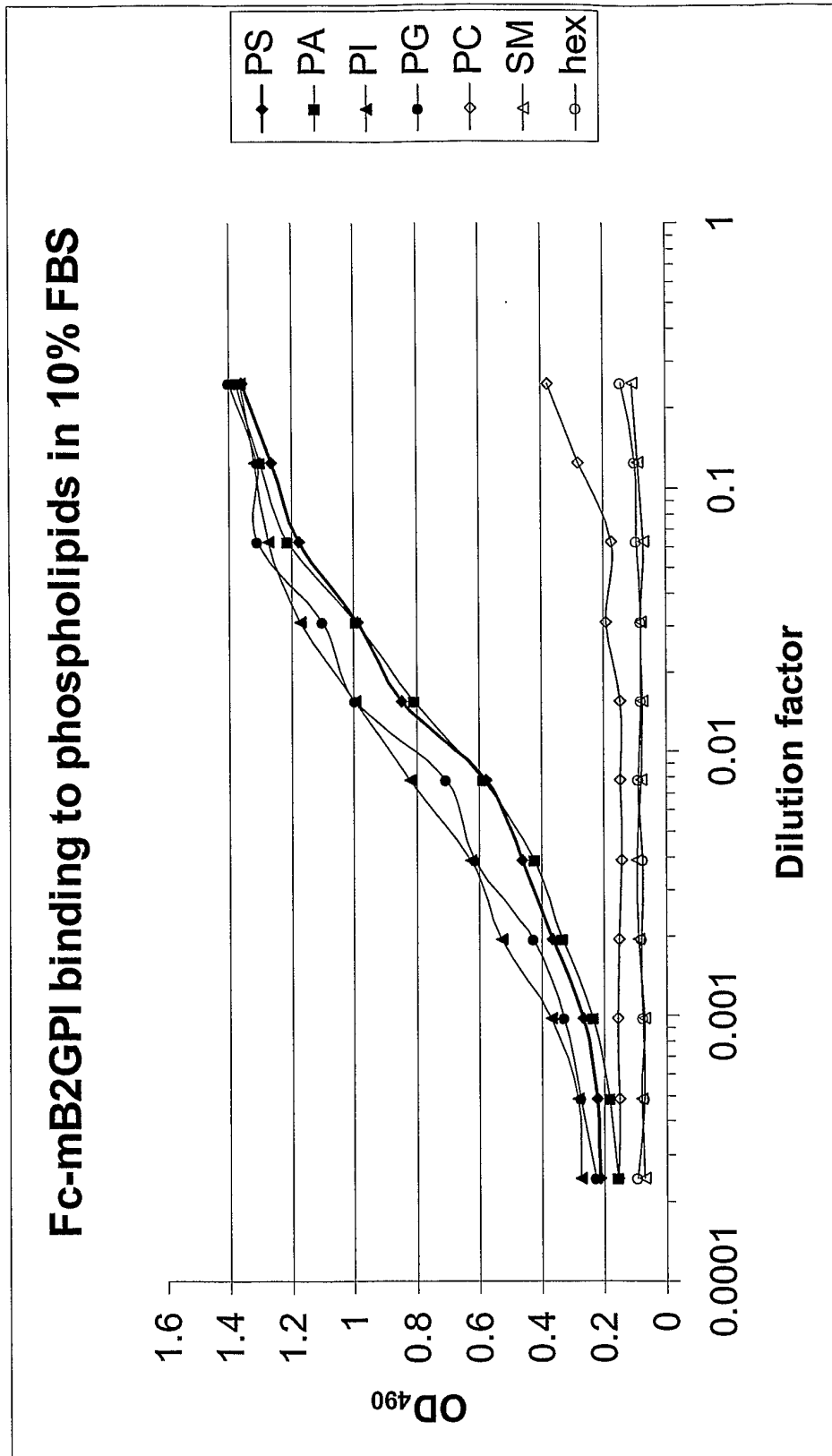


FIG. 21

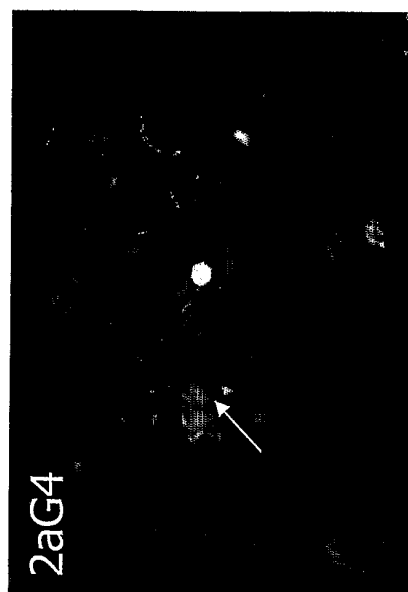


FIG. 22A

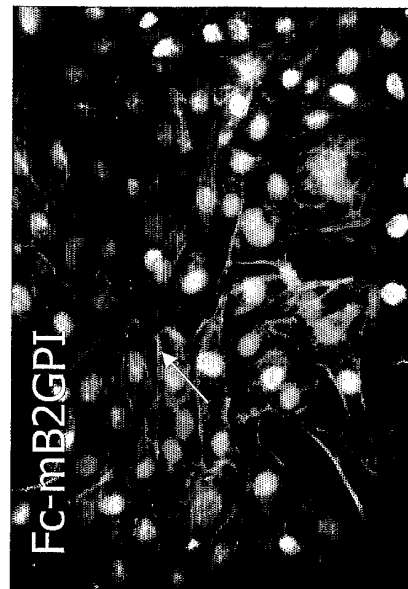


FIG. 22B



FIG. 22C



**FIG. 23B**



**FIG. 23A**

**FIG. 24**