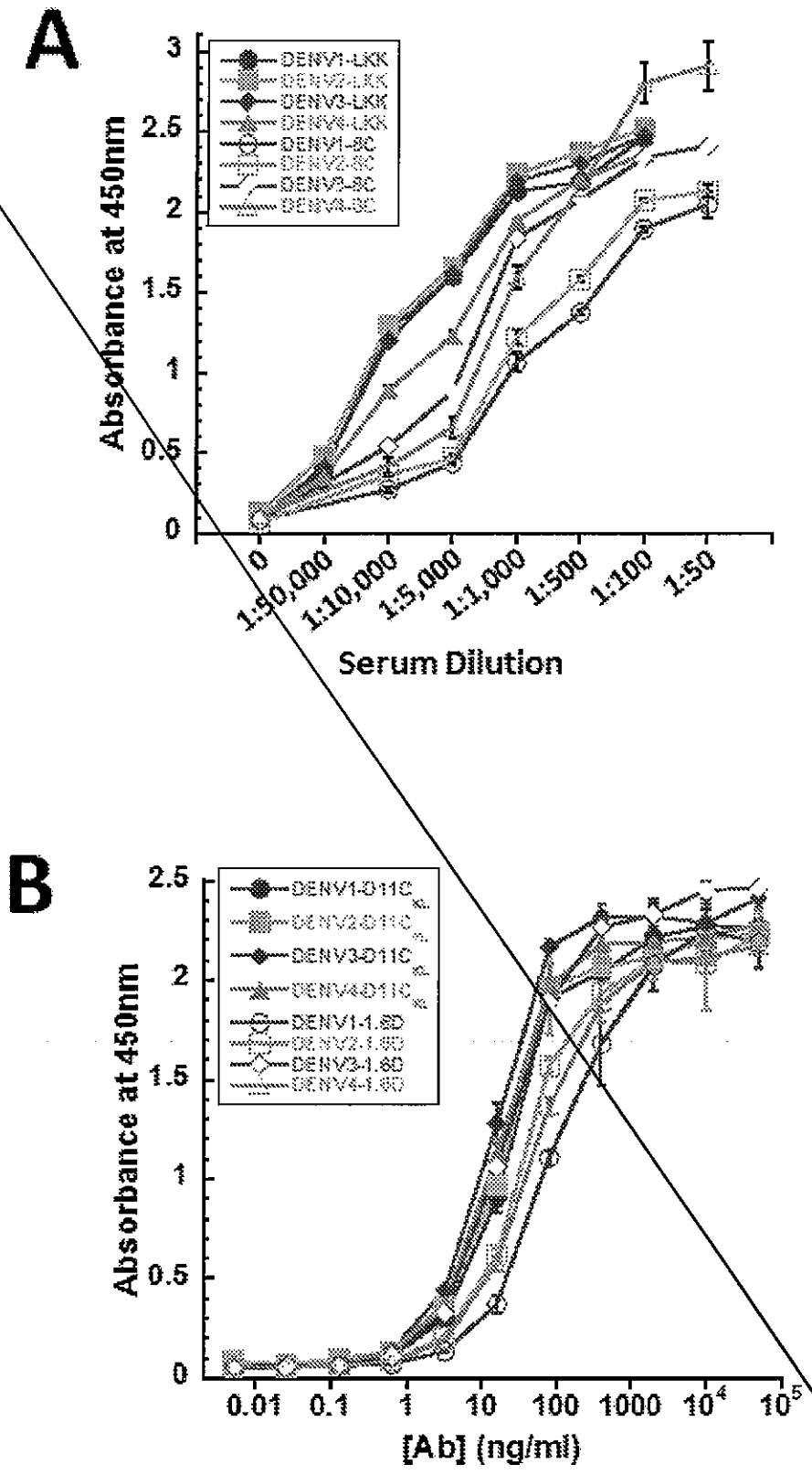

A
Absorbance at 450nm
3
2.5
2
1.5
1
0.5
0
DENV1-LKK
DENV2-LKK
DENV3-LKK
DENV4-LKK
DENV1-8C
DENV2-8C
DENV3-8C
DENV4-8C
0
1:50,000
1:10,000
1:5,000
1:1,000
1:500
1:100
1:50
Serum Dilution
B
Absorbance at 450nm
2.5
2
1.5
1
0.5
0
DENV1-D11C
DENV2-D11C
DENV3-D11C
DENV4-D11C
DENV1-1.6D
DENV2-1.6D
DENV3-1.6D
DENV4-1.6D
0.01
0.1
1
10
100
1000
10^4
10^5
[Ab] (ng/ml)

FIG. 1

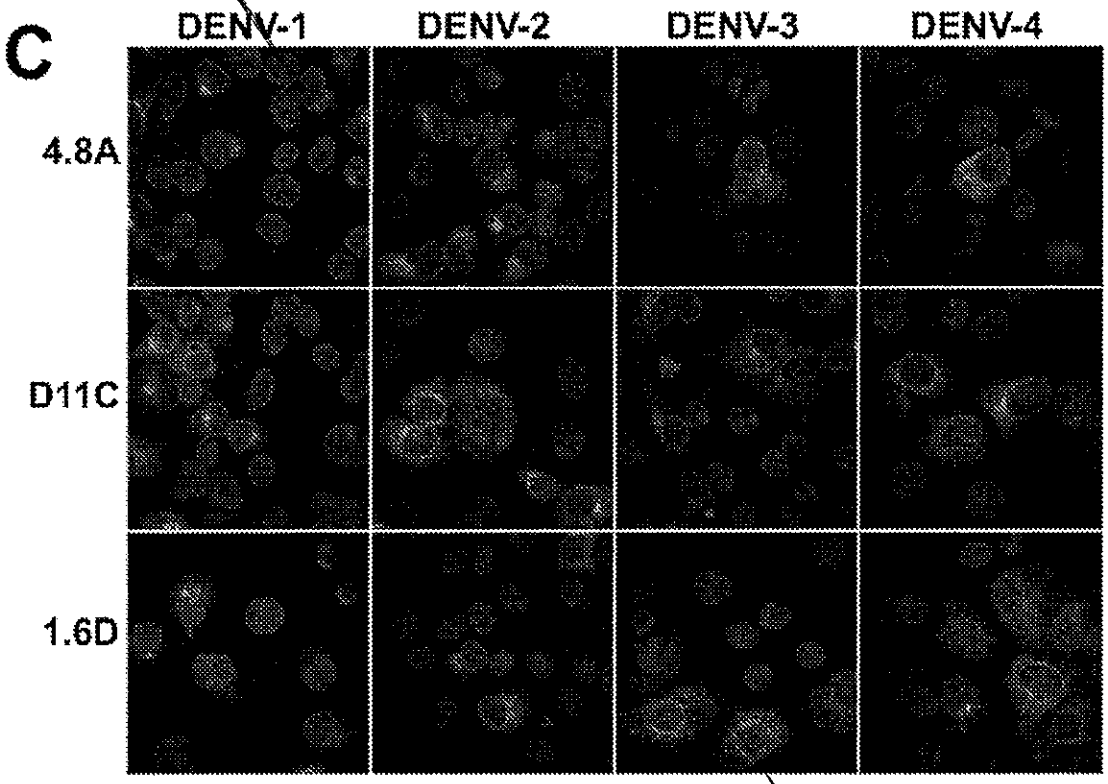


FIG. 2

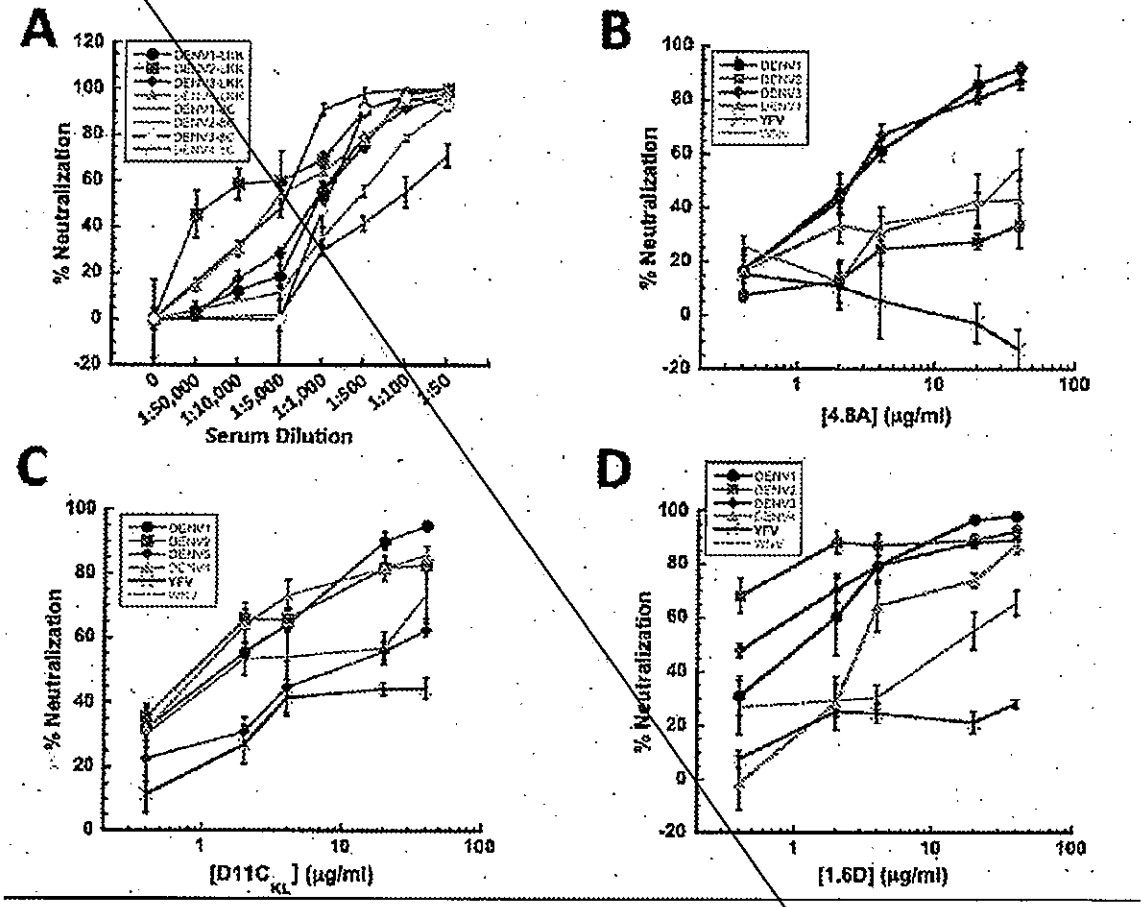

A
% Neutralization
Serum Dilution
B
% Neutralization
[4.8A] (µg/ml)
C
% Neutralization
[D11C KL] (µg/ml)
D
% Neutralization
[1.6D] (µg/ml)
YFV

FIG. 3

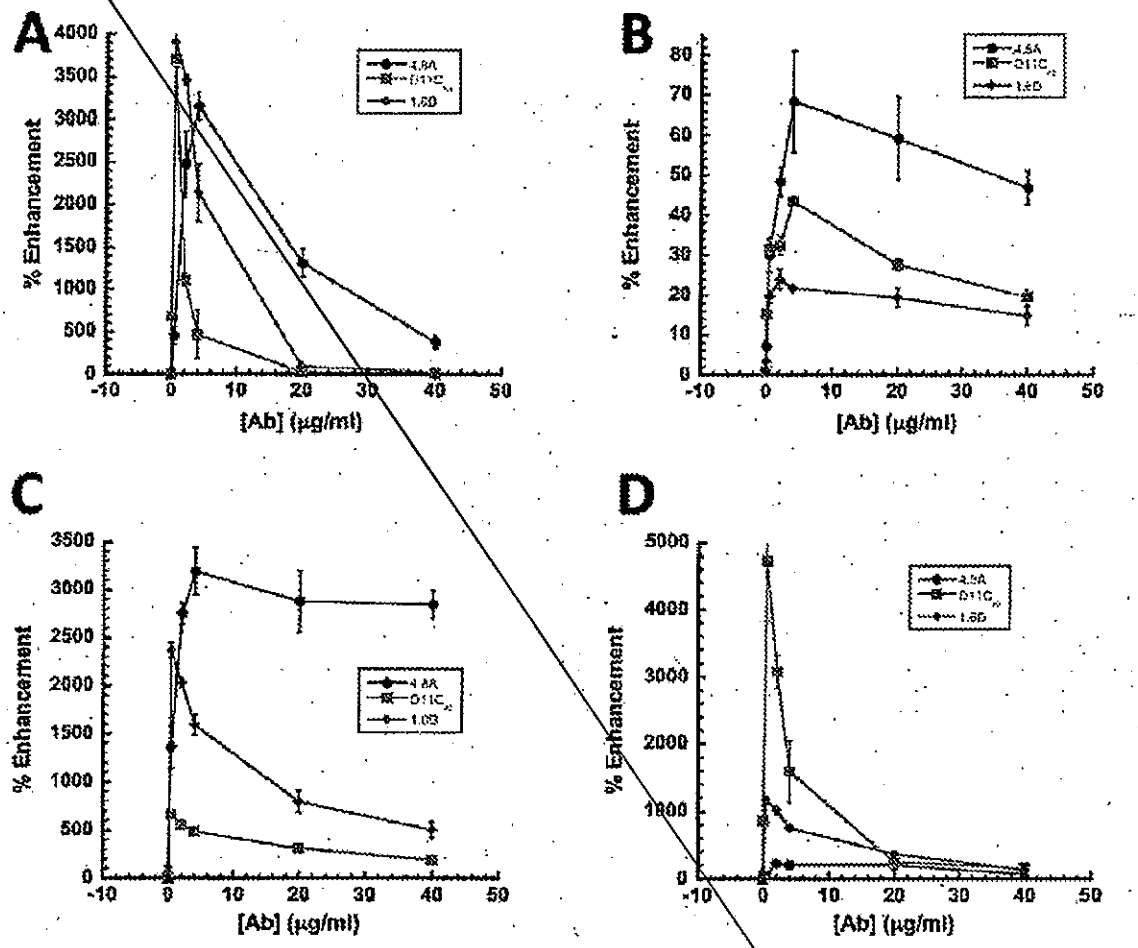


FIG. 4

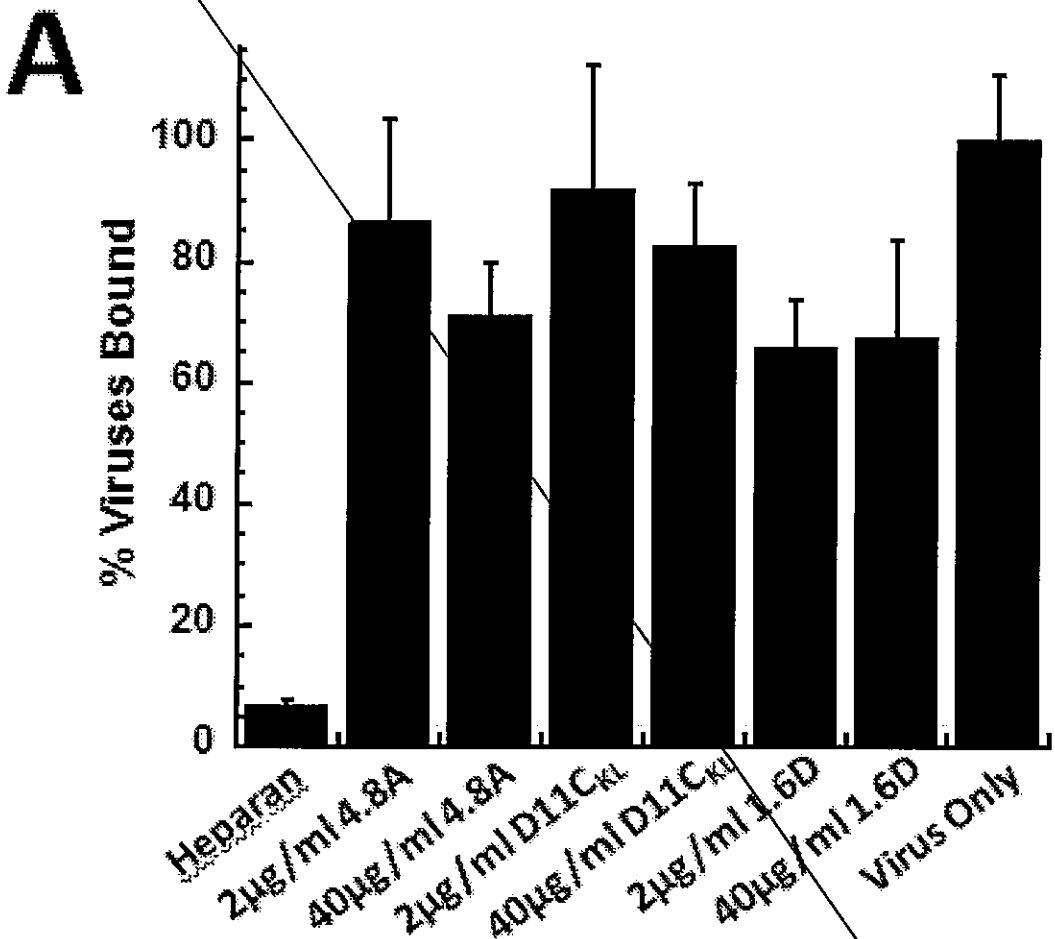

A
% Viruses Bound
0
20
40
60
80
100
Heparan
2µg/ml 4.8A
40µg/ml 4.8A
2µg/ml D11C$_{KL}$
40µg/ml D11C$_{KL}$
2µg/ml 1.6D
40µg/ml 1.6D
Virus Only

FIG. 5

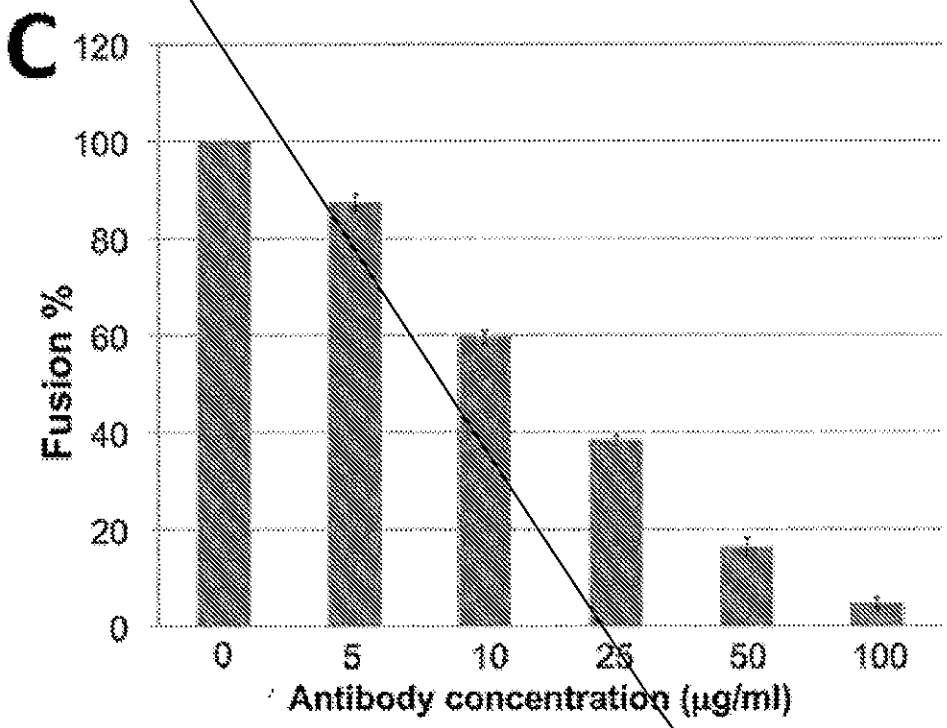

C
120
100
80
60
40
20
0
Fusion %
0
5
10
25
50
100
Antibody concentration (µg/ml)

FIG. 6

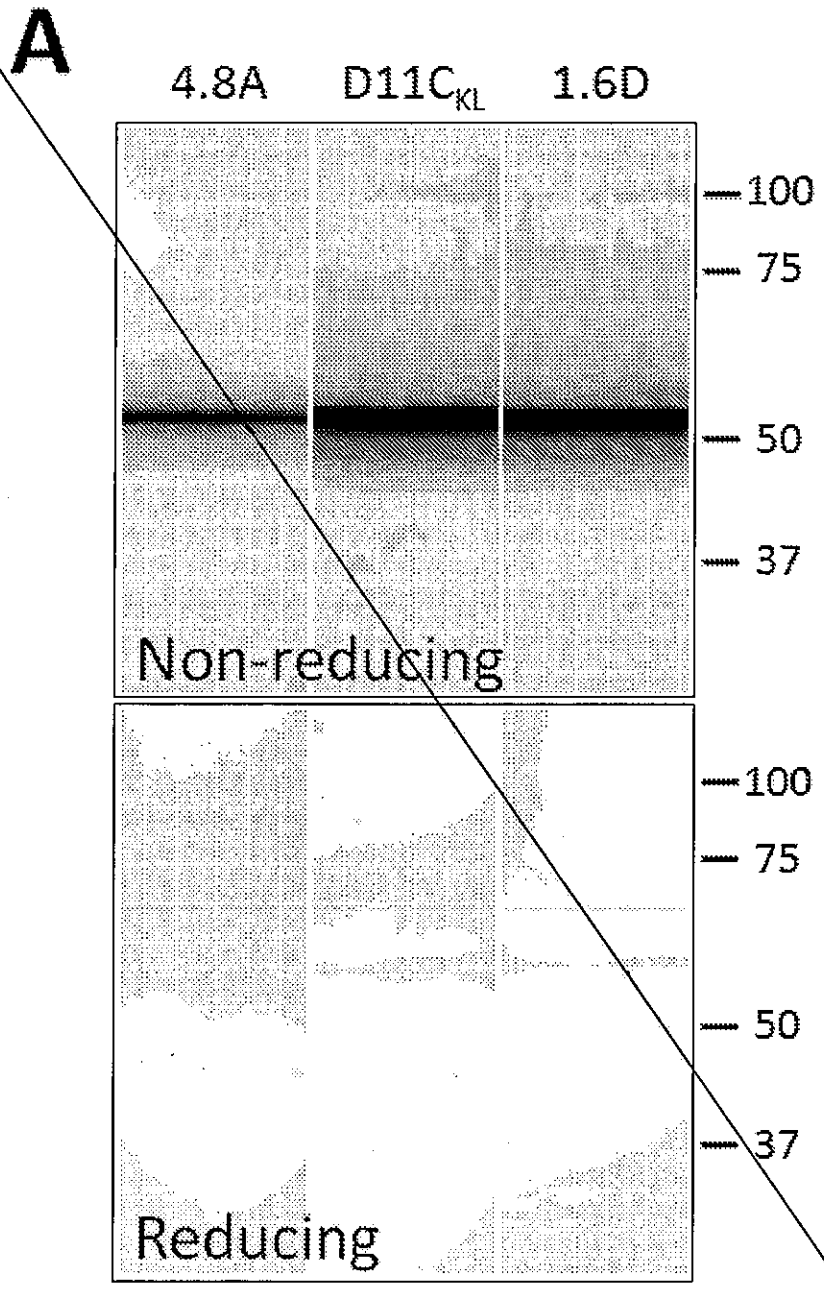

A
4.8A
D11C$_{KL}$
1.6D
100
75
50
37
Non-reducing
100
75
50
37
Reducing

FIG. 7

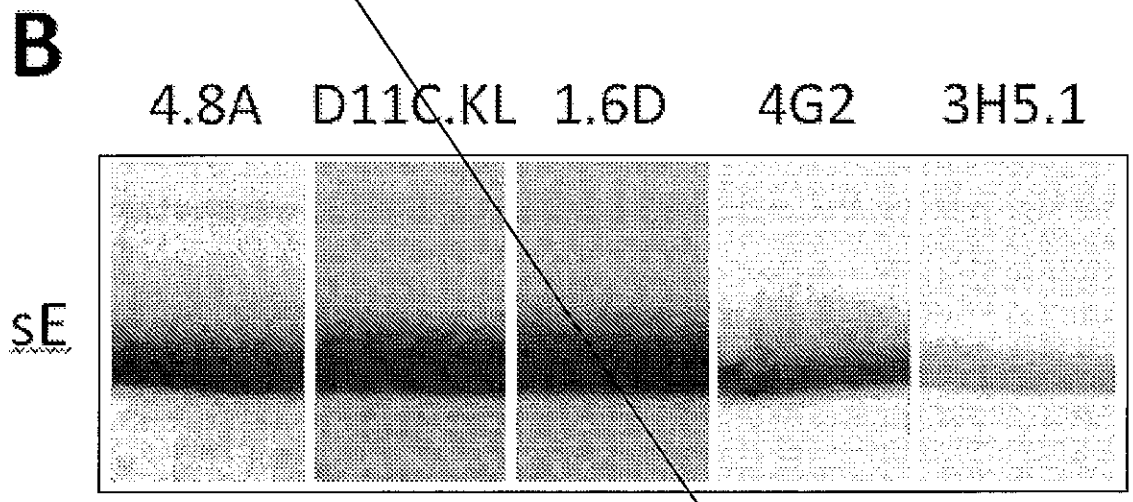


FIG. 8

	4.8A	D11C$_{KL}$	1.6D
DENV1	6.70175E-10	3.951E-10	2.75125E-10
DENV2	7.5382E-10	1.8205E-09	1.86987E-09
DENV3	1.43508E-09	3.293E-10	1.7884E-09
DENV4	1.15297E-09	4.7165E-10	1.619E-09

FIG. 9

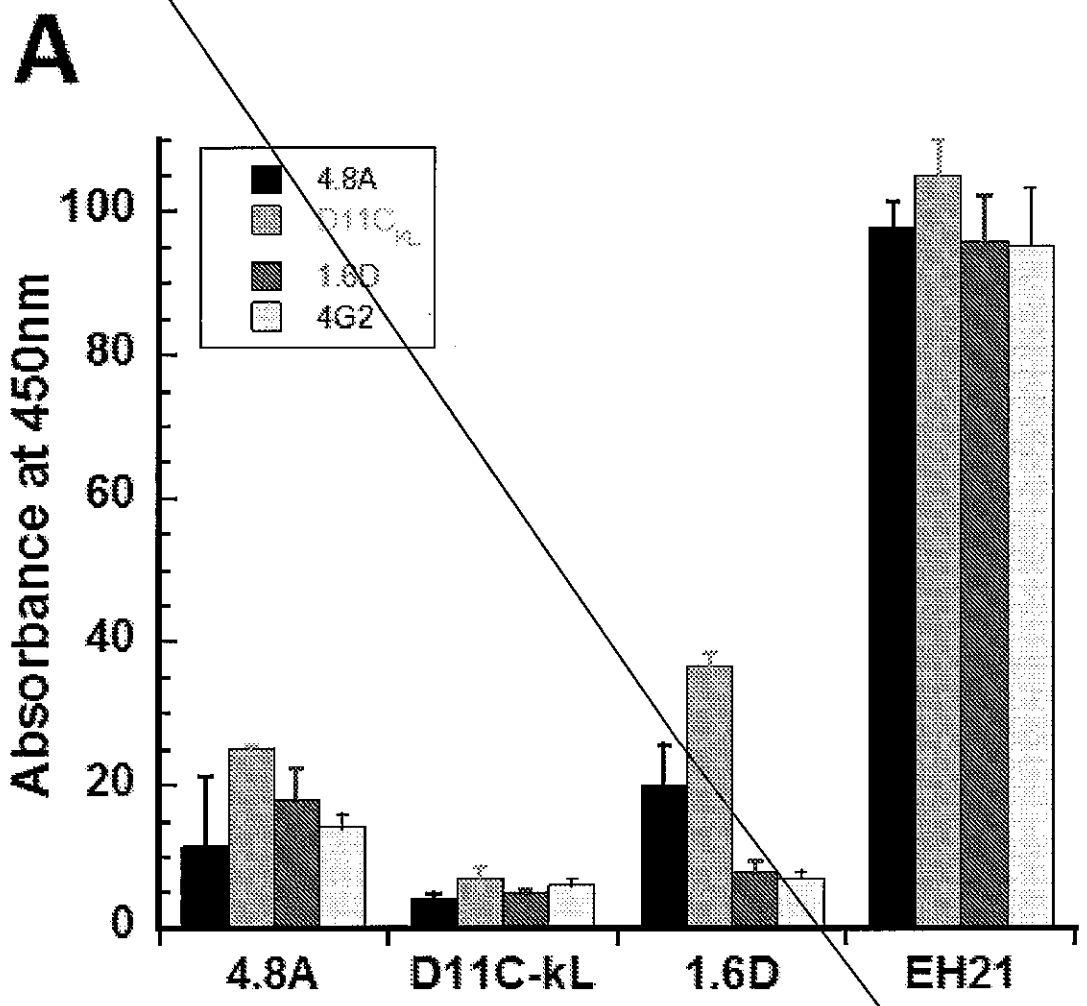

A
4.8A
D11C-kL
1.6D
4G2
Absorbance at 450nm
0
20
40
60
80
100
4.8A
D11C-kL
1.6D
EH21

FIG. 10

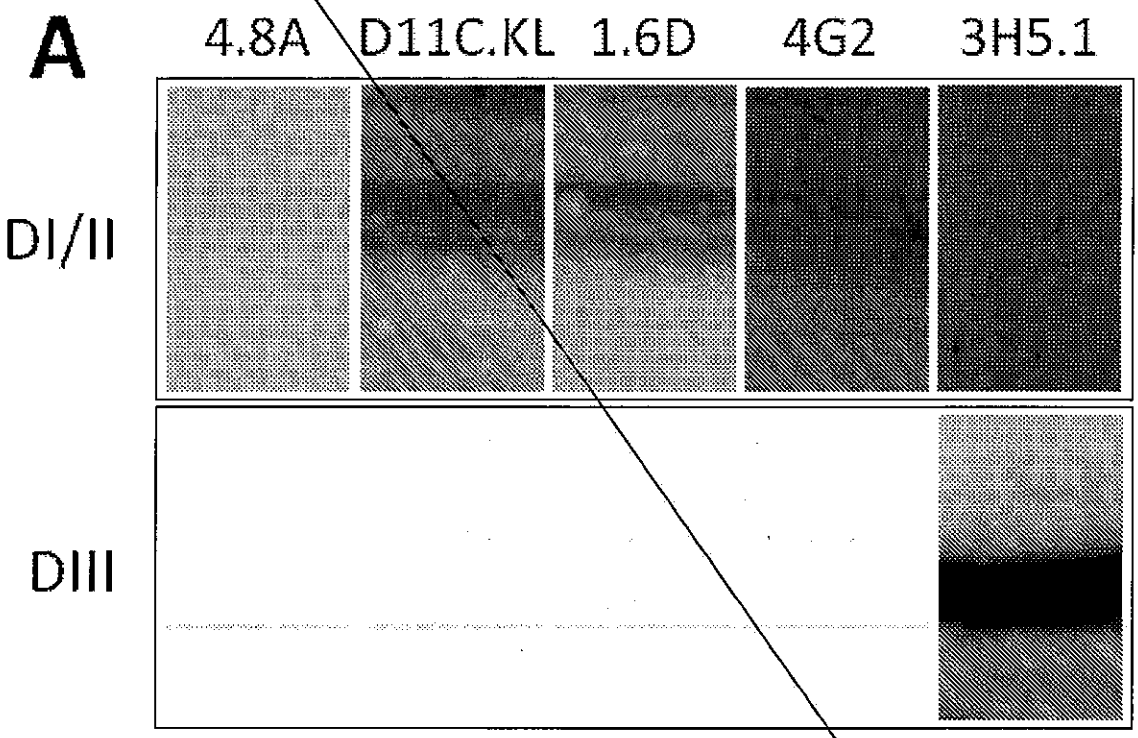


FIG. 11

B

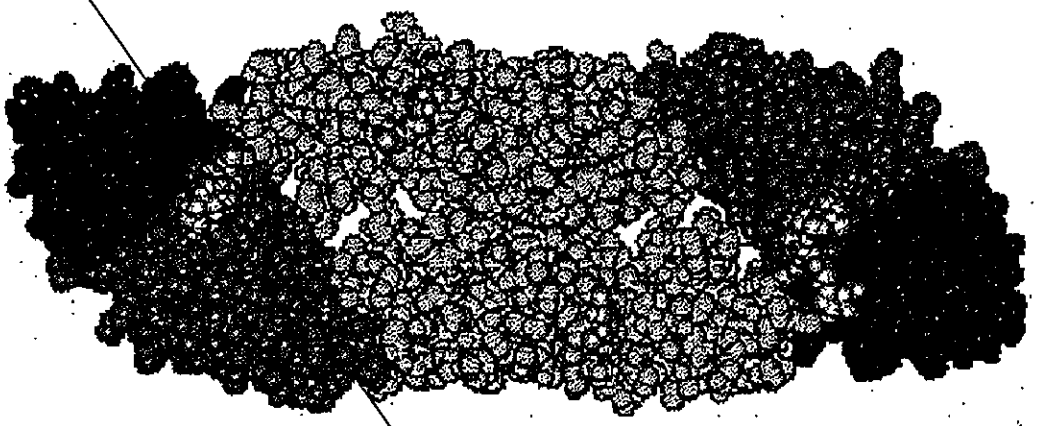


FIG. 12

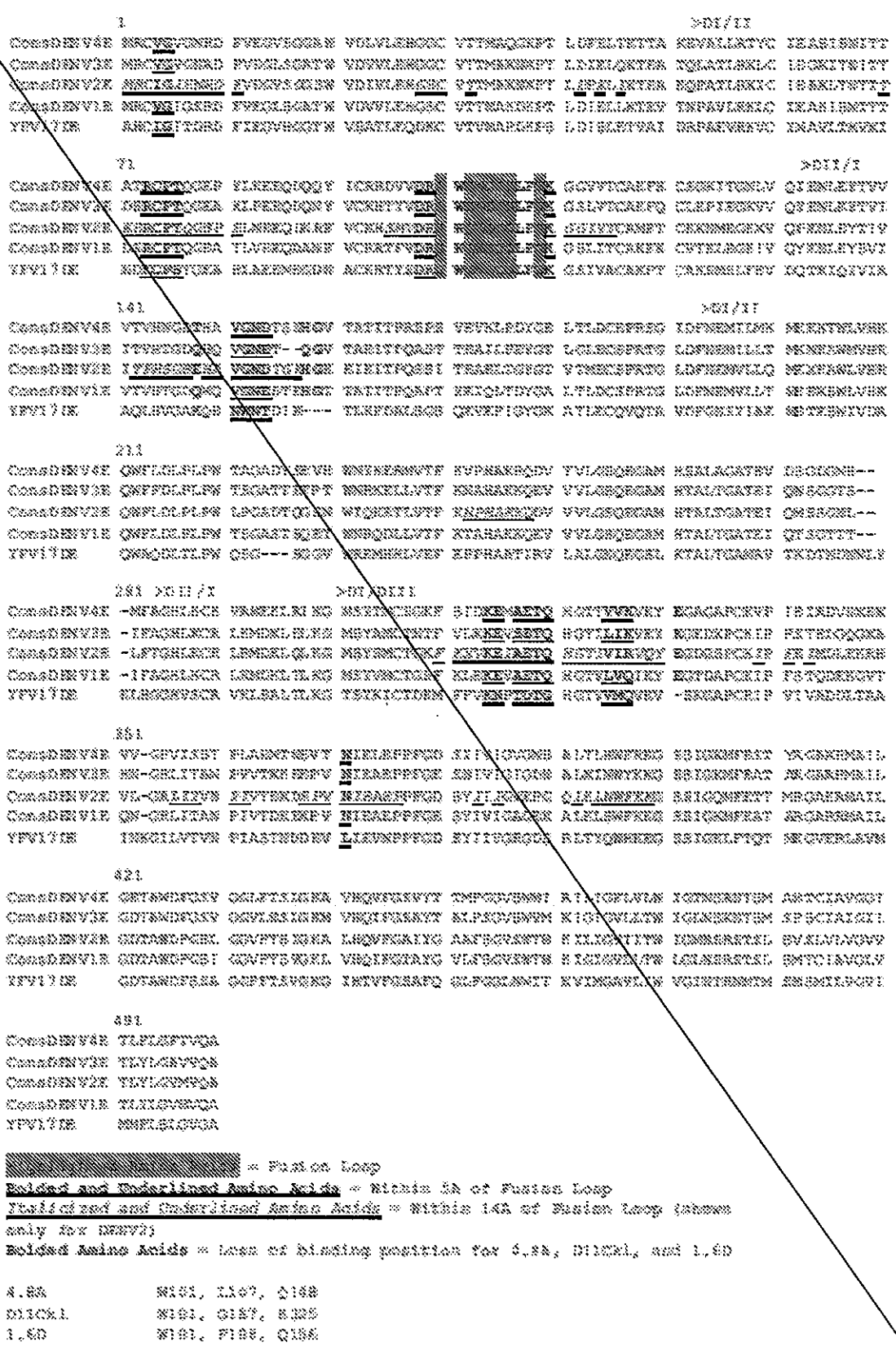

Dengue/yellow fever E protein alignment
= Fusion Loop
Bolded and Underlined Amino Acids = Within 5A of Fusion Loop
Bolded Amino Acids = Loss of binding position for 4.8A, DIIC&I, and 1.6D
4.8A W101, I147, Q188
DIICkI W101, Q187, E125
1.6D W101, F108, Q156

FIG. 13

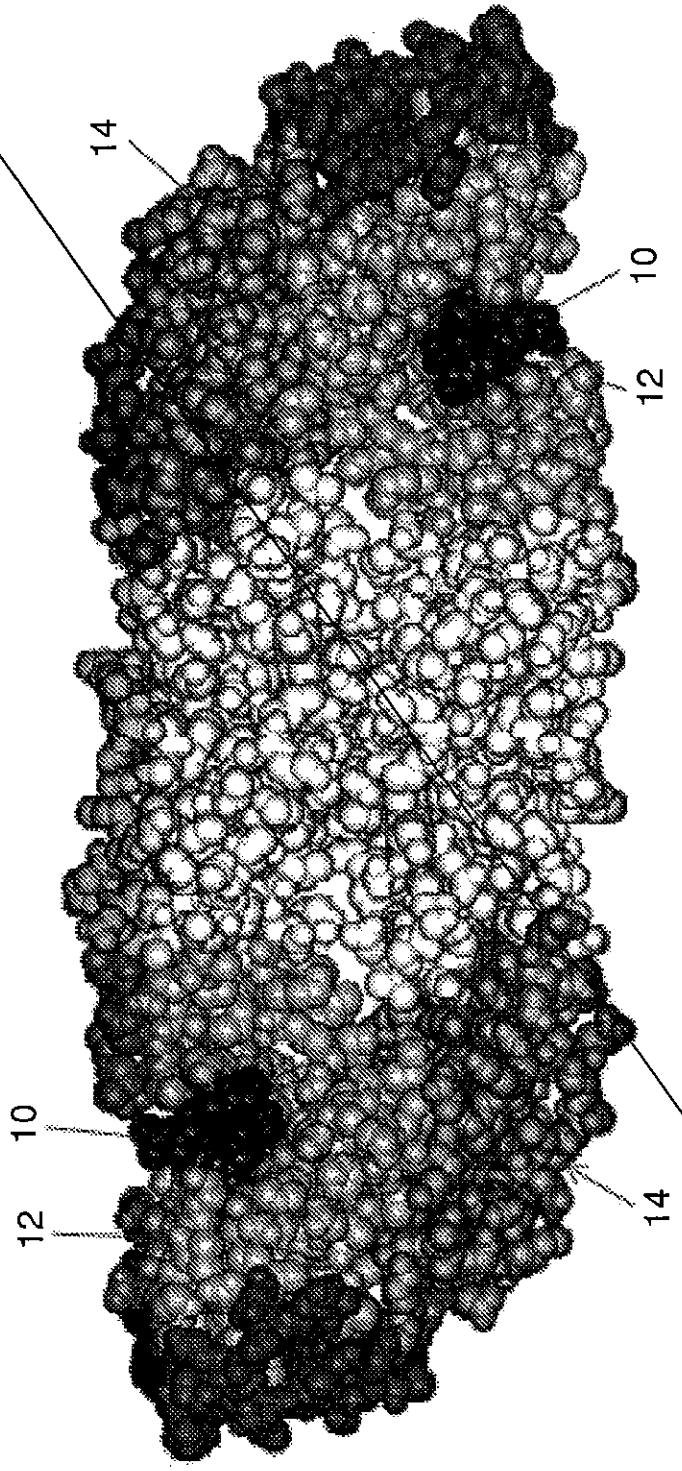
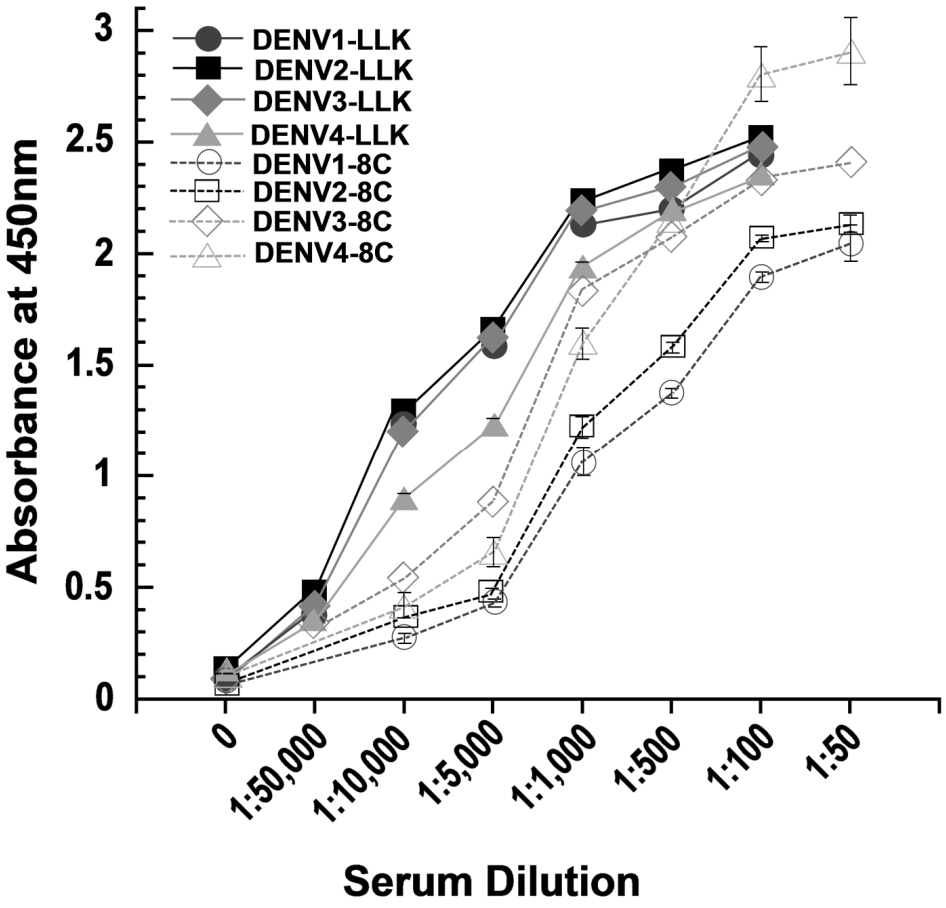


FIG. 14


DENV1-LLK
DENV2-LLK
DENV3-LLK
DENV4-LLK
DENV1-8C
DENV2-8C
DENV3-8C
DENV4-8C
Absorbance at 450nm
3
2.5
2
1.5
1
0.5
0
0
1:50,000
1:10,000
1:5,000
1:1,000
1:500
1:100
1:50
Serum Dilution

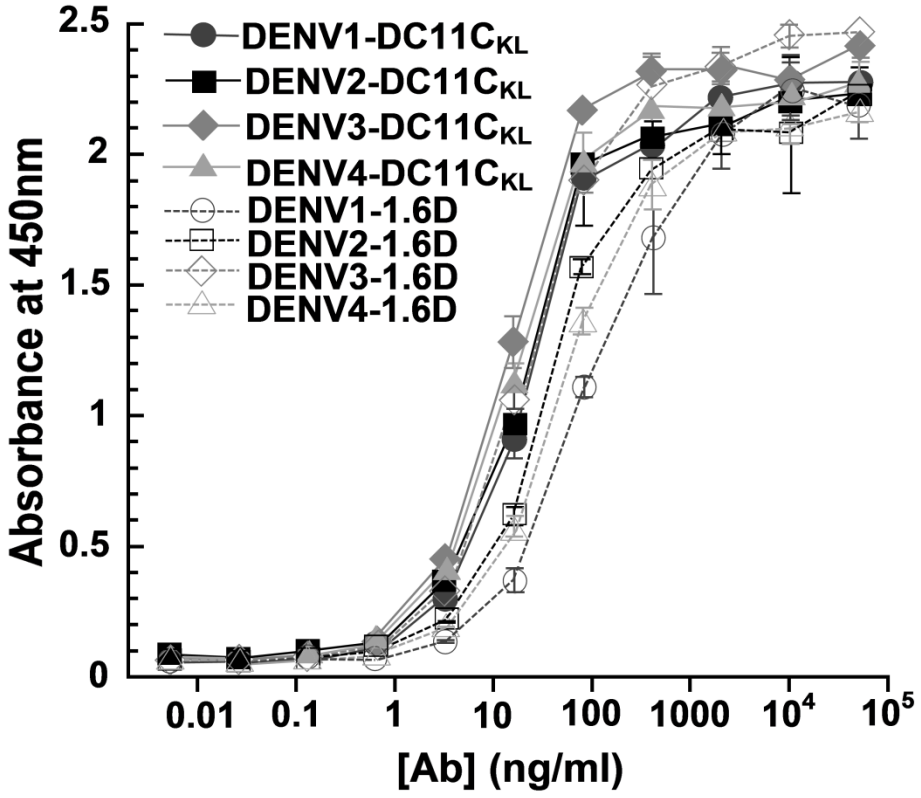

DENV1-DC11C$_{KL}$
DENV2-DC11C$_{KL}$
DENV3-DC11C$_{KL}$
DENV4-DC11C$_{KL}$
DENV1-1.6D
DENV2-1.6D
DENV3-1.6D
DENV4-1.6D
Absorbance at 450nm
2.5
2
1.5
1
0.5
0
0.01
0.1
1
10
100
1000
10^4
10^5
[Ab] (ng/ml)

FIG. 1

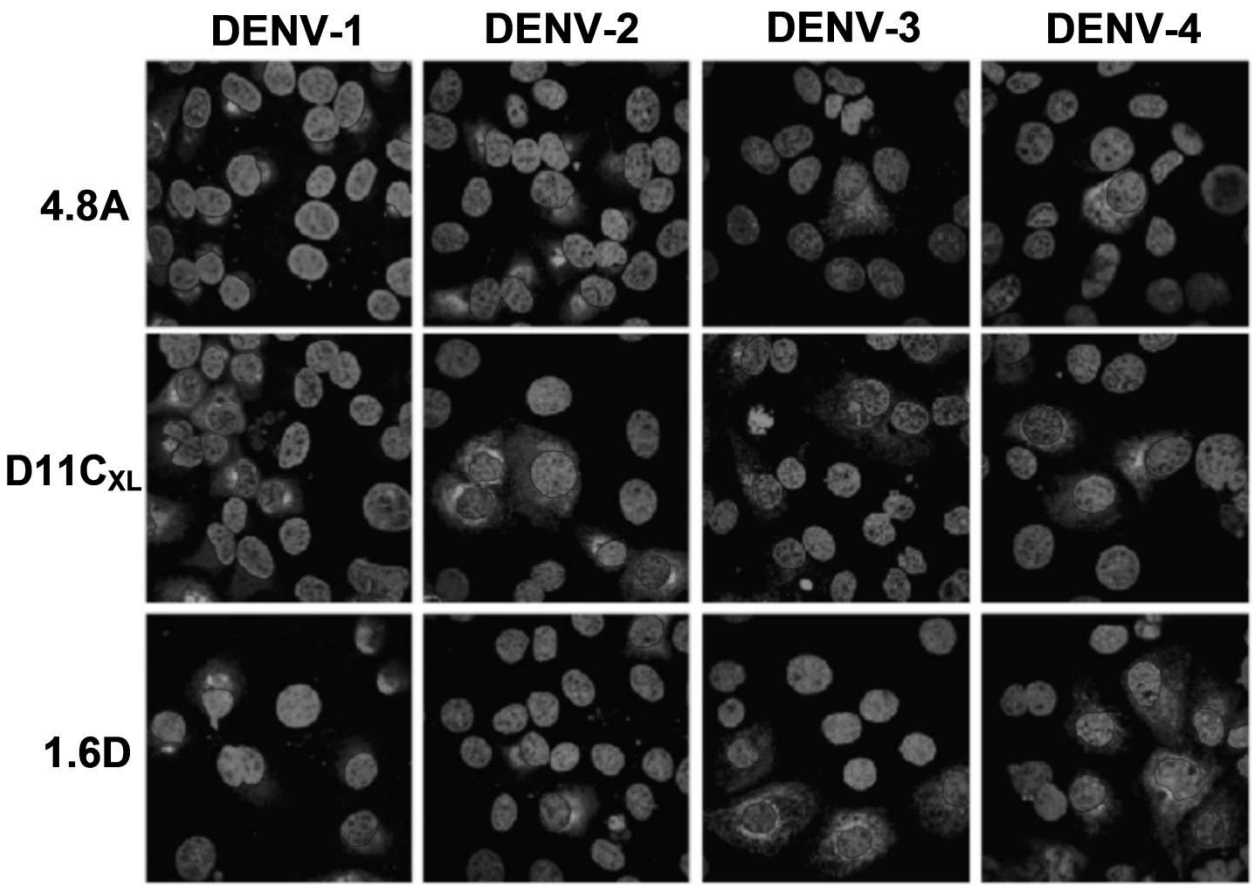
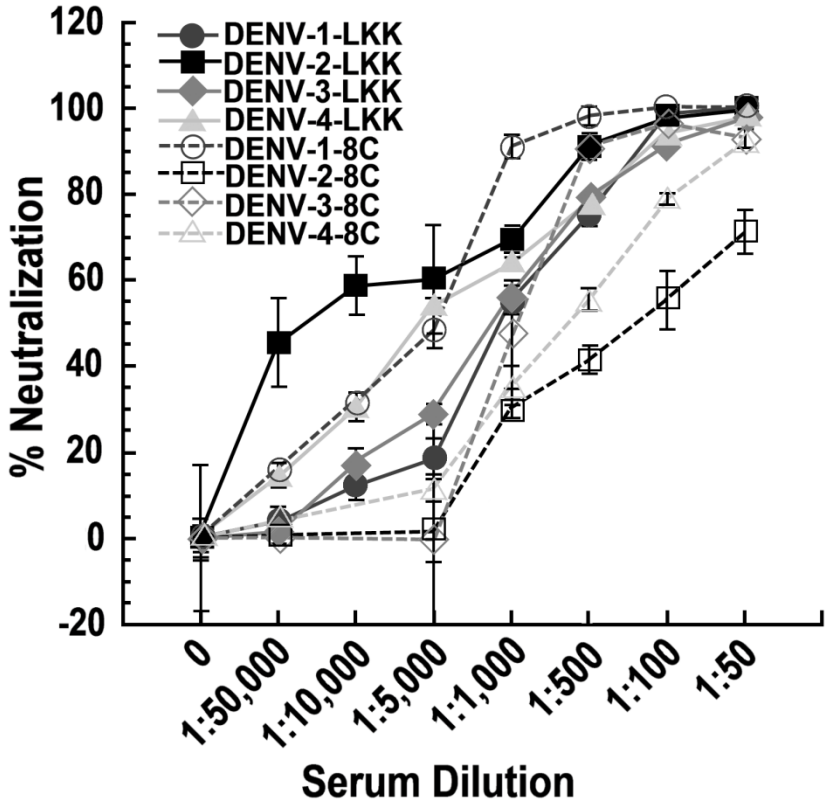
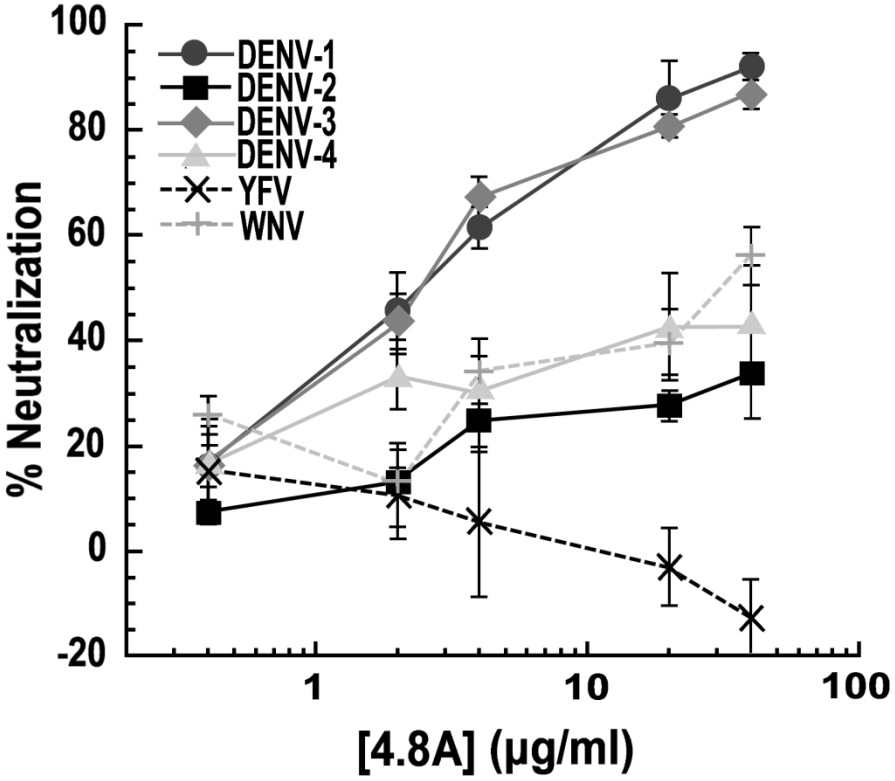


FIG. 2


DENV-1-LKK
DENV-2-LKK
DENV-3-LKK
DENV-4-LKK
DENV-1-8C
DENV-2-8C
DENV-3-8C
DENV-4-8C
% Neutralization
120
100
80
60
40
20
0
-20
0
1:50,000
1:10,000
1:5,000
1:1,000
1:500
1:100
1:50
Serum Dilution


DENV-1
DENV-2
DENV-3
DENV-4
YFV
WNV
% Neutralization
100
80
60
40
20
0
-20
1
10
100
[4.8A] (µg/ml)

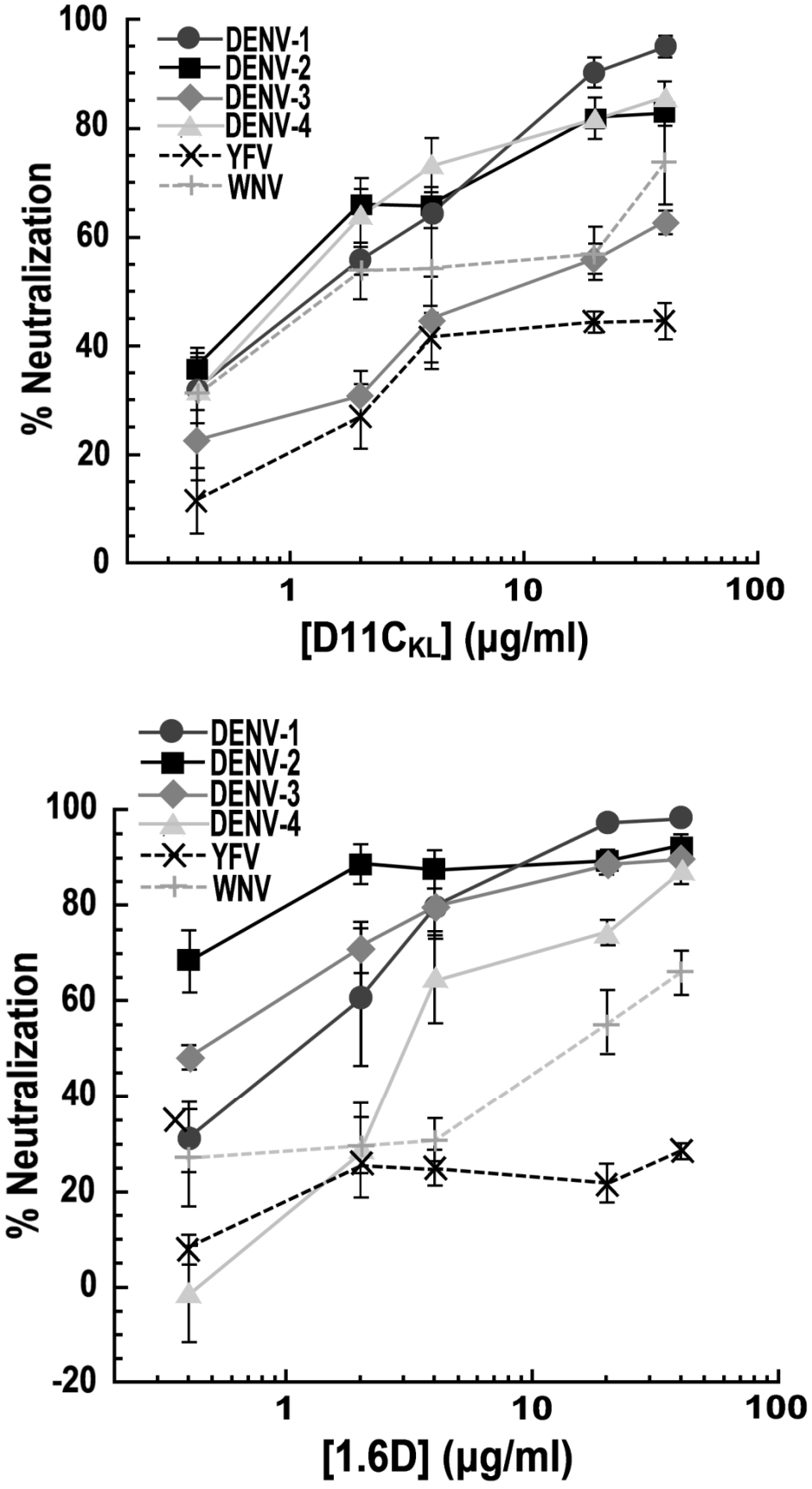
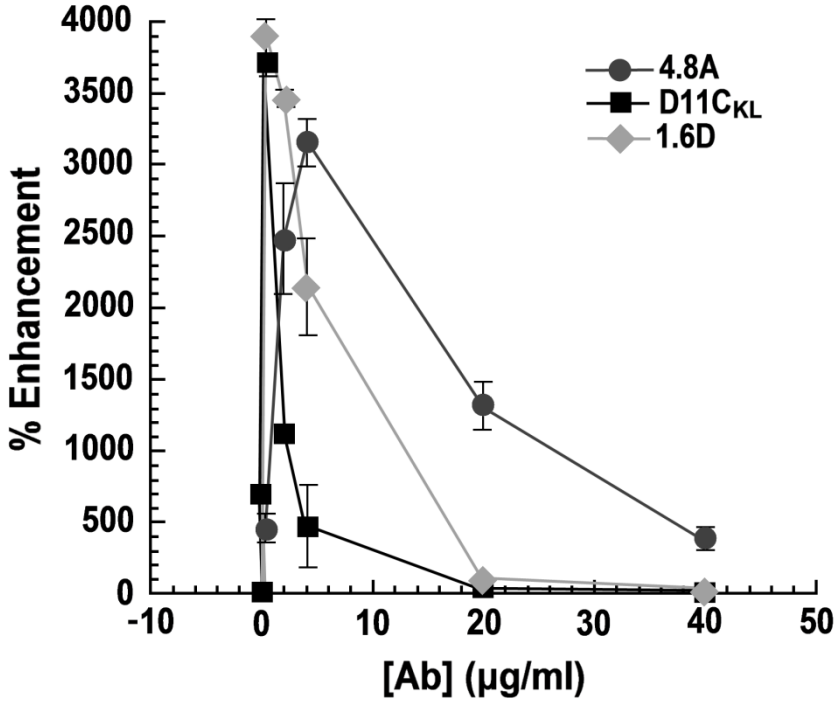
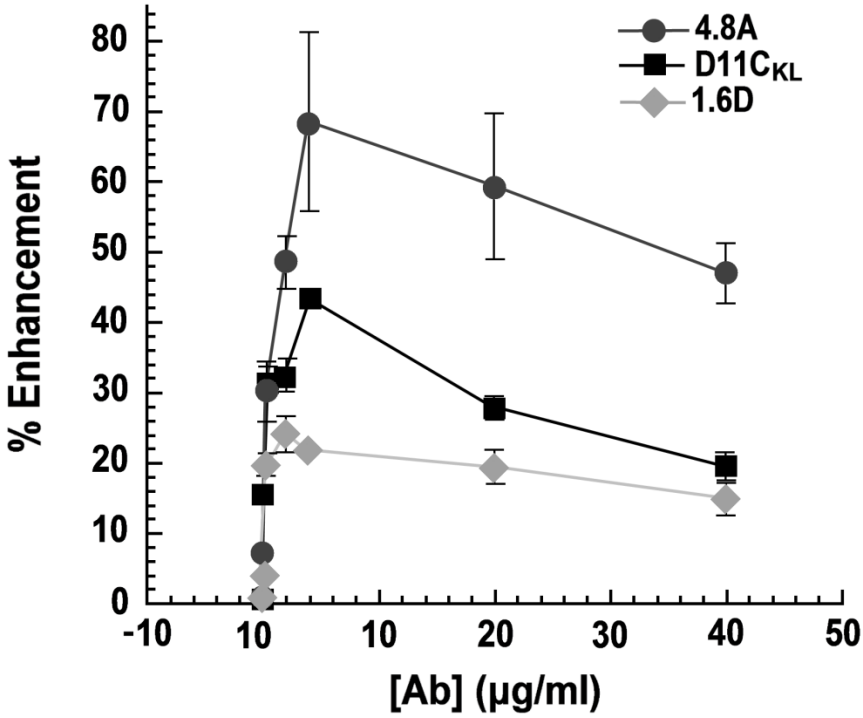

DENV-1
DENV-2
DENV-3
DENV-4
YFV
WNV
% Neutralization
100
80
60
40
20
0
1
10
100
[D11C$_{KL}$] (µg/ml)
DENV-1
DENV-2
DENV-3
DENV-4
YFV
WNV
% Neutralization
100
80
60
40
20
0
-20
1
10
100
[1.6D] (µg/ml)

FIG. 3


4000
3500
3000
2500
2000
1500
1000
500
0
% Enhancement
-10
0
10
20
30
40
50
[Ab] (µg/ml)
4.8A
D11C$_{KL}$
1.6D


80
70
60
50
40
30
20
10
0
% Enhancement
-10
10
10
20
30
40
50
[Ab] (µg/ml)
4.8A
D11C$_{KL}$
1.6D

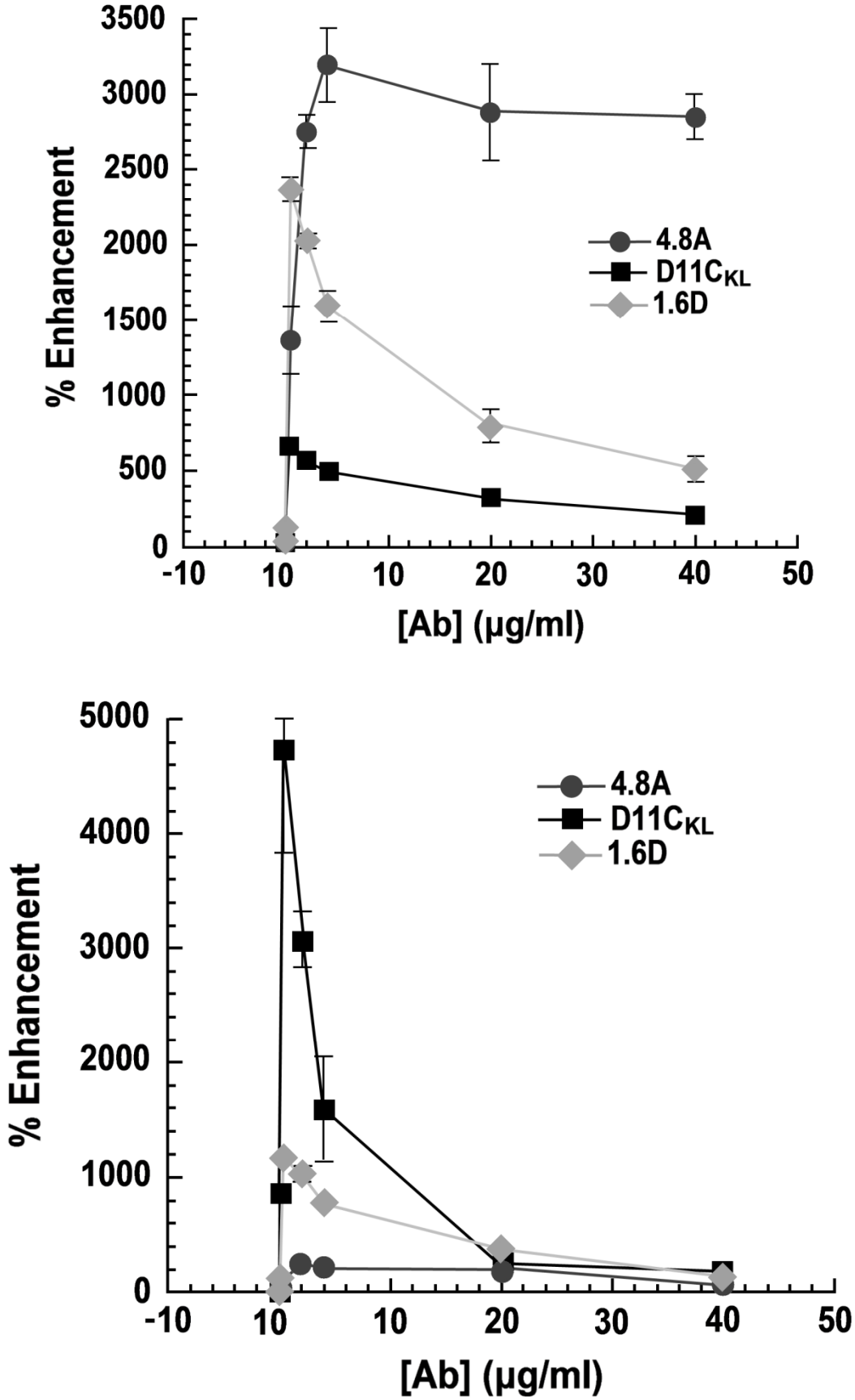

% Enhancement
3500
3000
2500
2000
1500
1000
500
0
-10
10
10
20
30
40
50
[Ab] (µg/ml)
4.8A
D11C$_{KL}$
1.6D
% Enhancement
5000
4000
3000
2000
1000
0
-10
10
10
20
30
40
50
[Ab] (µg/ml)
4.8A
D11C$_{KL}$
1.6D

FIG. 4

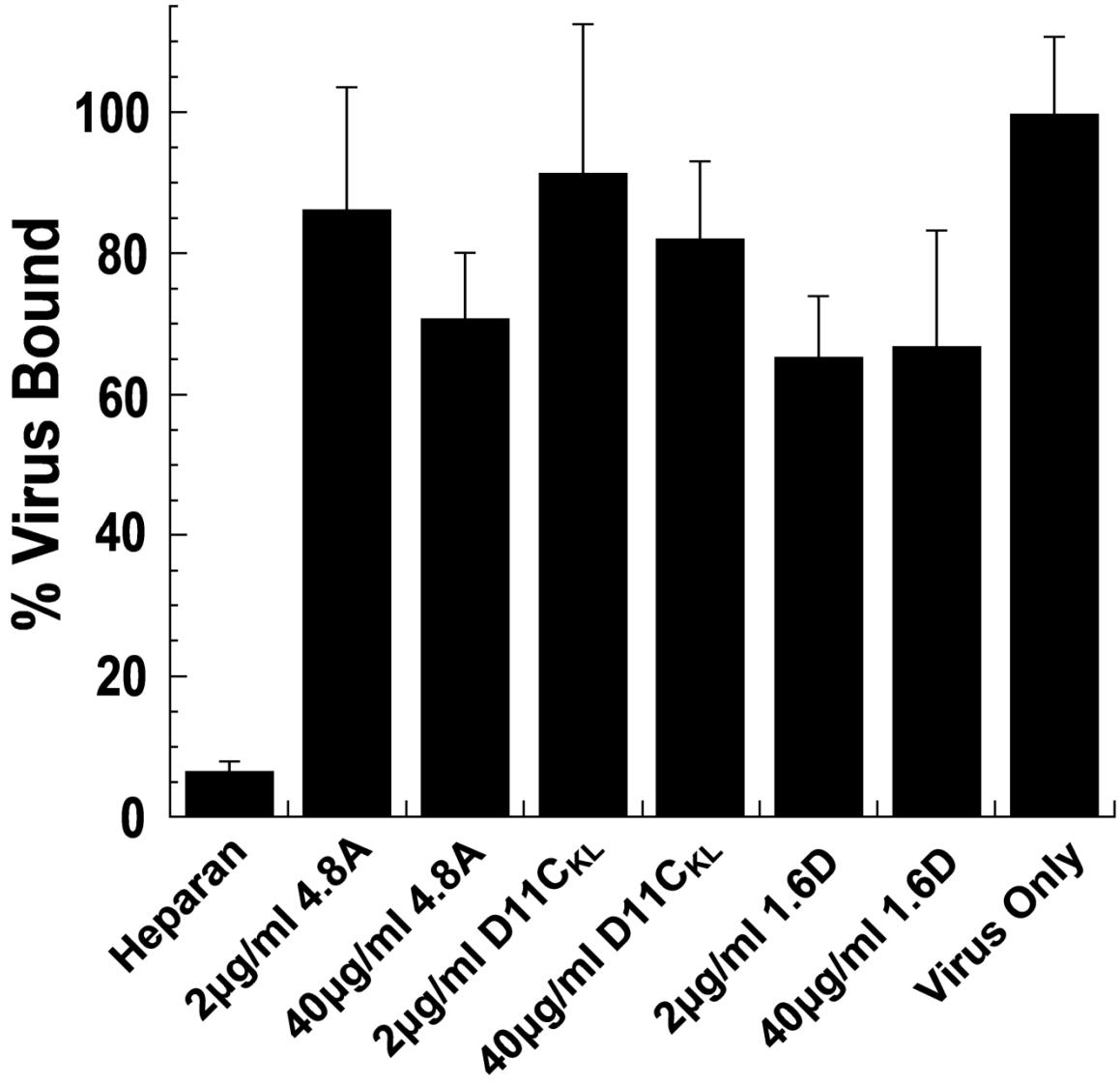

% Virus Bound
0
20
40
60
80
100
Heparan
2µg/ml 4.8A
40µg/ml 4.8A
2µg/ml D11C$_{KL}$
40µg/ml D11C$_{KL}$
2µg/ml 1.6D
40µg/ml 1.6D
Virus Only

FIG. 5

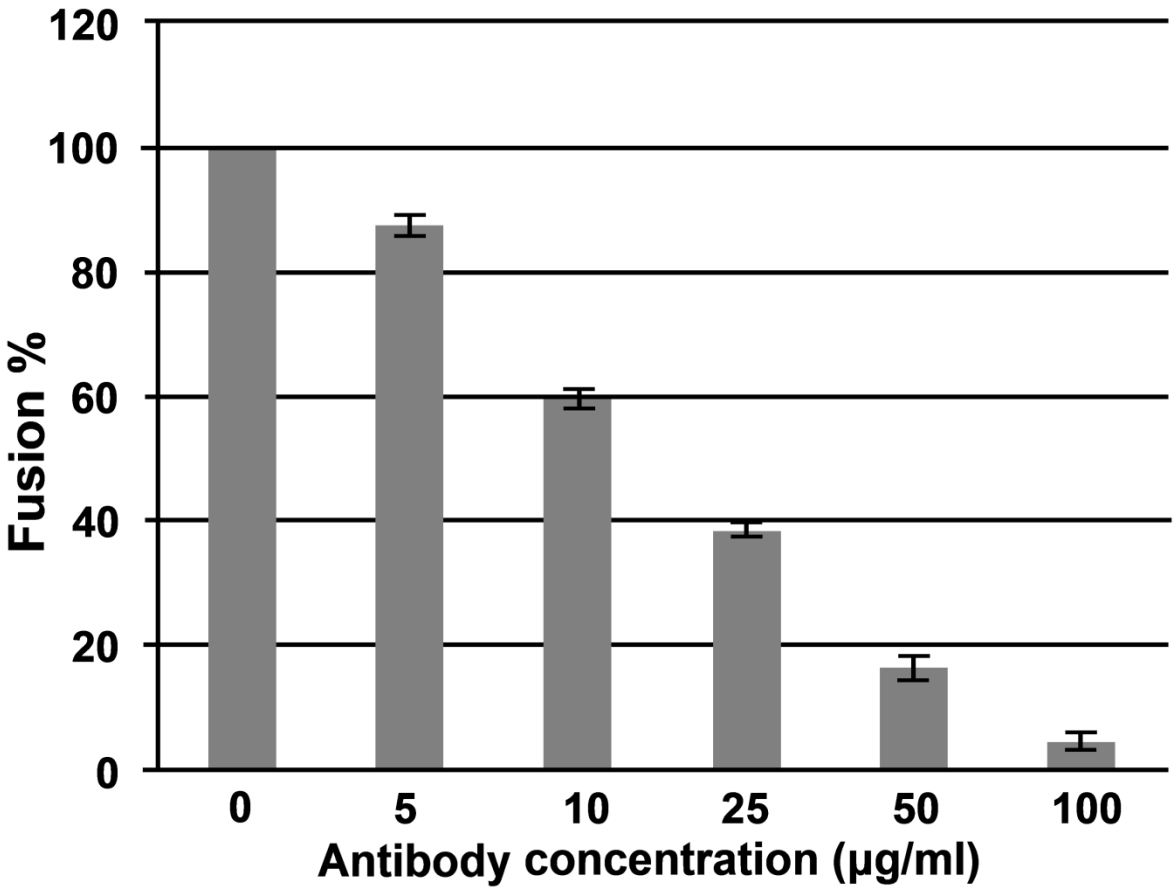

120
100
80
60
40
20
0
Fusion %
0
5
10
25
50
100
Antibody concentration (µg/ml)

FIG. 6

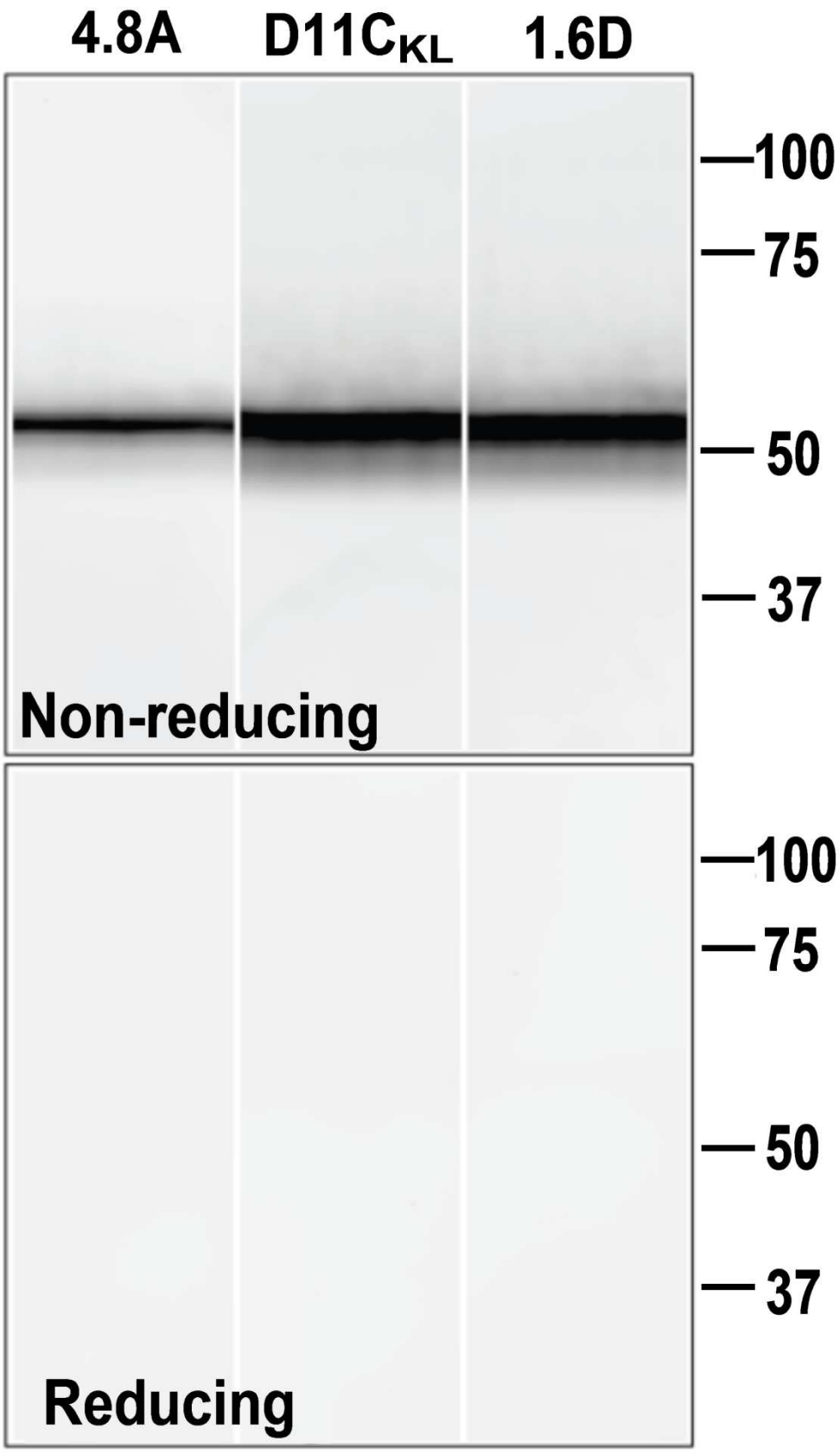


FIG. 7

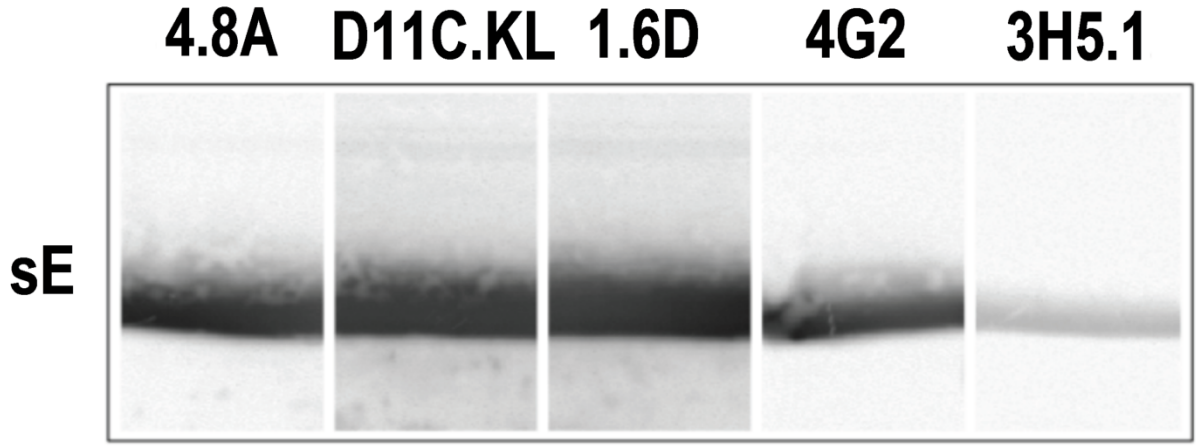


FIG. 8

	4.8A	$D11C_{KL}$	1.6D
DENV1	6.70175E-10	3.95E-10	2.75125E-10
DENV2	7.5382E-10	1.8205E-09	1.86987E-09
DENV3	1.43508E-09	3.293E-10	1.7884E-09
DENV4	1.15297E-09	4.7165E-10	1.619E-09

FIG. 9

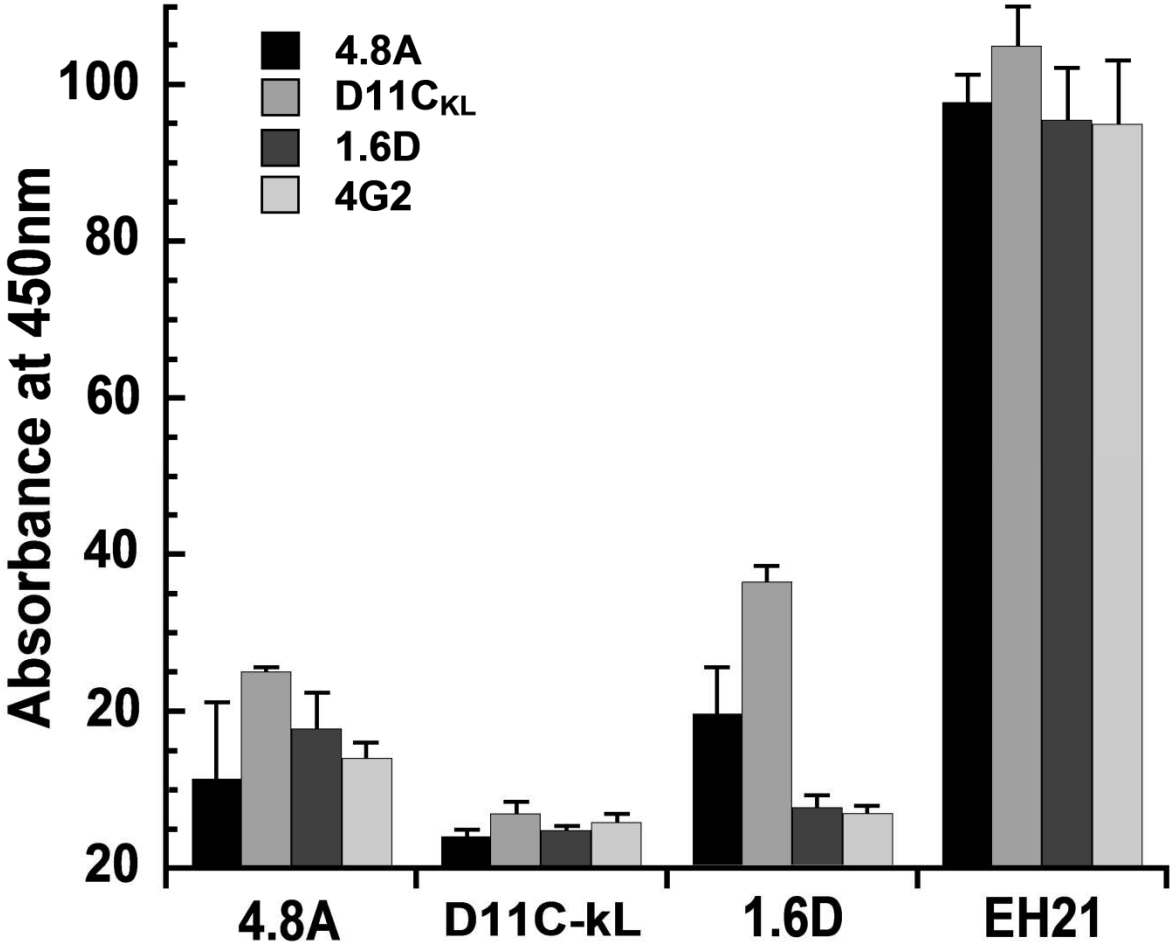

4.8A
D11C$_{KL}$
1.6D
4G2
Absorbance at 450nm
100
80
60
40
20
20
4.8A
D11C-kL
1.6D
EH21

FIG. 10

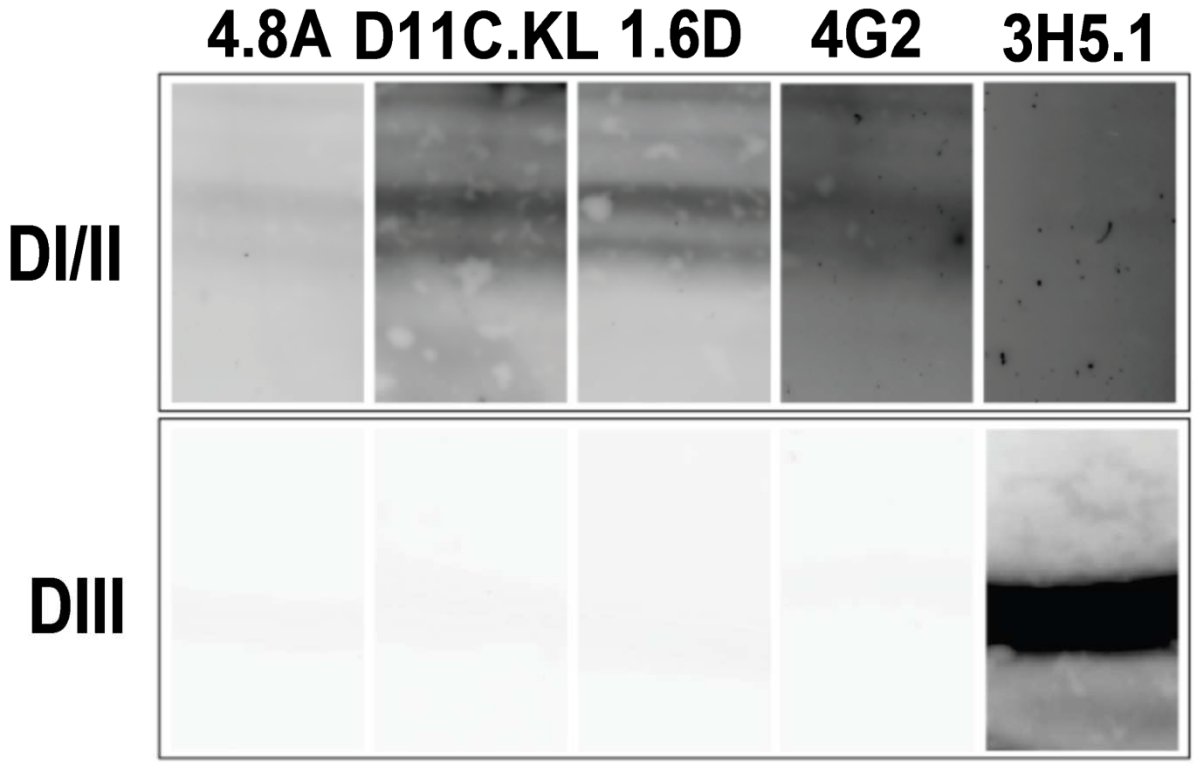


FIG. 11

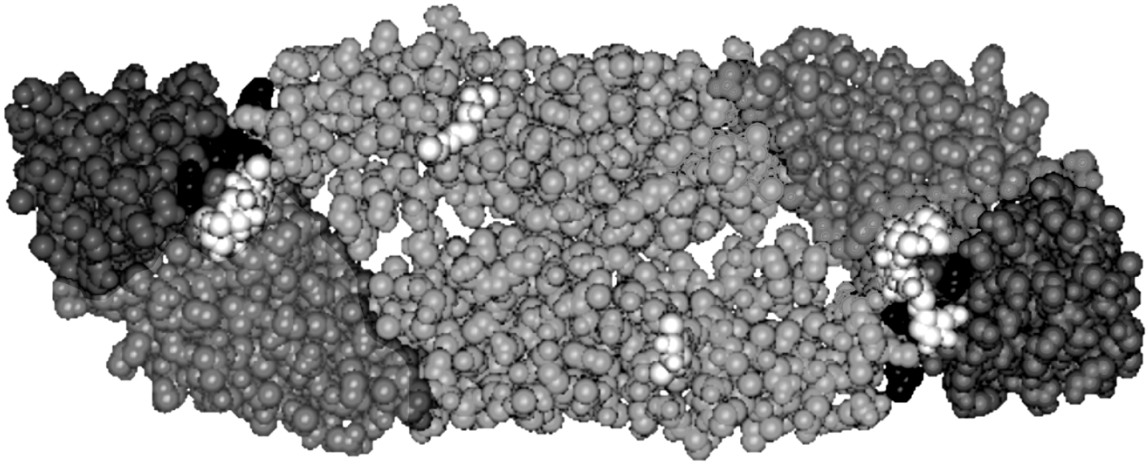


FIG. 12

Dengue/yellow fever E protein alignment

```
          1                                                        >DI/II
ConsDENV4E MRCVGVGNRD FVEGVSGGAW VDLVLEHGGC VTTMAQGKPT LDFELTKTTA KEVALLRTYC IEASISNITT
ConsDENV3E MRCVGVGNRD FVEGLSGATW VDVVLEHGGC VTTMAKNKPT LDIELQKTEA TQLATLRKLC IEGKITNITT
ConsDENV2E MRCIGISNRD FVEGVSGGSW VDIVLEHGSC VTTMAKNKPT LDFELIKTEA KQPATLRKYC IEAKLTNTTT
ConsDENV1E MRCVGIGSRD FVEGLSGATW VDVVLEHGSC VTTMAKDKPT LDIELLKTEV TNPAVLRKLC IEAKISNTTT
YFV17DE    AHCIGITDRD FIEGVHGGTW VSATLEQDKC VTVMAPDKPS LDISLETVAI DRPAEVRKVC YNAVLTHVKI
               71                                                      >DII/I
ConsDENV4E ATRCPTQGEP YLKEEQDQQY ICRRDVVDRG WGNGCGLFGK GGVVTCAKFS CSGKITGNLV QIENLEYTVV
ConsDENV3E DSRCPTQGEA XLPEEQDQNY VCKHTYVDRG WGNGCGLFGK GSLVTCAKFQ CLEPIEGKVV QYENLKYTVI
ConsDENV2E ESRCPTQGEP SLNEEQDKRF VCKHSMVDRG WGNGCGLFGK GGIVTCAMFT CKKNMEGKXV QPENLEYTIV
ConsDENV1E DSRCPTQGEA TLVEEQDANF VCRRTFVDRG WGNGCGLFGK GSLITCAKFK CVTKLEGKIV QYENLKYSVI
YFV17DE    NDKCPSTGEA HLAEENEGDN ACKRTYSDRG WGNGCGLFGK GSIVACAKFT CAKSMSLFEV DQTKIQYVIR
          141                                                      >DI/II
ConsDENV4E VTVHNGDTHA VGNDTSNHGV TATITPRSPS VEVKLPDYGE LTLDCEPRSG IDFNEMILMK MKKKTWLVHK
ConsDENV3E ITVHTGDQHQ VGNET--QGV TAEITPQAST TEAILPEYGT LGLECSPRTG LDFNEMILLT MKNKAWMVHR
ConsDENV2E ITPHSGEEHA VGNDTGKHGK EIKITPQSSI TEAELTGYGT VTMECSPRTG LDFNEMVLLQ MEXKAWLVHR
ConsDENV1E VTVHTGDQHQ VGNESTEHGT TATITPQAPT XEIQLTDYGA LTLDCSPRTG LDFNEMVLLT MKEKSWLVHK
YFV17DE    AQLHVGAKQE NWNTDIK--- TLKFDALSGS QEVEFIGYGK ATLECQVQTA VDFGNSYIAE METESWIVDR
          211
ConsDENV4E QWFLDLPLPW TAGADTSEVH WNYKERMVTF KVPHAKRQDV TVLGSQEGAM HSALAGATEV DSGDGNH---
ConsDENV3E QWFFDLPLPW TSGATTETPT WNRKELLVTF KNAHAKKQEV VVLGSQEGAM HTALTGATEI QNSGGTS---
ConsDENV2E QWFLDLPLPW LPGADTQGSN WIQKETLVTF KNPHAKKQDV VVLGSQEGAM HTALTGATEI QMSSGNL---
ConsDENV1E QWFLDLPLPW TSGASTSQET WNRQDLLVTF KTAHAKKQEV VVLGSQEGAM HTALTGATEI QTSGTTT---
YFV17DE    QWAQDLTLPW QSG---SGGV WREMHHLVEF EPPHAATIRV LALGNQEGSL KTALTGAMRV TKDTNDNNLY
          281 >DII/I            >DI/DIII
ConsDENV4E -MFAGHLKCK VRMEKLRIKG MSYTMCSGKF SIDKEMAETQ HGTTVVKVKY EGAGAPCKVP IEIRDVNKEK
ConsDENV3E -IFAGHLKCR LKMDKLELKG MSYAMCTNTF VLKKEVSETQ HGTILIKVEY KGEDXPCKIP FSTEDGQGKA
ConsDENV2E -LFTGHLKCR LRMDKLQLKG MSYSMCTGKF KXVKEIAETQ HGTIVIRVQY EGDGSPCKIP FEIMDLEKRH
ConsDENV1E -IFAGHLKCR LKMDKLTLKG MSYVMCTGSF KLEKEVAETQ HGTVLVQIKY EGTDAPCKIP FSTQDEKGVT
YFV17DE    KLHGGHVSCR VKLSALTLKG TSYKICTDKM FFVKNPTDTG HGTVVMQVKV -SKGAPCRIP VIVADDLTAA
          351
ConsDENV4E VV-GRVISST PLAENTNSVT NIELEPPFGD SYIVIGVGNS ALTLHWFRKG SSIGKMFEST YRGAKRMAIL
ConsDENV3E HN-GRLITAN PVVTKKEEPV NIEAEPPFGE SNIVIGIGDN ALKINWYKKG SSIGKMFEAT ARGARRMAIL
ConsDENV2E VL-GRLITVN PIVTEKDSPV NIEAEPPFGD SYIIIGVEPG QLKLNWFKKG SSIGQMFETT MRGAKRMAIL
ConsDENV1E QN-GRLITAN PIVTDKEKPV NIEAEPPFGE SYIVIGAGEK ALKLSWFKKG SSIGKMFEAT ARGARRMAIL
YFV17DE    INKGILVTVN PIASTNDDEV LIEVNPPFGD SYIIVGRGDS RLTYQWHKEG SSIGKLFTQT MKGVERLAVM
          421
ConsDENV4E GETAWDFGSV GGLFTSLGKA VHQVFGSVYT TMFGGVSWMI RILIGFLVLW IGTNSRNTSM AMTCIAVGGI
ConsDENV3E GDTAWDFGSV GGVLNSLGKM VHQIFGSAYT ALFSGVSWVM KIGIGVLLTW IGLNSKNTSM SFSCIAIGII
ConsDENV2E GDTAWDFGSL GGVFTSIGKA LHQVFGAIYG AAFSGVSWTM KILIGVIITW IGMNSRSTSL SVSLVLVGVV
ConsDENV1E GDTAWDFGSI GGVFTSVGKL VHQIFGTAYG VLFSGVSWTM KIGIGVLLTW LGLNSRSTSL SMTCIAVGLV
YFV17DE    GDTAWDFSSA GGFFTSVGKG IHTVFGSAFQ GLFGGLNWIT KVIMGAVLIW VGINTRNMTM SMSMILVGVI
491
ConsDENV4E TLFLGFTVQA
ConsDENV3E TLYLGAVVQA
ConsDENV2E TLYLGVMVQA
ConsDENV1E TLYLGVMVQA
YFV17DE    MMFLSLGVGA
```

Colored in grey background = Fusion Loop
Bolded and underlined Amino Acids= Within 5A of Fusion Loop
Italicized and Underlined Amino Acids = Within 14A of Fusion Loop (shown only for DENV2)
Bolded Amino Acids= Loss of binding position for 4.8A, D11Ckl, and 1.6D

4.8A	W101, L107, Q148
D11Ckl	W101, G157, K325
1.6D	W101, F108, Q156

FIG. 13

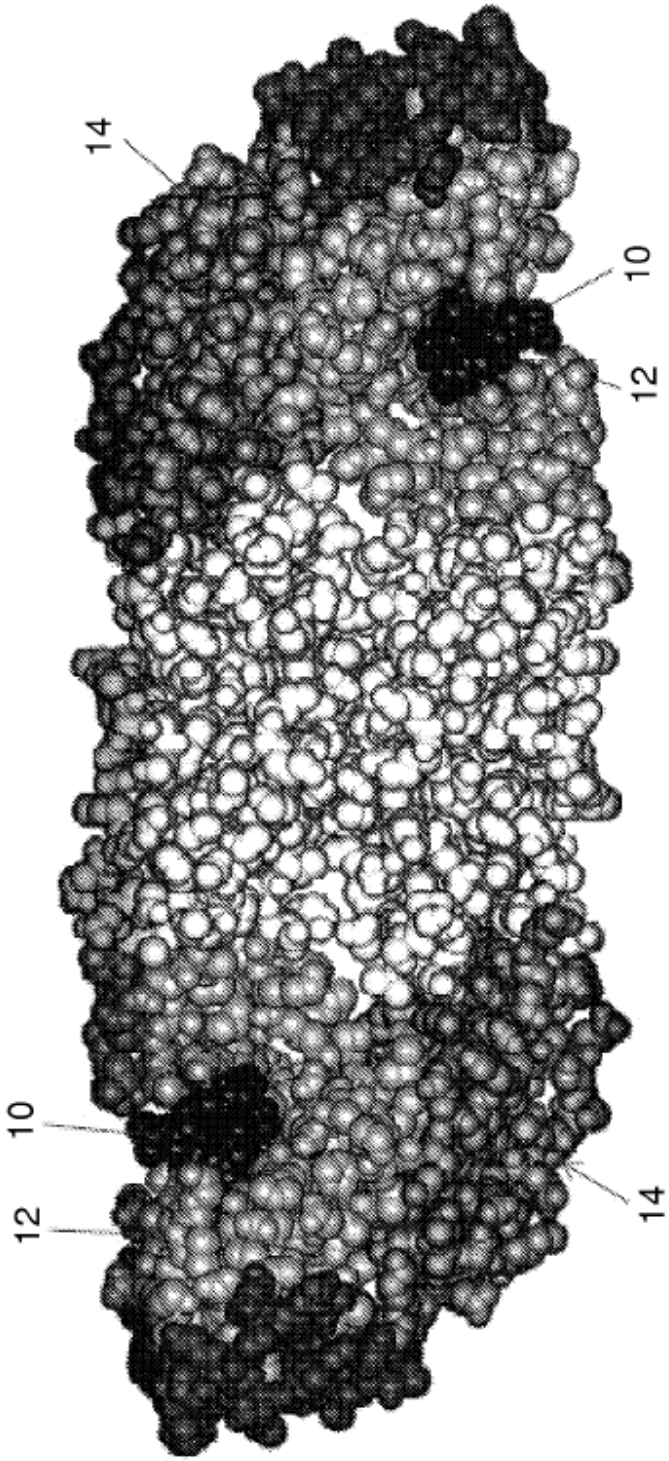


FIG. 14