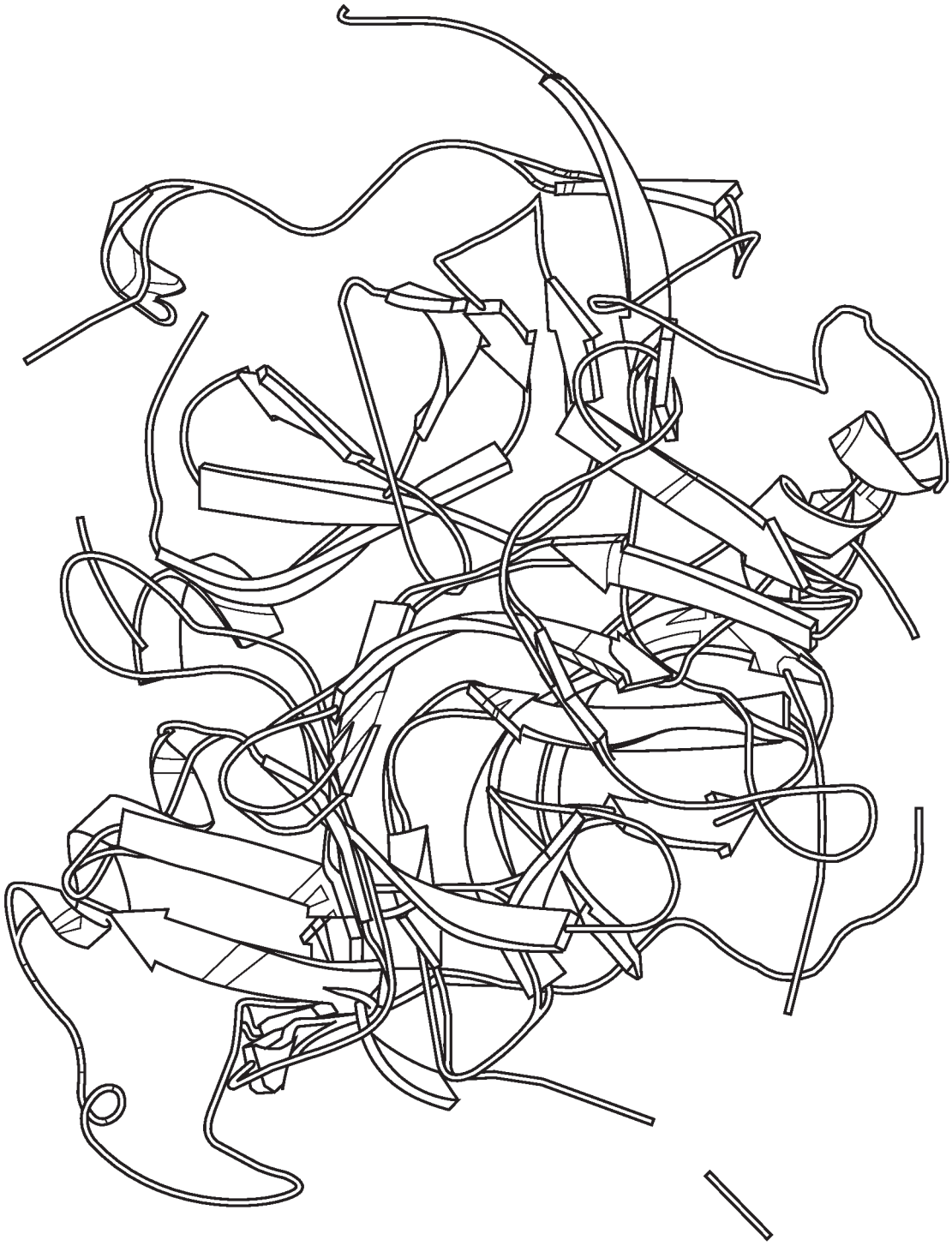


FIG. 1

```
M13-MKKLLFAIPLVVPFYSHSAETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATG 60
Fd- ------------------------------------------------------------ 60
F1- ------------------------------------------------------------ 60
Con MKKLLFAIPLVVPFYSHSAETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATG

M13-VVVCTGDETQCYGTWVPIGLAIPENEGGGSEGGGSEGGGSEGGGTKPPEYGDTPIPGYTY 120
Fd- ------------------------------------------------------------ 120
F1- ------------------------------------------------------------ 120
Con VVVCTGDETQCYGTWVPIGLAIPENEGGGSEGGGSEGGGSEGGGTKPPEYGDTPIPGYTY

M13-INPLDGTYPPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPV 180
Fd- ------------------------------------------------------------ 180
F1- ------------------------------------------------------------ 180
Con INPLDGTYPPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPV

M13-KTYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDPFVCEYQGQSSDLPQPPVNAGGGSG 240
Fd- ------------------------------------------------------------ 240
F1- ------------------------------------------------------------ 240
Con KTYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDPFVCEYQGQSSDLPQPPVNAGGGSG

M13-GGSGGGSEGGGSEGGGSEGGGSEGGGSGGGSGSGDFDYEKMANANKGAMTENADENALQS 300
Fd- ------------------------------------------------------------ 300
F1- ------------------------------------------------------------ 300
Con GGSGGGSEGGGSEGGGSEGGGSEGGGSGGGSGSGDFDYEKMANANKGAMTENADENALQS

M13-DAKGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDGDNSPLMNNFR 360
Fd- ------------------------------------------------------------ 360
F1- ------------------------------------------------------------ 360
Con DAKGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDGDNSPLMNNFR

M13-QYLPSLPQSVECRPFVFSAGKPYEFSIDCDKINLFRGVFAFLLYVATFMYVFSTFANILR 420
Fd- --------------Y--G-------------------------------------------- 420
F1- ----------------G-------------------------------------------- 420
Con QYLPSLPQSVECRPX--XAGKPYEFSIDCDKINLFRGVFAFLLYVATFMYVFSTFANILR

M13-NKES 424 (SEQ ID NO:1)
Fd- ---- 424 (SEQ ID NO:2)
F1- ---- 424 (SEQ ID NO:3)
Con NKES     (SEQ ID NO:4)
```

FIG. 2A

```
I2-2MKRKIIAISLFLYIPLSNADNWESITKSYYTGFAMSKTVESKDQDGKTVRKEVITQADLT 60
Ike ---------------------------------I--------K---P------------ 60
Con MKRKIIAISLFLYIPLSNADNWESITKSYYTGFAXSKTVESKDXDGKXVRKEVITQADLT

I2-2TACNDAKASAQDVFNQMKLTFSGIWPDSQFRLVTGDTCVYNGSPSEKTESWSIRAQVEGD 120
Ike -----------N----I---L--T-N------------------G--------------- 120
Con TACNDAKASAQXVFNQXKLTXSGXWXDSQFRLVTGDTCVYNGSPXEKTESWSIRAQVEGD

I2-2MQRSVPDEEPSEQTPEEICEAKPPIDGVFNNVSKGDEGGFYINYNGCEYEATGVTVCQND 180
Ike I-------------------------------F-------------------------- 180
Con XQRSVPDEEPSEQTPEEICEAKPPIDGVFNNVXKGDEGGFYINYNGCEYEATGVTVCQND

I2-2GTVCASSAWKPTGYVPESGESSSSPVKDGDTGGTGEGGSDTGGDTGGGDTGGGSTGGDTG 240
Ike ----S---------------P----L---------------------------------- 240
Con GTVCXSSAWKPTGYVPESGEXSSSPXKDGDTGGTGEGGSDTGGDTGGGDTGGGSTGGDTG

I2-2GSTGGGSTGGGSTGGSTGKSLTKEDVTAAIHDASPSIGDAVKDSLTEDNDQNDNQKKADE 300
Ike --S----S----------------------V------------------Y-------- 300
Con GSXGGGSXGGGSXGGSTGKSLTKEDVTAAIHXASPSIGDAVKDSLTEDNDQXDNQKKADE

I2-2QSAKASASVSDAISDGMRGVGNFVDDLGGESSQYGIGNSEMDLSVSLAKGQLGIDLEGHG 360
Ike -------------------------F--------T------------------R---- 360
Con QSAKASASVSDAISDGMRGVGNFVDDXGGESSQYGXGNSEMDLSVSLAKGQLGIDXEGHG

I2-2SAWESFLNDGALRPSIPSGHGCTDFVMFQGSVYQLDIGCDKLGDIKSVLSWVMYCLTFWY 420
Ike ----------------T-----N---Y------IE------NDIKSVLSWVMYCLTFWY 420
Con SAWESFLNDGALRPSIPXGHGCTXFVMXQGSVYQXXIGCDKLXDIKSVLSWVMYCLTFWY

I2-2VFQSATSLLRKGEQ 434  (SEQ ID NO:5)
Ike ----V--------- 434  (SEQ ID NO:6)
Con VFQSXTSLLRKGEQ      (SEQ ID NO:7)
```

FIG. 2B

```
MKKIIIALFFAPFFTHATTDAECLSKPAFDGTLSNVWKEGDSRYANFENCIYELSGIGIG  60
YDNDTSCNGHWTPVRAADGSGNGGDDNSSGGGSNGDSGNNSTPDTVTPGQTVNLPSDLST 120
LSIPANVVKSDSIGSQFSLYTNASCTMCSGYYLSNNADSIAIANITETVKADYNQPDMWF 180
EQTDSDGNHVKILQNSYKAVSYNVESKQSDVNNPTYINYSYSVNVKQVSYDTSNVCIMNW 240
ETFQNKCDASRAVLITDTVTPSYSRNITIQSNINYQGSNGSGGSGGSGGSGNDGGGTGNN 300
GNGTGDFDYVKMANANKDALTESFDLSALQADTGASLDGSVQGTLDSLSGFSDSIGGLVG 360
NGSAISGEFAGSSAAMNAIGEGDKSPLLDSLSFLKDGLFPALPEFKQCTPFVFAPGKEYE 420
FIIECKYIDMFKGIFAFILYFWTFVTVYDSFSGILRKGRG  (SEQ ID NO:8)      460
```

FIG. 2C

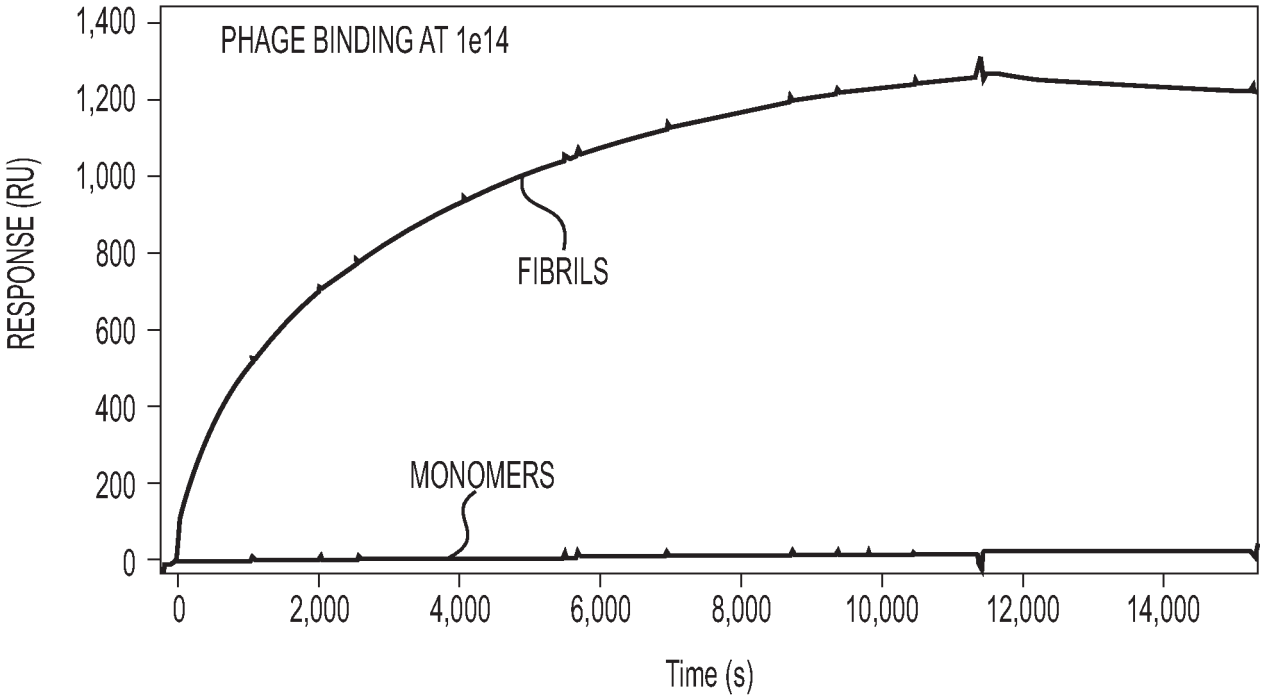


FIG. 3A

PARAMETER	VALUE
K_a	2572 (6)
K_d	9.234E-6
K_D	3.589 (8) nM

FIG. 3B

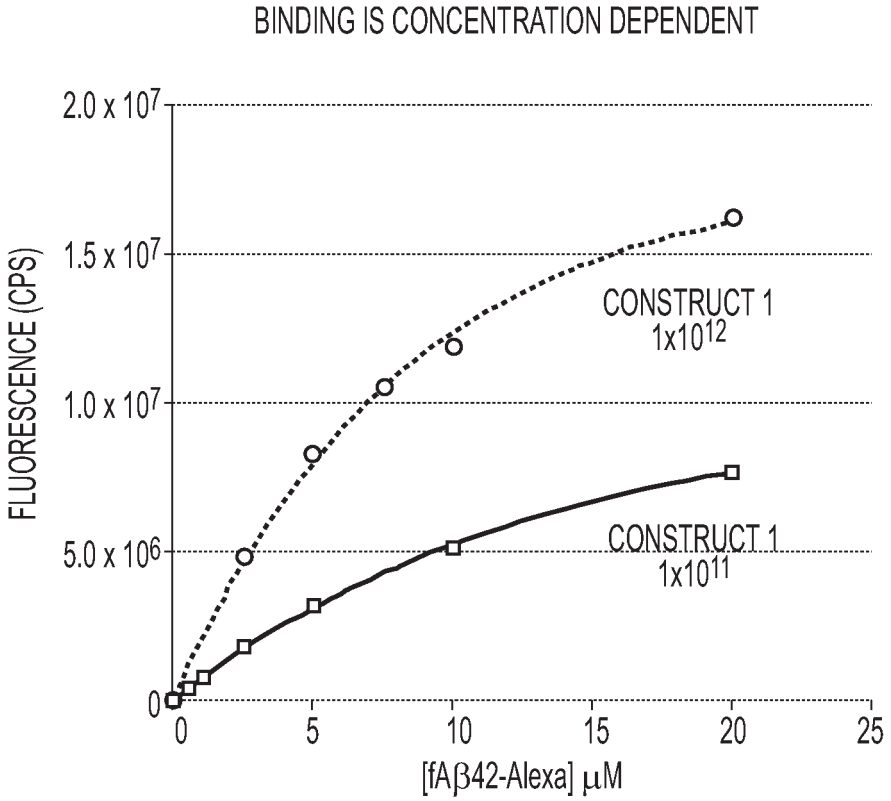

BINDING IS CONCENTRATION DEPENDENT
2.0 x 10^7
1.5 x 10^7
1.0 x 10^7
5.0 x 10^6
0
FLUORESCENCE (CPS)
CONSTRUCT 1
1x10^12
CONSTRUCT 1
1x10^11
0
5
10
15
20
25
[fAβ42-Alexa] μM

FIG. 4A

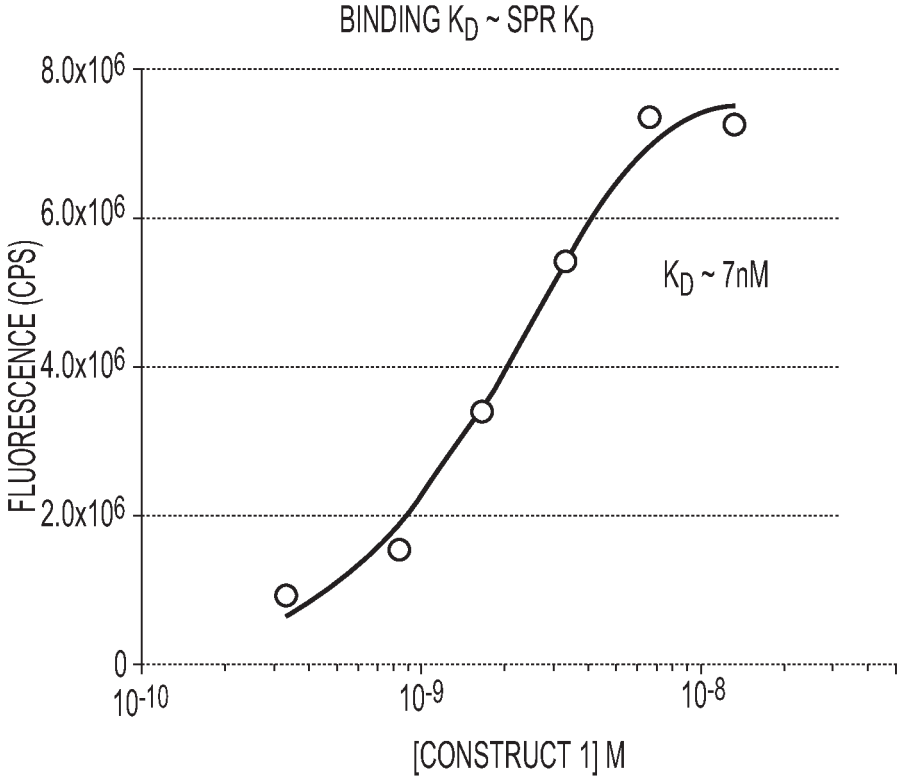

BINDING K_D ~ SPR K_D
8.0x10^6
6.0x10^6
4.0x10^6
2.0x10^6
0
FLUORESCENCE (CPS)
K_D ~ 7nM
10^-10
10^-9
10^-8
[CONSTRUCT 1] M

FIG. 4B

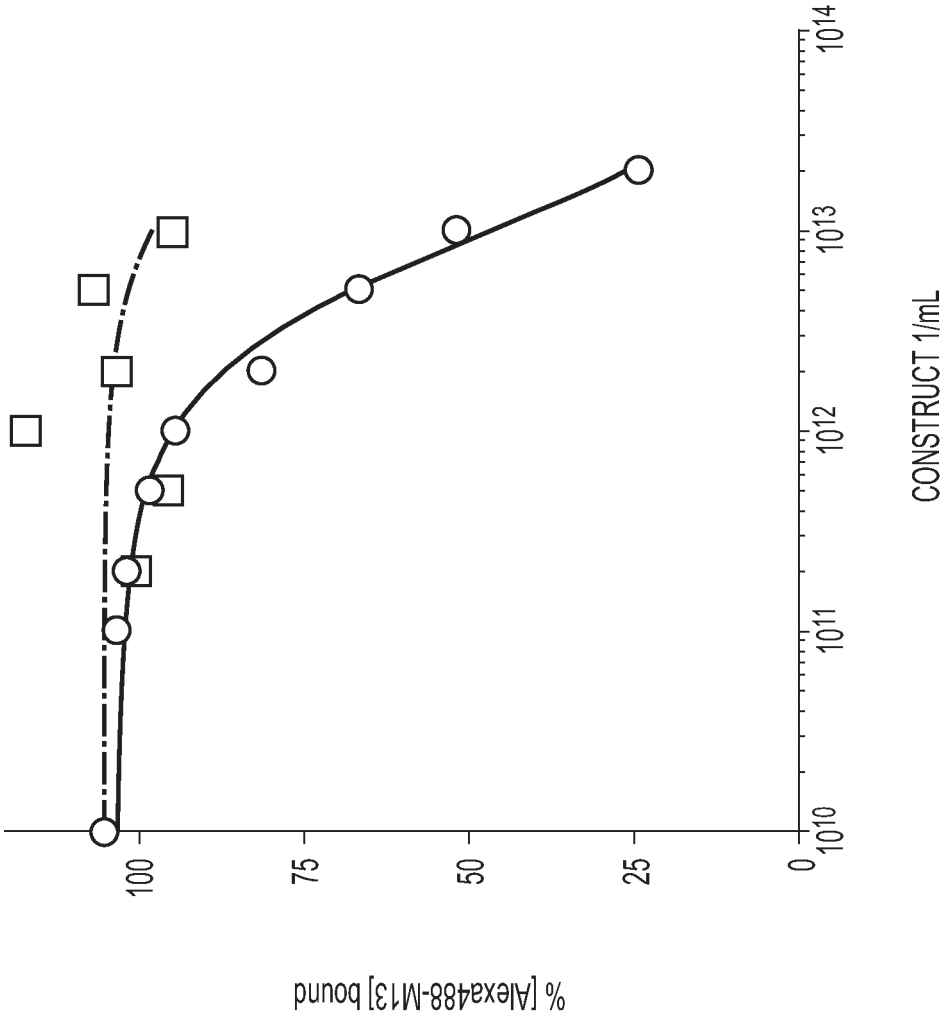

% [Alexa488-M13] bound
100
75
50
25
0
10^{10}
10^{11}
10^{12}
10^{13}
10^{14}
CONSTRUCT 1/mL

FIG. 5

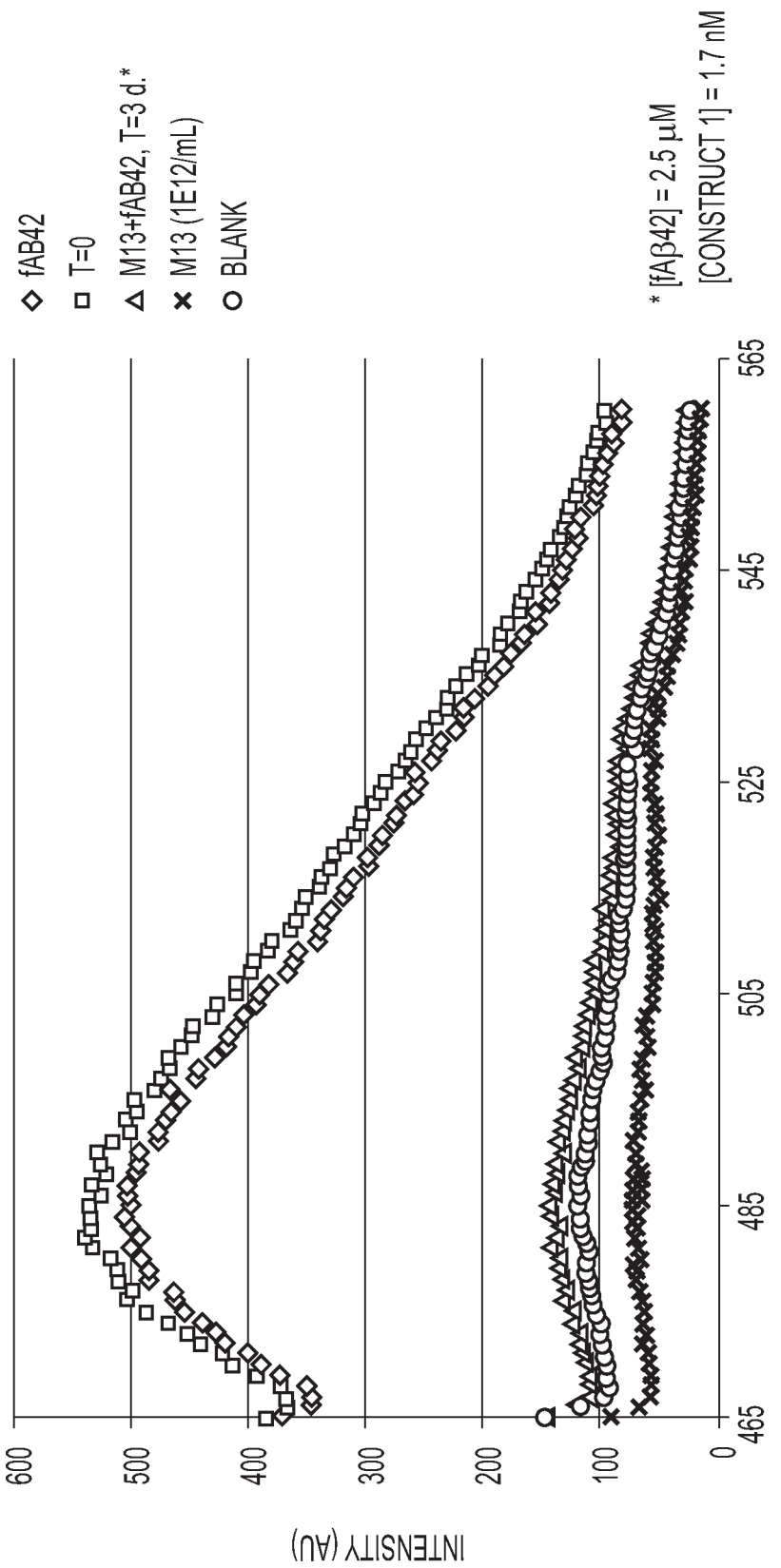

fAB42
T=0
M13+fAB42, T=3 d.*
M13 (1E12/mL)
BLANK
* [fAβ42] = 2.5 µM
[CONSTRUCT 1] = 1.7 nM
INTENSITY (AU)
600
500
400
300
200
100
0
465
485
505
525
545
565
WAVELENGTH (nm)

FIG. 6

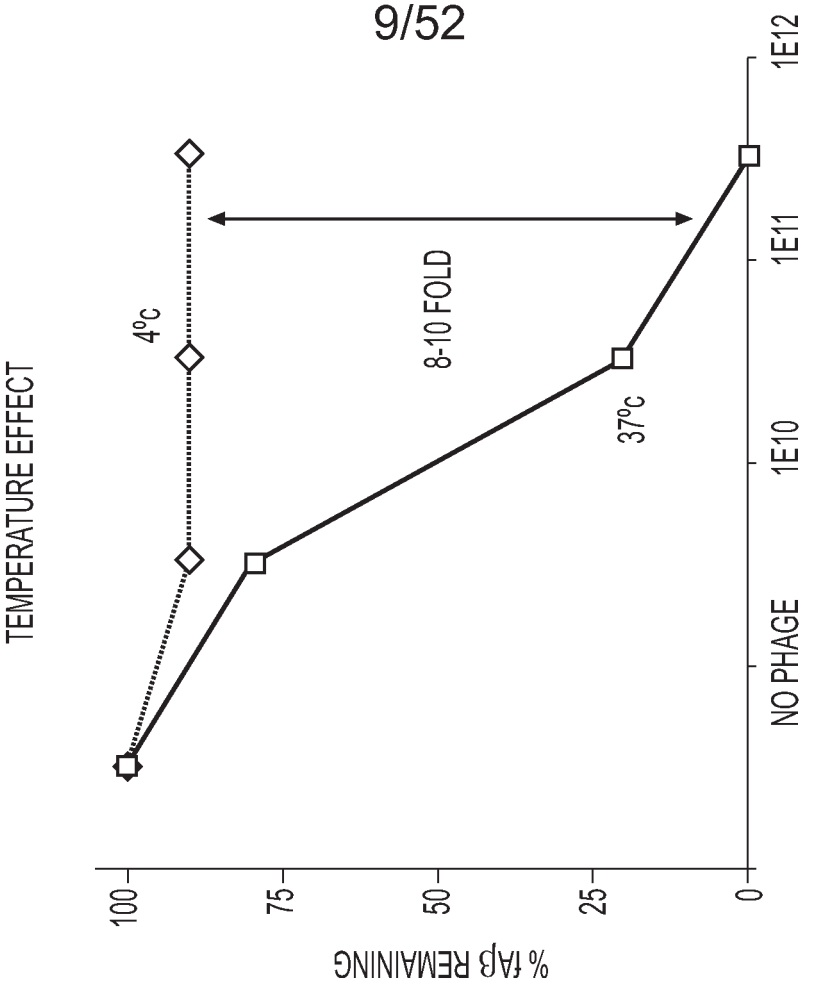

TEMPERATURE EFFECT
4°c
8-10 FOLD
37°c
% fAβ REMAINING
100
75
50
25
0
NO PHAGE
1E10
1E11
1E12

FIG. 7B

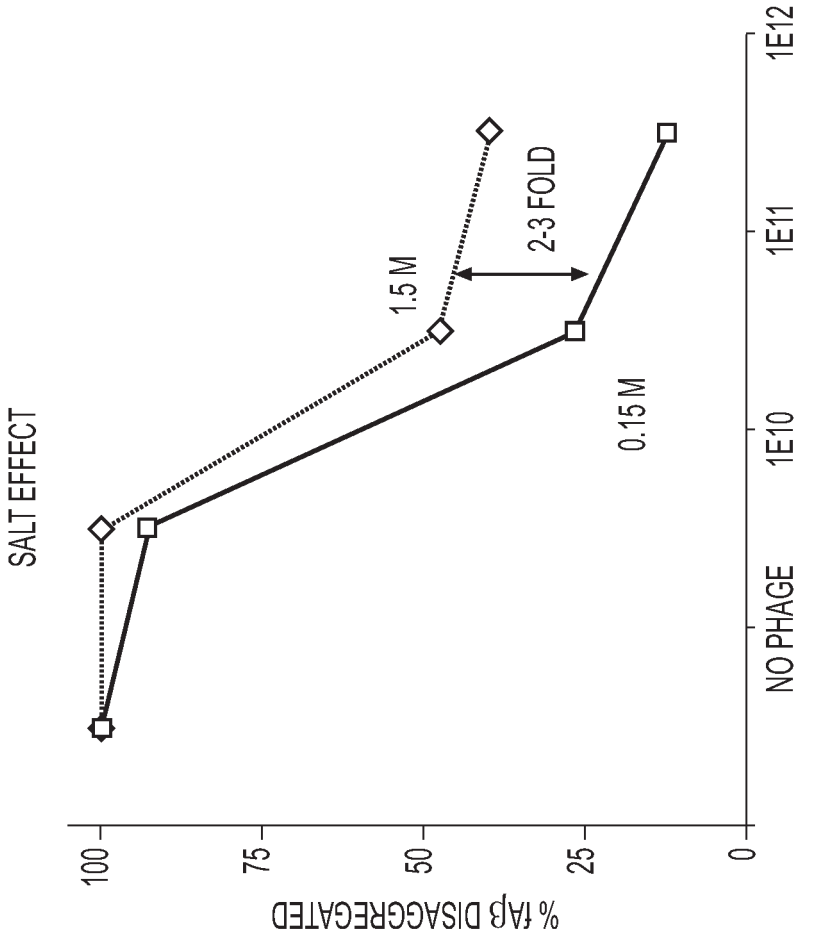

SALT EFFECT
1.5 M
2-3 FOLD
0.15 M
% fAβ DISAGGREGATED
100
75
50
25
0
NO PHAGE
1E10
1E11
1E12

FIG. 7A

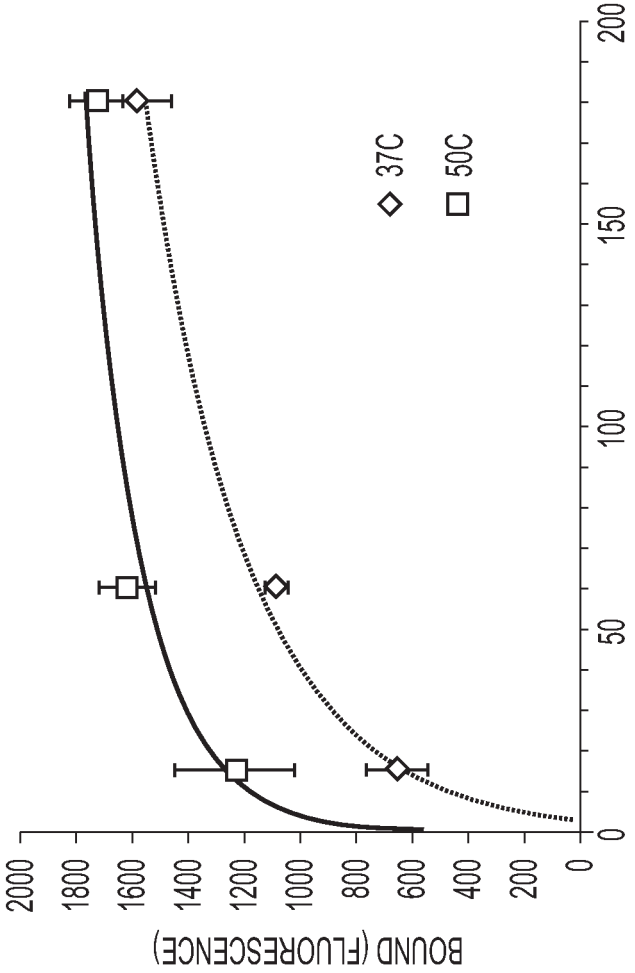

BOUND (FLUORESCENCE)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
0
50
100
150
200
BINDING INCUBATION TIME (min)
37C
50C

FIG. 8B

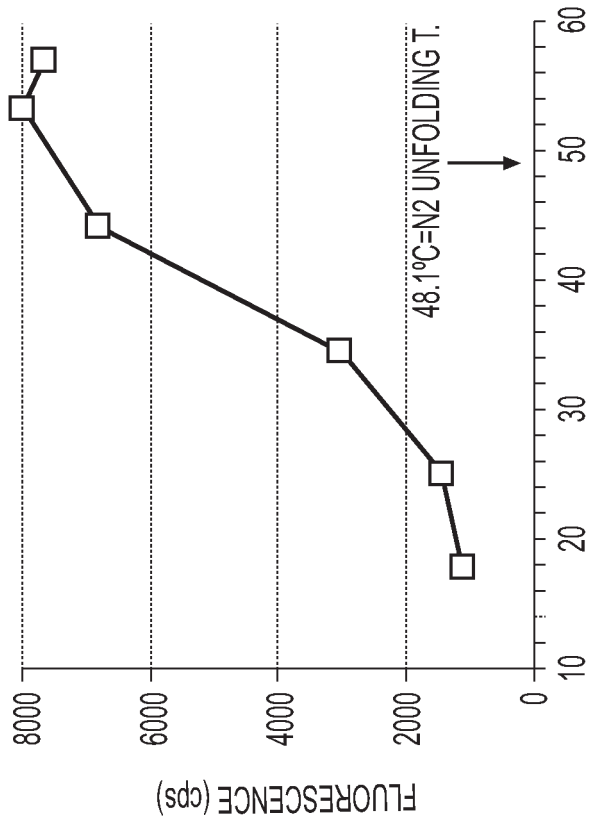

FLUORESCENCE (cps)
8000
6000
4000
2000
0
10
20
30
40
50
60
INCUBATION TEMP (°C)
48.1°C=N2 UNFOLDING T.

FIG. 8A

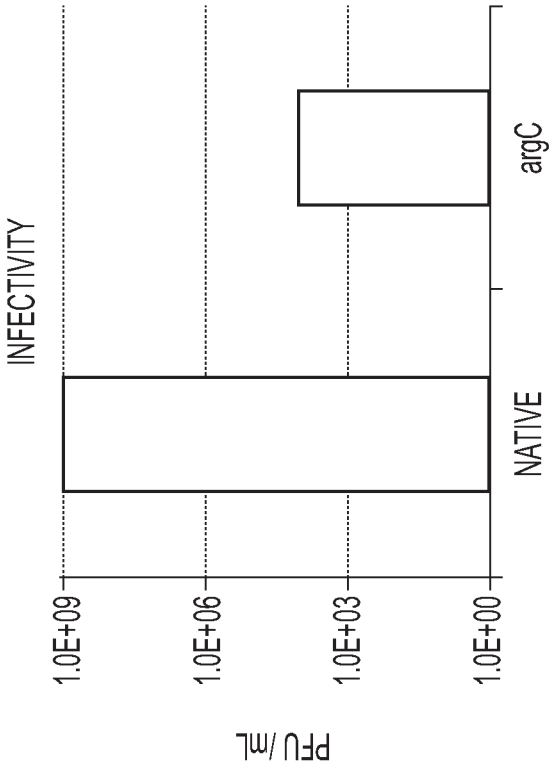


FIG. 9B

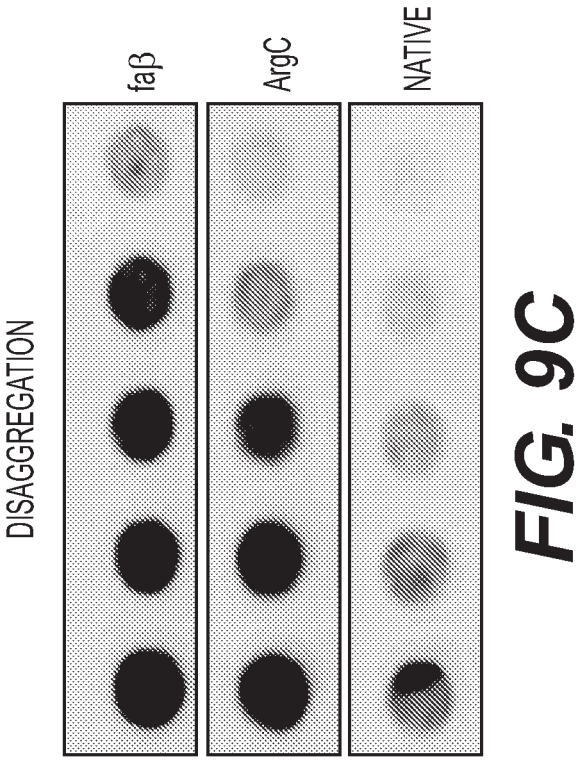


FIG. 9C

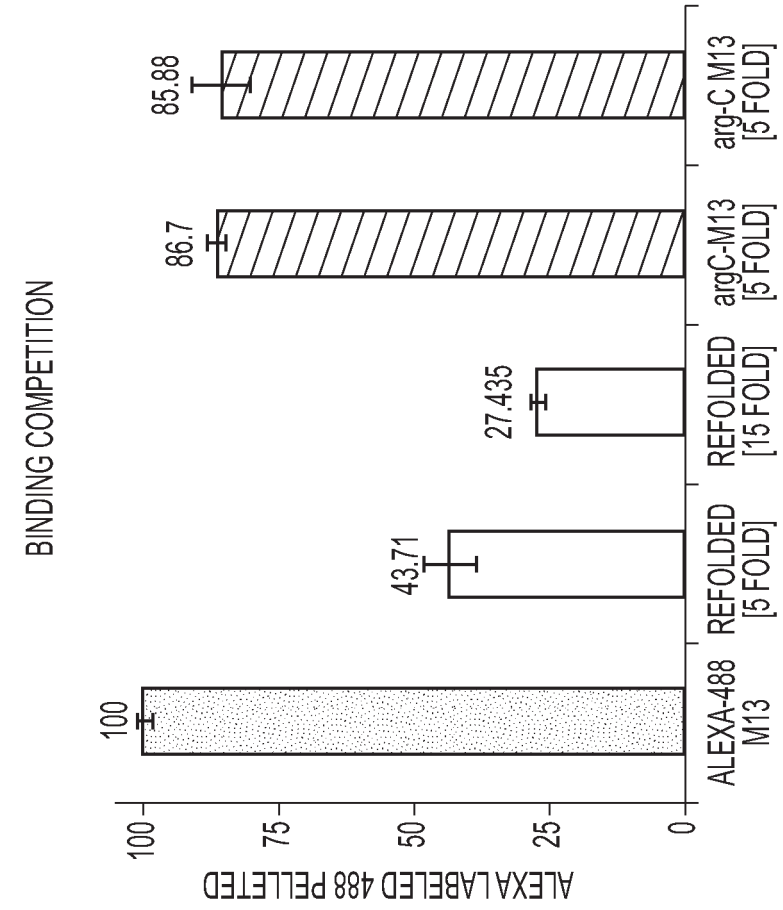


FIG. 9A

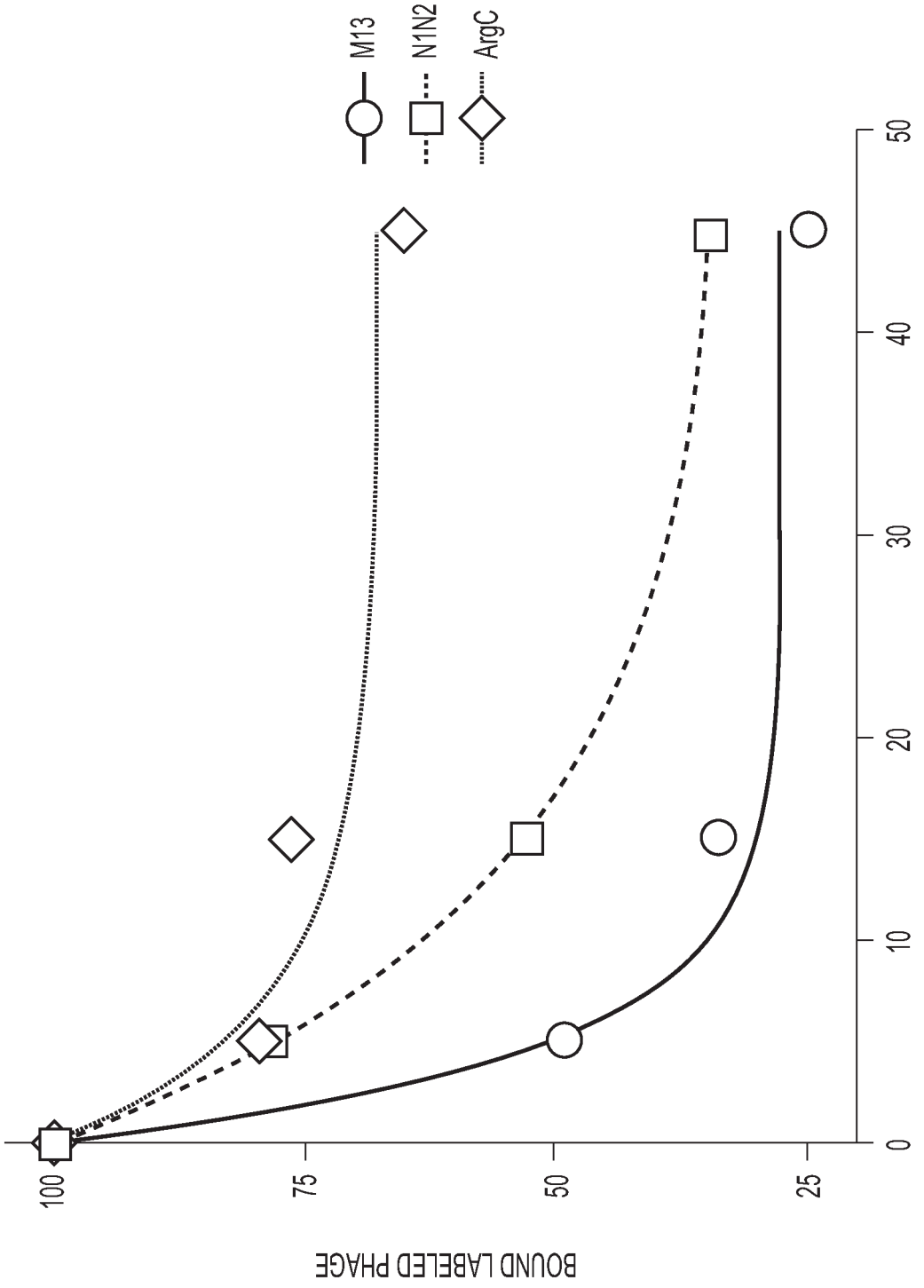

M13
N1N2
ArgC
BOUND LABELED PHAGE
100
75
50
25
0
10
20
30
40
50
COMPETITOR [MOLAR EXCESS]

FIG. 10A

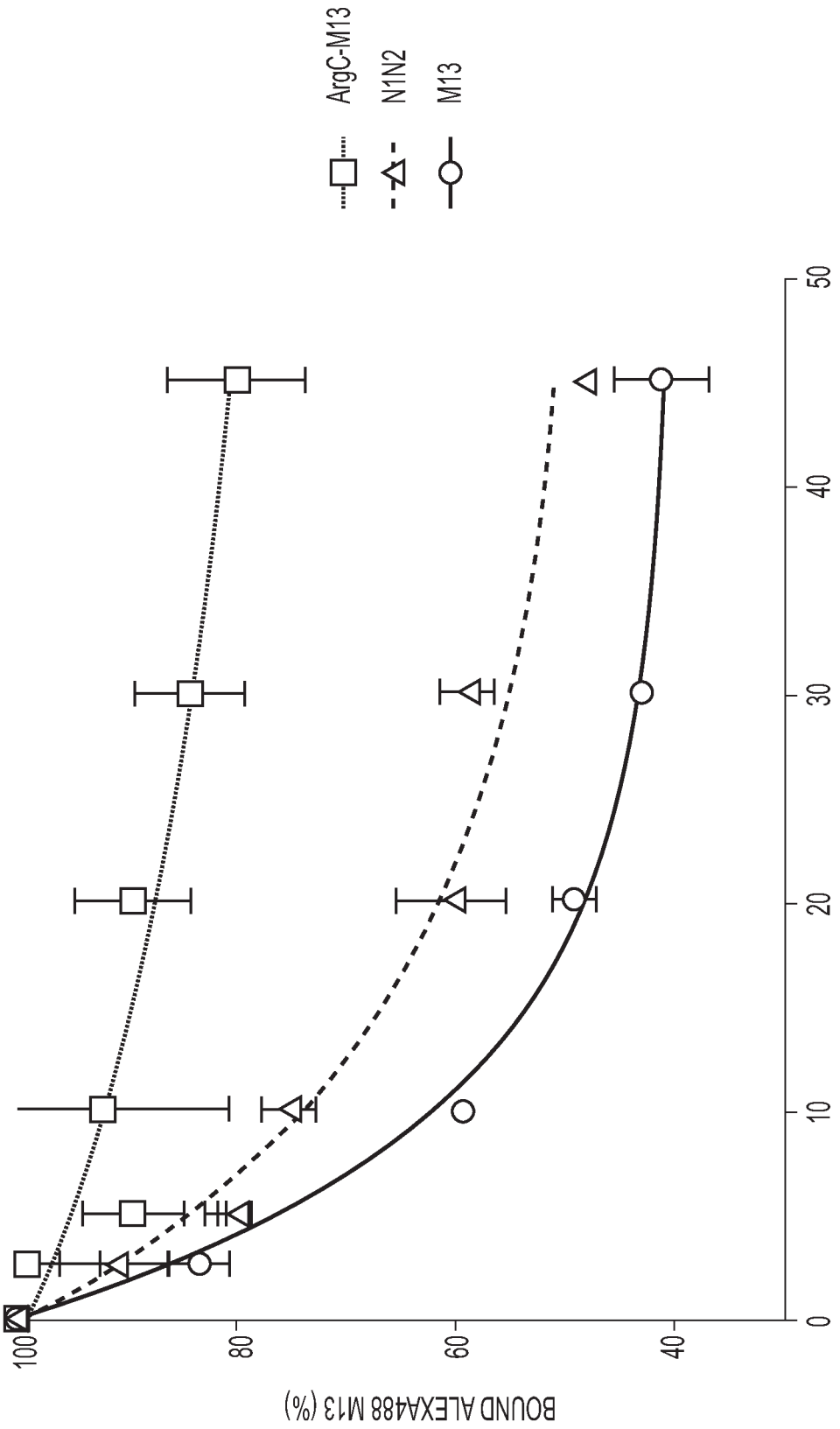

ArgC-M13
N1N2
M13
BOUND ALEXA488 M13 (%)
100
80
60
40
0
10
20
30
40
50
MOLAR EXCESS OF COMPETITOR

FIG. 10B

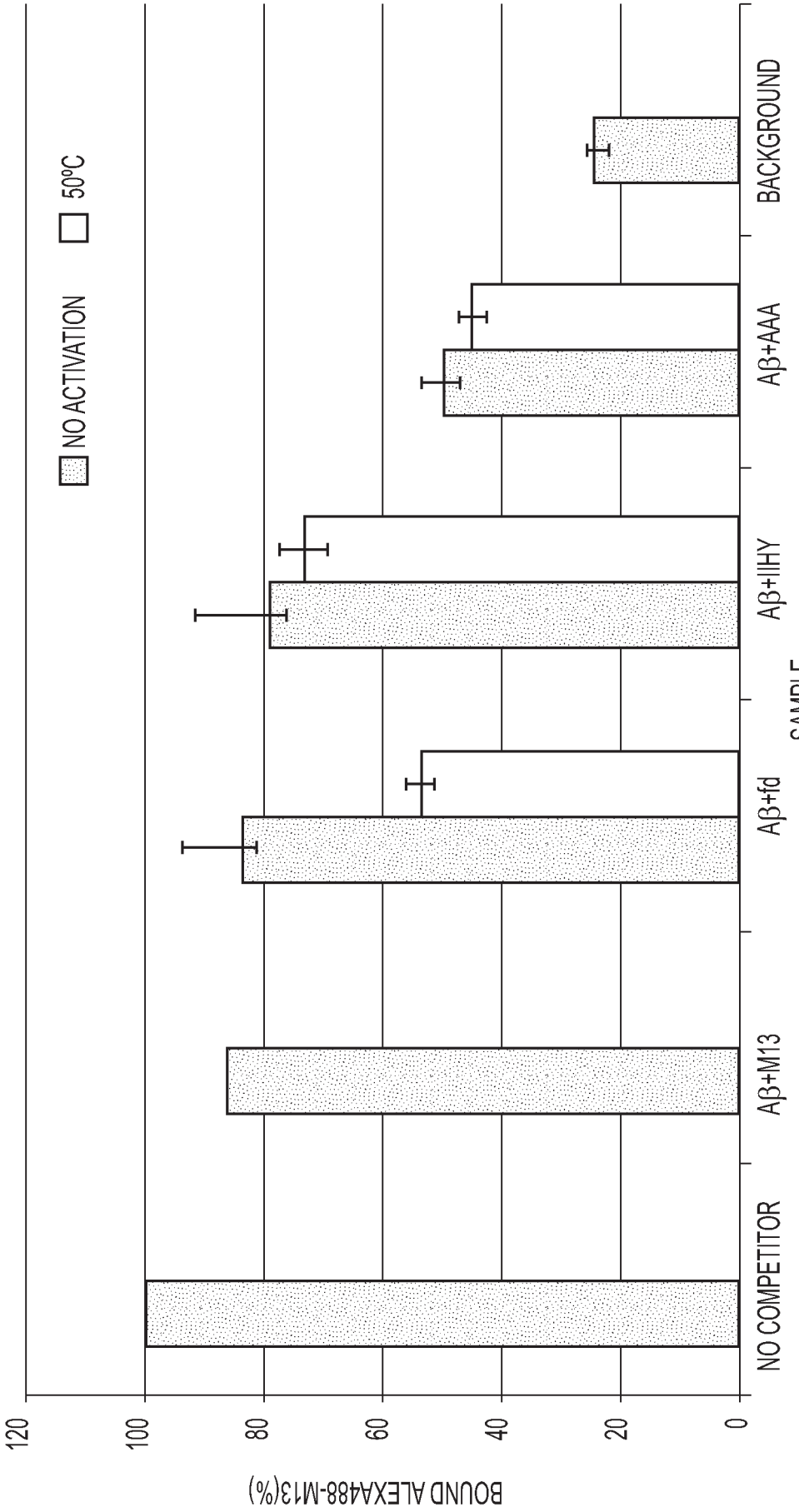
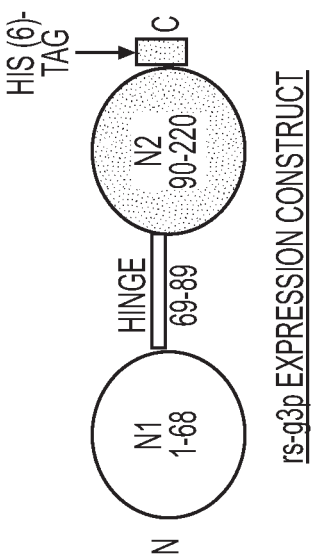

NO ACTIVATION
50°C
BOUND ALEXA488-M13(%)
120
100
80
60
40
20
0
NO COMPETITOR
Aβ+M13
Aβ+fd
Aβ+IIHY
Aβ+AAA
BACKGROUND
SAMPLE

FIG. 11



rs-g3p EXPRESSION CONSTRUCT

FIG. 12A

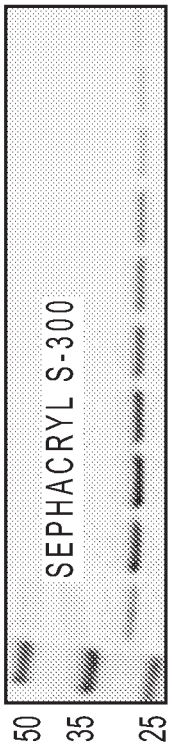


FIG. 12C

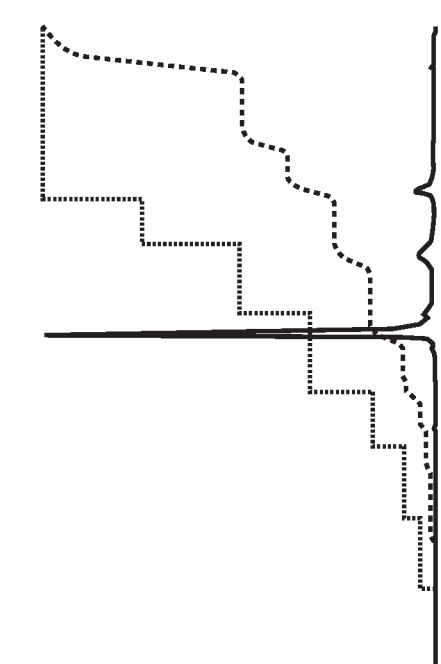


FIG. 12B

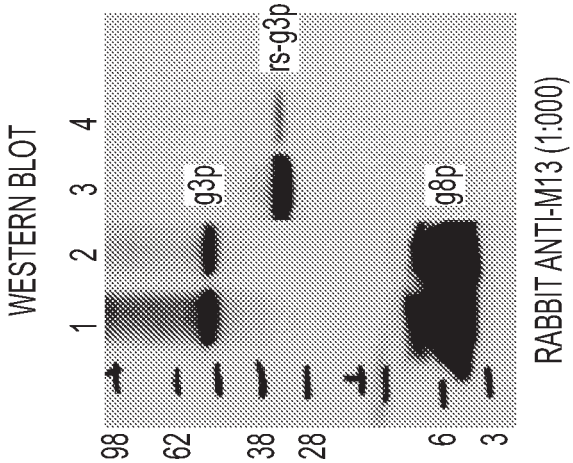


FIG. 12D

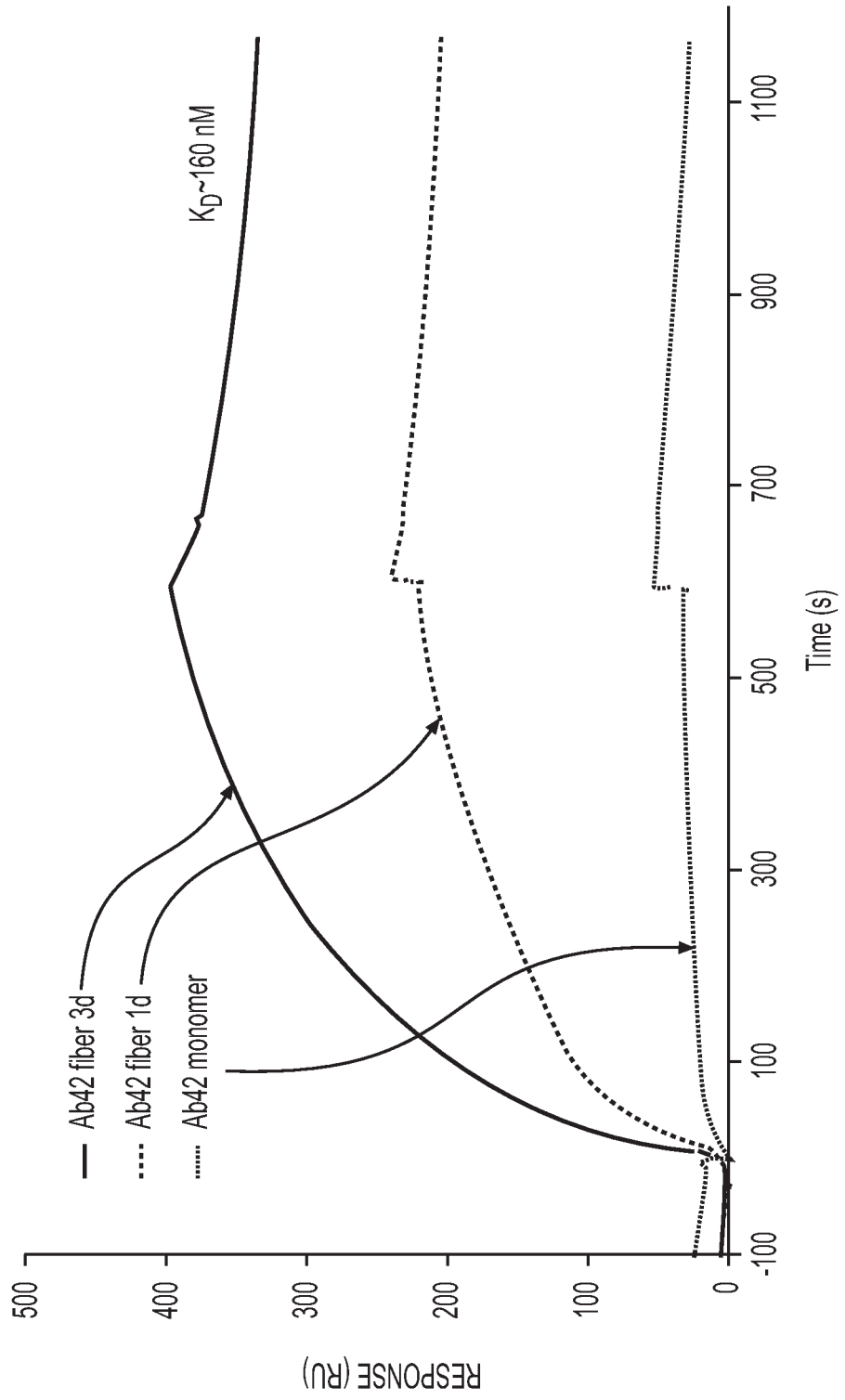

RESPONSE (RU)
500
400
300
200
100
0
-100
100
300
500
700
900
1100
Time (s)
Ab42 fiber 3d
Ab42 fiber 1d
Ab42 monomer
K_D~160 nM

FIG. 13

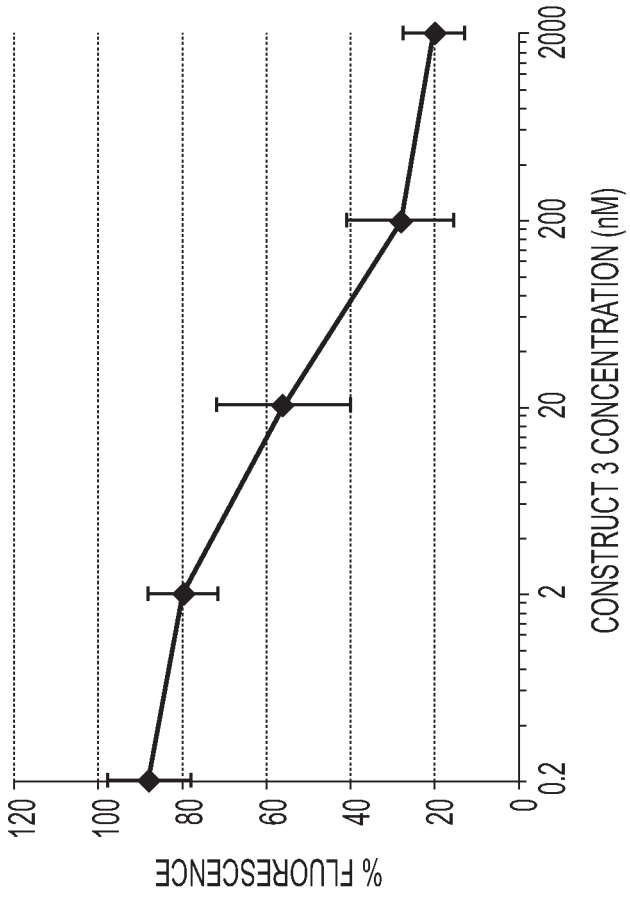


FIG. 14B

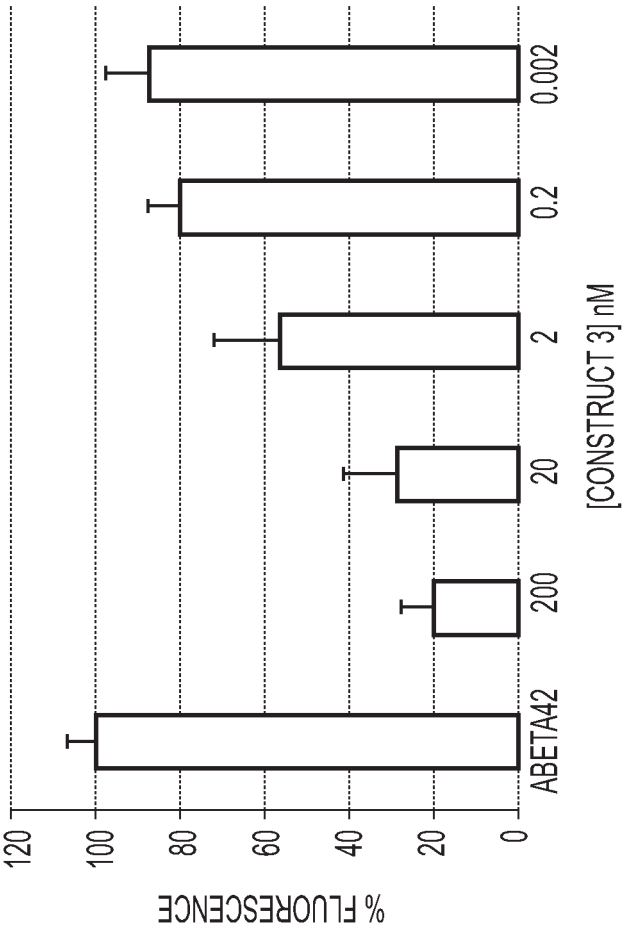


FIG. 14A

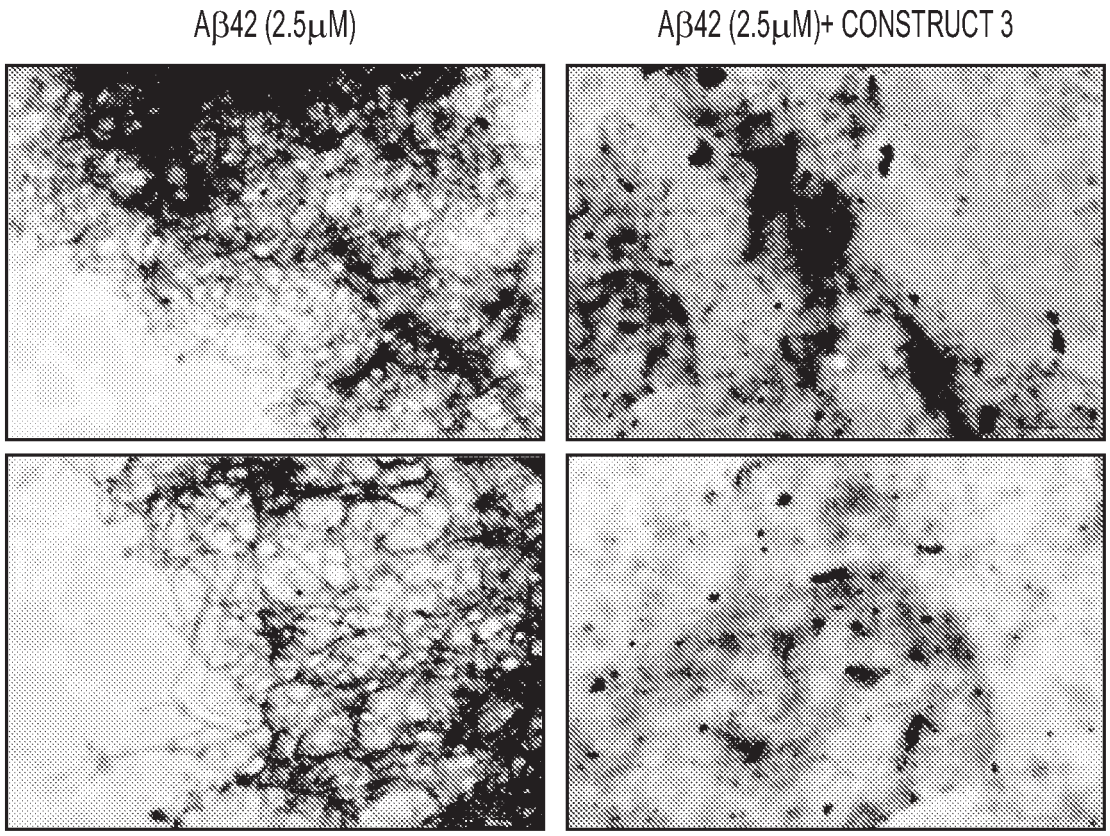


FIG. 15A

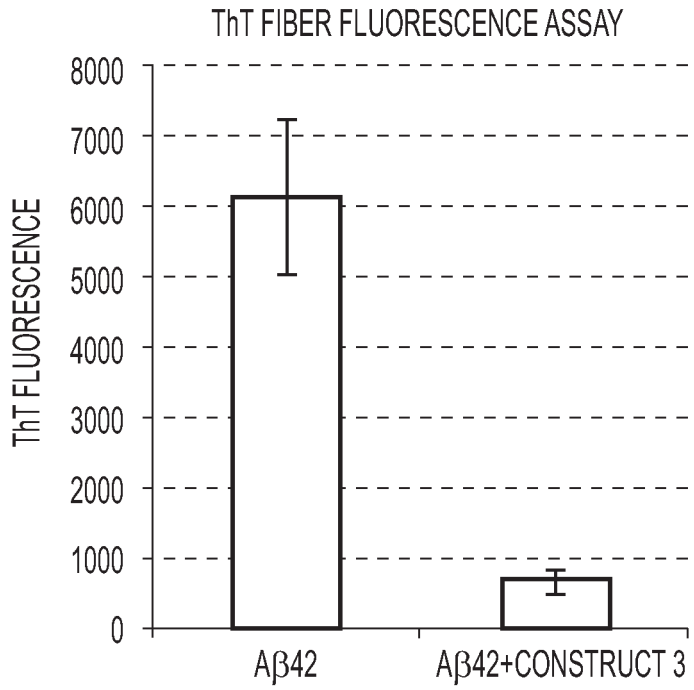


FIG. 15B

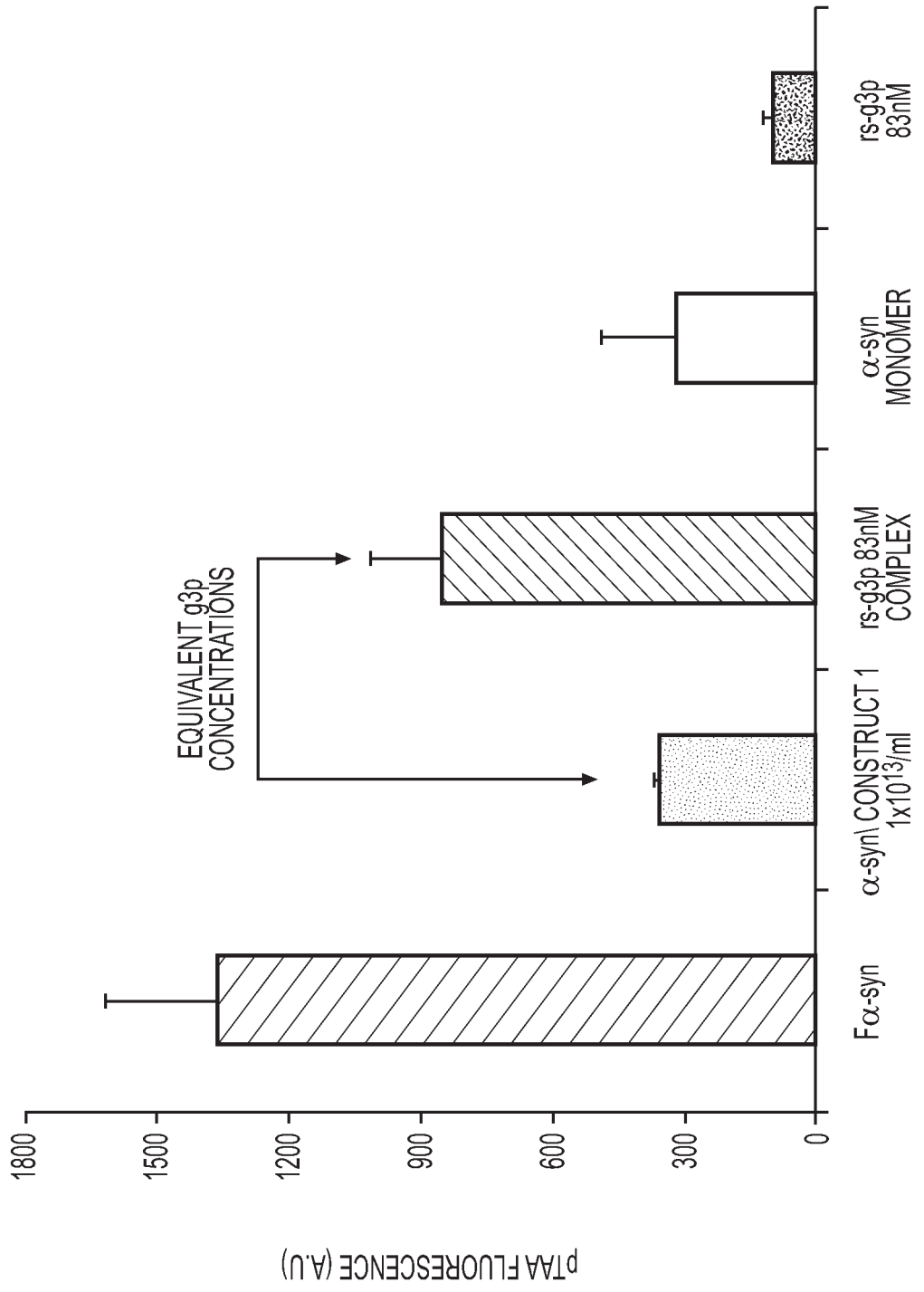

pTAA FLUORESCENCE (A.U)
1800
1500
1200
900
600
300
0
Fα-syn
α-syn\ CONSTRUCT 1
1x10^13/ml
rs-g3p 83nM
COMPLEX
α-syn
MONOMER
rs-g3p
83nM
EQUIVALENT g3p
CONCENTRATIONS

FIG. 16

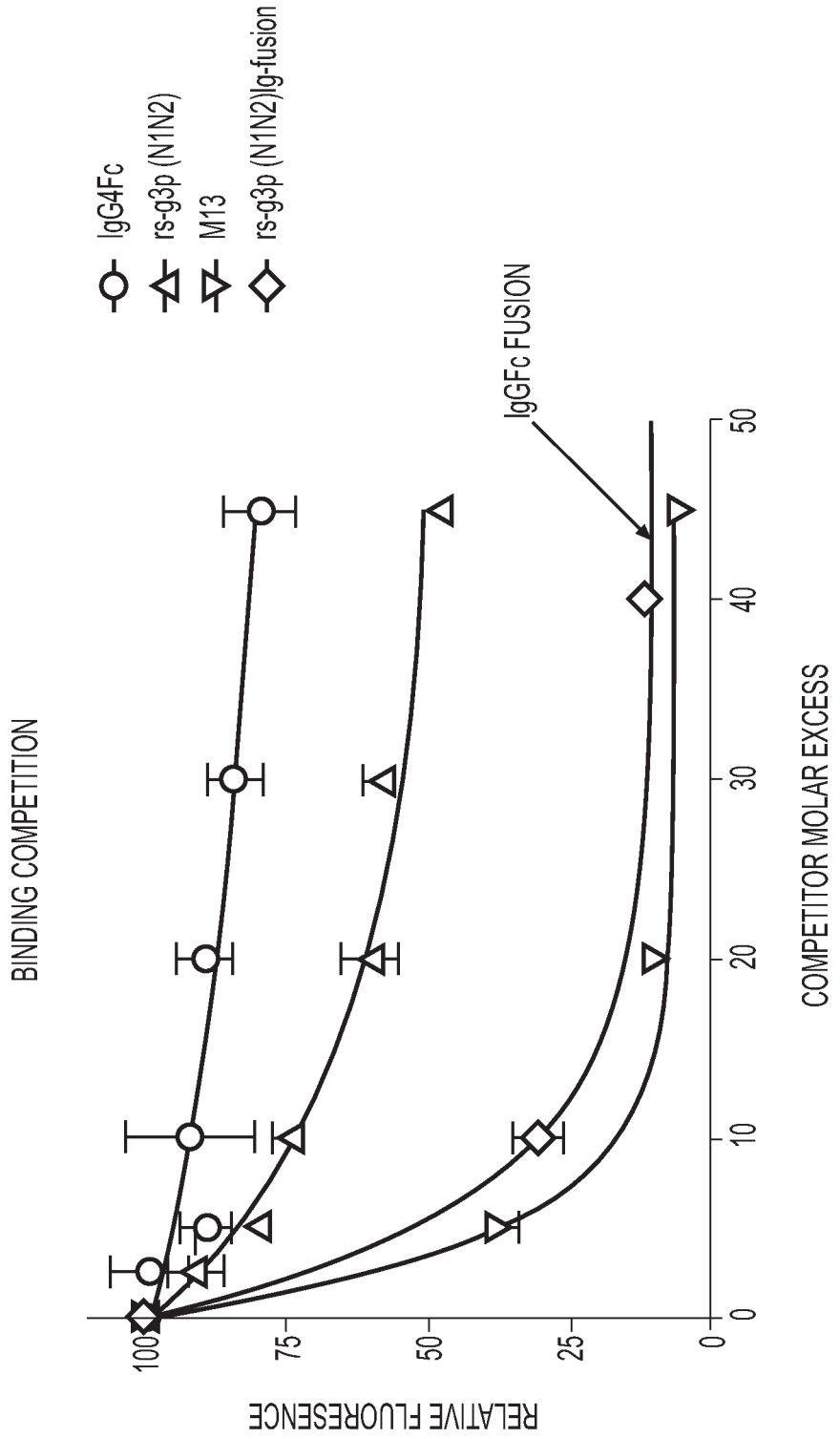

BINDING COMPETITION
RELATIVE FLUORESCENCE
100
75
50
25
0
0
10
20
30
40
50
COMPETITOR MOLAR EXCESS
IgGFc FUSION
IgG4Fc
rs-g3p (N1N2)
M13
rs-g3p (N1N2)Ig-fusion

FIG. 17

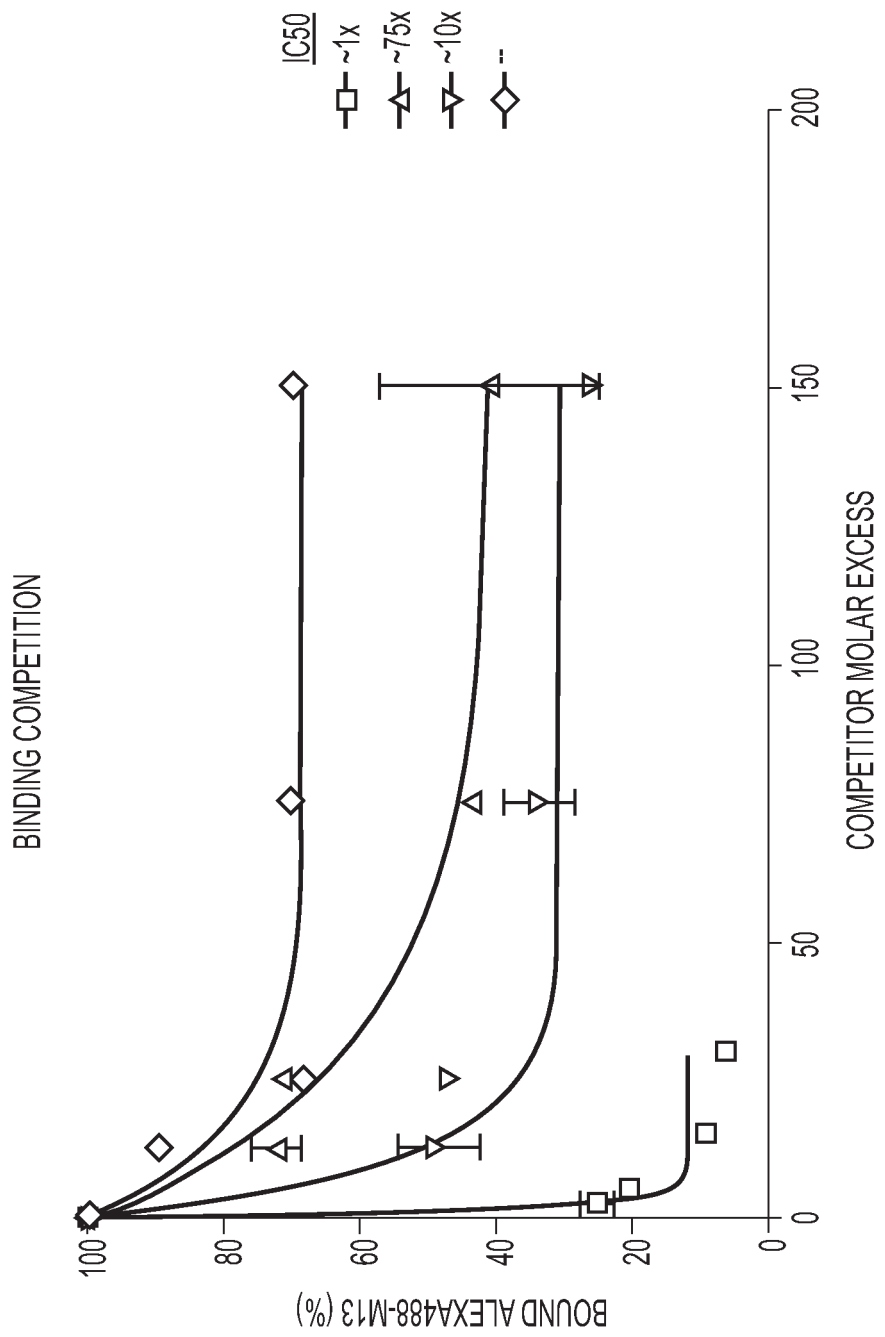

BINDING COMPETITION
BOUND ALEXA488-M13 (%)
100
80
60
40
20
0
0
50
100
150
200
COMPETITOR MOLAR EXCESS
IC50
~1x
~75x
~10x
--

FIG. 18

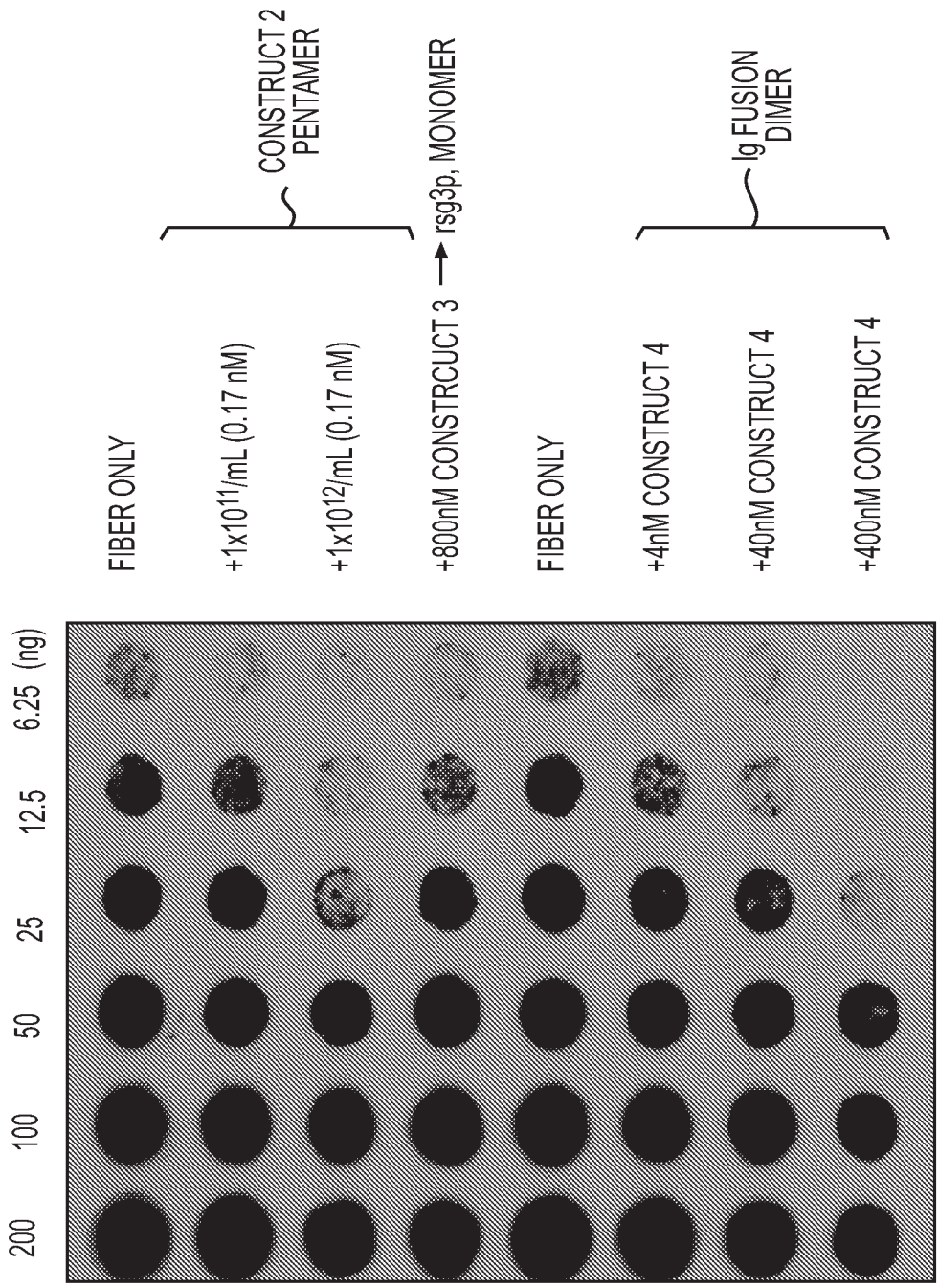

FIBER ONLY
+1x10^11/mL (0.17 nM)
+1x10^12/mL (0.17 nM)
+800nM CONSTRCUCT 3
FIBER ONLY
+4nM CONSTRUCT 4
+40nM CONSTRUCT 4
+400nM CONSTRUCT 4
CONSTRUCT 2 PENTAMER
rsg3p, MONOMER
Ig FUSION DIMER
200
100
50
25
12.5
6.25 (ng)

FIG. 19

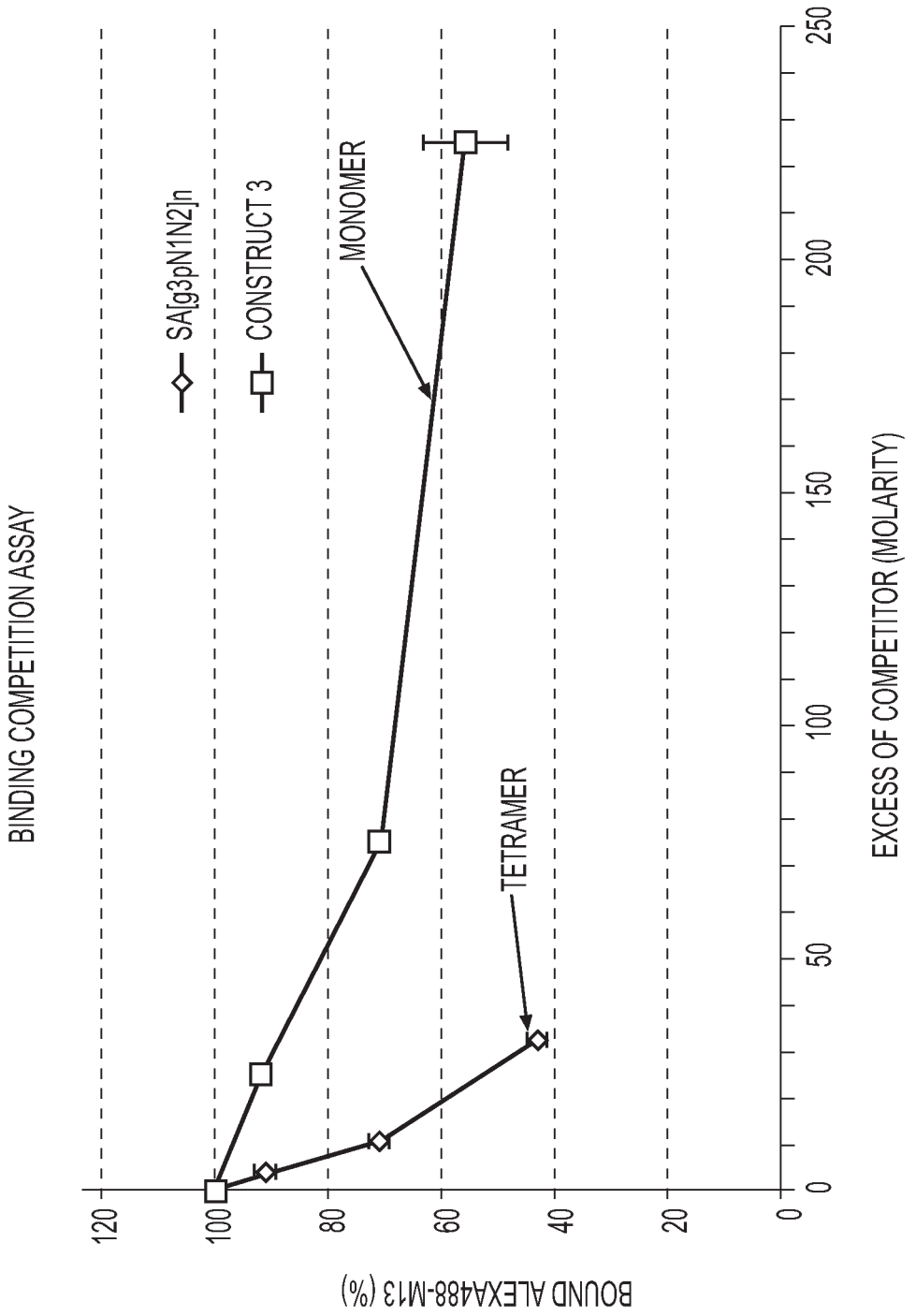

BINDING COMPETITION ASSAY
SA[g3pN1N2]n
CONSTRUCT 3
MONOMER
TETRAMER
BOUND ALEXA488-M13 (%)
120
100
80
60
40
20
0
0
50
100
150
200
250
EXCESS OF COMPETITOR (MOLARITY)

FIG. 20

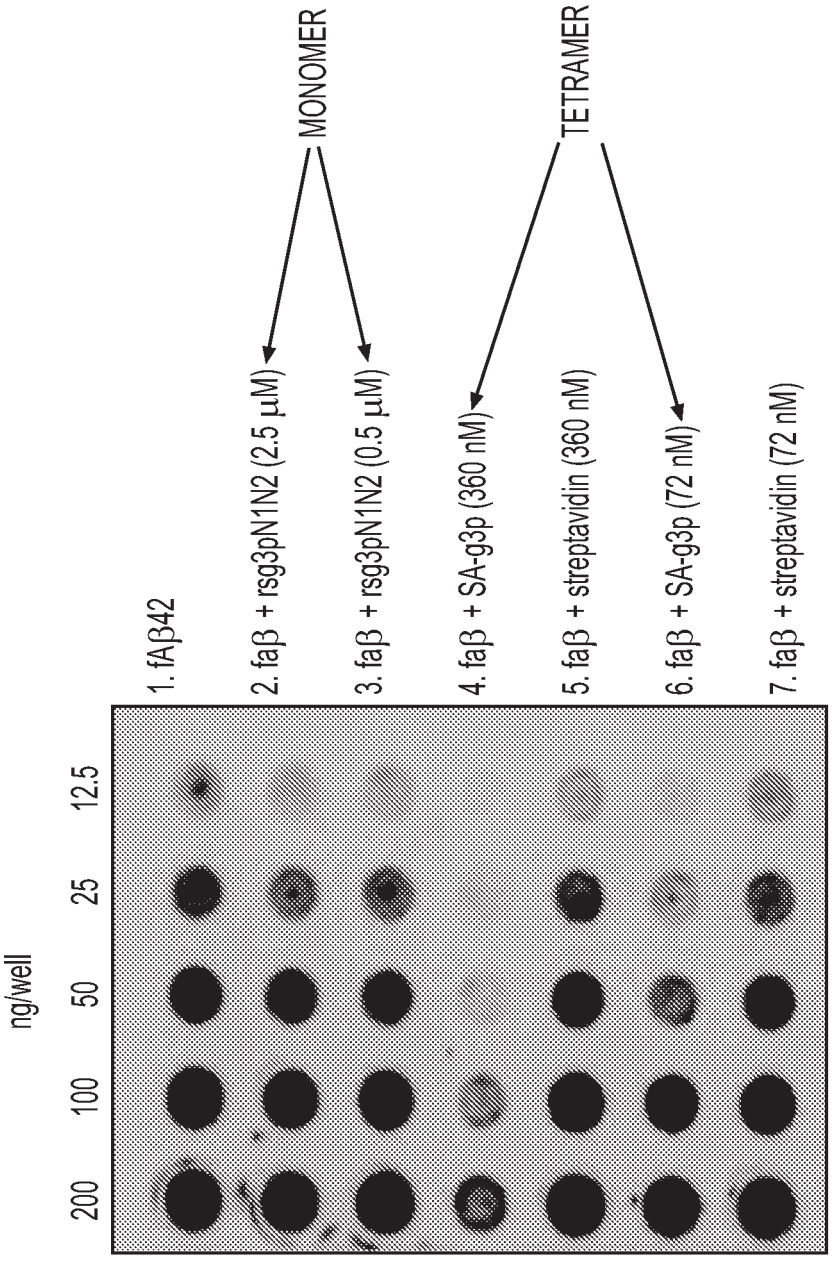

MONOMER
TETRAMER
1. fAβ42
2. faβ + rsg3pN1N2 (2.5 μM)
3. faβ + rsg3pN1N2 (0.5 μM)
4. faβ + SA-g3p (360 nM)
5. faβ + streptavidin (360 nM)
6. faβ + SA-g3p (72 nM)
7. faβ + streptavidin (72 nM)
ng/well
200
100
50
25
12.5

FIG. 21

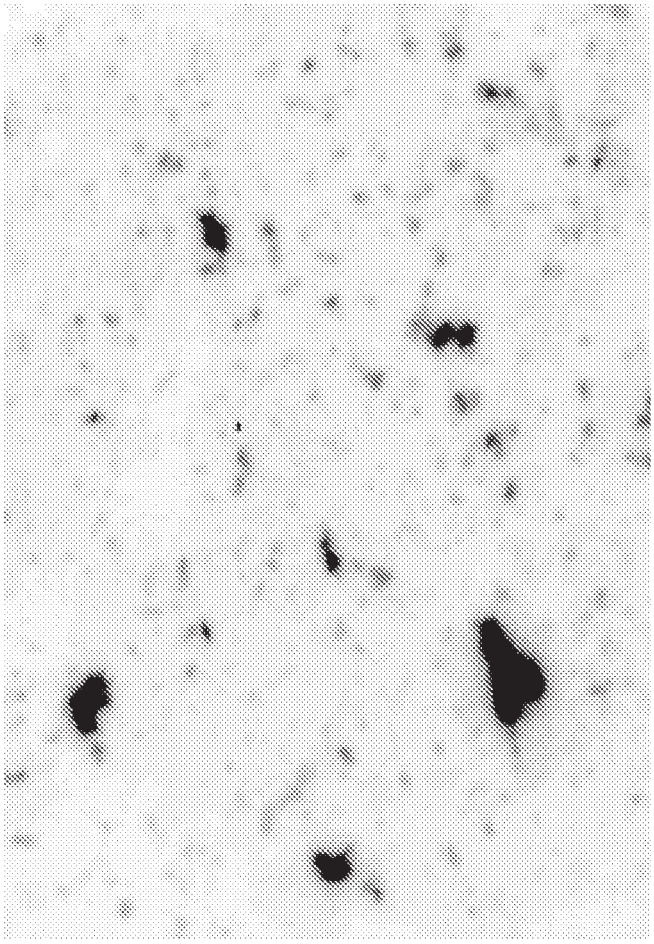


FIG. 22B

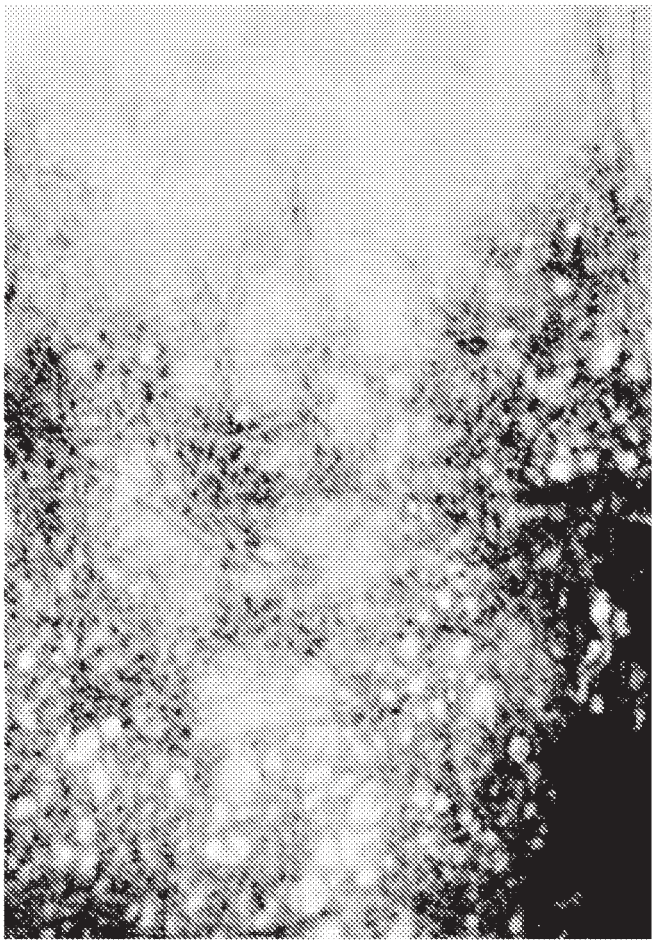


FIG. 22A

M Y R M Q L L S C I A L S L A L V T N S M A E T V E S C L A K P H T E N
S F T N V W K D D K T L D R Y A N Y E G C L W N A T G V V V C T G D E T
Q C Y G T W V P I G L A I P E N E G G G S E G G G S E G G G S E G G G T
K P P E Y G D T P I P G Y T Y I N P L D G T Y P P G T E Q N P A N P N P
S L E E S Q P L N T F M F Q N N R F R N R Q G A L T V Y T G T V T Q G T
D P V K T Y Y Q Y T P V S S K A M Y D A Y W N G K F R D C A F H S G F N
E D P F V C E Y Q G Q S S D L P Q P P V N A G G G S G G G S G G G S E G
G G S E G G G S E G G G S E G G G S G G G S G S G A M V R S P P C P S C
P A P E F L G G P S V F L F P P K P K D T L M I S R T P E V T C V V V D
V S Q E D P E V Q F N W Y V D G V E V H N A K T K P R E E Q F N S T Y R
V V S V L T V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S
K A K G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y
P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S R
L T V D K S R W Q E G N V F S C S V M H E A L H N H Y T Q K S L S L S P
G K (SEQ ID NO:9)

FIG. 23

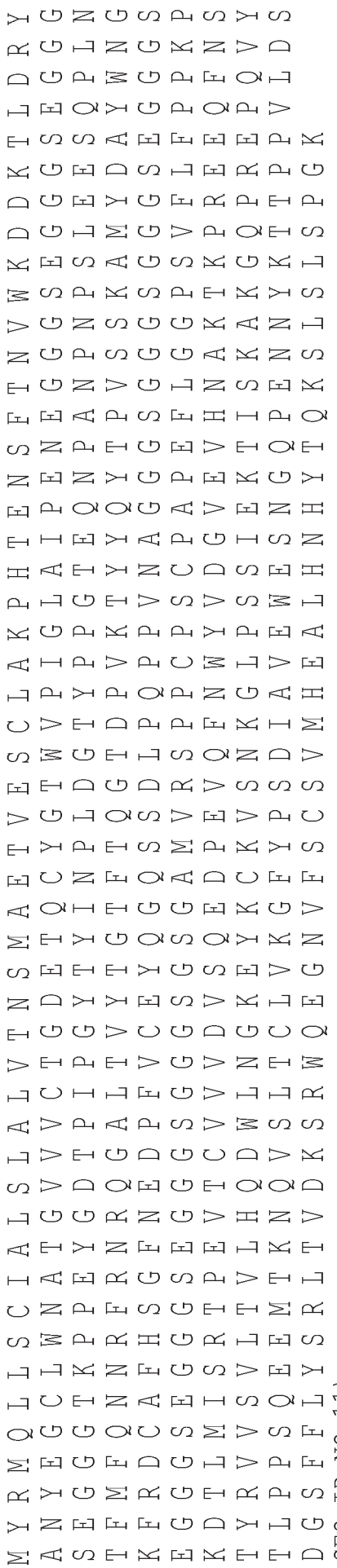

MYRMQLLSCIALSLALVTNSMAETVESCLAKPHTENSFTNVWKDDKTLDRY
ANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENEGGGNPANPNPSLEESKAMYDAYWNGG
SEGGGGTKPPEYGDTPIPGYITGTFEQNPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO:11)

FIG. 24

MYRMQLLSCIALSLALVTNSMAETVESCLAKPHTENSFTNVWKDDKTL
DRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENEGGGSEGG
GSEGGGGSEGGGTKPPEYGDTPIPGYTYINPLDGTYPPPGTEQNPANPNP
SLEESQPLNTFMFQNNRFRNRQGALTVYTGTFTQGTDPVKTYYQYTPV
SSKAMYDAYWNGKFRDCAFHSGFNEDPFVCEYQGQSSDLPQPPVNAGG
GSGGGGSEGGGSEGGGSSEGGGGSSEGGGSSGGAMVRSDKTHTC
PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 13)

FIG. 25

```
fd          TKPPEYGDTPIPGYTYINPLDGTYPPGTEQNPAN
f1          TKPPEYGDTPIPGYTYINPLDGTYPPGTEQNPAN
M13         TKPPEYGDTPIPGYTYINPLDGTYPPGTEQNPAN
Ike         S-PGEKTESWSIRAQVEGDIQRSVPD--EEPSEQ
I2-2        S-PSEKTESWSIRAQVEGDMQRSVPD--EEPSEQ
If1         STPDTVTPGQTVNLPSDLSTLSIPANVVKSDSIG
                 .*      .  :: .

fd          PNPSLEE----------SQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPVKTY
f1          PNPSLEE----------SQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPVKTY
M13         PNPSLEE----------SQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPVKTY
Ike         TPEEICE----------AKPPIDGVFNNVFKGDEGGFYINYNGCEYEATGVTVCQ
I2-2        TPEEICE----------AKPPIDGVFNNVSKGDEGGFYINYNGCEYEATGVTVCQ
If1         SQFSLYTNASCTMCSGYYLSNNADSIAIANITETVKADYNQPDMWFEQTDSDGNHVKILQ
              .  ::          :..   : :   :    :   :..

fd          YQYTPVSS----------KAMYDAYWNGKFRDCAFHSG----FNEDPFVCEYQGQSSDL
f1          YQYTPVSS----------KAMYDAYWNGKFRDCAFHSG----FNEDPFVCEYQGQSSDL
M13         YQYTPVSS----------KAMYDAYWNGKFRDCAFHSG----FNEDPFVCEYQGQSSDL
Ike         NDGTVCSS----------SAWKPTGYVPESGEPSSSPL----KDGDTGGTGEGGSDTGG
I2-2        NDGTVCAS----------SAWKPTGYVPESGESSSSPV----KDGDTGGTGEGGSDTGG
If1         NSYKAVSYNVFESKQSDVNNPTYINYSYSVNVKQVSYDTSNVCIMNWETFQNKCDASRAVL
              . .  ::          :   : :: : :  .    : ::.    .. ::

fd          PQPPVNA (SEQ ID NO:14)
f1          PQPPVNA (SEQ ID NO:15)
M13         PQPPVNA (SEQ ID NO:16)
Ike         DTGGGDT (SEQ ID NO:17)
I2-2        DTGGGDT (SEQ ID NO:18)
If1         ITDTVTP (SEQ ID NO:19)
```

FIG. 26

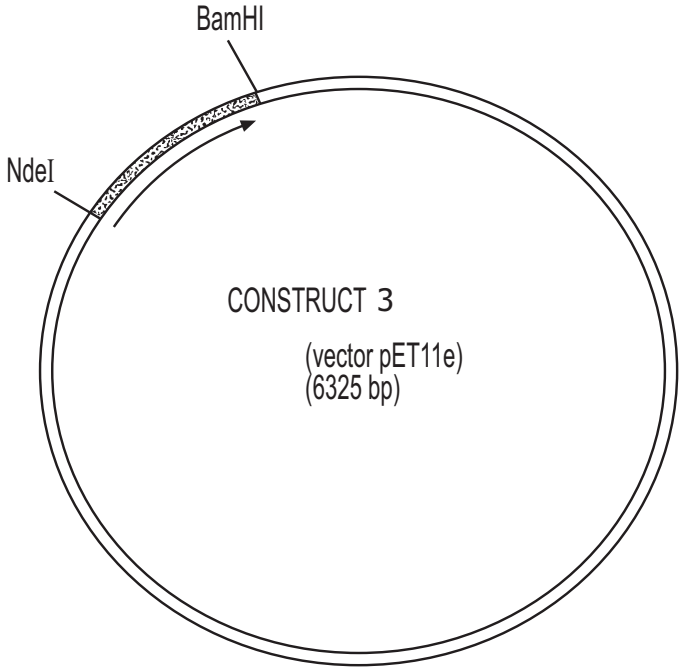


FIG. 27A

atgGCTGAAACTGTTGAAAGTTGTTTAGCAAAATCCCATACAGAAAATTCATTTACTAACGTCTGGAAAGACGACAA
AACTTTAGATCGTTACGCTAACTATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGTAGTTTGTACTGGTGACGAAA
CTCAGTGTTACGGTACATGGGTTCCTATTGGGCTTGCTATCCCTGAAAATGAGGGTGGTGGCTCTGAGGGTGGCGGT
TCTGAGGGTGGCGGTTCTGAGGGTGGCGGTACTAAACCTCCTGAGTACGGTGATACACCTATTCCGGGCTATACTTA
TATCAACCCTCTCGACGGCACTTATCCGCCTGGTACTGAGCAAAACCCCGCTAATCCTAATCCTTCTCTTGAGGAGT
CTCAGCCTCTTAATACTTTCATGTTTCAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATACGGGCA
CTGTTACTCAAGGCACTGACCCCGTTAAAACTTATTACCAGTACACTCCTGTATCATCAAAAGCCATGTATGACGCTT
ACTGGAACGGTAAATTCAGAGACTGCGCTTTCCATTCTGGCTTTAATGAGGATTTATTTGTTTGTGAATATCAAGGCC
AATCGTCTGACCTGCCTCAACCTCCTGTCAATGCTCCGTCCgggcatcatcatcatcattaa(SEQIDNO:23)

FIG. 27B

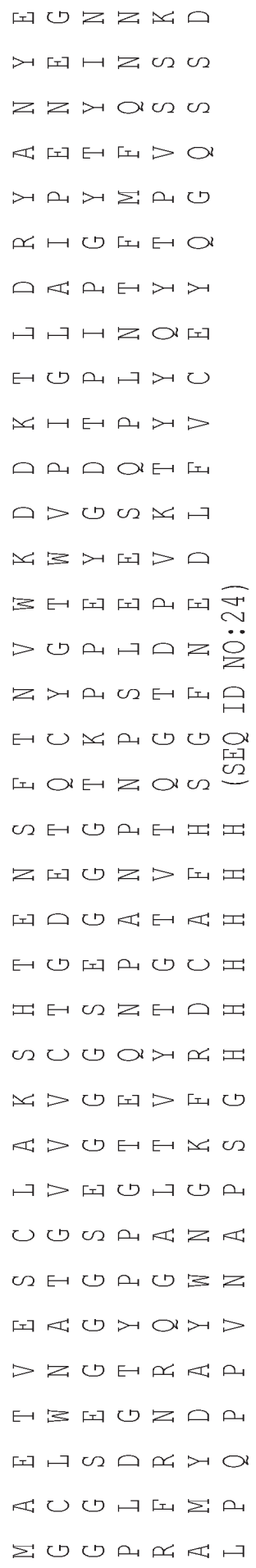

MAETVESCLAKSHTENSFTNVWKDDKTLDRYANYEG
GCCLWNATGVVVCTGDETQCYGTWVPIGLAIPEENEGG
GGGSEGGGTYPPPGTEQNPPSLEEESQPPLNTFEMFQNNN
PLDDGTYPPPGTTVYYQLYTGGYTPVSSSK
RFRRNRQGGALTVYTGSGKFRDCAFHSGFNEDLFVCEYQGQD
AMYDAYWNGKFRDCAFHSGFNEDLFVCEYQGQ
LPQPPVNAPSGHHHHHH (SEQ ID NO:24)

FIG. 27C

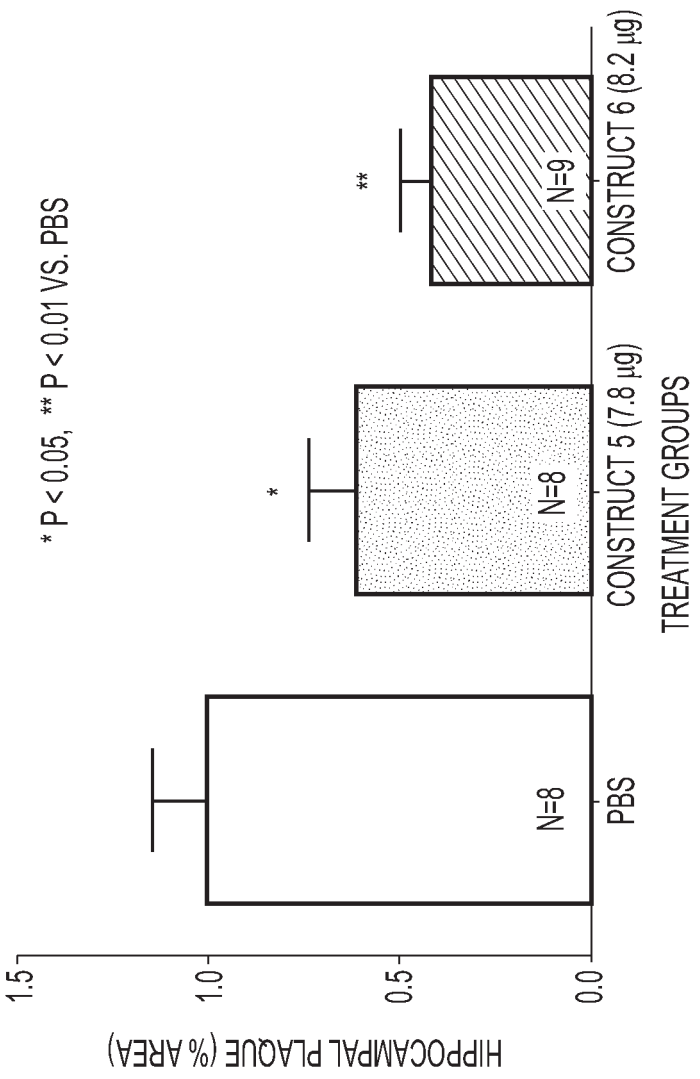

* P < 0.05, ** P < 0.01 VS. PBS
HIPPOCAMPAL PLAQUE (% AREA)
1.5
1.0
0.5
0.0
*
**
N=8
N=8
N=9
PBS
CONSTRUCT 5 (7.8 µg)
CONSTRUCT 6 (8.2 µg)
TREATMENT GROUPS

FIG. 28

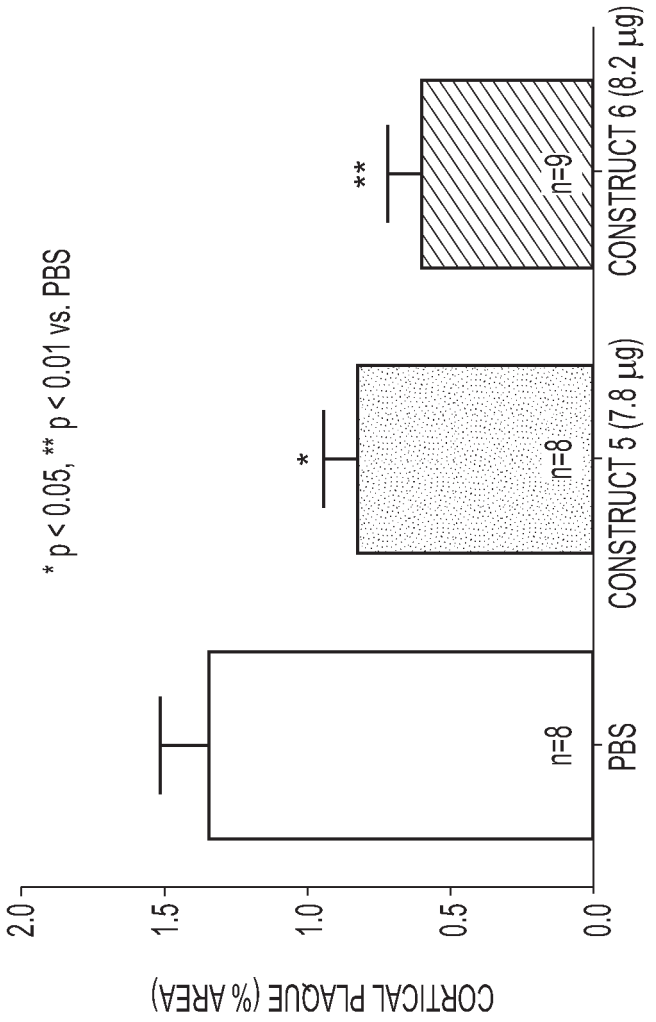

CORTICAL PLAQUE (% AREA)
2.0
1.5
1.0
0.5
0.0
* p < 0.05, ** p < 0.01 vs. PBS
*
**
n=8
n=8
n=9
PBS
CONSTRUCT 5 (7.8 µg)
CONSTRUCT 6 (8.2 µg)
TREATMENT GROUPS

FIG. 29

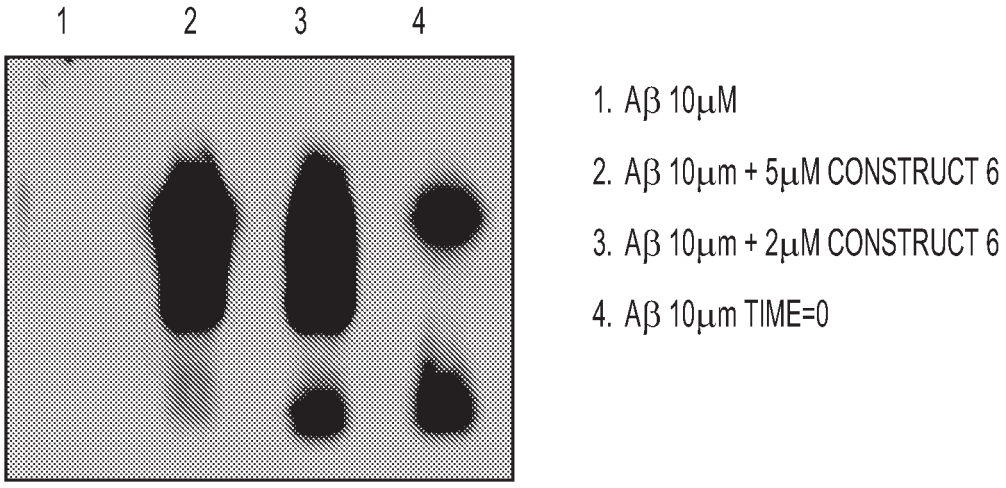


FIG. 30A

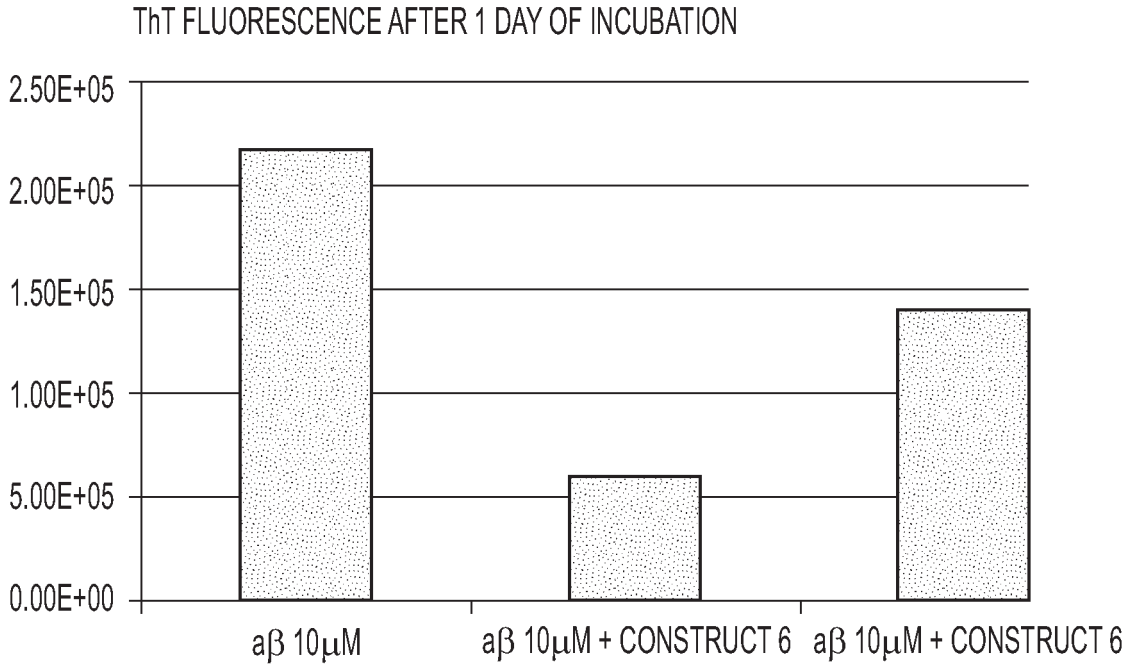


FIG. 30B

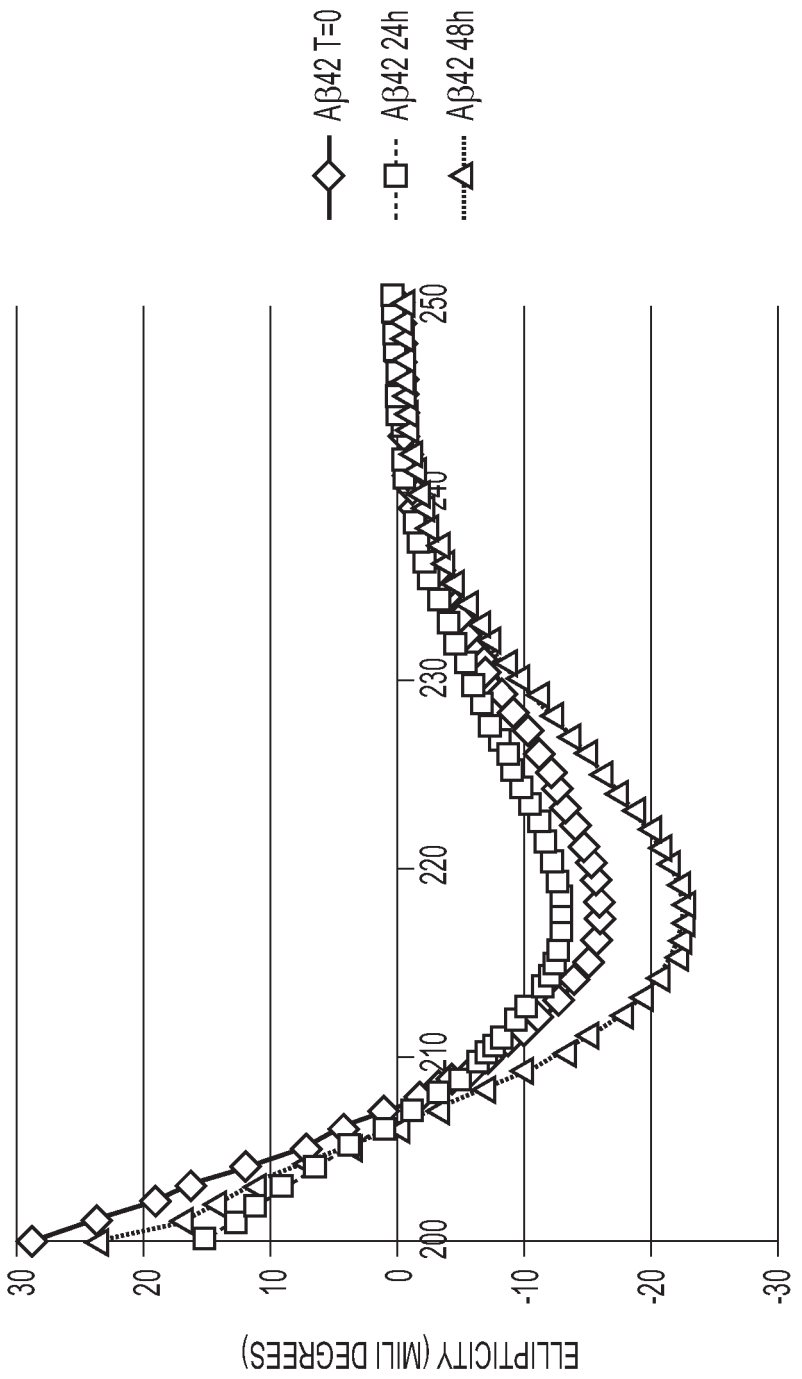

Aβ42 T=0
Aβ42 24h
Aβ42 48h
30
20
10
0
-10
-20
-30
200
210
220
230
240
250
ELLIPTICITY (MILLI DEGREES)
WAVELENGTH (nm)

FIG. 31A

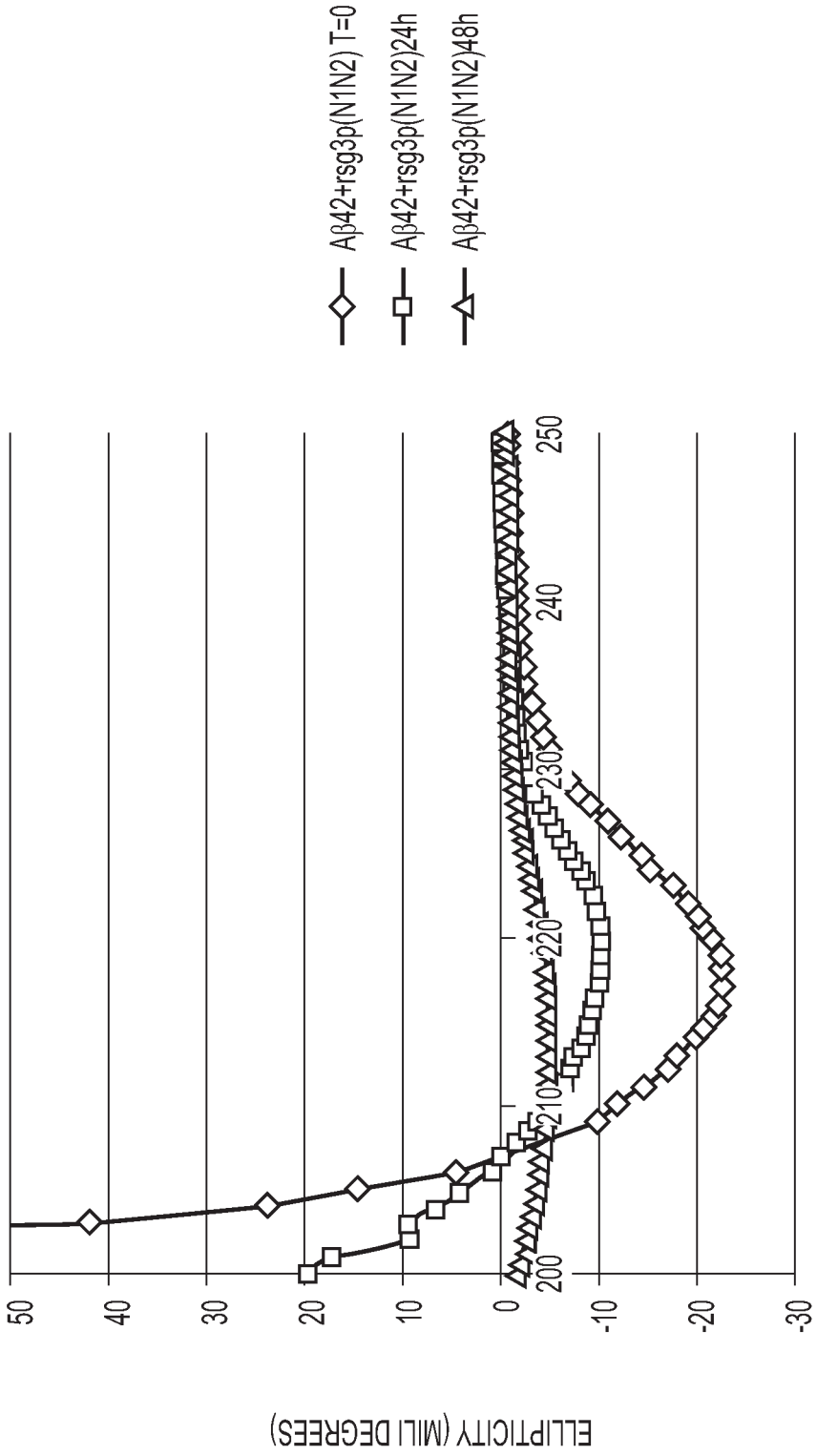

Aβ42+rsg3p(N1N2) T=0
Aβ42+rsg3p(N1N2)24h
Aβ42+rsg3p(N1N2)48h
ELLIPTICITY (MILLI DEGREES)
50
40
30
20
10
0
-10
-20
-30
200
210
220
230
240
250

FIG. 31B

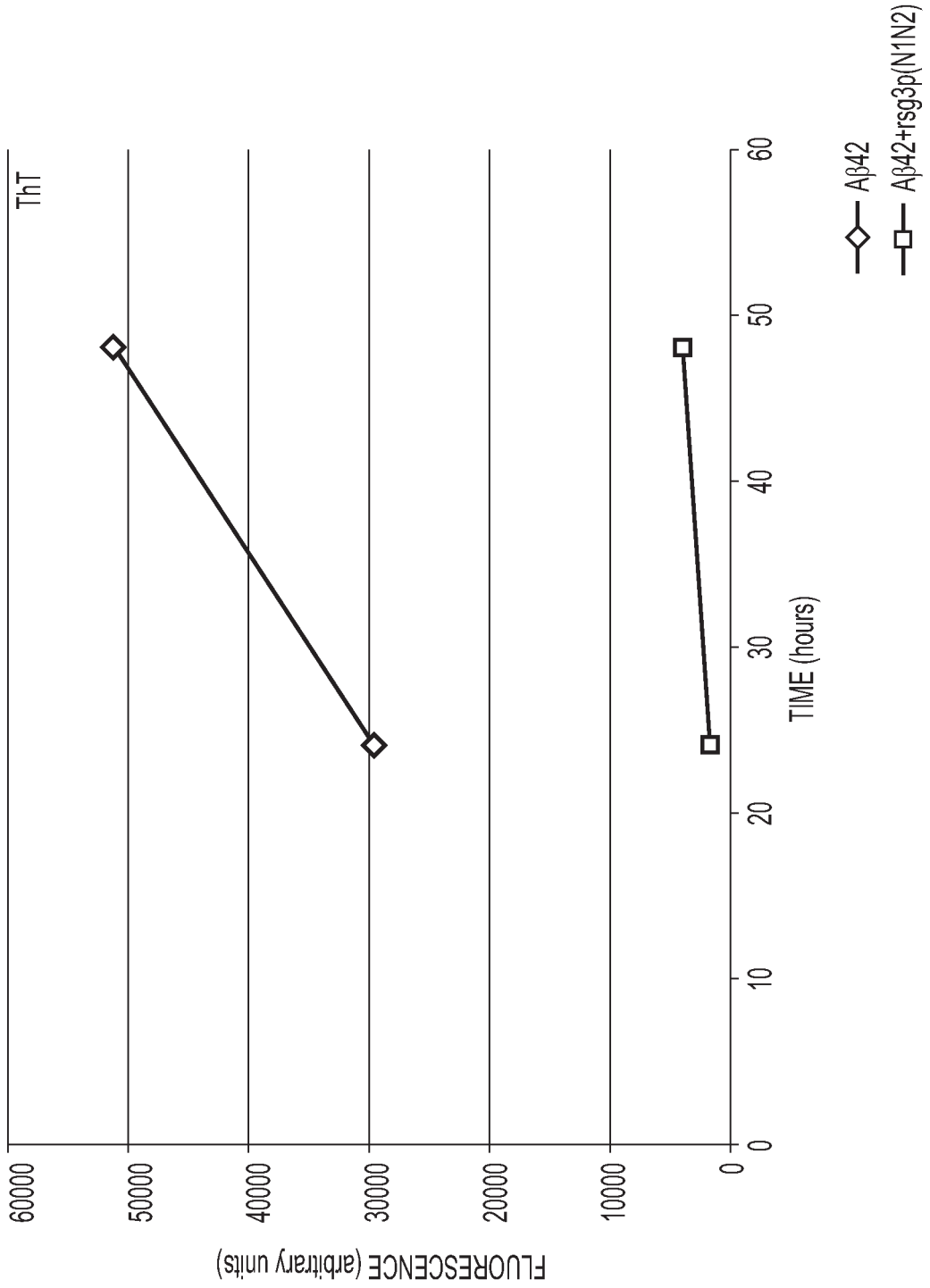

ThT
FLUORESCENCE (arbitrary units)
60000
50000
40000
30000
20000
10000
0
0
10
20
30
40
50
60
TIME (hours)
Aβ42
Aβ42+rsg3p(N1N2)

FIG. 31C

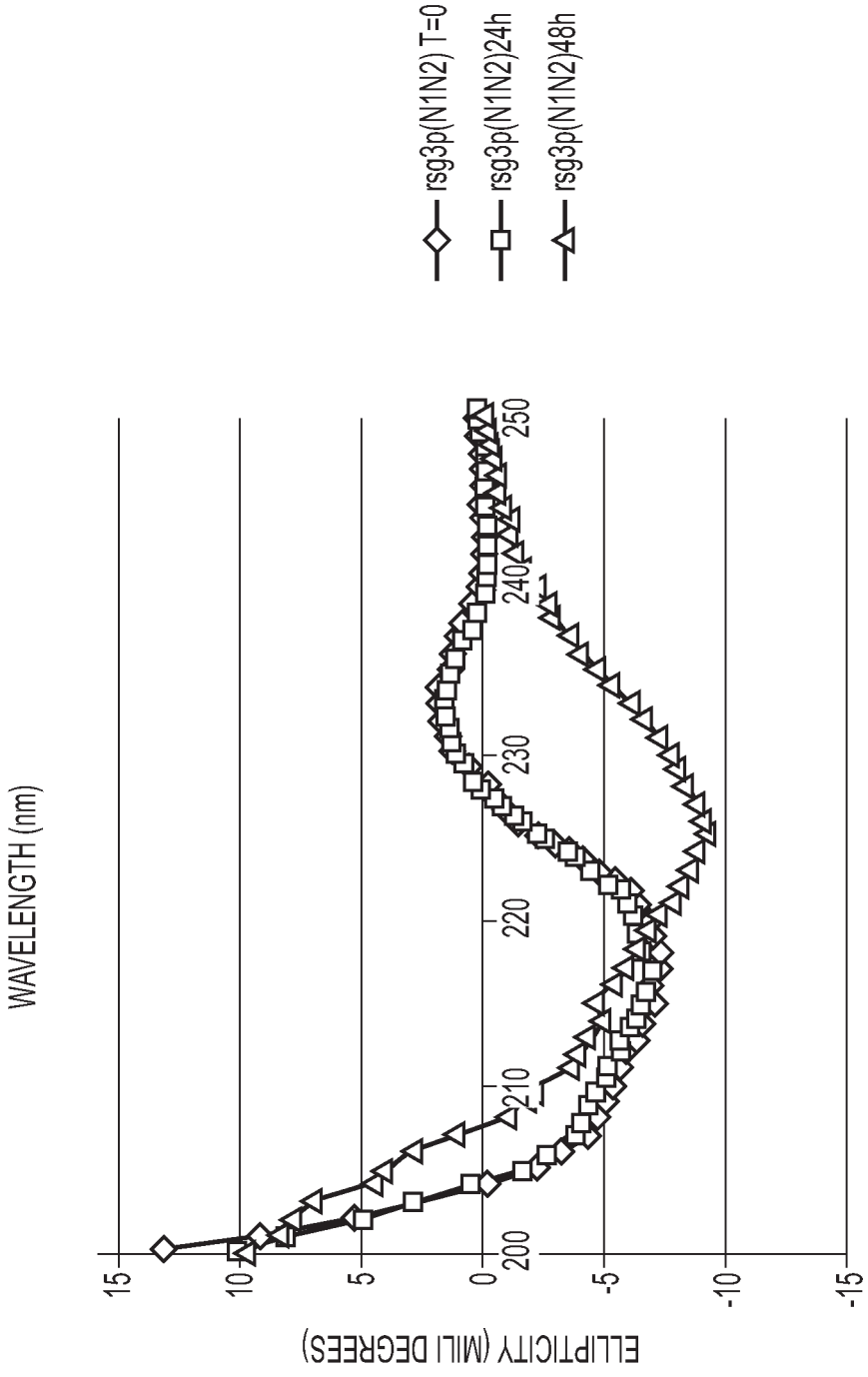

rsg3p(N1N2) T=0
rsg3p(N1N2)24h
rsg3p(N1N2)48h
WAVELENGTH (nm)
ELLIPTICITY (MILLI DEGREES)
WAVELENGTH (nm)
15
10
5
0
-5
-10
-15
200
210
220
230
240
250

FIG. 31D

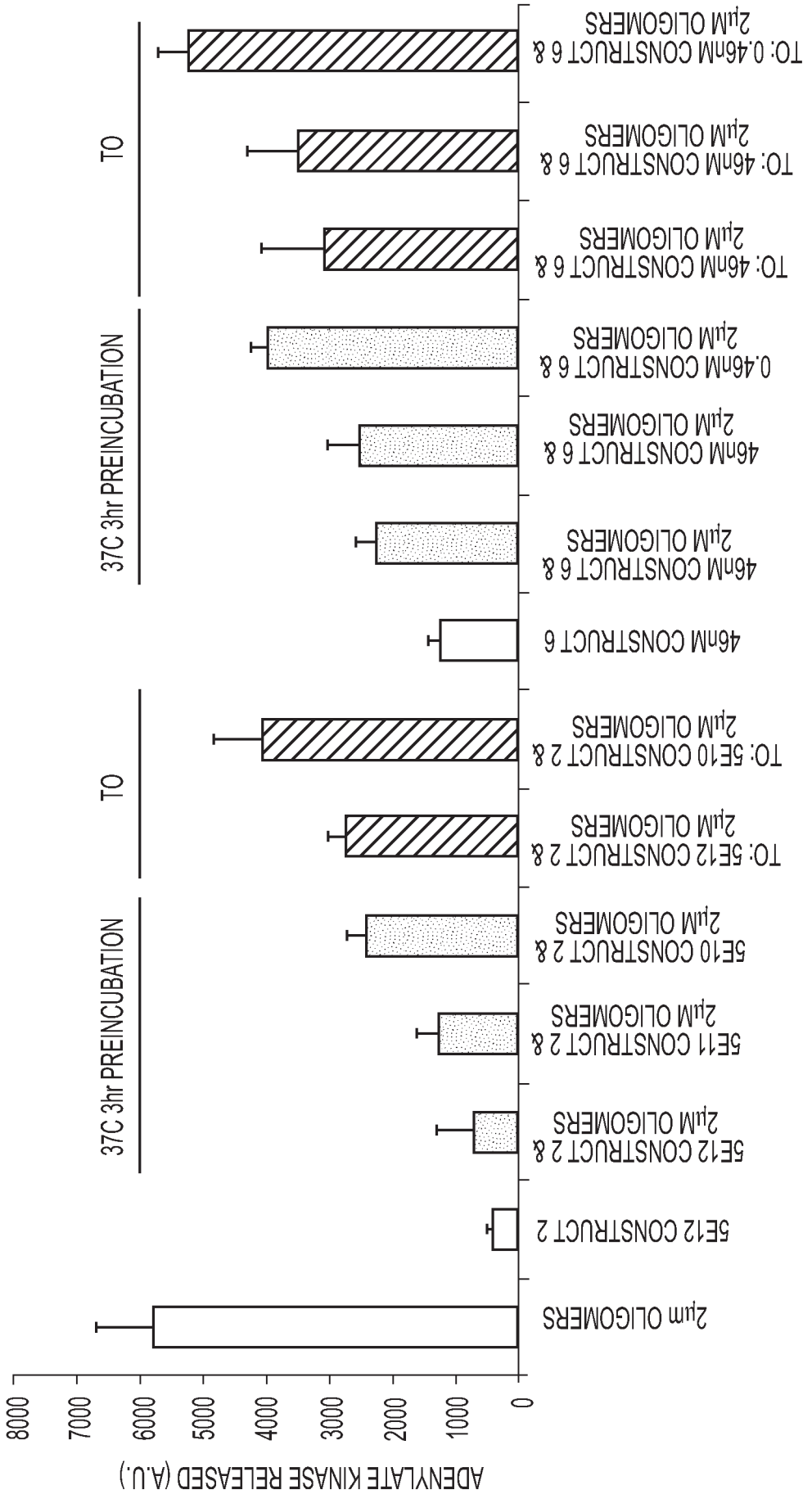

ADENYLATE KINASE RELEASED (A.U.)
8000
7000
6000
5000
4000
3000
2000
1000
0
2μm OLIGOMERS
5E12 CONSTRUCT 2
5E12 CONSTRUCT 2 & 2μM OLIGOMERS
5E11 CONSTRUCT 2 & 2μM OLIGOMERS
5E10 CONSTRUCT 2 & 2μM OLIGOMERS
TO: 5E12 CONSTRUCT 2 & 2μM OLIGOMERS
TO: 5E10 CONSTRUCT 2 & 2μM OLIGOMERS
46nM CONSTRUCT 6
46nM CONSTRUCT 6 & 2μM OLIGOMERS
46nM CONSTRUCT 6 & 2μM OLIGOMERS
0.46nM CONSTRUCT 6 & 2μM OLIGOMERS
TO: 46nM CONSTRUCT 6 & 2μM OLIGOMERS
TO: 46nM CONSTRUCT 6 & 2μM OLIGOMERS
TO: 0.46nM CONSTRUCT 6 & 2μM OLIGOMERS
37C 3hr PREINCUBATION
TO
37C 3hr PREINCUBATION
TO

FIG. 32

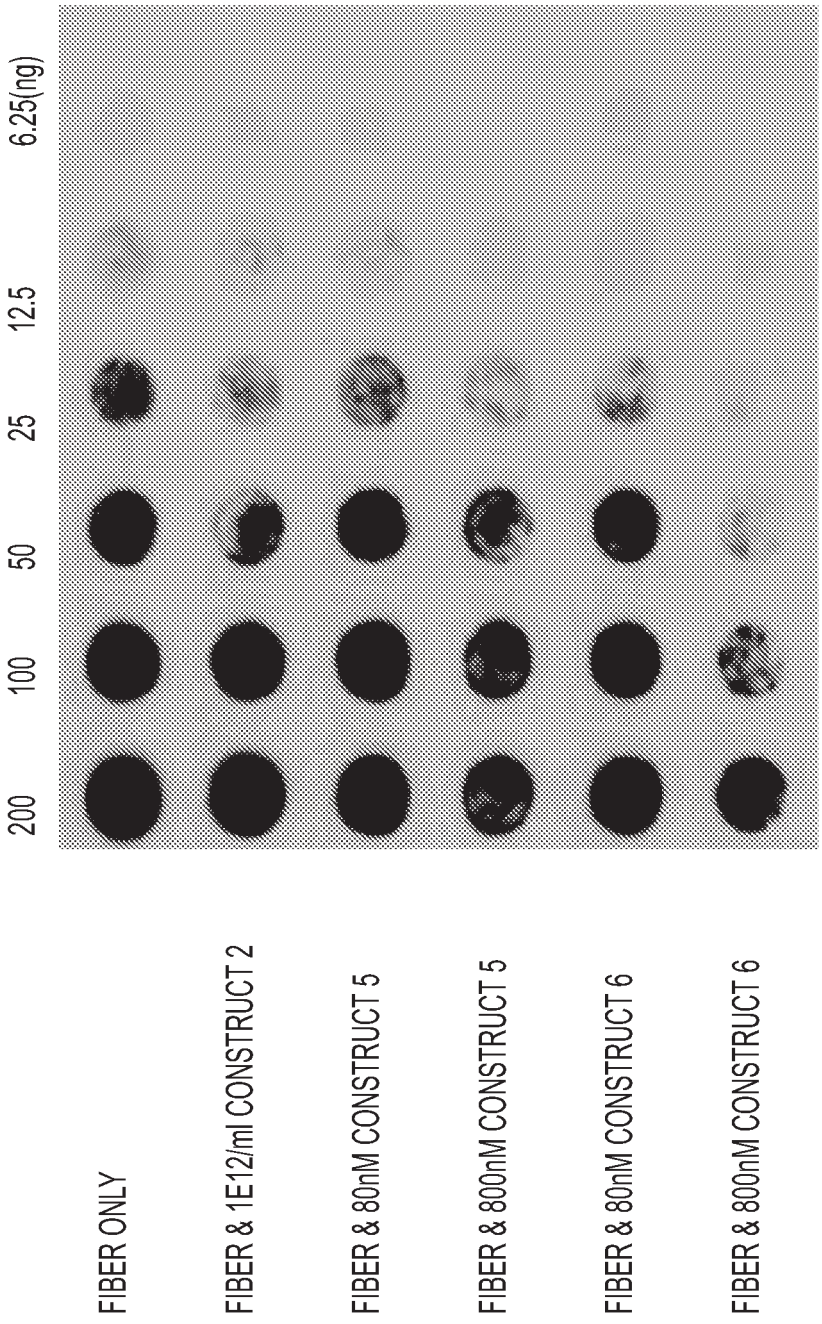

200
100
50
25
12.5
6.25(ng)
FIBER ONLY
FIBER & 1E12/ml CONSTRUCT 2
FIBER & 80nM CONSTRUCT 5
FIBER & 800nM CONSTRUCT 5
FIBER & 80nM CONSTRUCT 6
FIBER & 800nM CONSTRUCT 6

FIG. 33

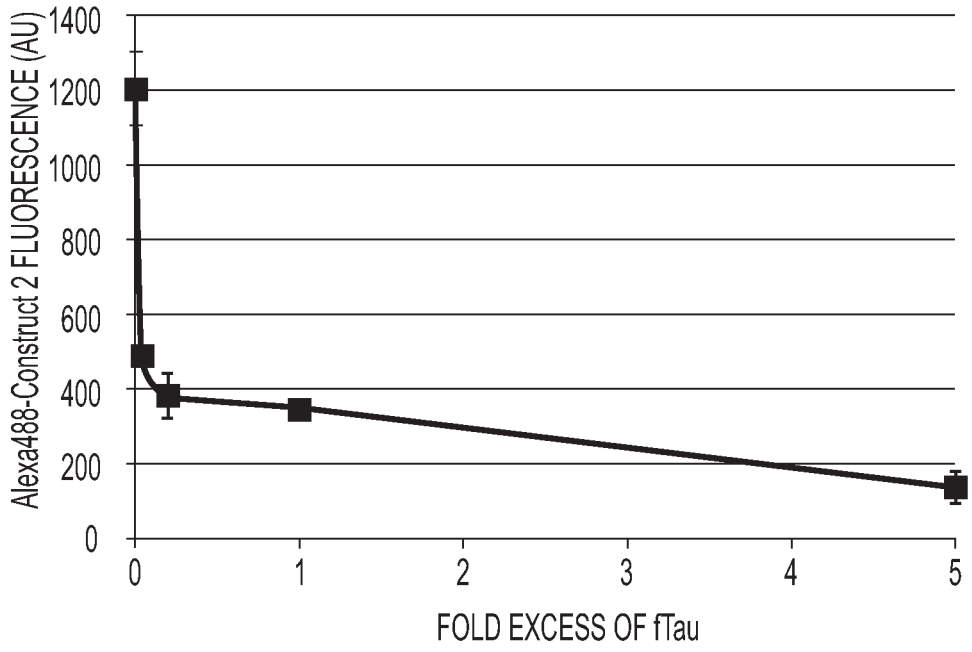


FIG. 34A

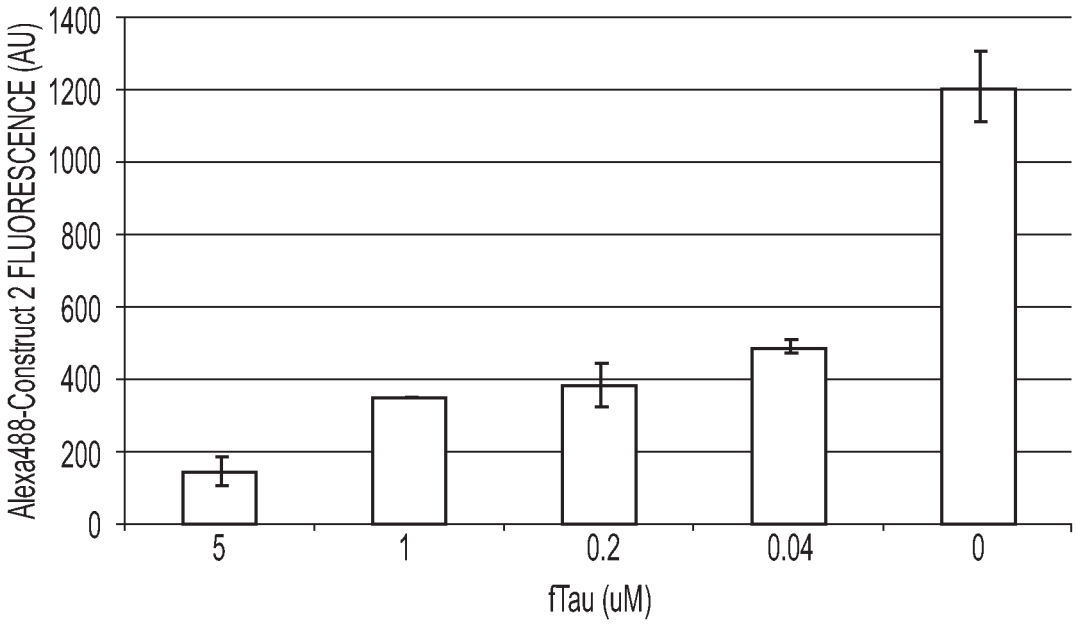


FIG. 34B

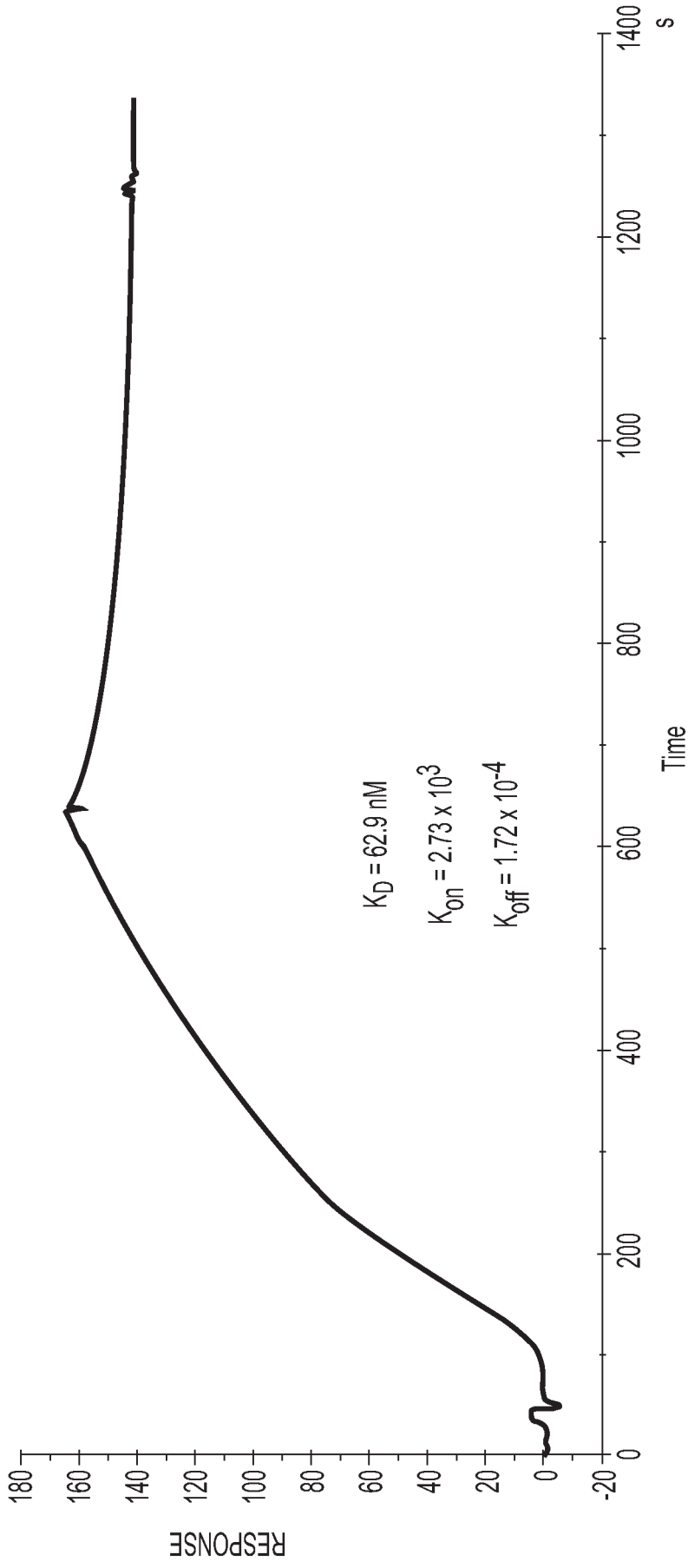

RESPONSE
180
160
140
120
100
80
60
40
20
0
-20
0
200
400
600
800
1000
1200
1400
s
Time
K_D = 62.9 nM
K_{on} = 2.73 x 10^3
K_{off} = 1.72 x 10^{-4}

FIG. 35

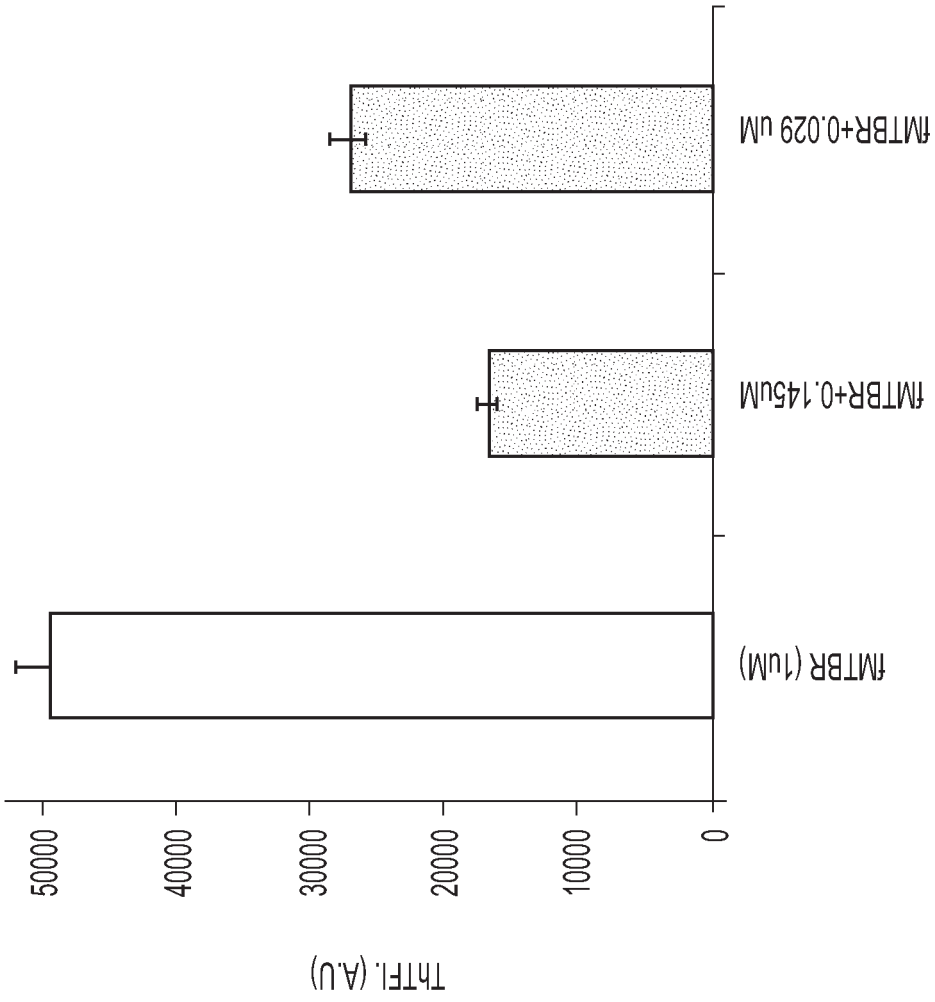

ThTFl. (A.U)
50000
40000
30000
20000
10000
0
fMTBR (1uM)
fMTBR+0.145uM
fMTBR+0.029 uM

FIG. 36A

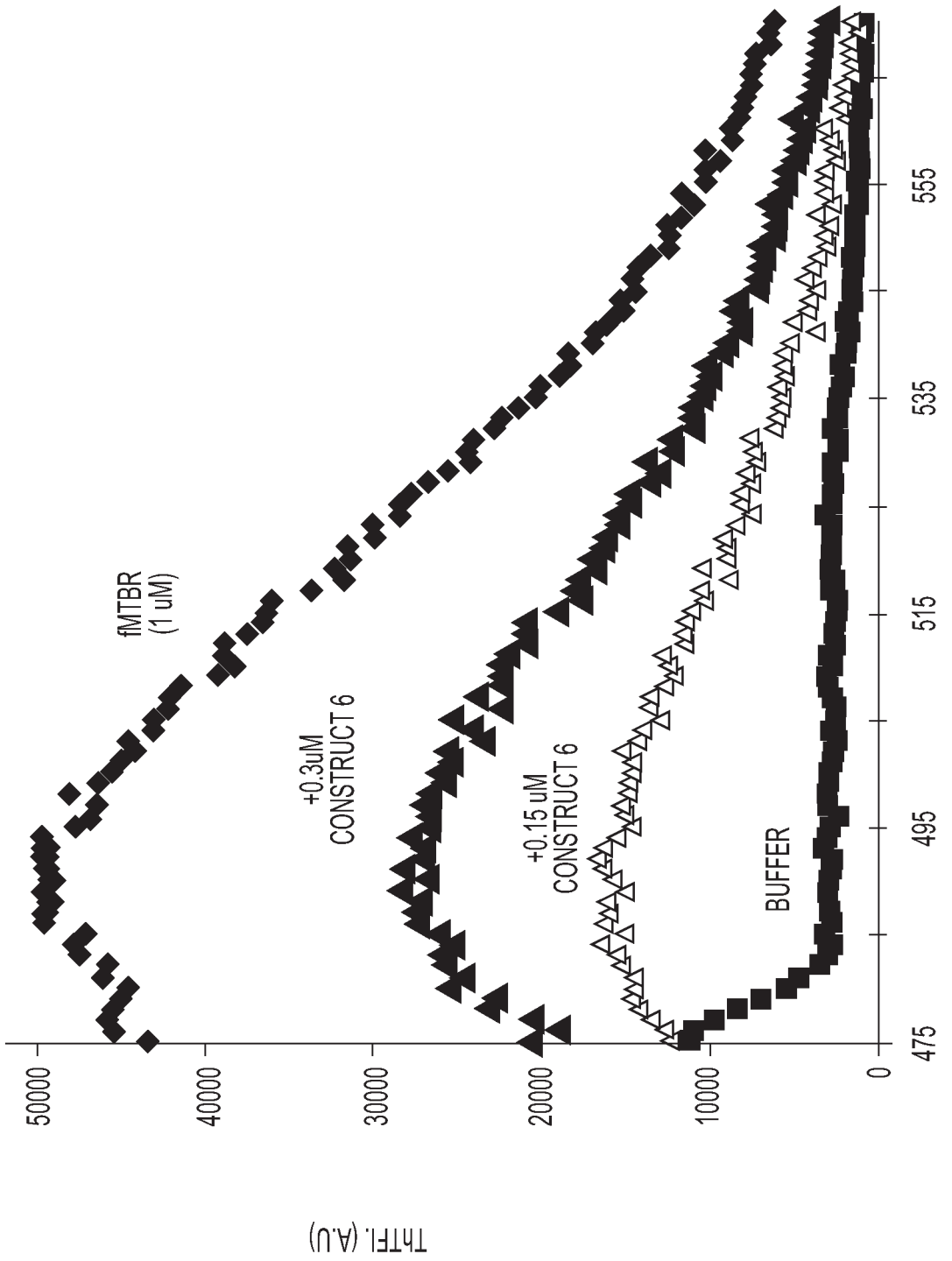

fMTBR
(1 uM)
+0.3uM
CONSTRUCT 6
+0.15 uM
CONSTRUCT 6
BUFFER
50000
40000
30000
20000
10000
0
475
495
515
535
555
WAVELENGTH (nm)
INTENSITY (A.U)

FIG. 36B

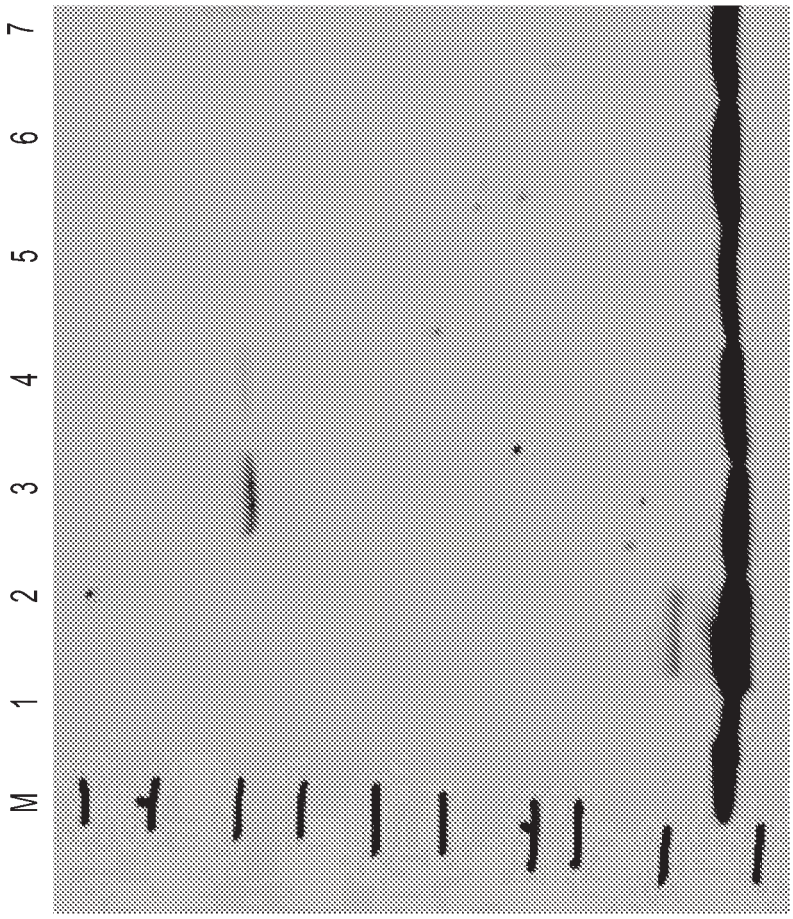

M
1
2
3
4
5
6
7
1. Aβ42 1μM
2. Aβ42 1μM T=0
3. Aβ42 + CONSTRUCT 6 0.5μM
4. Aβ + CONSTRUCT 6 0.2μM
5. Aβ + CONSTRUCT 6 0.05μM
6. Aβ + CONSTRUCT 6 1μM
7. Aβ + CONSTRUCT 6 0.1μM

FIG. 37A

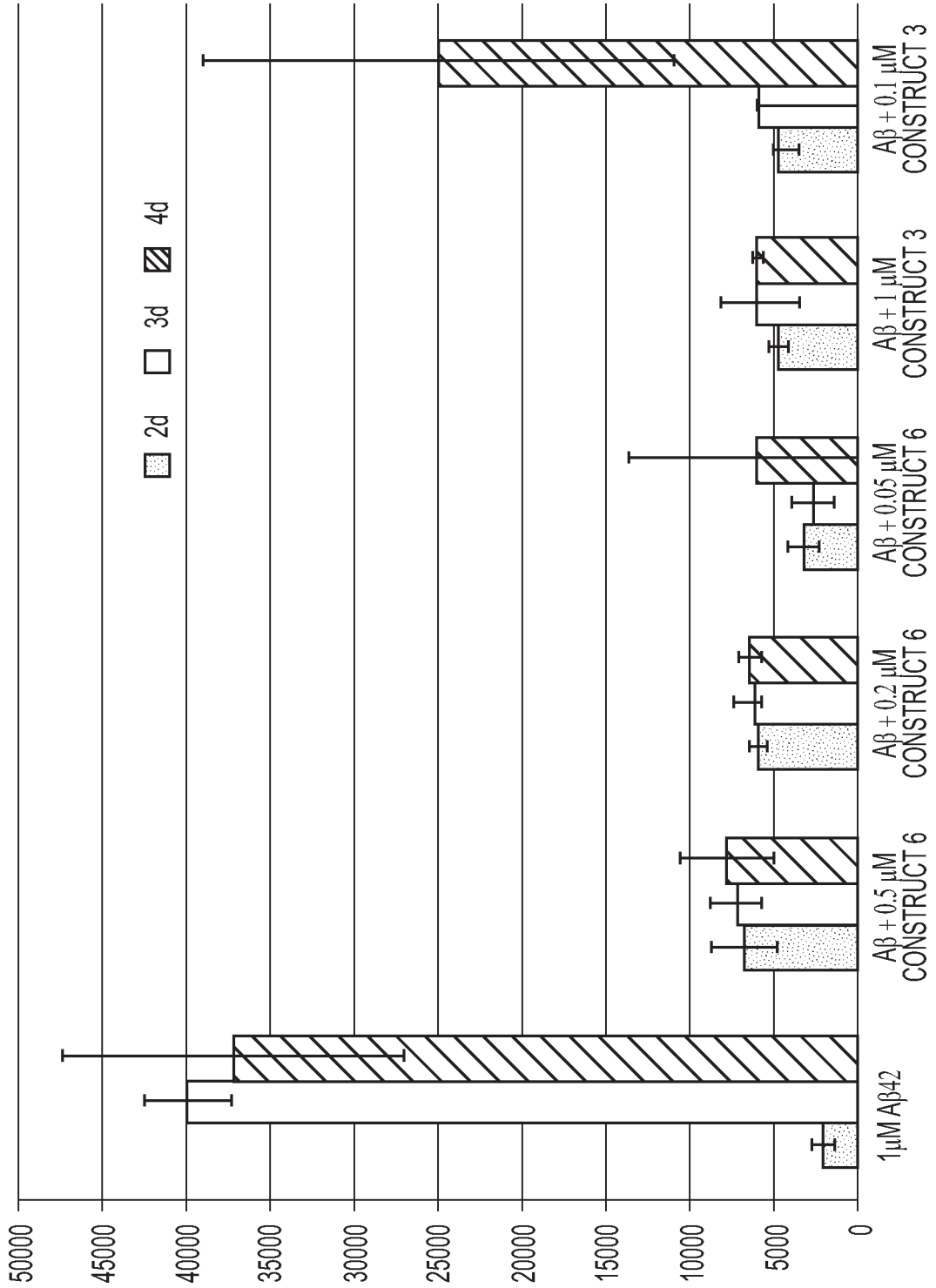

50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
2d
3d
4d
1μM Aβ42
Aβ + 0.5 μM CONSTRUCT 6
Aβ + 0.2 μM CONSTRUCT 6
Aβ + 0.05 μM CONSTRUCT 6
Aβ + 1 μM CONSTRUCT 3
Aβ + 0.1 μM CONSTRUCT 3

FIG. 37B

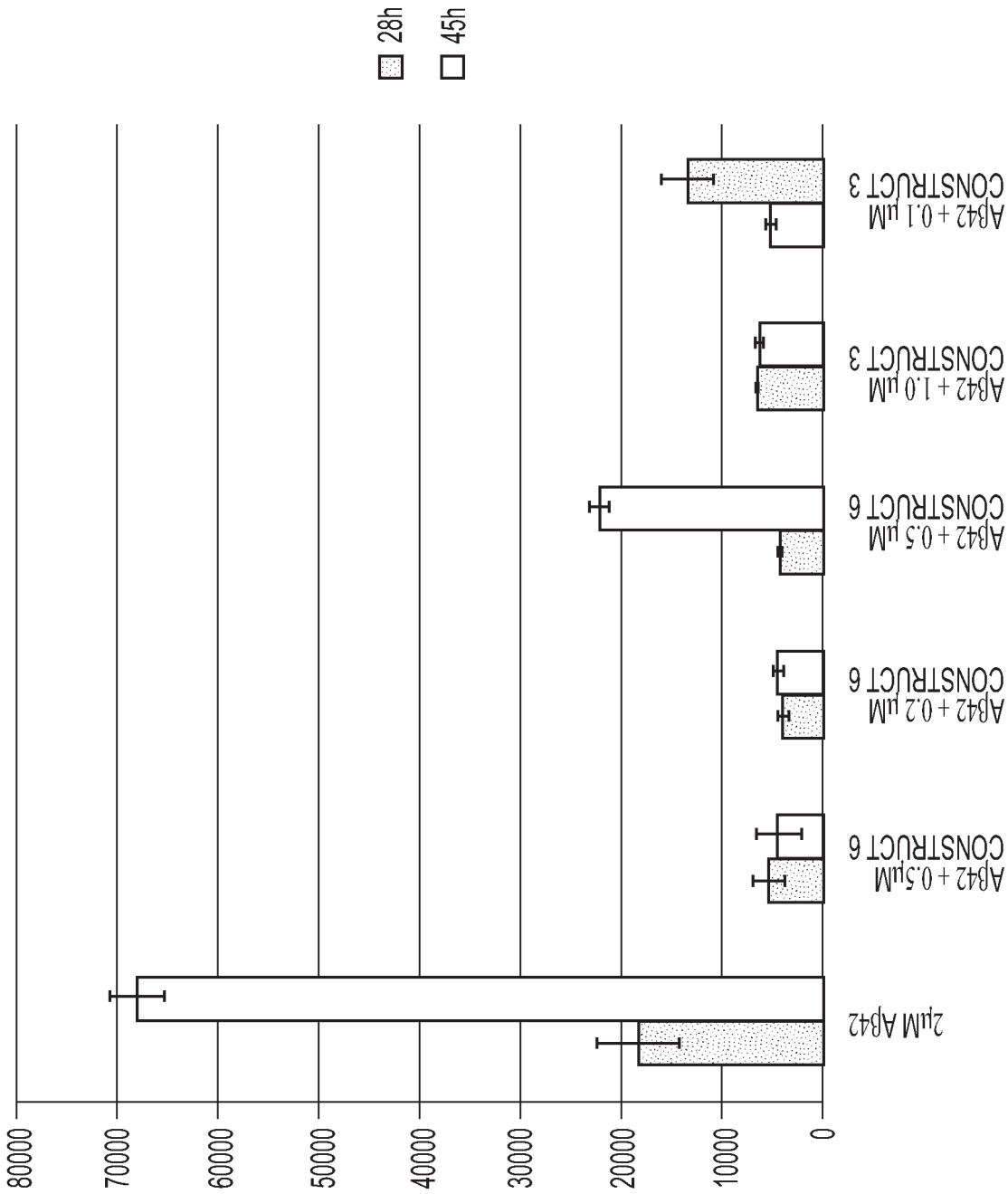

28h
45h
80000
70000
60000
50000
40000
30000
20000
10000
0
2μM Aβ42
Aβ42 + 0.5μM CONSTRUCT 6
Aβ42 + 0.2 μM CONSTRUCT 6
Aβ42 + 0.5 μM CONSTRUCT 6
Aβ42 + 1.0 μM CONSTRUCT 3
Aβ42 + 0.1 μM CONSTRUCT 3

FIG. 37C

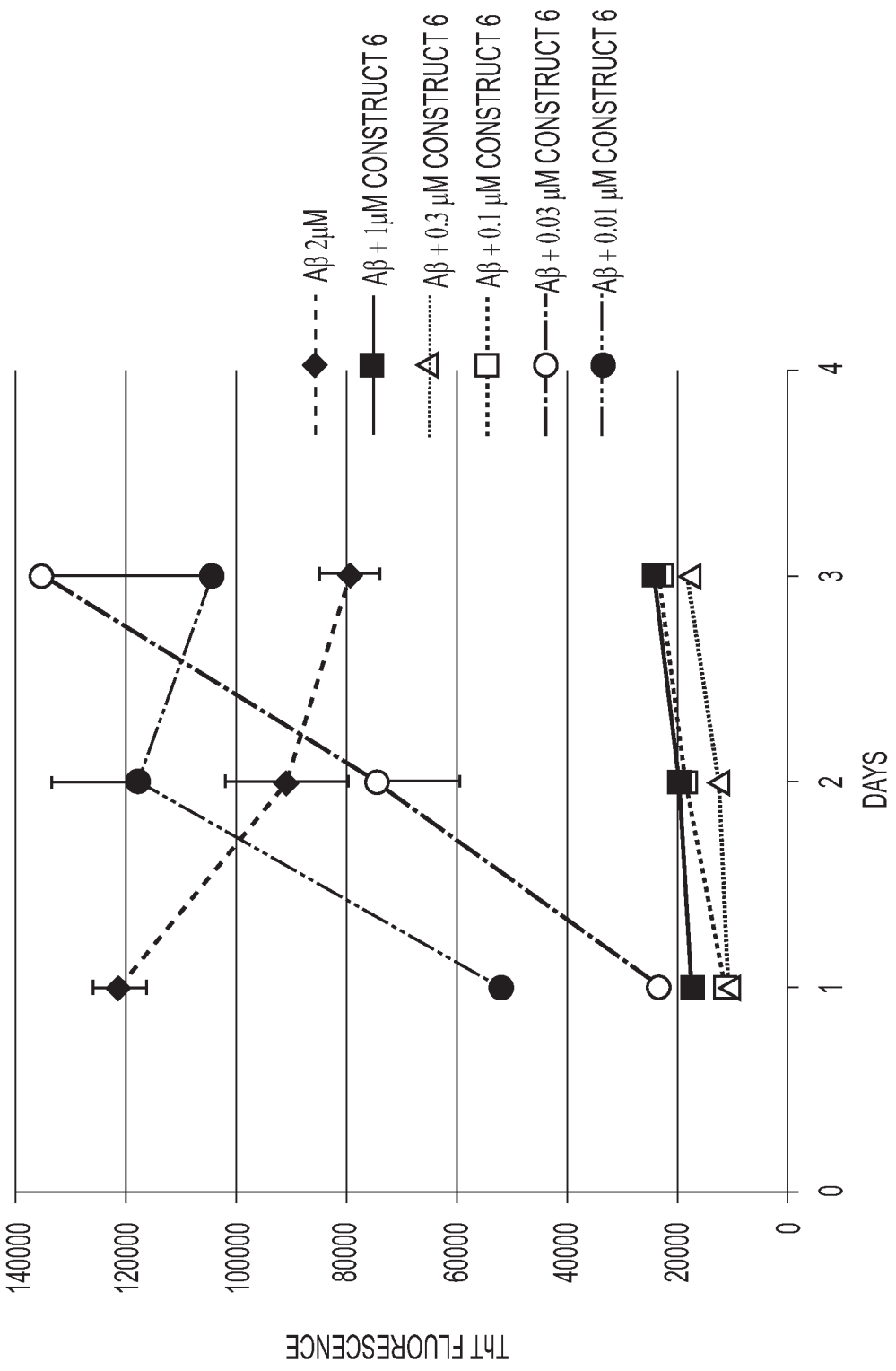

Aβ 2μM
Aβ + 1μM CONSTRUCT 6
Aβ + 0.3 μM CONSTRUCT 6
Aβ + 0.1 μM CONSTRUCT 6
Aβ + 0.03 μM CONSTRUCT 6
Aβ + 0.01 μM CONSTRUCT 6
140000
120000
100000
80000
60000
40000
20000
0
0
1
2
3
4
DAYS
THT FLUORESCENCE

FIG. 37D

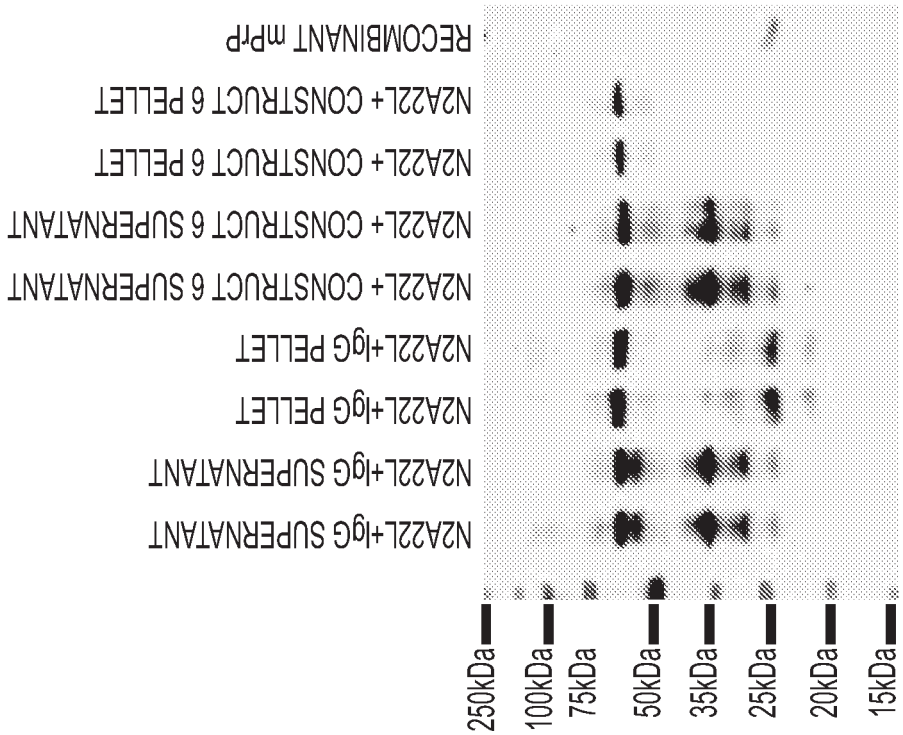

RECOMBINANT mPrP
N2A22L+ CONSTRUCT 6 PELLET
N2A22L+ CONSTRUCT 6 PELLET
N2A22L+ CONSTRUCT 6 SUPERNATANT
N2A22L+ CONSTRUCT 6 SUPERNATANT
N2A22L+IgG PELLET
N2A22L+IgG PELLET
N2A22L+IgG SUPERNATANT
N2A22L+IgG SUPERNATANT
250kDa
100kDa
75kDa
50kDa
35kDa
25kDa
20kDa
15kDa

FIG. 38A

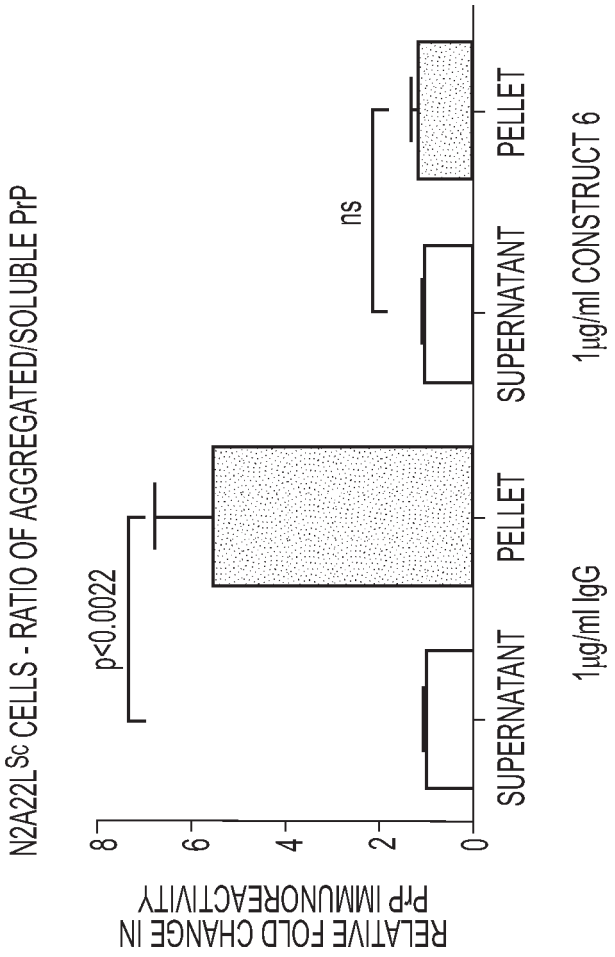

N2A22L Sc CELLS - RATIO OF AGGREGATED/SOLUBLE PrP
RELATIVE FOLD CHANGE IN PrP IMMUNOREACTIVITY
8
6
4
2
0
p<0.0022
ns
SUPERNATANT
PELLET
SUPERNATANT
PELLET
1µg/ml IgG
1µg/ml CONSTRUCT 6

FIG. 38B

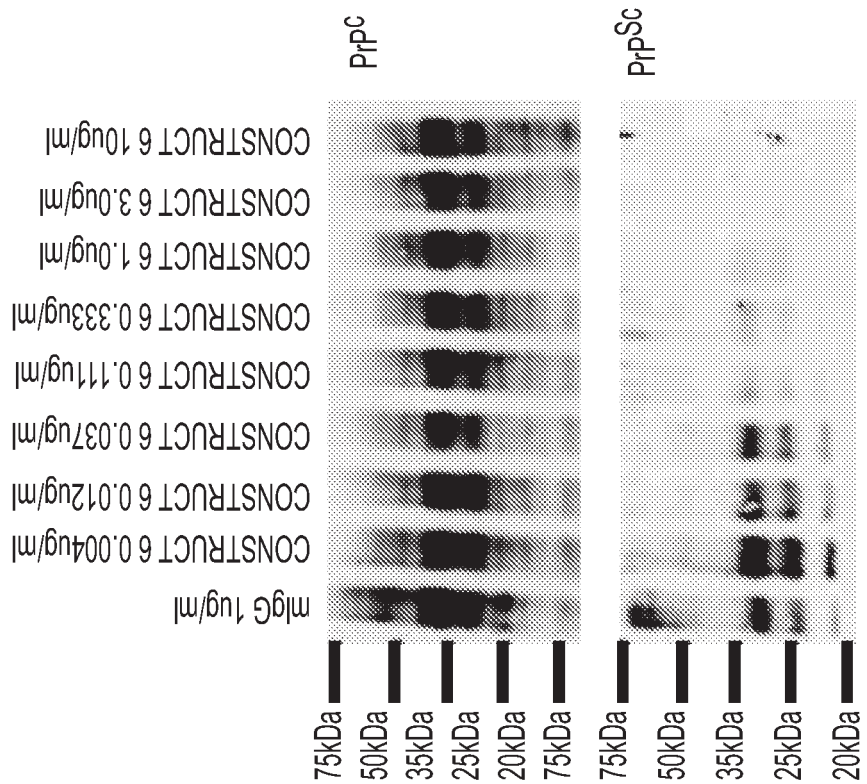

PrPC
PrPSc
mIgG 1ug/ml
CONSTRUCT 6 0.004ug/ml
CONSTRUCT 6 0.012ug/ml
CONSTRUCT 6 0.037ug/ml
CONSTRUCT 6 0.111ug/ml
CONSTRUCT 6 0.333ug/ml
CONSTRUCT 6 1.0ug/ml
CONSTRUCT 6 3.0ug/ml
CONSTRUCT 6 10ug/ml
75kDa
50kDa
35kDa
25kDa
20kDa
75kDa
50kDa
35kDa
25kDa
20kDa

FIG. 39A

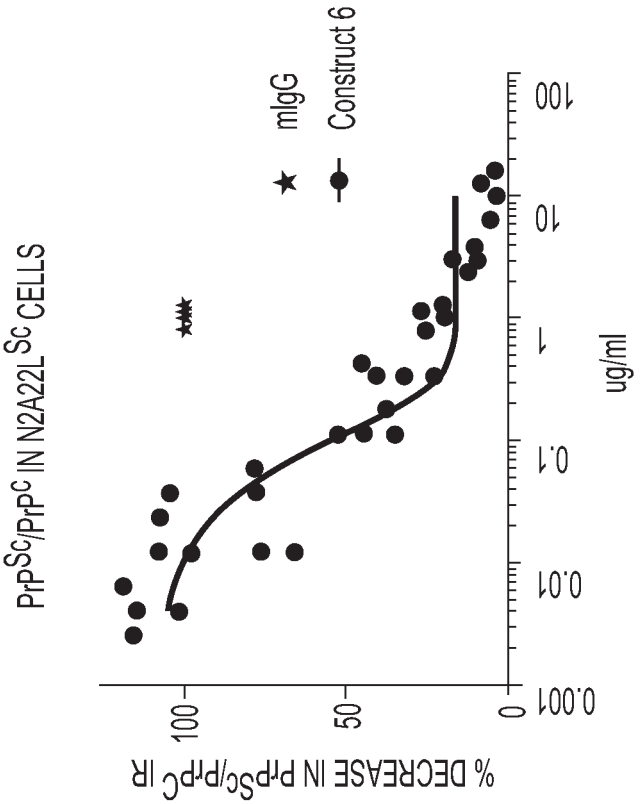

% DECREASE IN PrPSc/PrPC IR
100
50
0
0.001
0.01
0.1
1
10
100
ug/ml
mIgG
Construct 6
PrPSc/PrPC IN N2A22L Sc CELLS

FIG. 39B