FIG. 1

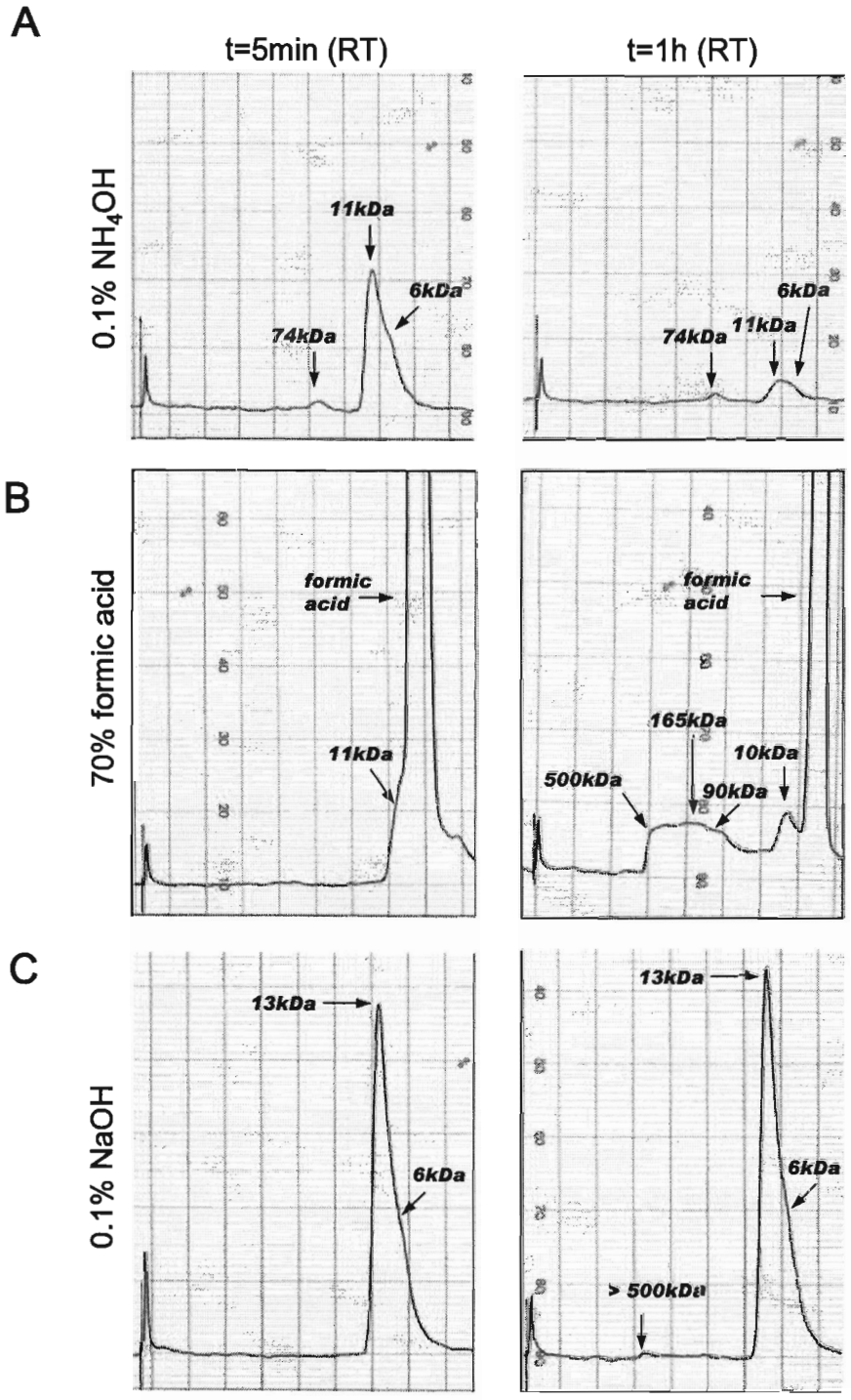

A
t=5min (RT)
t=1h (RT)
0.1% NH4OH
11kDa
6kDa
74kDa
74kDa
11kDa
6kDa
B
70% formic acid
formic acid
11kDa
formic acid
165kDa
10kDa
500kDa
90kDa
C
0.1% NaOH
13kDa
6kDa
13kDa
6kDa
> 500kDa

FIG. 1

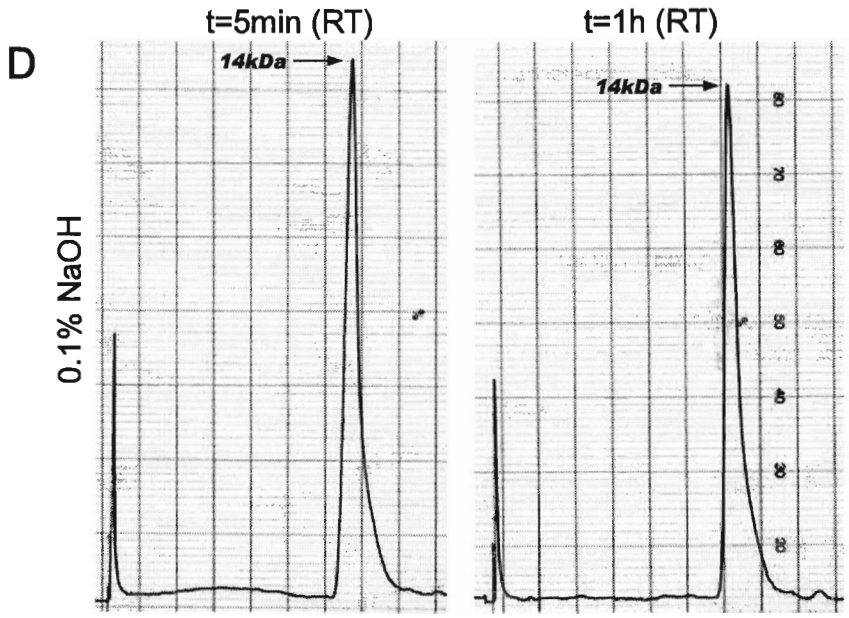
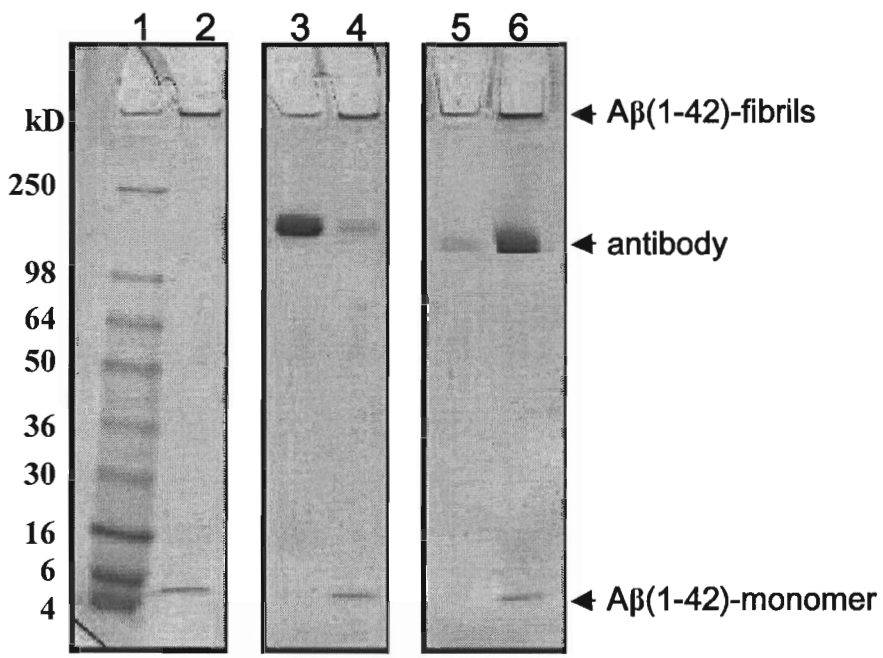


FIG. 2

A



B

	antibody bound to fibrils [%]
6E10	98
5F7	7
2F2	15
6A2	22
4D10	6
10F11	7
3B10	5
7C6	2
7E5	3
10C1	5

FIG. 3

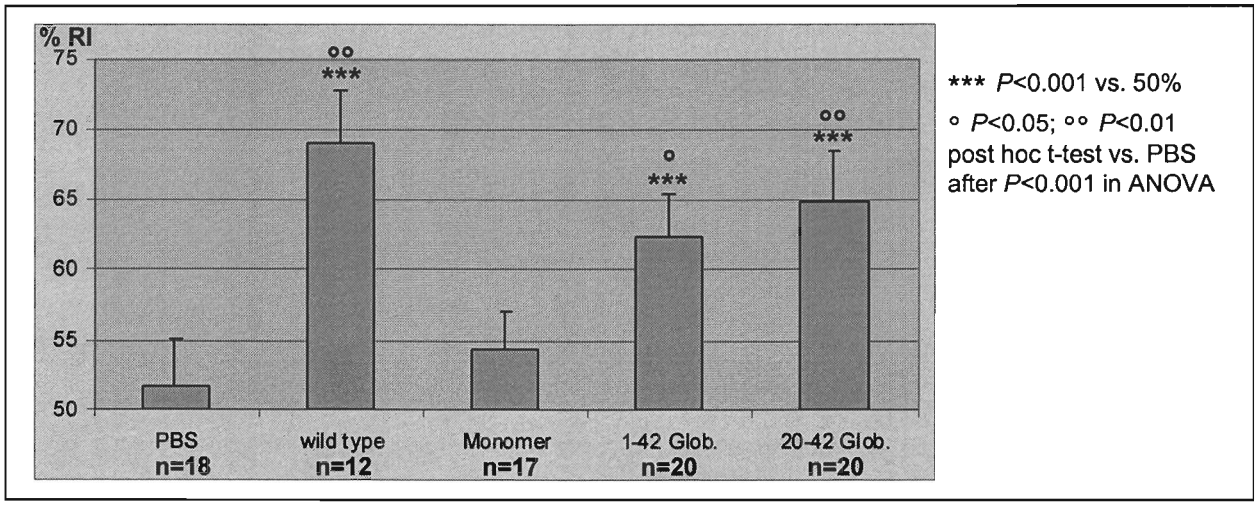

% RI
75
70
65
60
55
50
°°
***
°
***
°°
***
PBS
n=18
wild type
n=12
Monomer
n=17
1-42 Glob.
n=20
20-42 Glob.
n=20
*** P<0.001 vs. 50%
° P<0.05; °° P<0.01
post hoc t-test vs. PBS
after P<0.001 in ANOVA

FIG. 4

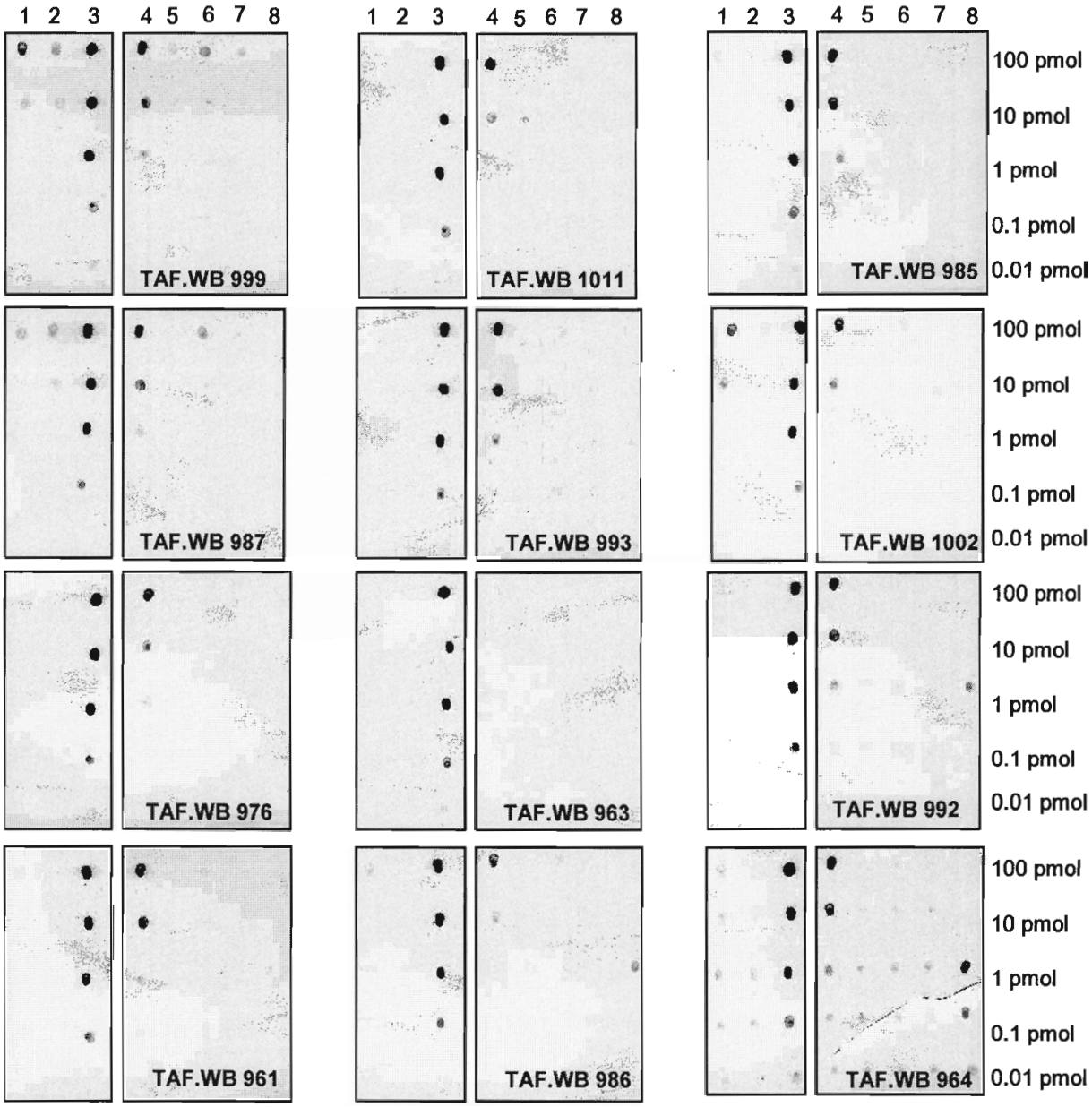

1 2 3 4 5 6 7 8
TAF.WB 999
TAF.WB 1011
TAF.WB 985
TAF.WB 987
TAF.WB 993
TAF.WB 1002
TAF.WB 976
TAF.WB 963
TAF.WB 992
TAF.WB 961
TAF.WB 986
TAF.WB 964
100 pmol
10 pmol
1 pmol
0.1 pmol
0.01 pmol

FIG. 5

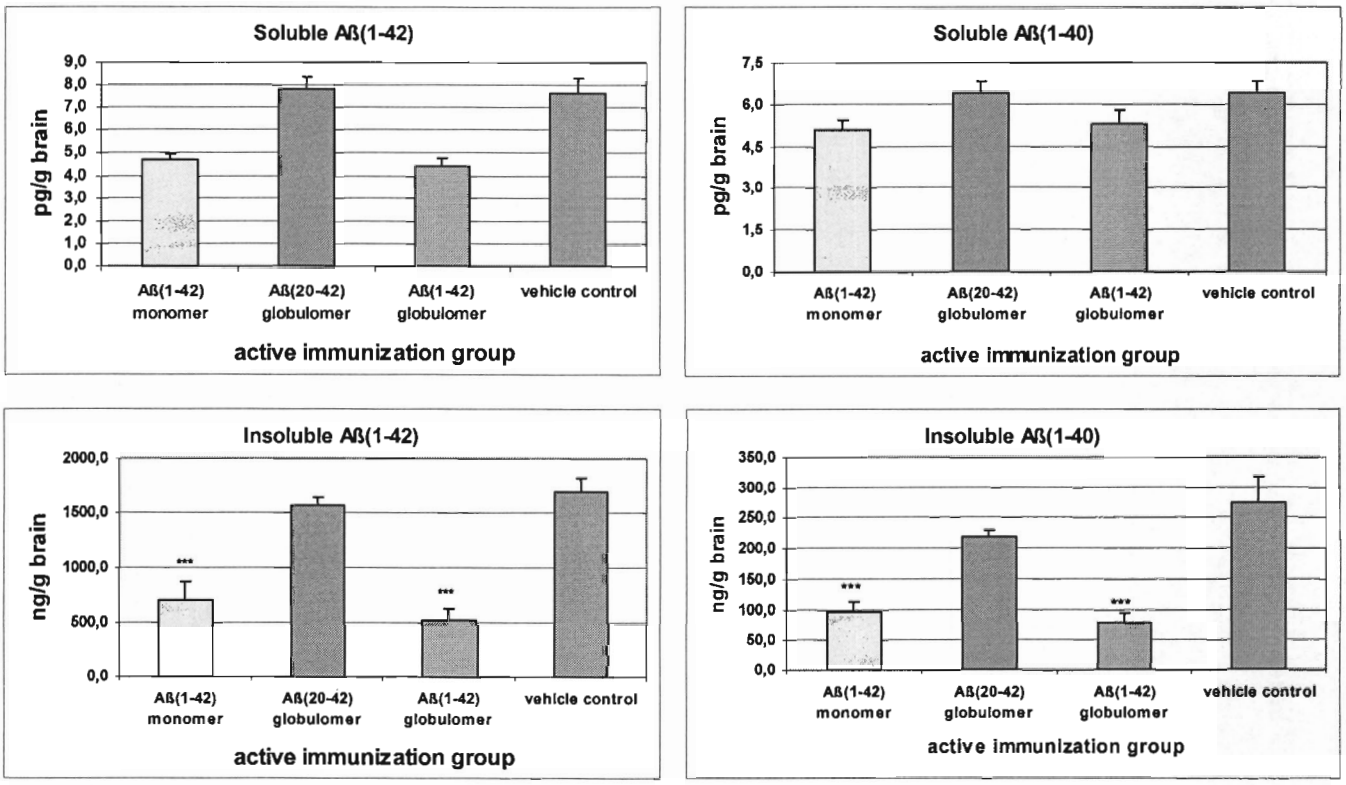
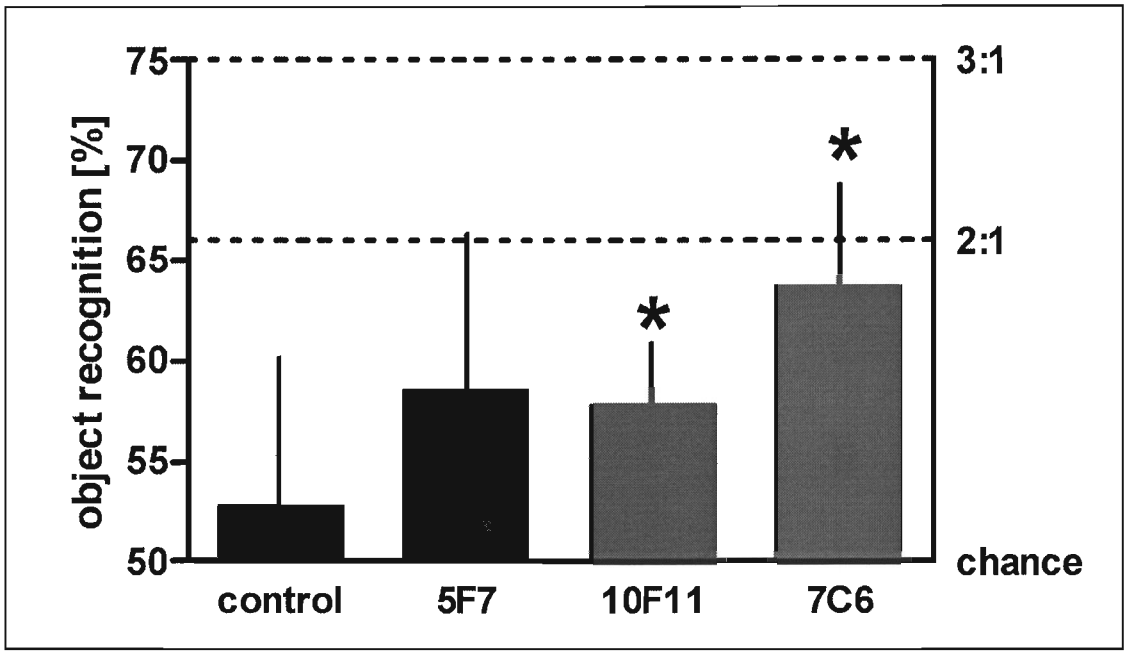

Soluble Aß(1-42)
pg/g brain
9,0
8,0
7,0
6,0
5,0
4,0
3,0
2,0
1,0
0,0
Aß(1-42) monomer
Aß(20-42) globulomer
Aß(1-42) globulomer
vehicle control
active immunization group
Soluble Aß(1-40)
pg/g brain
7,5
6,0
4,5
3,0
1,5
0,0
Aß(1-42) monomer
Aß(20-42) globulomer
Aß(1-42) globulomer
vehicle control
active immunization group
Insoluble Aß(1-42)
ng/g brain
2000,0
1500,0
1000,0
500,0
0,0
***
***
Aß(1-42) monomer
Aß(20-42) globulomer
Aß(1-42) globulomer
vehicle control
active immunization group
Insoluble Aß(1-40)
ng/g brain
350,0
300,0
250,0
200,0
150,0
100,0
50,0
0,0
***
***
Aß(1-42) monomer
Aß(20-42) globulomer
Aß(1-42) globulomer
vehicle control
active immunization group

FIG. 6

A


75
70
65
60
55
50
object recognition [%]
3:1
2:1
chance
*
*
control
5F7
10F11
7C6

B

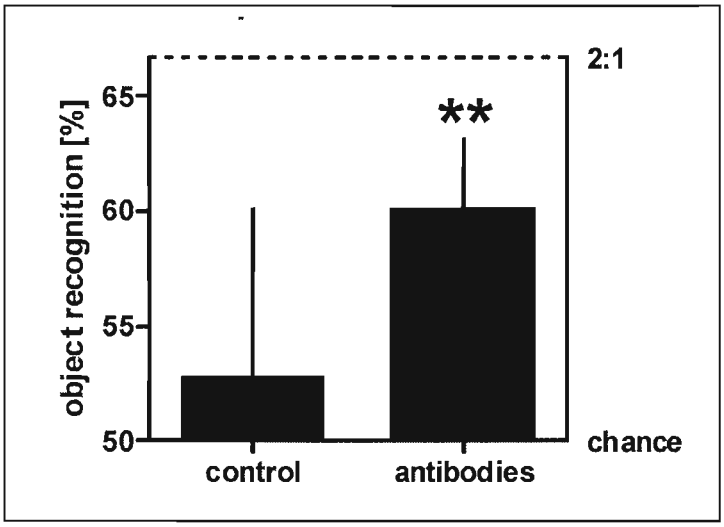
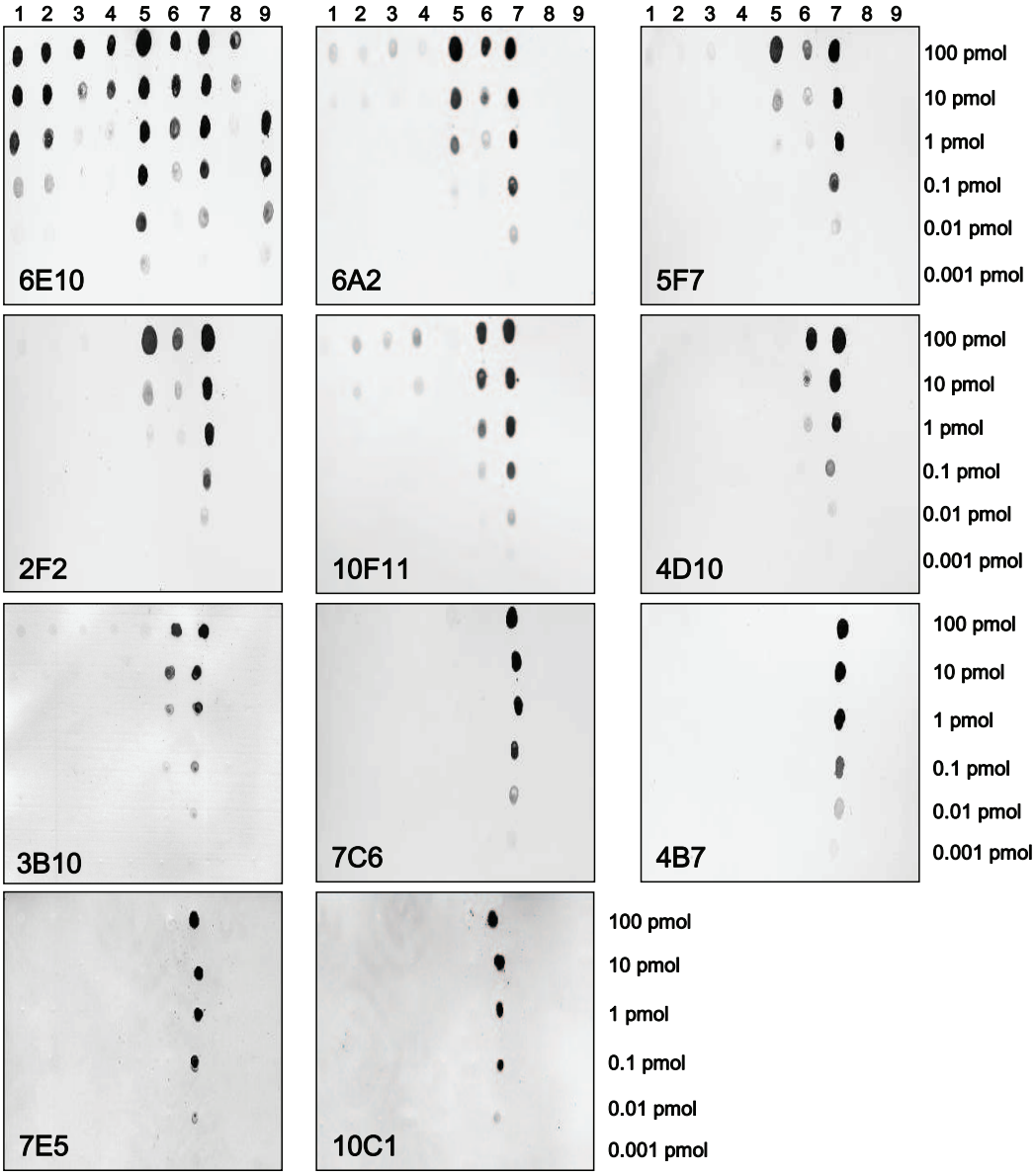

65
60
55
50
object recognition [%]
2:1
chance
**
control
antibodies

FIG. 7

A



B

	Aβ(1-42) monomer, 0.1% NH_4OH	Aβ(1-40) monomer, 0.1% NH_4OH	Aβ(1-42) monomer, 0.1% NaOH	Aβ(1-40) monomer, 0.1% NaOH	Aβ(1-42) globulomer	Aβ(12-42) globulomer	Aβ(20-42) globulomer	Aβ(1-42) fibril	sAPPα
6E10	10	17	505	322	0.2	9	1	510	0.3
6A2	7 840	5 078	7 717	38 583	47	138	1	337 931	> 1 000
5F7	26 955	> 10 000	23 455	164 182	226	242	1	> 10 000	> 100
2F2	36 827	> 10 000	> 10 000	> 10 000	195	274	1	> 10 000	> 100
10F11	83 267	3 719	17 417	2 233	77 985	12	1	294 366	> 1 000
4D10	> 10 000	43 535	> 10 000	35 069	> 10 000	29	1	> 10 000	> 100
3B10	16 364	22 500	45 000	> 10 000	30 000	14	1	> 10 000	> 100
7C6	> 100 000	> 100 000	> 100 000	> 100 000	94 052	> 100 000	1	> 100 000	> 1 000
4B7	> 100 000	> 457 971	> 100 000	> 100 000	> 100 000	> 100 000	1	> 100 000	> 1 000
7E5	> 100 000	> 100 000	> 100 000	> 100 000	> 100 000	> 100 000	1	> 100 000	> 1 000
10C1	> 100 000	> 100 000	> 100 000	> 100 000	40 000	> 100 000	1	> 100 000	> 1 000

FIG. 8

A

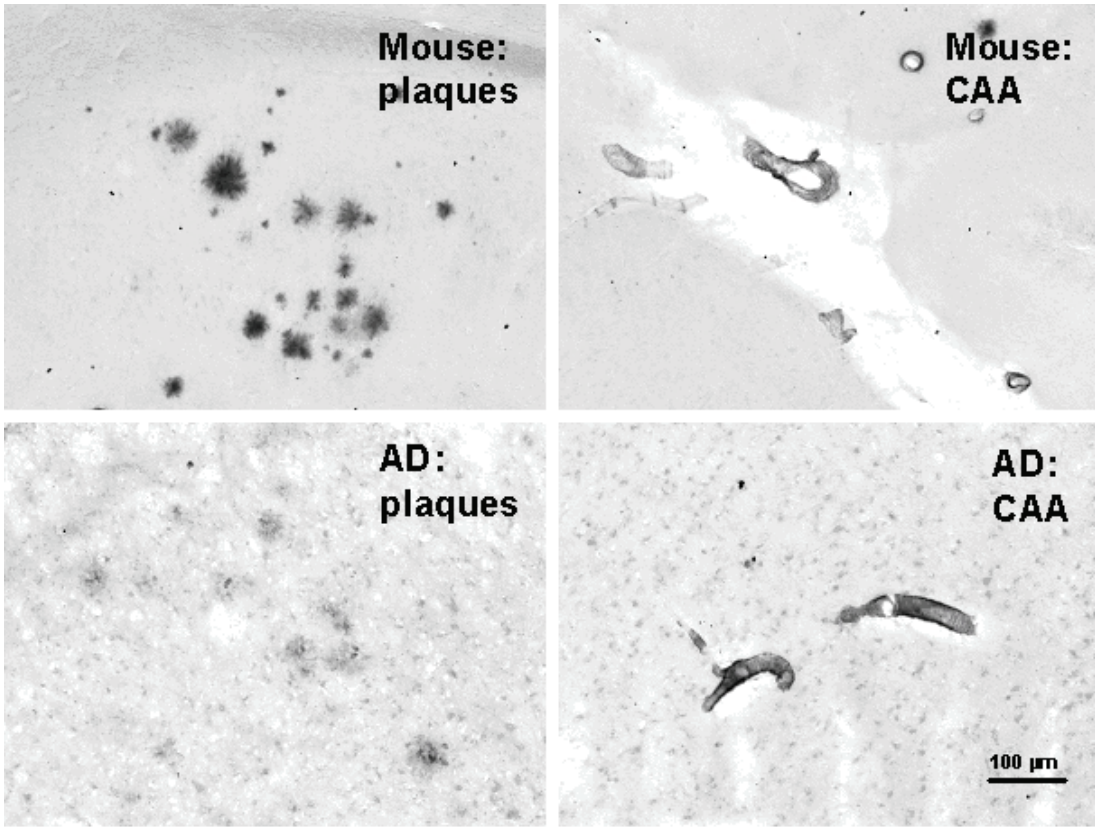


FIG. 8

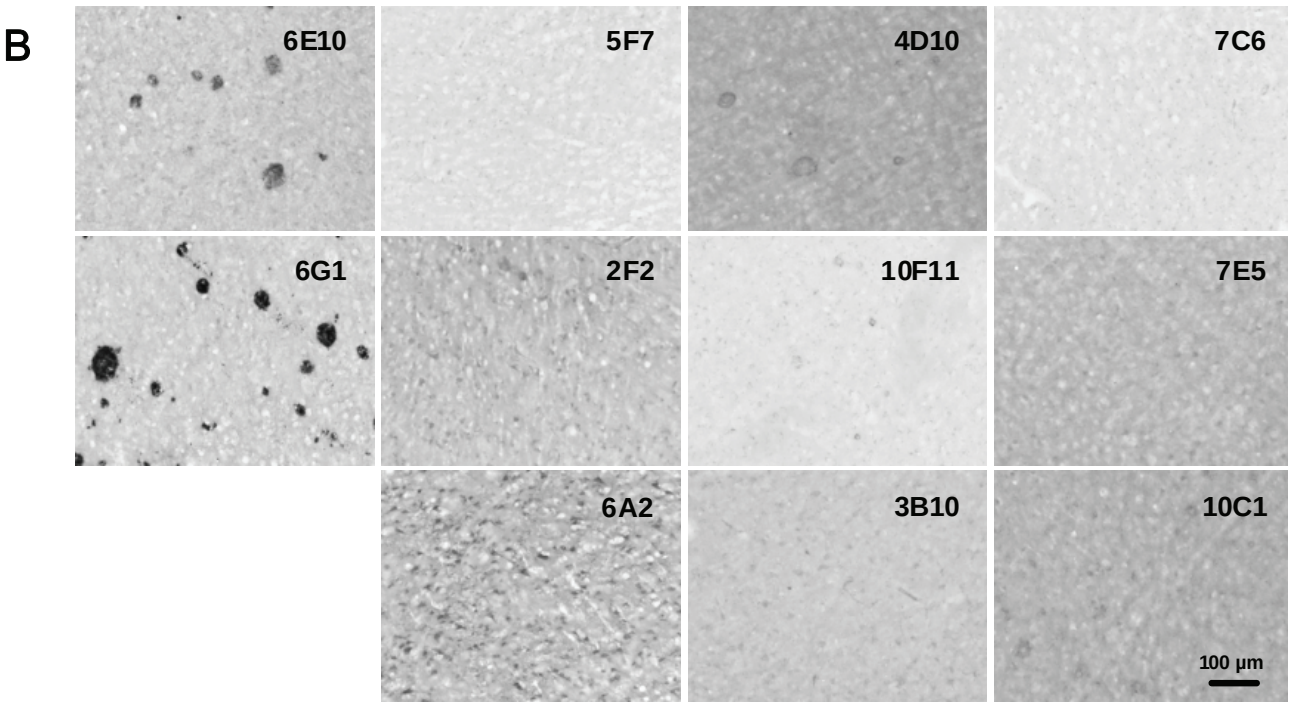


FIG. 8

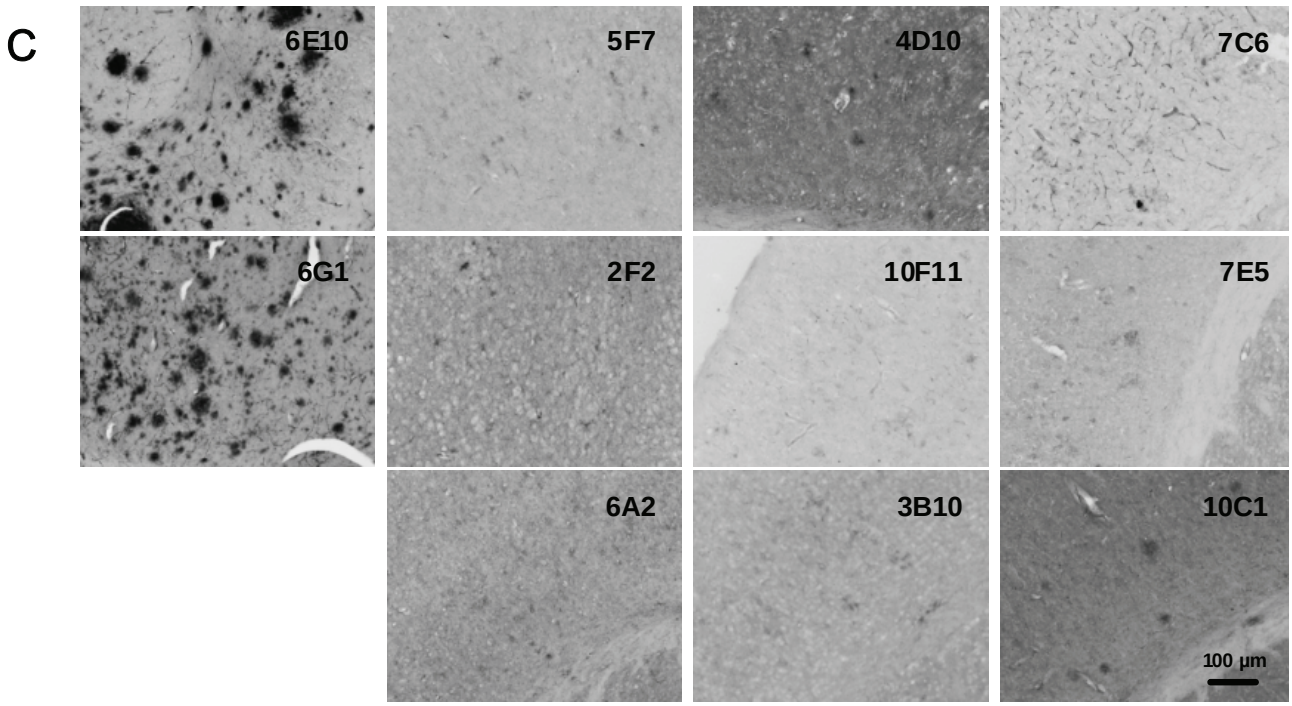
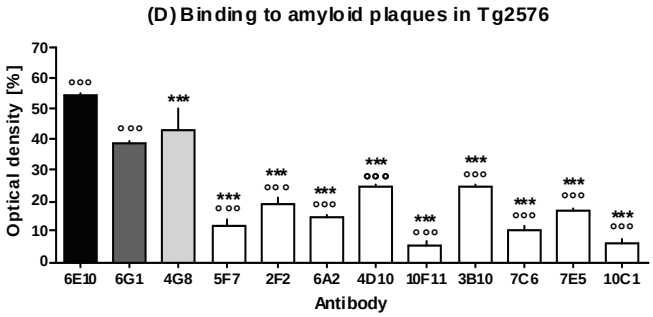
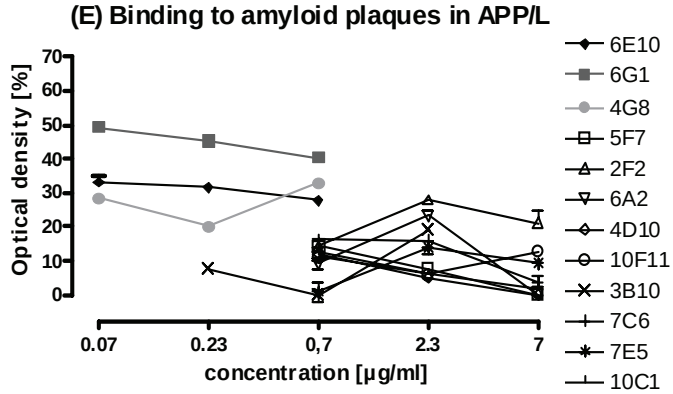
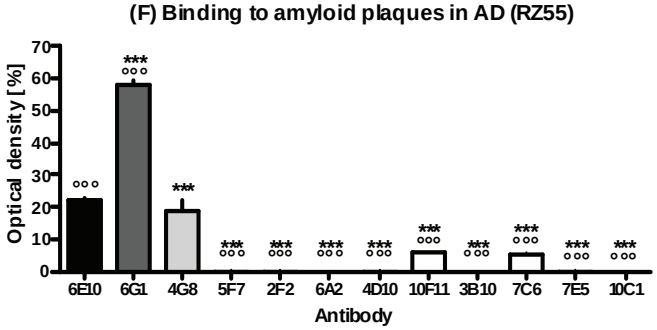


FIG. 8 (D-H)


(D) Binding to amyloid plaques in Tg2576
Optical density [%]
Antibody
6E10
6G1
4G8
5F7
2F2
6A2
4D10
10F11
3B10
7C6
7E5
10C1


(E) Binding to amyloid plaques in APP/L
Optical density [%]
concentration [µg/ml]
0.07
0.23
0,7
2.3
7
6E10
6G1
4G8
5F7
2F2
6A2
4D10
10F11
3B10
7C6
7E5
10C1


(F) Binding to amyloid plaques in AD (RZ55)
Optical density [%]
Antibody
6E10
6G1
4G8
5F7
2F2
6A2
4D10
10F11
3B10
7C6
7E5
10C1

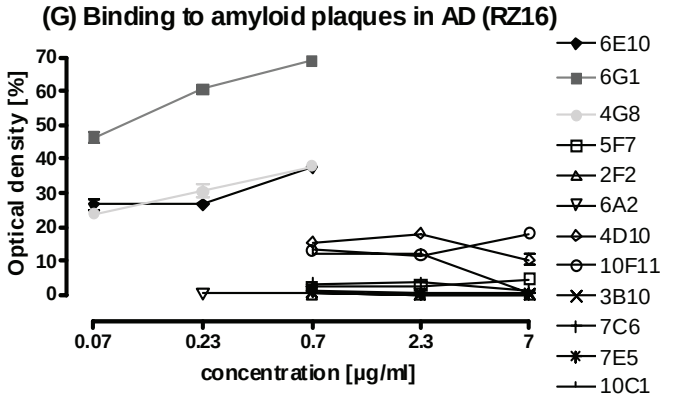

(G) Binding to amyloid plaques in AD (RZ16)
Optical density [%]
concentration [µg/ml]
0.07
0.23
0.7
2.3
7
6E10
6G1
4G8
5F7
2F2
6A2
4D10
10F11
3B10
7C6
7E5
10C1

FIG. 8

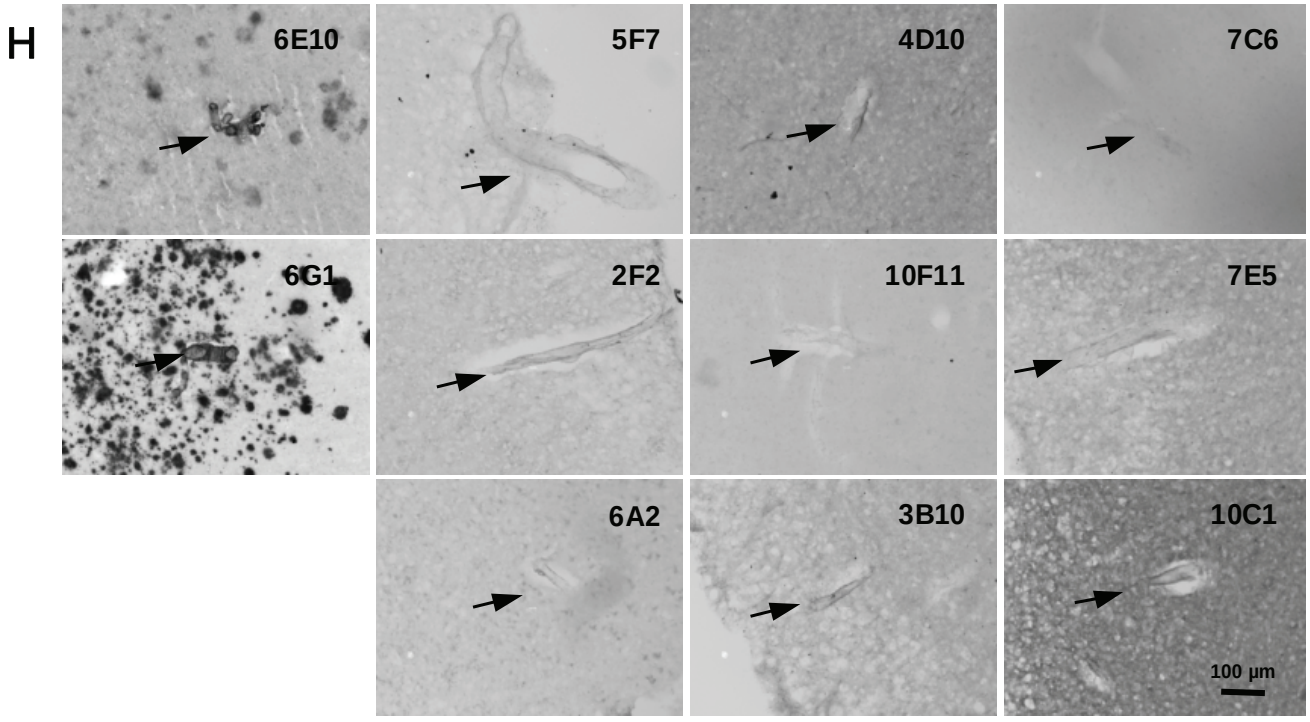


FIG. 9

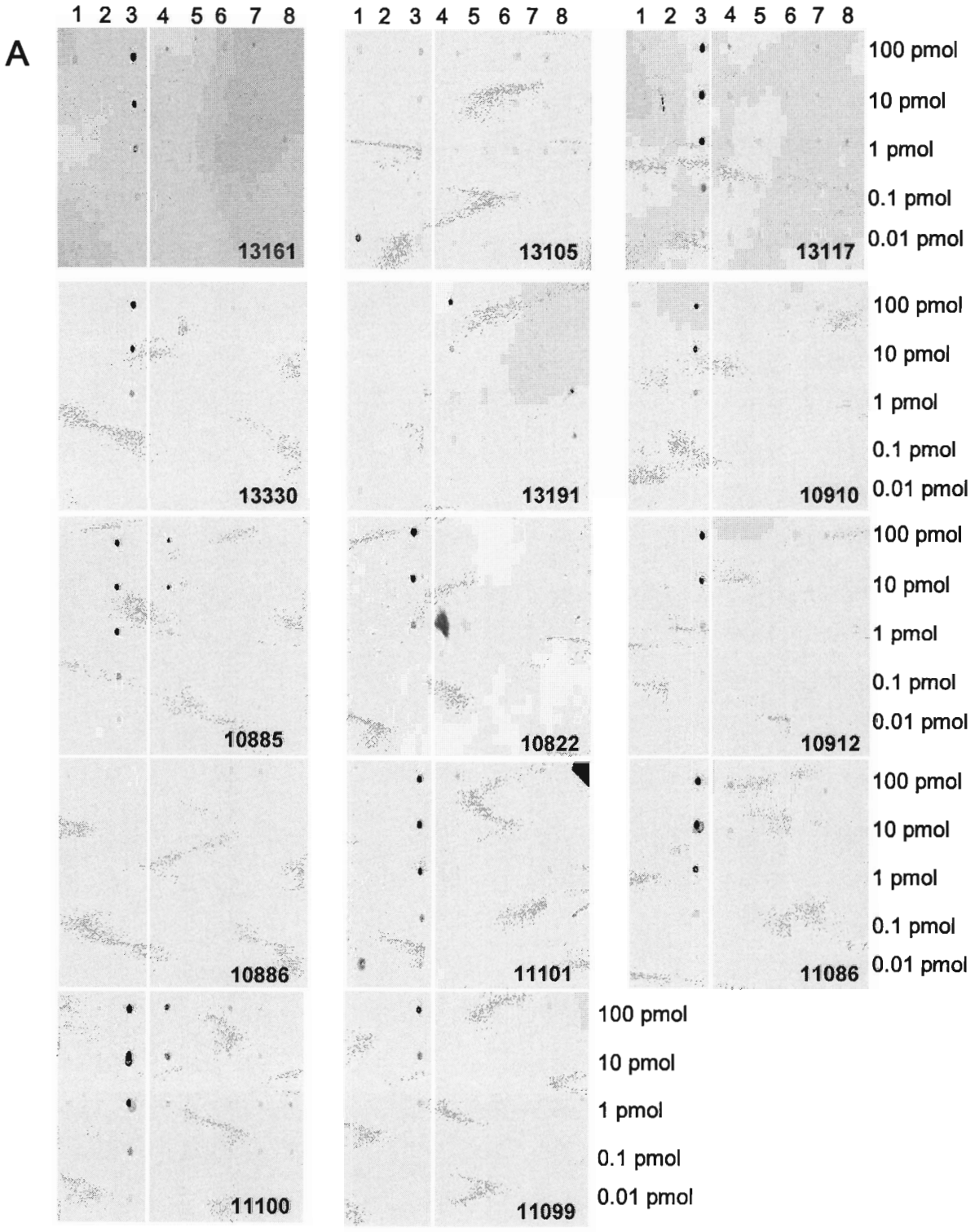

A
1 2 3 4 5 6 7 8
13161
13105
13117
13330
13191
10910
10885
10822
10912
10886
11101
11086
11100
11099
100 pmol
10 pmol
1 pmol
0.1 pmol
0.01 pmol

FIG. 9

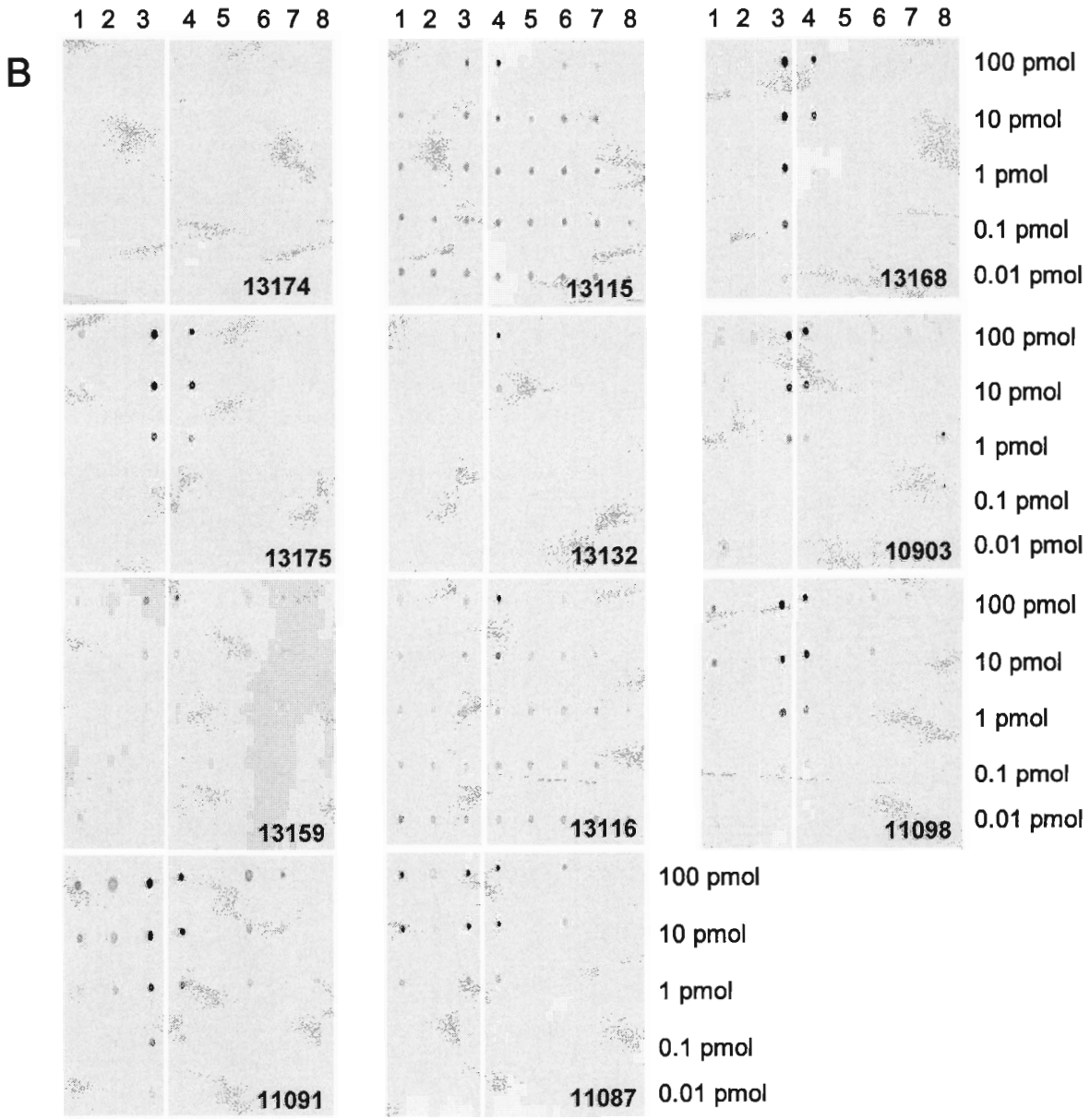

B
1 2 3 4 5 6 7 8
13174
13115
13168
13175
13132
10903
13159
13116
11098
11091
11087
100 pmol
10 pmol
1 pmol
0.1 pmol
0.01 pmol

FIG. 9

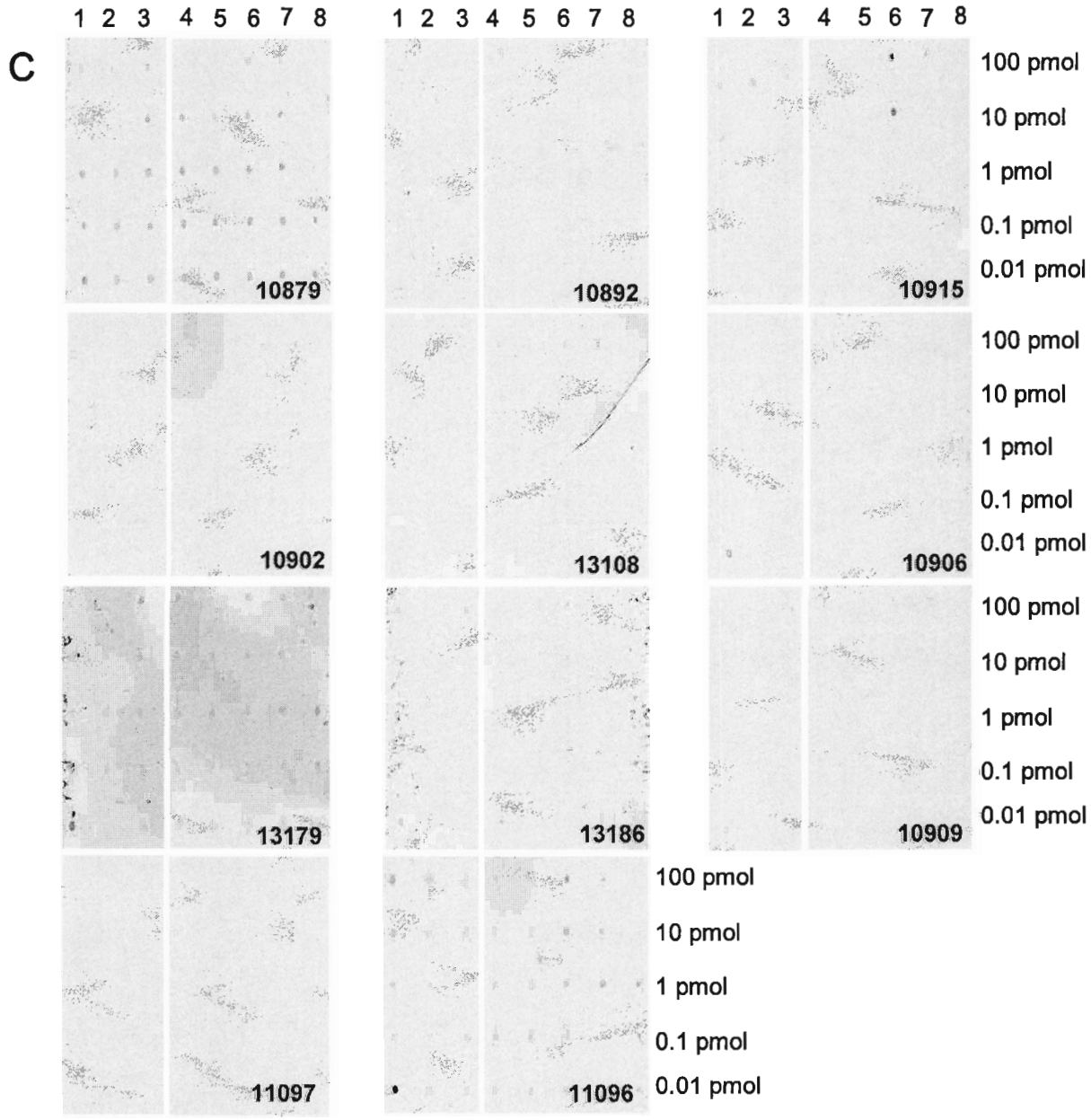

C
1 2 3 4 5 6 7 8
10879
10892
10915
10902
13108
10906
13179
13186
10909
11097
11096
100 pmol
10 pmol
1 pmol
0.1 pmol
0.01 pmol

FIG. 9

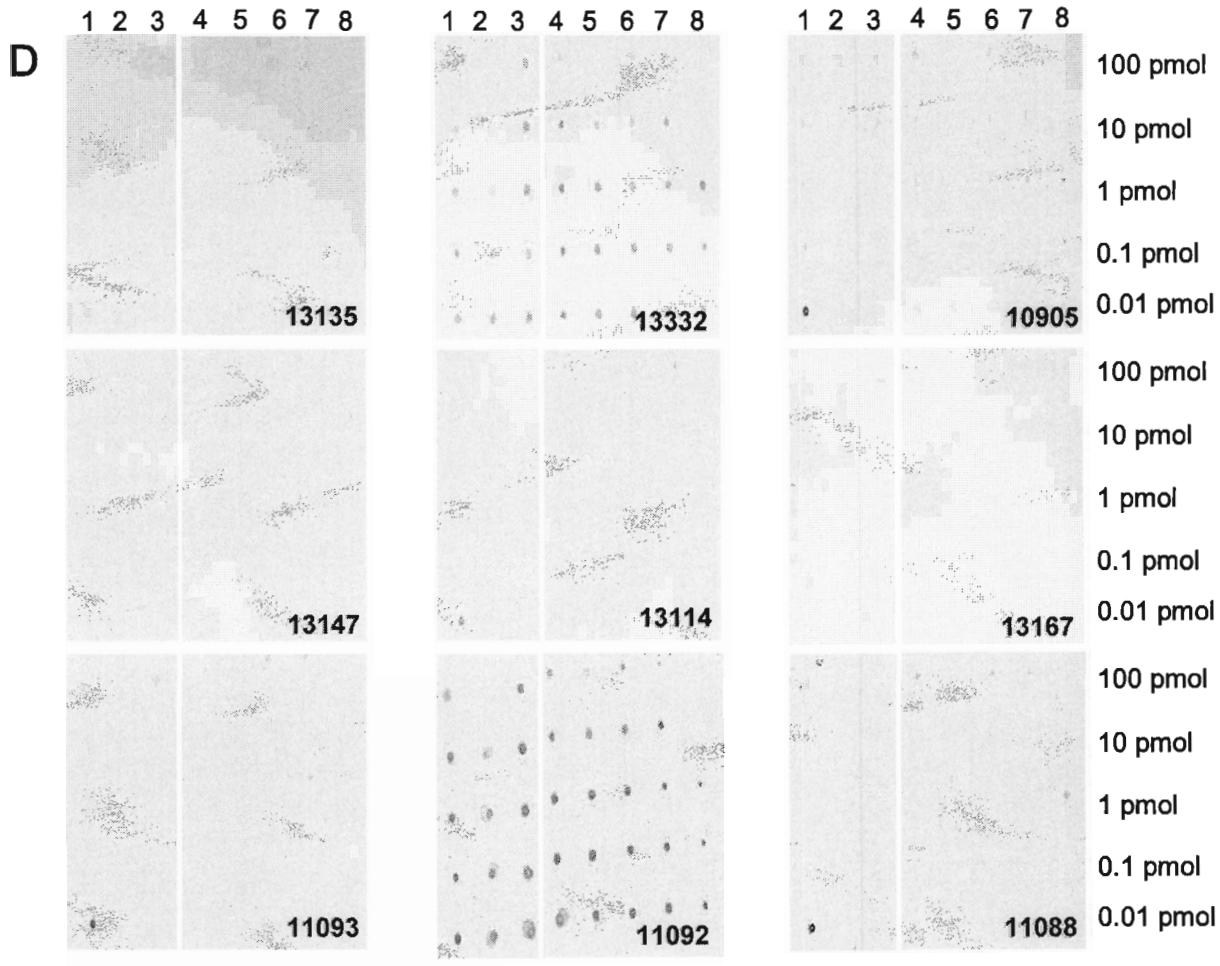

D
1 2 3 4 5 6 7 8
13135
13332
10905
13147
13114
13167
11093
11092
11088
100 pmol
10 pmol
1 pmol
0.1 pmol
0.01 pmol

FIG. 10

	7C6 ->BA199 Aβ(20-42) globulomer [pmol/g] brain tissue	10F11->BA199 Aβ(20-42) globulomer [pmol/g] brain tissue	5F7 ->BA199 Aβ(20-42) globulomer [pmol/g] brain tissue
RZ16 (AD)	50,1	10,6	10,2
RZ 52 (AD)	43,9	14,3	13,9
RZ 55 (AD)	13,9	2,9	3,6
RZ 92 (control)	< 0,2	< 0,06	< 0,06

FIG. 11

A1) VH ML15-5F7

SEQ ID NO:1

CAGGTCCAGCTGAAGCAGTCTGGAGCTGAGCTGGTGAGGCCTGGGACTTC
AGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACTACCTTCTATAT
ACACTGGGTGAAGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATG
ATTGGTCCTGGAAGTGGTAATACTTACTACAATGAGATGTTCAAGGACAA
GGCCACATTGACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCA
GCAGCCTCACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGCAAAG
TCAGCTCGGGCGGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCAC
TGTCTCTGCA

SEQ ID NO:3

QVQLKQSGAELVRPGTSVKMSCKASGYTFTTFYIHWVKQRPGQGLEWIGMI
GPGSGNTYYNEMFKDKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARAKSAR
AAWFAYWGQGTLVTVSA

A2) VL ML15-5F7

SEQ ID NO:2

GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGAT
CAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCGTTGTACAGAGTAATGG
AAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGC
TCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCA
GTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGA
GGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCTCC
CACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:4

DVLMTQTPLSLPVSLGDQASISCRSSQSVVQSNGNTYLEWYLQKPGQSPKLLI
YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGG
TKLEIKR

B1) VH ML15-10F11

SEQ ID NO:5

CAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTC
AGTGAAGATGTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTAT
GCACTGGGTGAAGCAGAGGCCTGGGCAGGGCCTTGAGTGGATTGGATATA
TTTATCCTTACAATGATGGTACTAAGTACAATGAGAAGTTCAAAGGCAAG
GCCACACTGACTTCAGACAAATCCTCCAGCACAGTATATATGGAGCTCAG
CAGCCTGACCTCTGAGGACTCTACAGTCTATTACTGTACAGTAGAGGGTG
CTACCTGGGACGGGTACTTCGATGTCTGGGGCACAGGGACCACGGTCACC
GTCTCCTCA

SEQ ID NO:7

QVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQRPGQGLEWIGYI
YPYNDGTKYNEKFKGKATLTSDKSSSTVYMELSSLTSEDSTVYYCTVEGATW
DGYFDVWGTGTTVTVSS

B2) VL ML15-10F11

SEQ ID NO:6

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAA
TCAGCCTCTATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAAAGGA
AAAACCTATTTGAATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGCG
CCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCAC
TGGCAGTGGATCAGGAACAGATTTTACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATTTGGGAGTTTATTACTGCGTGCAAGGTACACATTTTCCTCAC
ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:8

DVVMTQTPLTLSVTIGQSASISCKSSQSLLYSKGKTYLNWLLQRPGQSPKRLI
YLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPHTFGG
GTKLEIKR

C1) VH ML13-7C6

SEQ ID NO:9

GAAGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGT
CCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAGCTATGCCA
TGTCTTGGGTTCGCCAGACTCCAGCGAAGAGGCTAGAGTGGGTCGCGTCC
ATTCATAATAGAGGTACTATCTTCTATCTAGACAGTGTGAAGGGCCGATTC
ACCATCTCCAGAGATAATGTCAGGAACACCCTGTACCTGCAAATGAGCAG
TCTGAGGTCTGAGGACACGGCCATATATTACTGTACAAGAGGCCGGAGTA
ACTCCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCT
CG

SEQ ID NO:11

EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPAKRLEWVASIH
NRGTIFYLDSVKGRFTISRDNVRNTLYLQMSSLRSEDTAIYYCTRGRSNSYAM
DYWGQGTSVTVSS

C2) VL ML13-7C6

SEQ ID NO:10

GATGTTTTGGTGACCCAATCTCCACTCTCCCTGCCTGTCAGGCTTGGAGAT
CAAGCCTCCATCTCTTGCCGATCTACTCAGACCCTTGTACATCGTAATGGA
GACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGTC
CCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAG
CGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAG
GCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCGTAC
ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:12

DVLVTQSPLSLPVRLGDQASISCRSTQTLVHRNGDTYLEWYLQKPGQSPKSLI
YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGG
TKLEIKR

D1) VH ML15-4B7

SEQ ID NO:13

GAGGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGCTC
CCGGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTGACTACGAAAT
GGTGTGGGTTCGACAGGCTCCAGGGGAGGGGCTGGAGTGGGTTGCATACA
TTAGTAGTGGCAGTCGTACCATCCACTATGCAGACACAGTGAAGGGCCGA
TTCACCATCTCCAGAGACAATCCCAAGAACACCCTGTTCCTGCAAATGAG
CAGTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGGACATTAC
TACGGCTACACTTTGACTACTGGGGCCAAGGCACCATTCTCACAGTCTCCT
CA

SEQ ID NO:15

EVKLVESGGGLVQPGGSRKLSCAASGFTFSDYEMVWVRQAPGEGLEWVAYI
SSGSRTIHYADTVKGRFTISRDNPKNTLFLQMSSLRSEDTAMYYCARTLLRLH
FDYWGQGTILTVSS

D2) VL ML15-4B7

SEQ ID NO:14

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAG
AAGGTTACTATGAGCTGCAGGTCCAGTCAGAGCCTTTTCTATAGGAGCAA
TCAAAAGAACTTCTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTA
AACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCT
TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTG
AAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTATCC
GTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGG

SEQ ID NO:16

DIVMSQSPSSLAVSVGEKVTMSCRSSQSLFYRSNQKNFLAWYQQKPGQSPKL
LIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPWTFG
GGTKLEIKR

E1) VH ML15-2F2

SEQ ID NO:17

CAGGTCCAGCTGAAGCAGTCTGGAGCTGAGCTGGTGAGGCCTGGGACTTC
AGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACTACCTTCTATAT
ACACTGGGTGAAGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATG
ATTGGTCCTGGAAGTGGTAATACTTACTACAATGAGATGTTCAAGGACAA
GGCCACATTGACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCA
GCAGCCTCACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGCAAAG
TCAGCTCGGGCGGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCAC
TGTCTCTGCA

SEQ ID NO:19

QVQLKQSGAELVRPGTSVKMSCKASGYTFTTFYIHWVKQRPGQGLEWIGMI
GPGSGNTYYNEMFKDKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARAKSAR
AAWFAYWGQGTLVTVSA

E2) VL ML15-2F2

SEQ ID NO:18

GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGAT
CAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCGTTGTACAGAGTAATGG
AAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGC
TCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCA
GTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGA
GGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCTCC
CACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:20

DVLMTQTPLSLPVSLGDQASISCRSSQSVVQSNGNTYLEWYLQKPGQSPKLLI
YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGG
TKLEIKR

F1) VH ML15-6A2

SEQ ID NO:21

CAGGTCCAGCTGCAGCAGTCTGGAGCTGAGCTGGTGAGGCCTGGGACTTC
AGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTCACTACCTTCTATAT
ACACTGGGTGAGGCAGAGGCCTGGACAGGGCCTTGAGTGGATTGGAATG
ATTGGTCCTGGAAGTGGTAATACTTACTACAATGAGATGTTCAAGGACAA
GGCCACATTGACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCA
GCAGCCTCACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAGCAAAG
TCACATCGGGCGGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCAC
TGTCTCTGCA

SEQ ID NO:23

QVQLQQSGAELVRPGTSVKMSCKASGYTFTTFYIHWVRQRPGQGLEWIGMI
GPGSGNTYYNEMFKDKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARAKSHR
AAWFAYWGQGTLVTVSA

F2) VL ML15-6A2

SEQ ID NO:22

GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGAT
CAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCGTTGTACAGAGTAATGG
AAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGC
TCCTGATCTACAAAGTTTCCAACCGATTTTTTGGGGTCCCAGACAGGTTCA
GTGGCAGTAGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGA
GGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCTCC
CACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:24

DVLMTQTPLSLPVSLGDQASISCRSSQSVVQSNGNTYLEWYLQKPGQSPKLLI
YKVSNRFFGVPDRFSGSRSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGG
TKLEIKR

G1) VH ML13-4D10

SEQ ID NO:25

CAGGTGCAGCTGAAGCAGTCAGGACCTAGCCTAATACAGCCCTCACAGAG
CCTGTCCATAACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGT
ACACTGGGTTCGCCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGA
TATGGAGAGGTGGAAGGATAGACTATAATGCAGCTTTCATGTCCAGACTG
AGCATCACCAAGGACAACTCCAAGAGCCAAGTTTTCTTTAAAATGAACAG
TCTGCAAGCTGATGACACTGCCATATACTACTGTGCCAGAAACTCCGATG
TCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA

SEQ ID NO:27

QVQLKQSGPSLIQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWR
GGRIDYNAAFMSRLSITKDNSKSQVFFKMNSLQADDTAIYYCARNSDVWGT
GTTVTVSS

G2) VL ML13-4D10

SEQ ID NO:26

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAA
CCAGCCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATATTGATGGA
AAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCG
CCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCAC
TGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAG
GCTGAGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCGTAC
ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG

SEQ ID NO:28

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDIDGKTYLNWLLQRPGQSPKRLIY
LVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGG
TKLEIKR

H1) VH ML15-7E5

SEQ ID NO:29

GAGGTGAAGCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGCTC
CCGGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTGACTACGAAAT
GGTGTGGGTTCGACAGGCTCCAGGGGAGGGGCTGGAGTGGGTTGCATACA
TTAGTAGTGGCAGTCGTACCATCCACTATGCAGACACAGTGAAGGGCCGG
TTCACCATCTCCAGAGACAATCCCAAGAACACCCTGTTCCTGCAAATGAG
CAGTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGGACATTAC
TACGGCTACACTTTGACTACTGGGGCCAAGGCACCATTCTCACAGTCTCCT
CA

SEQ ID NO:31

EVKLVESGGGLVQPGGSRKLSCAASGFTFSDYEMVWVRQAPGEGLEWVAYI
SSGSRTIHYADTVKGRFTISRDNPKNTLFLQMSSLRSEDTAMYYCARTLLRLH
FDYWGQGTILTVSS

H2) VL ML15-7E5

SEQ ID NO:30

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAG
AAGGTTACTATGAGCTGCAGGTCCAGTCAGAGCCTTTTCTATAGGAGCAA
TCAAAAGAACTTCTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTA
AACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCT
TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTG
AAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTATCC
GTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGG

SEQ ID NO:32

DIVMSQSPSSLAVSVGEKVTMSCRSSQSLFYRSNQKNFLAWYQQKPGQSPKL
LIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSYPWTFG
GGTKLEIKR

I1) VH ML15-10C1

SEQ ID NO:33

GAGGTGAAGCTGGTGGAGTCTGGGGGAGGTTTAGTGCAGCCTGGAGGCTC
CCGGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTGACTACGAAAT
GGTGTGGGTTCGACAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCATACA
TTAATAGTGGCAGTGGTACCATCCACTATGCAGACACAGTGAAGGGCCGA
TTCACCATCTCCAGAGACAATCCCAAGAACACCCTGTTCCTGCAAATGAG
CAGTCTAAGGTCTGAGGACACGGCCATGTATTACTGTGCAAGGACATTAC
TACGGCTACACTTTGACTACTGGGGCCAAGGCACCATTCTCACTGTCTCCT
CA

SEQ ID NO:35

EVKLVESGGGLVQPGGSRKLSCAASGFTFSDYEMVWVRQAPGKGLEWVAYI
NSGSGTIHYADTVKGRFTISRDNPKNTLFLQMSSLRSEDTAMYYCARTLLRLH
FDYWGQGTILTVSS

I2) VL ML15-10C1

SEQ ID NO:34

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAG
AAGGTTACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTCTATAGTCGCAAT
CAAAAGAACTTCTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAA
ACTGCTGATTTACTGGGCATCCACTGGGGAATCTGGGGTCCCTGATCGCTT
CACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGA
AGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTTTAGCTATCCGT
GGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGG

SEQ ID NO:36

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLFYSRNQKNFLAWYQQKPGQSPKL
LIYWASTGESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYFSYPWTFG
GGTKLEIKR

J1) VH ML15-3B10

SEQ ID NO:37

CAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTC
AGTGAAGATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTATGTTAT
ACACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGAGTGGATTGGATATA
TTAATCCTTACAATGATGGTACTCAGTACAATGAGAAGTTCAAAGGCAAG
GCCACACTGACTTCAGACAAATCCTCCAGCACAGTCTACATGGAGCTCAG
CAGTCTGACCTCTGAGGACTCTACAGTCTACTACTGTACAGTAGAGGGTG
GTACCTGGGACGGGTATTTCGATGTCTGGGGCACAGGGACCACGGTCACC
GTCTCCTCA

SEQ ID NO:38

QVQLQQSGPELVKPGASVKMSCKASGYTFTDYVIHWVKQKPGQGLEWIGYI
NPYNDGTQYNEKFKGKATLTSDKSSSTVYMELSSLTSEDSTVYYCTVEGGTW
DGYFDVWGTGTTVTVSS