FIG. 1

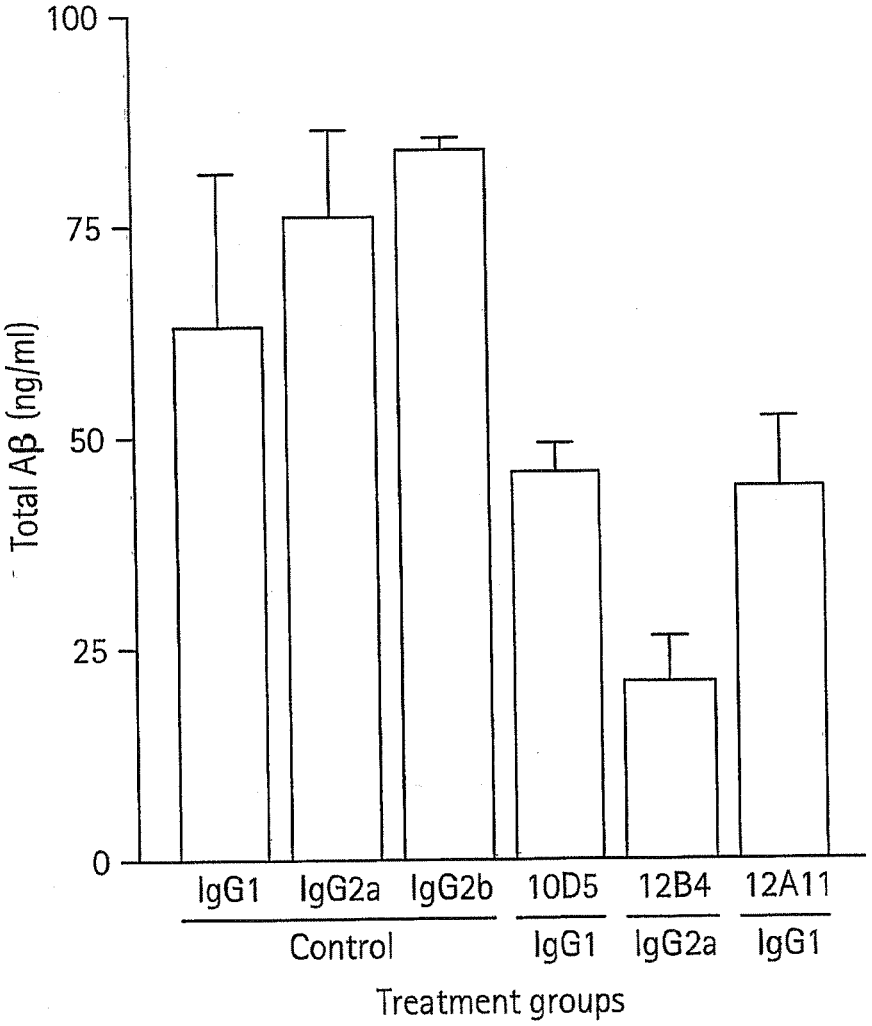

100
75
50
25
0
Total Aβ (ng/ml)
IgG1
IgG2a
IgG2b
10D5
12B4
12A11
Control
IgG1
IgG2a
IgG1
Treatment groups

FIG. 2A

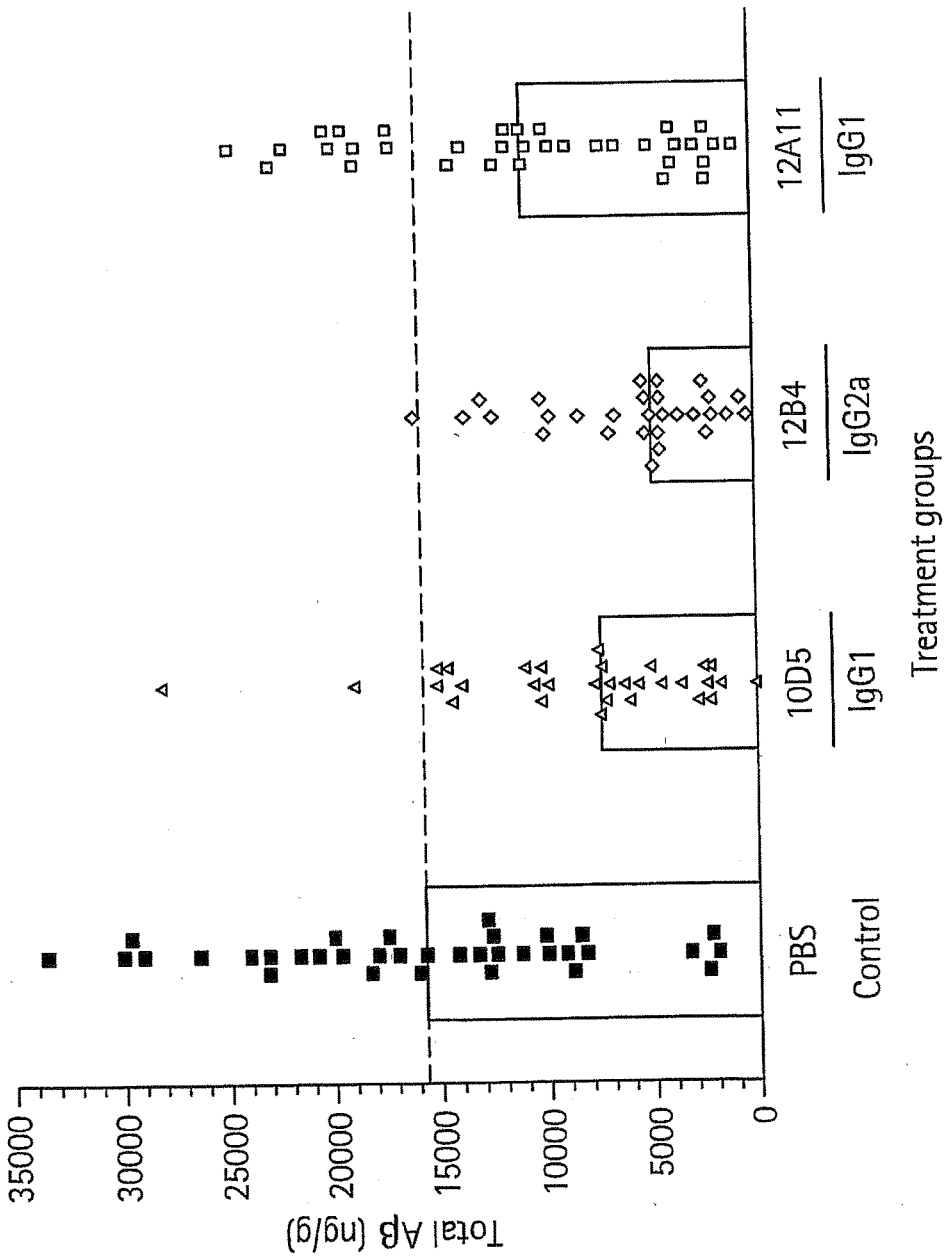

Total Aβ (ng/g)
35000
30000
25000
20000
15000
10000
5000
0
PBS
Control
10D5
IgG1
12B4
IgG2a
12A11
IgG1
Treatment groups

FIG. 2B

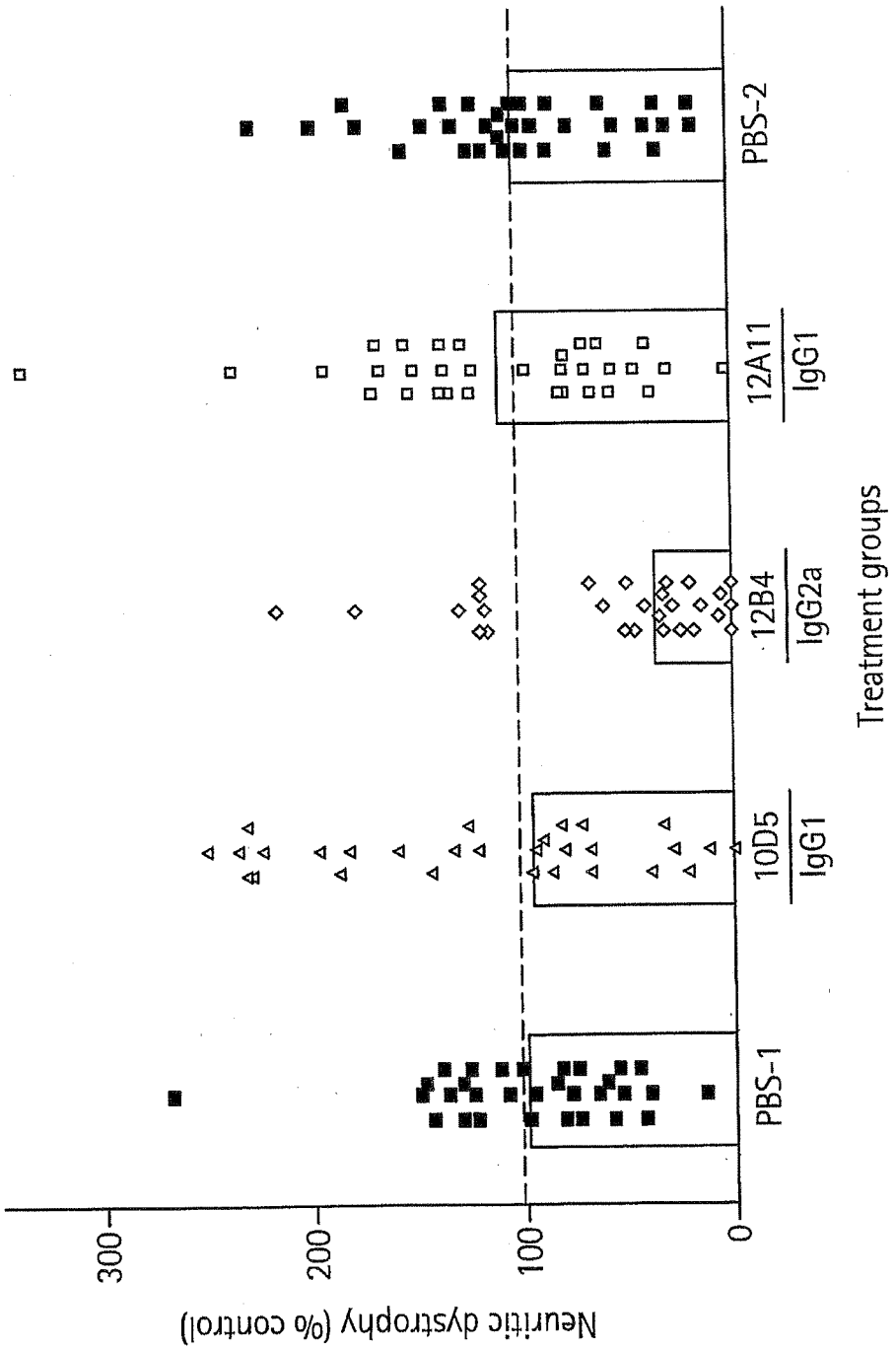

Neuritic dystrophy (% control)
300
200
100
0
PBS-1
10D5
IgG1
12B4
IgG2a
12A11
IgG1
PBS-2
Treatment groups

FIG. 3A


HindIII
CMGMAAGCTTGCCGCCACCATGAAGTTGCCTGTTAGGCTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTTTGATGACCCAAACTCCA 100
M K L P V R L L V L M F W I P A S S S D V L M T Q T P
VL
KpnI
CTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTACTTAGAATGGTACC 200
L S L P V S L G D Q A S I S C R S S Q S I V H S N G N T Y L E W Y
VL
CDR
L1
PstI
EcoO109I
TGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGA 300
L Q K P G Q S P K L L I Y K V S N R F S G V P D R F S G S G S G T D
VL
CDR
L2
TTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAATTTATTACTGCTTTCAAAGTTCACATGTTCCTCTCACGTTCGGTGCTGGGACCAAG 400
F T L K I S R V E A E D L G I Y Y C F Q S S H V P L T F G A G T K
VL
CDR
L3
BamHI
CTGGAGCTGAAACGTGAGTGGATCCTMGR 429
L E L K
VL

FIG. 3B

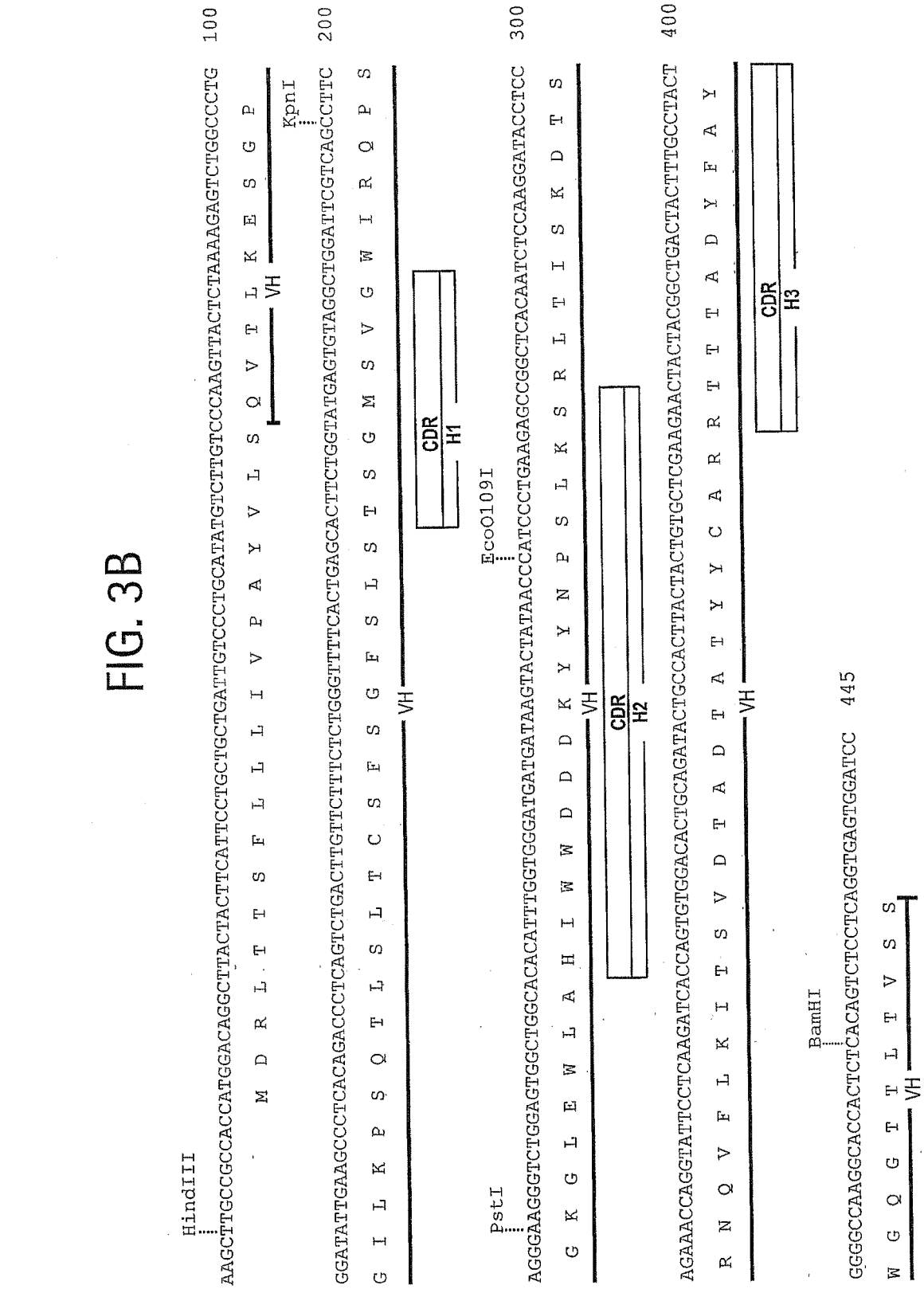

HindIII
AAGCTTGCCGCCACCATGGACAGGCTTACTTCCTCATTCCTGCTGCTGATTGTCCCTGCATATGTCTTGTCCCAAGTTACTCTAAAAGAGTCTGGCCCTG 100
M D R L T T S F L L L I V P A Y V L S Q V T L K E S G P
VH
KpnI
GGATATTGAAGCCCTCACAGACCCTCAGTCTGACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGAGTGTAGGCTGGATTCGTCAGCCTTC 200
G I L K P S Q T L S L T C S F S G F S L S T S G M S V G W I R Q P S
VH
CDR
H1
PstI
EcoO109I
AGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATGATAAGTACTATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC 300
G K G L E W L A H I W W D D D K Y Y N P S L K S R L T I S K D T S
VH
CDR
H2
AGAAACCAGGTATTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACTTACTACTGTGCTCGAAGAACTACTACGGCTGACTACTTTGCCTACT 400
R N Q V F L K I T S V D T A D T A T Y Y C A R R T T T A D Y F A Y
VH
CDR
H3
BamHI
GGGGCCAAGGCACCACTCTCACAGTCTCCTCAGGTGAGTGGATCC 445
W G Q G T T L T V S S
VH

FIG. 4

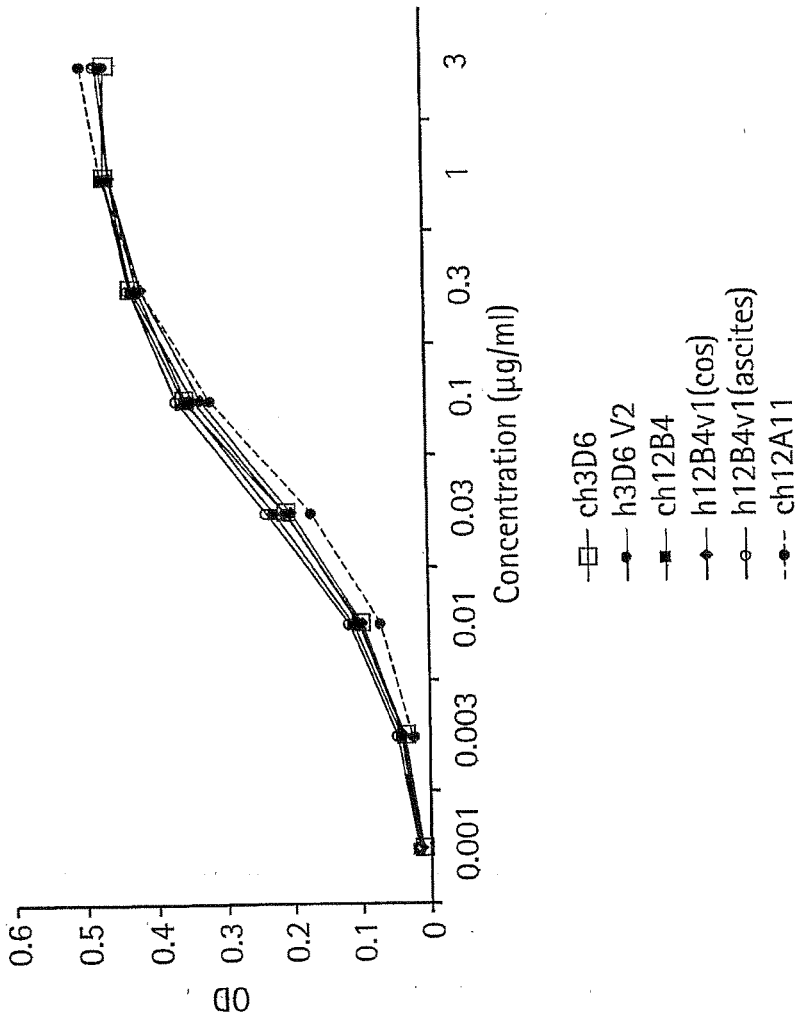

Aß 1-42 Binding Assay
ch3D6/h3D6v2/ch12B4/h12B4v1/ch12A11
OD
0.6
0.5
0.4
0.3
0.2
0.1
0
0.001
0.003
0.01
0.03
0.1
0.3
1
3
Concentration (µg/ml)
ch3D6
h3D6 V2
ch12B4
h12B4v1(cos)
h12B4v1(ascites)
ch12A11

FIG. 5A

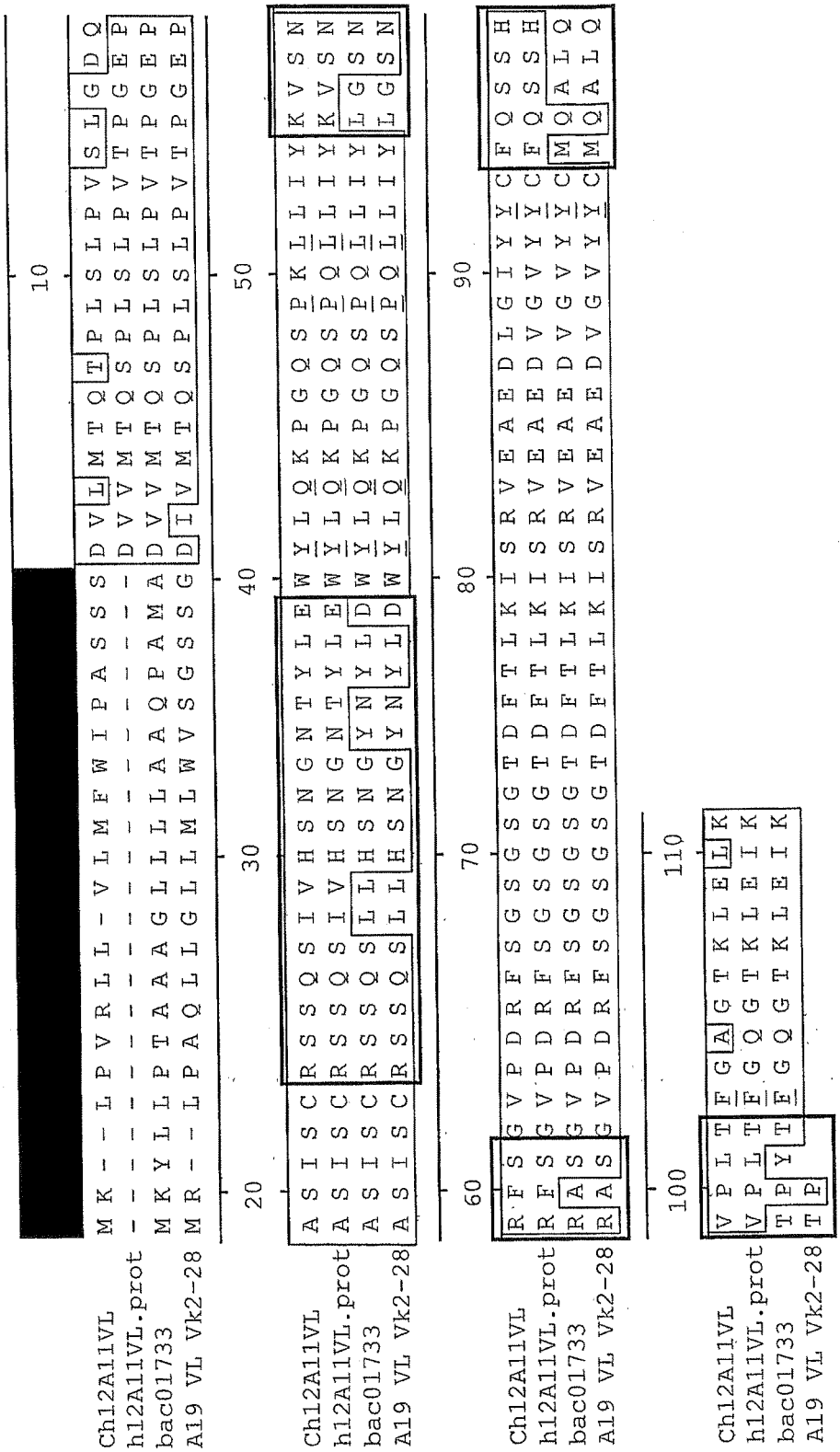

h12A11 VL Design
Ch12A11VL
h12A11VL.prot
bac01733
A19 VL Vk2-28

FIG. 5B

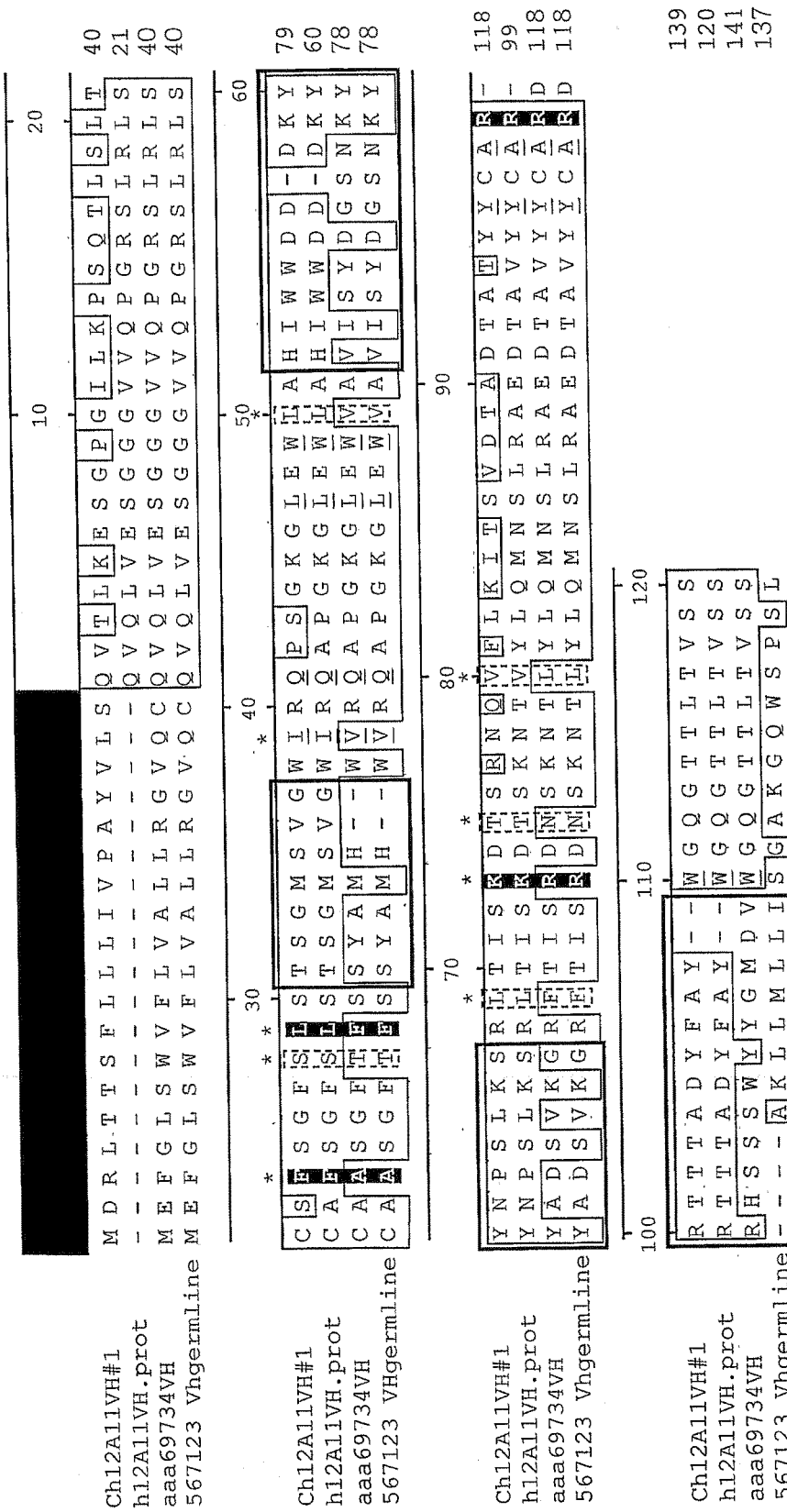

Ch12A11VH#1
h12A11VH.prot
aaa69734VH
567123 Vhgermline
10
20
30
40
50
60
70
80
90
100
110
120
40
21
40
40
79
60
78
78
118
99
118
118
139
120
141
137

FIG.6A

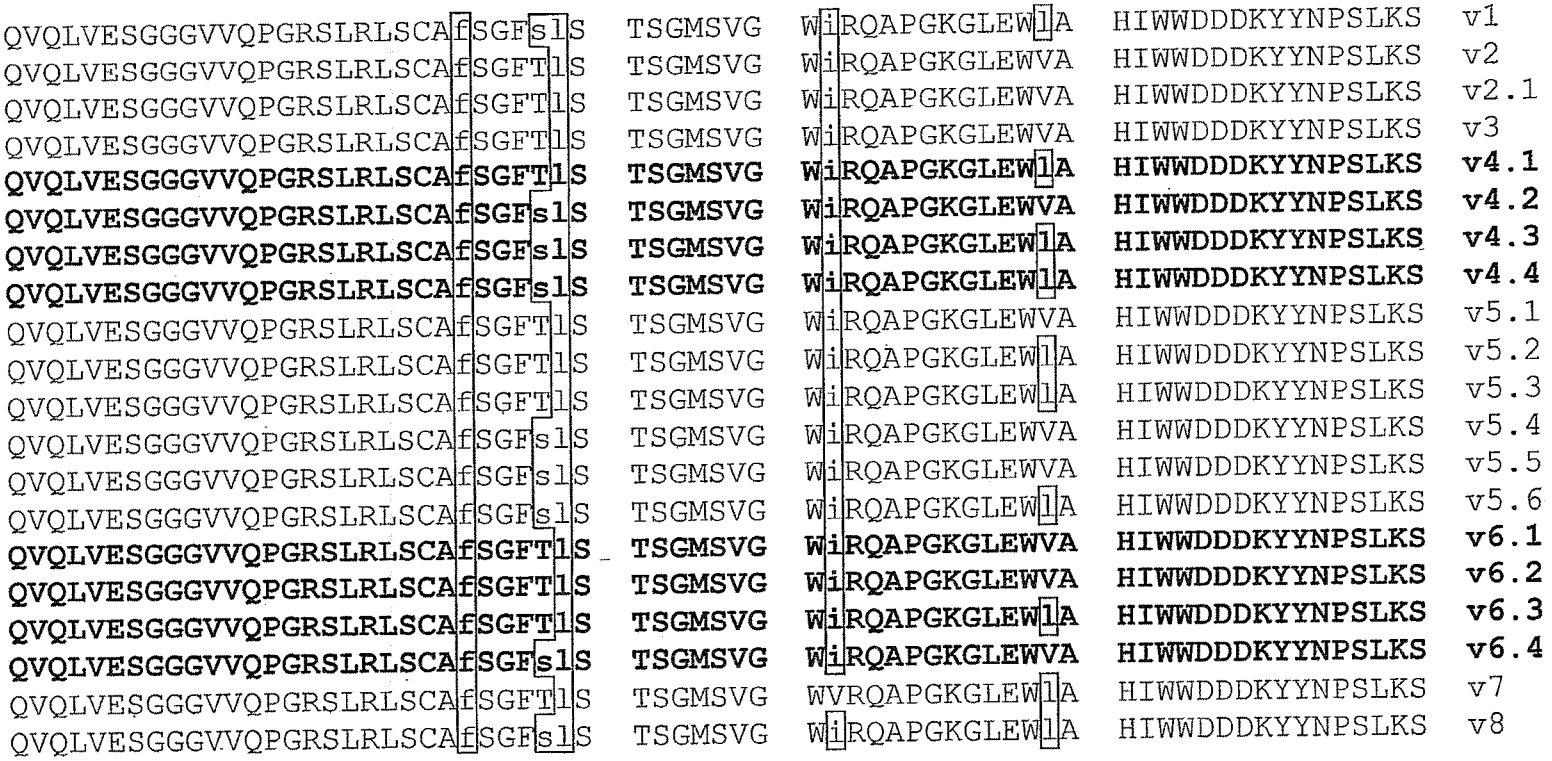

QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v1
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v2
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v2.1
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v3
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v4.1
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v4.2
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v4.3
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v4.4
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v5.1
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v5.2
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v5.3
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v5.4
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v5.5
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v5.6
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v6.1
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v6.2
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v6.3
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWVA HIWWDDDKYYNPSLKS v6.4
QVQLVESGGGVVQPGRSLRLSCAfSGFTlS TSGMSVG WVRQAPGKGLEWlA HIWWDDDKYYNPSLKS v7
QVQLVESGGGVVQPGRSLRLSCAfSGFslS TSGMSVG WiRQAPGKGLEWlA HIWWDDDKYYNPSLKS v8

FIG. 6B

R[I]TIS[k]D[t]S[K]NT[V]YLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v1
RFTIS[k]D[t]S[K]NTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v2
RFTIS[k]DNSKNTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v2.1
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v3
R[I]TIS[k]D[t]S[K]NT[V]YLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v4.1**
R[I]TIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v4.2**
R[I]TIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v4.3**
RFTIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v4.4**
R[I]TIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v5.1**
R[I]TIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v5.2
RFTIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v5.3
R[I]TIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v5.4
RFTIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v5.5
R[I]TIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v5.6
RFTIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	**v6.1**
RFTIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v6.2**
R[I]TIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v6.3**
RFTIS[k]D[t]SKNTLYLQMNSLRAEDTAVYYCAR	**RTTTADYFAY**	**WGQGTTVTVSS**	**v6.4**
R[I]TIS[k]D[t]SKNTVYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v7
R[I]TIS[k]DNSKNTVYLQMNSLRAEDTAVYYCAR	RTTTADYFAY	WGQGTTVTVSS	v8

FIG. 6C

>vh design	A24F	T28S	F29L	V37I	V48L	F67L	R71K	N73T	L78V - version 1
>vh design	A24F		F29L	V37I			R71K	N73T	- version 2
>vh design	A24F		F29L	V37I			R71K		- version 2.1
>vh design	A24F		F29L	V37I					- version 3
>vh design	**A24F**		**F29L**	**V37I**	**V48L**	**F67L**	**R71K**	**N73T**	**L78V - version 4.1**
>vh design	**A24F**	**T28S**	**F29L**	**V37I**		**F67L**	**R71K**	**N73T**	**L78V - version 4.2**
>vh design	**A24F**	**T28S**	**F29L**	**V37I**	**V48L**		**R71K**	**N73T**	**L78V - version 4.3**
>vh design	**A24F**	**T28S**	**F29L**	**V37I**	**V48L**	**F67L**	**R71K**	**N73T**	**- version 4.4**
>vh design	A24F		F29L	V37I		F67L	R71K	N73T	L78V - version 5.1
>vh design	A24F		F29L	V37I	V48L		R71K	N73T	L78V - version 5.2
>vh design	A24F		F29L	V37I	V48L	F67L	R71K	N73T	- version 5.3
>vh design	A24F	T28S	F29L	V37I			R71K	N73T	L78V - version 5.4
>vh design	A24F	T28S	F29L	V37I		F67L	R71K	N73T	- version 5.5
>vh design	A24F	T28S	F29L	V37I	V48L		R71K	N73T	- version 5.6
>vh design	**A24F**		**F29L**	**V37I**			**R71K**	**N73T**	**L78V - version 6.1**
>vh design	**A24F**		**F29L**	**V37I**		**F67L**	**R71K**	**N73T**	**- version 6.2**
>vh design	**A24F**		**F29L**	**V37I**	**V48L**		**R71K**	**N73T**	**- version 6.3**
>vh design	**A24F**	**T28S**	**F29L**	**V37I**			**R71K**	**N73T**	**- version 6.4**
>vh design	A24F		F29L		V48L	F67L	R71K	N73T	L78V - version 7
>vh design	A24F	T28S	F29L	V37I	V48L	F67L	R71K		L78V - version 8

FIG. 7

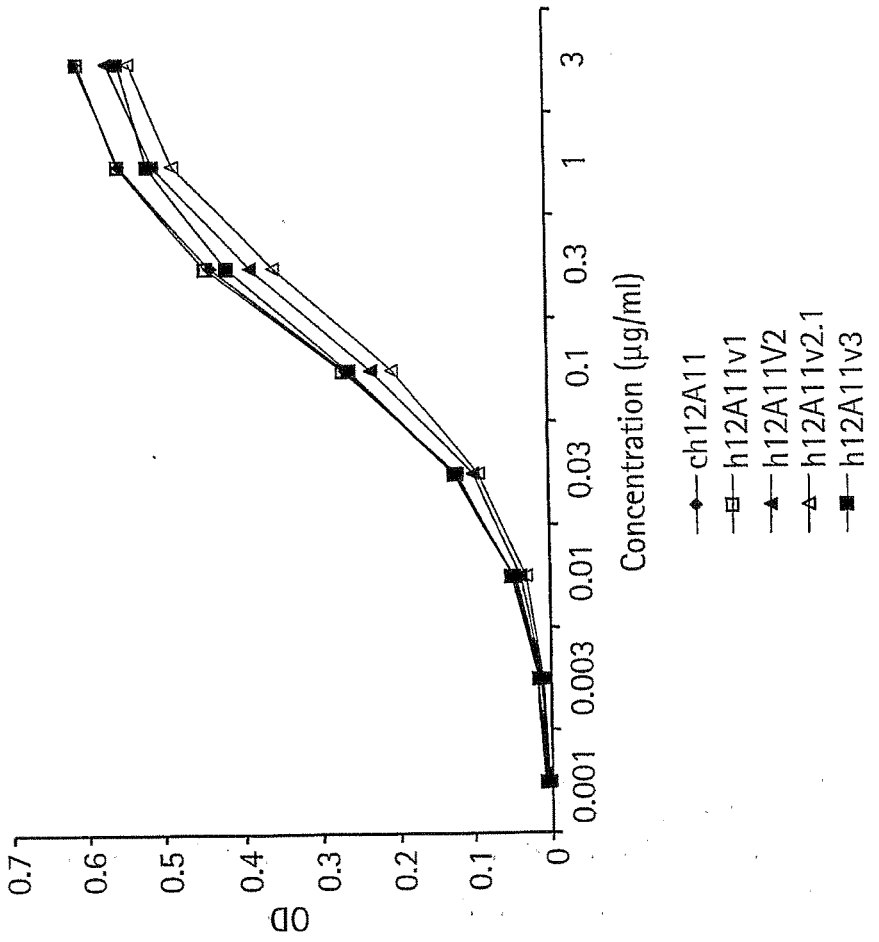
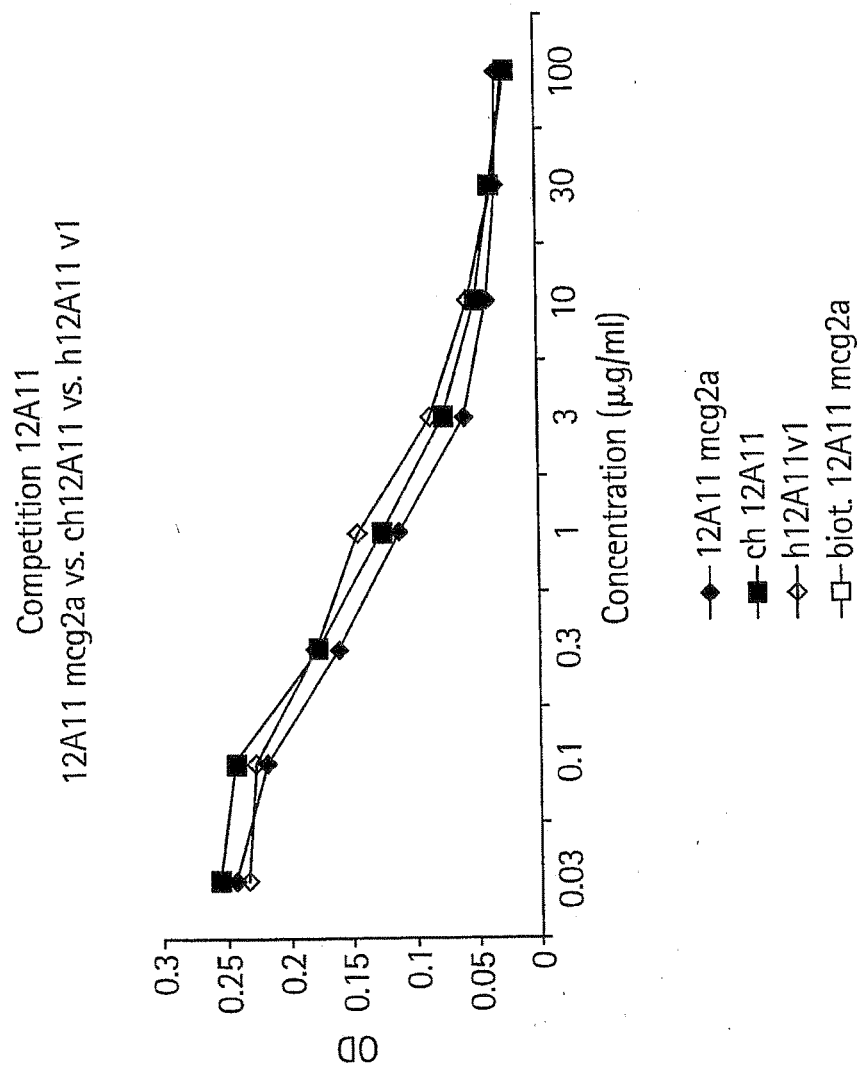

Aß (1-42) Binding Assay
ch12A11 vs h12A11 v1 vs. h12a11v2, v2.1, v3
OD
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.001
0.003
0.01
0.03
0.1
0.3
1
3
Concentration (µg/ml)
ch12A11
h12A11v1
h12A11V2
h12A11v2.1
h12A11v3

FIG. 8


Competition 12A11
12A11 mcg2a vs. ch12A11 vs. h12A11 v1
OD
0.3
0.25
0.2
0.15
0.1
0.05
0
0.03
0.1
0.3
1
3
10
30
100
Concentration (µg/ml)
12A11 mcg2a
ch 12A11
h12A11v1
biot. 12A11 mcg2a

SEQUENCE LISTING

<110> Neuralab Limited, Wyeth et al.

<120> HUMANIZED ANTIBODIES THAT RECOGNIZE BETA AMYLOID PEPTIDE

<130> ELN-028PC

<150> 60/474654
<151> 2003-05-30

<160> 35

<170> FastSEQ for Windows Version 4.0

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<211> 393
<212> DNA
<213> Murine

<220>

<221> CDS
<222> (1)...(393)

<220>

<221> sig_peptide
<222> (1)...(57)

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atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct gct   48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15                 -10                 -5

tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc   96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
            1               5                  10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc att   144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
     15                  20                  25

gta cat agt aat gga aac acc tac tta gaa tgg tac ctg cag aaa cca   192
Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 30                  35                  40                  45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct   240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca   288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75

ctc aag atc agc aga gtg gag gct gag gat ctg gga att tat tac tgc   336
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
```

```
ttt caa agt tca cat gtt cct ctc acg ttc ggt gct ggg acc aag ctg   384
Phe Gln Ser Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
     95                  100                 105

                                                                 393
gag ctg aaa
Glu Leu Lys
110
```

<210> 2
<211> 131
<212> PRT
<213> Murine

<220>
<221> SIGNAL
<222> (1)...(19)

```
<400> 2
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                -15                 -10                 -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
             1                   5                  10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
    15                  20                  25
Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
                50                  55                  60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            65                  70                  75
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
        80                  85                  90
Phe Gln Ser Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                  100                 105
Glu Leu Lys
110
```

<210> 3
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<212> DNA
<213> Murine

<220>
<221> CDS
<222> (1)...(417)

<220>
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Met Asp Arg Leu Thr Thr Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
                -15                 -10                 -5

gtc ttg tcc caa gtt act cta aaa gag tct ggc cct ggg ata ttg aag   96
Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys
             1                   5                  10
```

```
ccc tca cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg   144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
     15                  20                  25

agc act tct ggt atg agt gta ggc tgg att cgt cag cct tca ggg aag   192
Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 30                  35                  40                  45

ggt ctg gag tgg ctg gca cac att tgg tgg gat gat gat aag tac tat   240
Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
                 50                  55                  60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga   288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
             65                  70                  75

aac cag gta ttc ctc aag atc acc agt gtg gac act gca gat act gcc   336
Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
         80                  85                  90

act tac tac tgt gct cga aga act act acg gct gac tac ttt gcc tac   384
Thr Tyr Tyr Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr
     95                  100                 105

tgg ggc caa ggc acc act ctc aca gtc tcc tca                       417
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

110                 115                 120
```

<210> 4
<211> 139
<212> PRT
<213> Murine

<220>
<221> SIGNAL
<222> (1)...(19)

```
<400> 4
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                -15                 -10                  -5
Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys
                 1                   5                  10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
     15                  20                  25
Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 30                  35                  40                  45
Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
                 50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
             65                  70                  75
Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
         80                  85                  90
Thr Tyr Tyr Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr
     95                  100                 105
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
110                 115                 120
```

<210> 5
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<213> Artificial Sequence

<220>
<223> synthetic

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tggagatcaa gcctccatct cttgcagatc tagtcagagc attgtacata gtaatggaaa 180
cacctactta gaatggtacc tgcagaaacc aggccagtct ccaaagctcc tgatctacaa 240
agtttccaac cgattttctg gggtcccaga caggttcagt ggcagtggat cagggacaga 300
tttcacactc aagatcagca gagtggaggc tgaggatctg ggaatttatt actgctttca 360
aagttcacat gttcctctca cgttcggtgc tgggaccaag ctggagctga aacgtgagtg 420
gatcctmgr 429

<210> 6
<211> 445
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 6
aagcttgccg ccaccatgga caggcttact acttcattcc tgctgctgat tgtccctgca 60
tatgtcttgt cccaagttac tctaaaagag tctggccctg ggatattgaa gccctcacag 120
accctcagtc tgacttgttc tttctctggg ttttcactga gcacttctgg tatgagtgta 180
ggctggattc gtcagccttc agggaagggt ctggagtggc tggcacacat ttggtgggat 240
gatgataagt actataaccc atccctgaag agccggctca caatctccaa ggatacctcc 300
agaaaccagg tattcctcaa gatcaccagt gtggacactg cagatactgc cacttactac 360
tgtgctcgaa gaactactac ggctgactac tttgcctact ggggccaagg caccactctc 420
acagtctcct caggtgagtg gatcc 445

<210> 7
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v1 - VL region

<400> 7
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Ser
85 90 95
Ser His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 8
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(22)

<400> 8
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
-20 -15 -10
Ala Gln Pro Ala Met Ala Asp Val Val Met Thr Gln Ser Pro Leu Ser
-5 1 5 10
Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
15 20 25
Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
30 35 40
Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn
45 50 55
Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
60 65 70
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
75 80 85 90
Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Tyr Thr Phe Gly Gln Gly
95 100 105
Thr Lys Leu Glu Ile Lys
110

<210> 9
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(20)

<400> 9
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Ser
-20 -15 -10 -5
Gly Ser Ser Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
1 5 10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
15 20 25
Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
30 35 40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
Cys Met Gln Ala Leu Gln Thr Pro
95 100

<210> 10
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> h12A11v1 - VH region

<400> 10
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 11
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 11
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
-15 -10 -5
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Arg Asp Arg His Ser Ser Ser Trp Tyr Tyr Gly Met
95 100 105
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120

<210> 12
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> (1)...(19)

<400> 12
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
-15 -10 -5
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Arg Asp Ala Lys Leu Leu Met Leu Leu Ile Ser Gly
95 100 105
Ala Lys Gly Gln Trp Ser Pro Ser Leu
110 115

<210> 13
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v2

<400> 13
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v2.1

<400> 14
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 15
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v3

<400> 15
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 16
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v4.1

<400> 16
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 17
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v4.2

<400> 17
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 18
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v4.3

<400> 18
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

```
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 19
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v4.4

<400> 19

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 20
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.1

<400> 20

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65                  70                  75                  80
```

```
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 21
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.2

```
<400> 21
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 22
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.3

```
<400> 22
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser Val
        115                 120
```

<210> 23
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.4

<400> 23
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Val
115 120

<210> 24
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.5

<400> 24
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 25
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v5.6

<400> 25
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 26
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A116.1

<400> 26
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
35 40 45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 27
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v6.2

<400> 27
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 28
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v6.3

```
<400> 28
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 29
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v6.4

```
<400> 29
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Val Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
```

```
Leu Lys Ser Arg Phe Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Leu
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 30
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v7

```
<400> 30
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Thr Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Thr Val
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 31
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic h12A11v8

```
<400> 31
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30
Gly Met Ser Val Gly Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu
        35                  40                  45
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
    50                  55                  60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val
65                  70                  75                  80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
Cys Ala Arg Arg Thr Thr Thr Ala Asp Tyr Phe Ala Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 32
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic igg hinge region

<400> 32
Leu Leu Gly Gly Pro
1 5

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic igg hinge region

<400> 33
Leu Glu Gly Gly Pro
1 5

<210> 34
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized 12A11 v1 VL sequence

<220>
<221> sig_peptide
<222> (1)...(60)

<400> 34
atgaggctcc ctgctcagct cctggggctg ctgatgctct gggtctctgg ctccagtggg 60
gatgttgtga tgacccaatc tccactctcc ctgcctgtca ctcctggaga gccagcctcc 120
atctcttgca gatctagtca gagcattgtg catagtaatg gaaacaccta cctggaatgg 180
tacctgcaga aaccaggcca gtctccacag ctcctgatct acaaagtttc caaccgattt 240
tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 300
agcagagtgg aggctgagga tgtgggagtt tattactgct ttcaaagttc acatgttcct 360
ctcaccttcg gtcaggggac caagctggag atcaaa 396

<210> 35
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> humanized 12A11 v1 VH sequence

<220>
<221> sig_peptide
<222> (1)...(57)

<400> 35
atggagtttg ggctgagctg ggttttcctc gttgctcttc tgagaggtgt ccagtgtcaa 60
gttcagctgg tggagtctgg cggcggggtg gtgcagcccg gacggtccct caggctgtct 120
tgtgctttct ctgggttttc actgagcact tctggtatga gtgtgggctg gattcgtcag 180
gctccaggga agggtctgga gtggctggca cacatttggt gggatgatga taagtactat 240
aacccatccc tgaagagccg gctcacaatc tccaaggata cctccaaaaa caccgtgtac 300
ctccagatga acagtctgcg ggctgaagat actgccgtgt actactgtgc tcgaagaact 360
actaccgctg actactttgc ctactggggc caaggcacca ctgtcacagt ctcctca 417