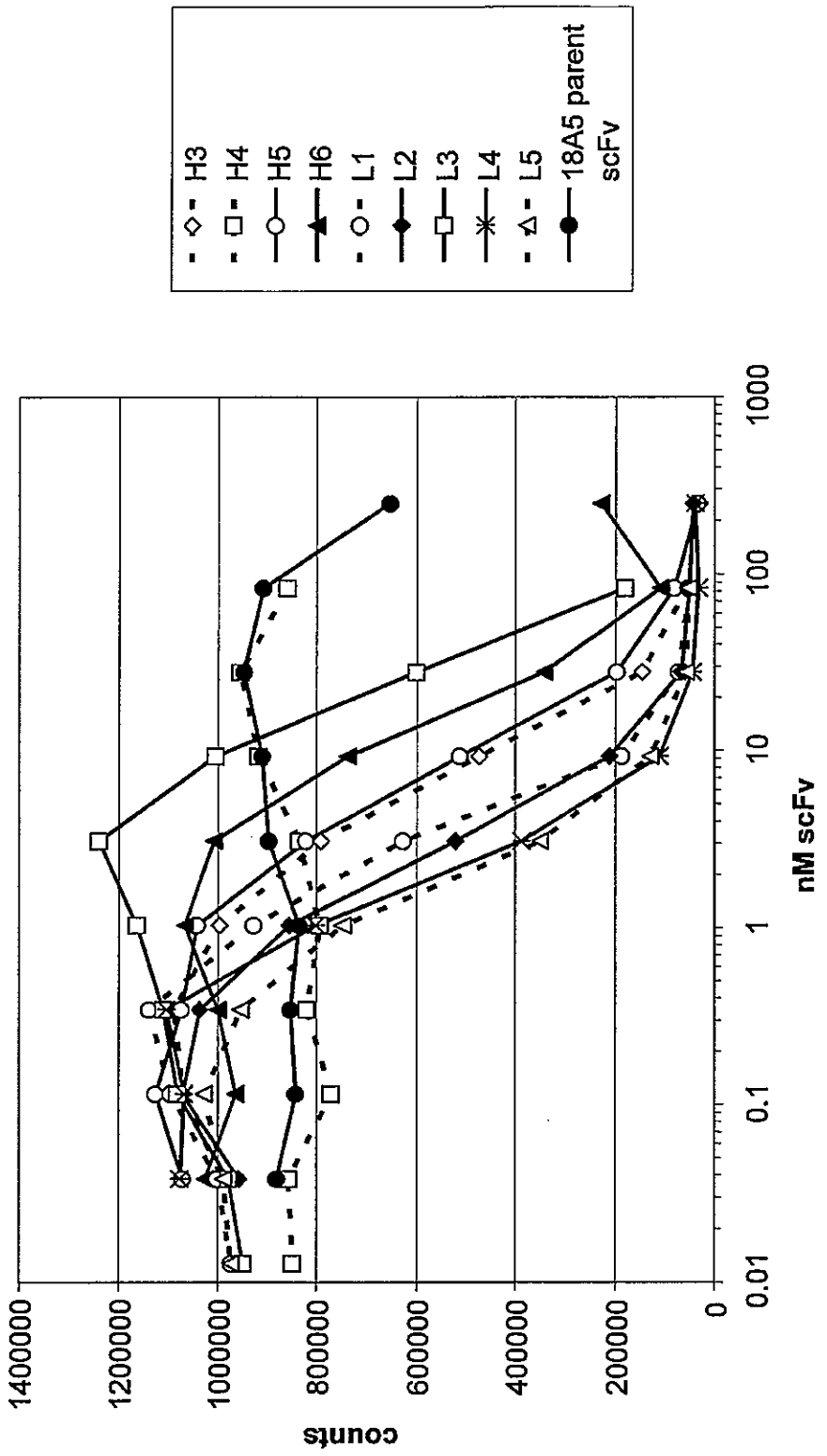

H3
H4
H5
H6
L1
L2
L3
L4
L5
18A5 parent scFv
counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
100
1000
nM scFv

Figure 1a

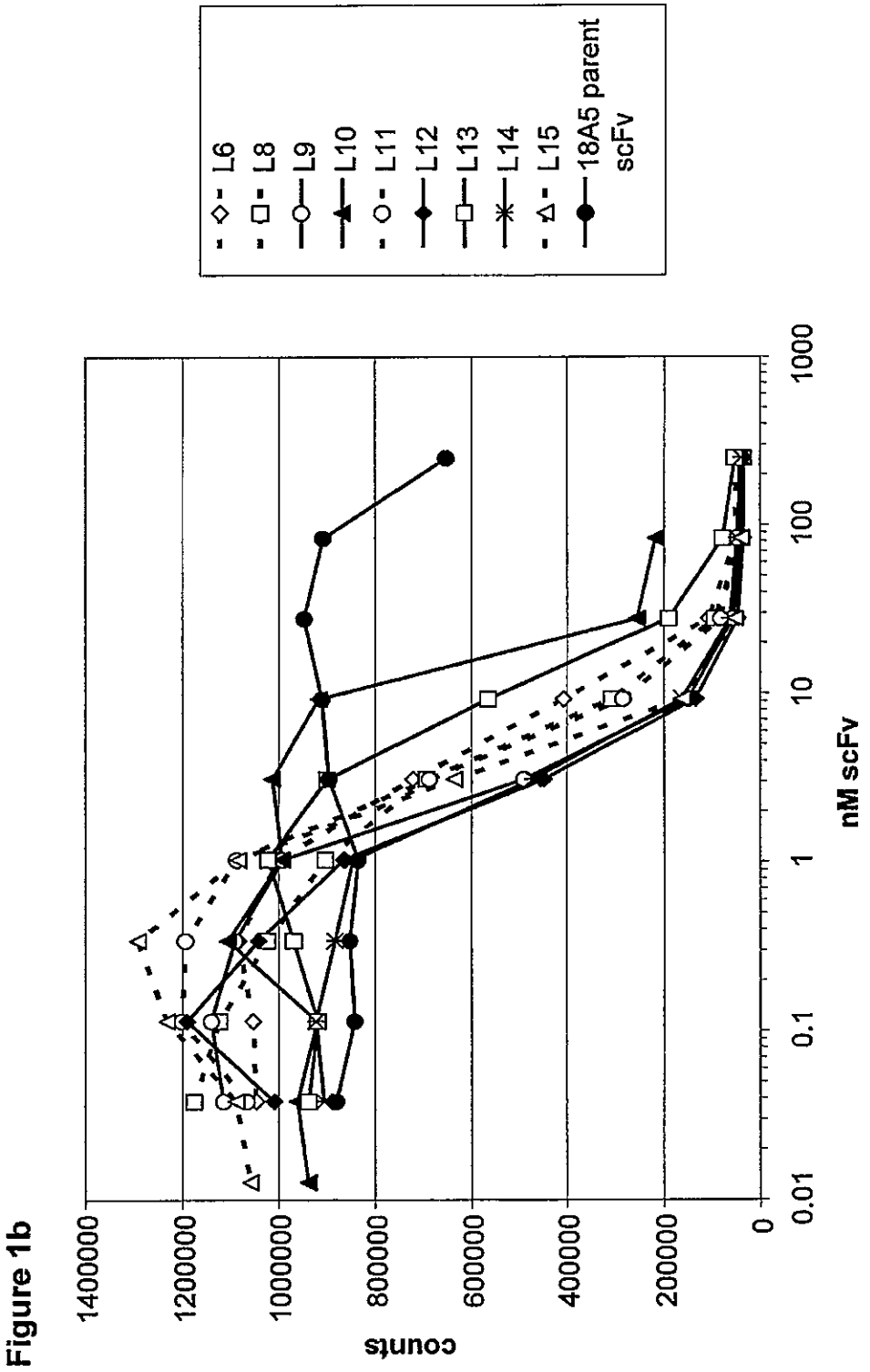

L6
L8
L9
L10
L11
L12
L13
L14
L15
18A5 parent scFv
counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
100
1000
nM scFv

Figure 1b

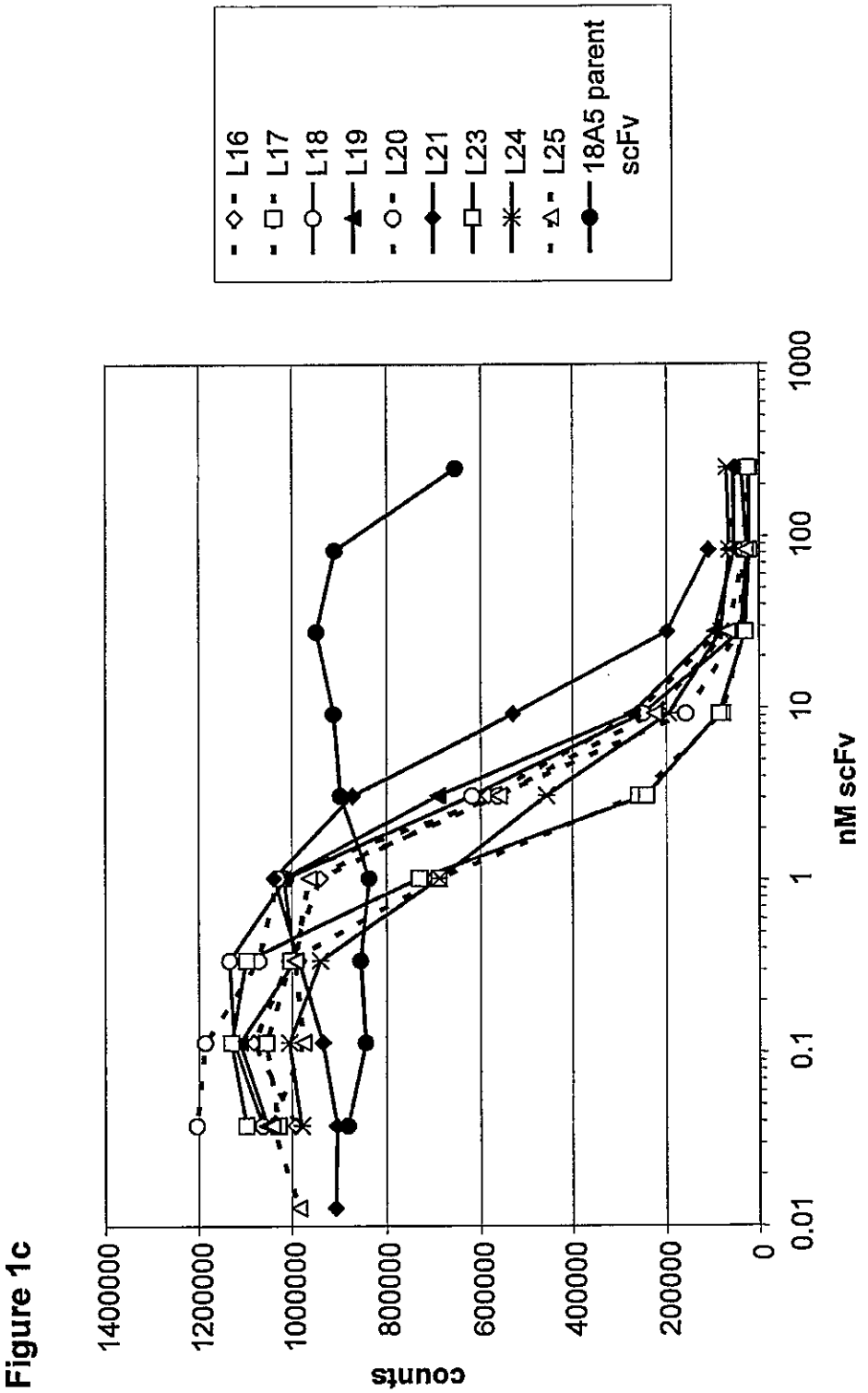

L16
L17
L18
L19
L20
L21
L23
L24
L25
18A5 parent scFv
counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
100
1000
nM scFv

Figure 1c

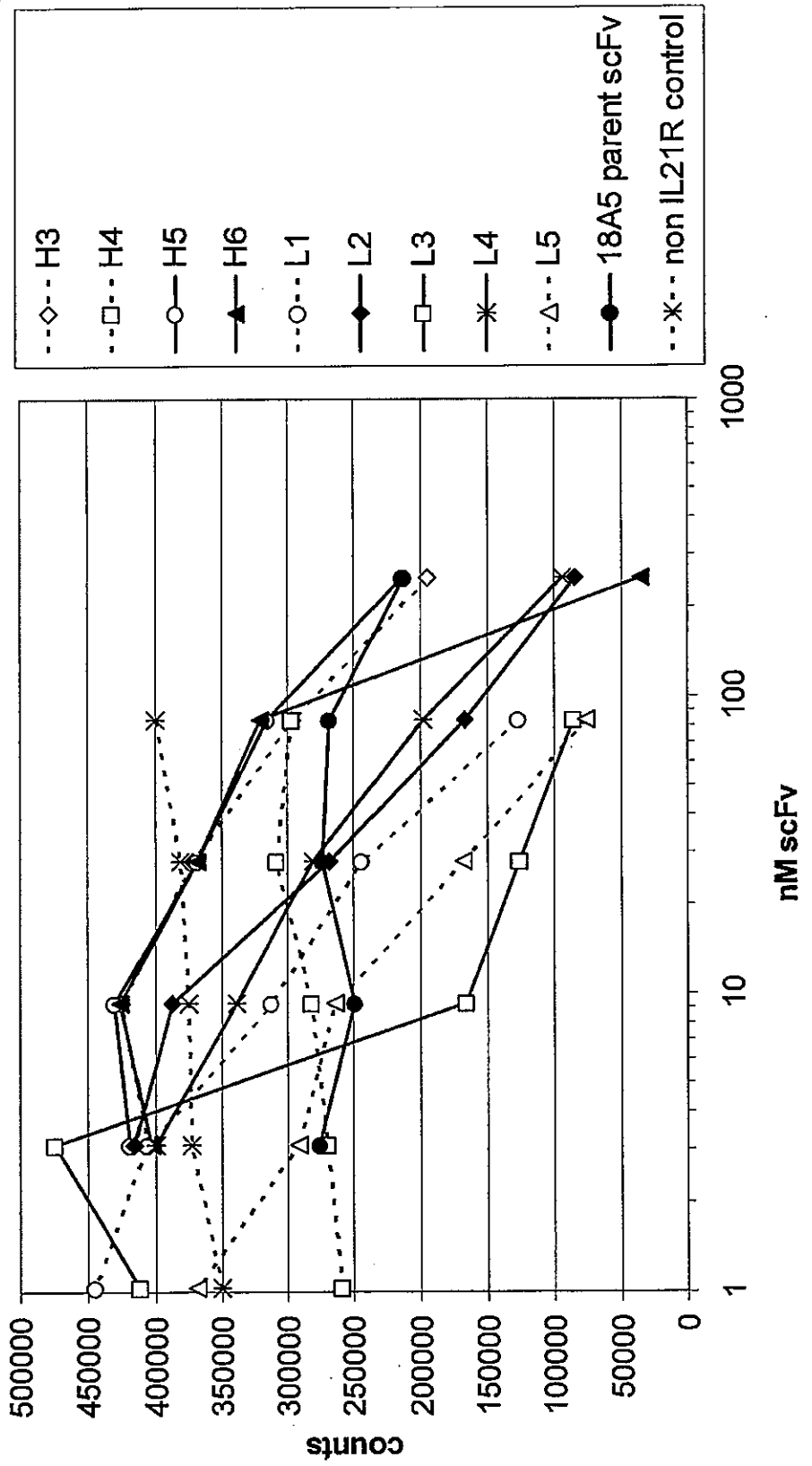

H3
H4
H5
H6
L1
L2
L3
L4
L5
18A5 parent scFv
non IL21R control
counts
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
1
10
100
1000
nM scFv

Figure 2a

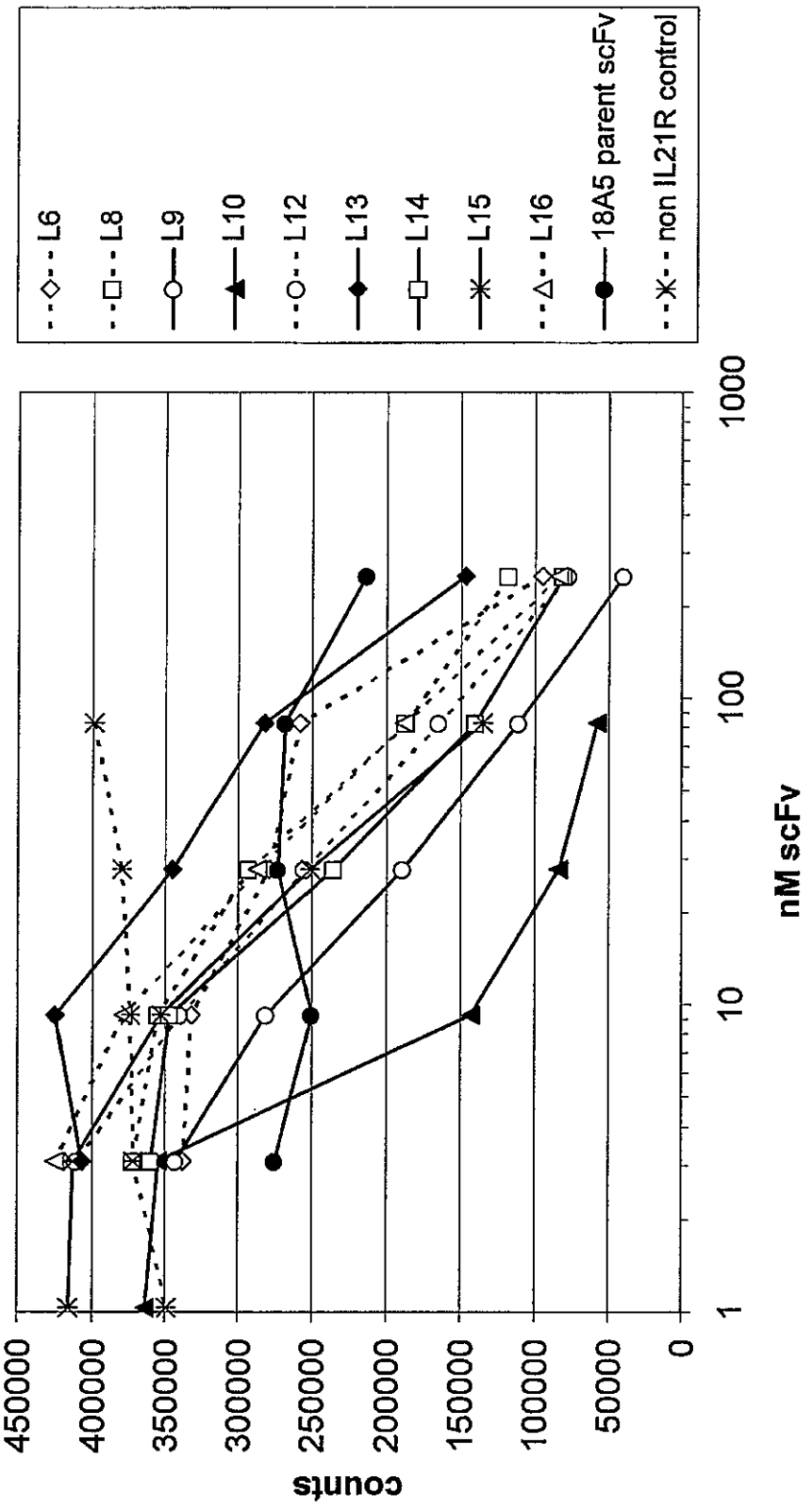

L6
L8
L9
L10
L12
L13
L14
L15
L16
18A5 parent scFv
non IL21R control
counts
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
1
10
100
1000
nM scFv

Figure 2b

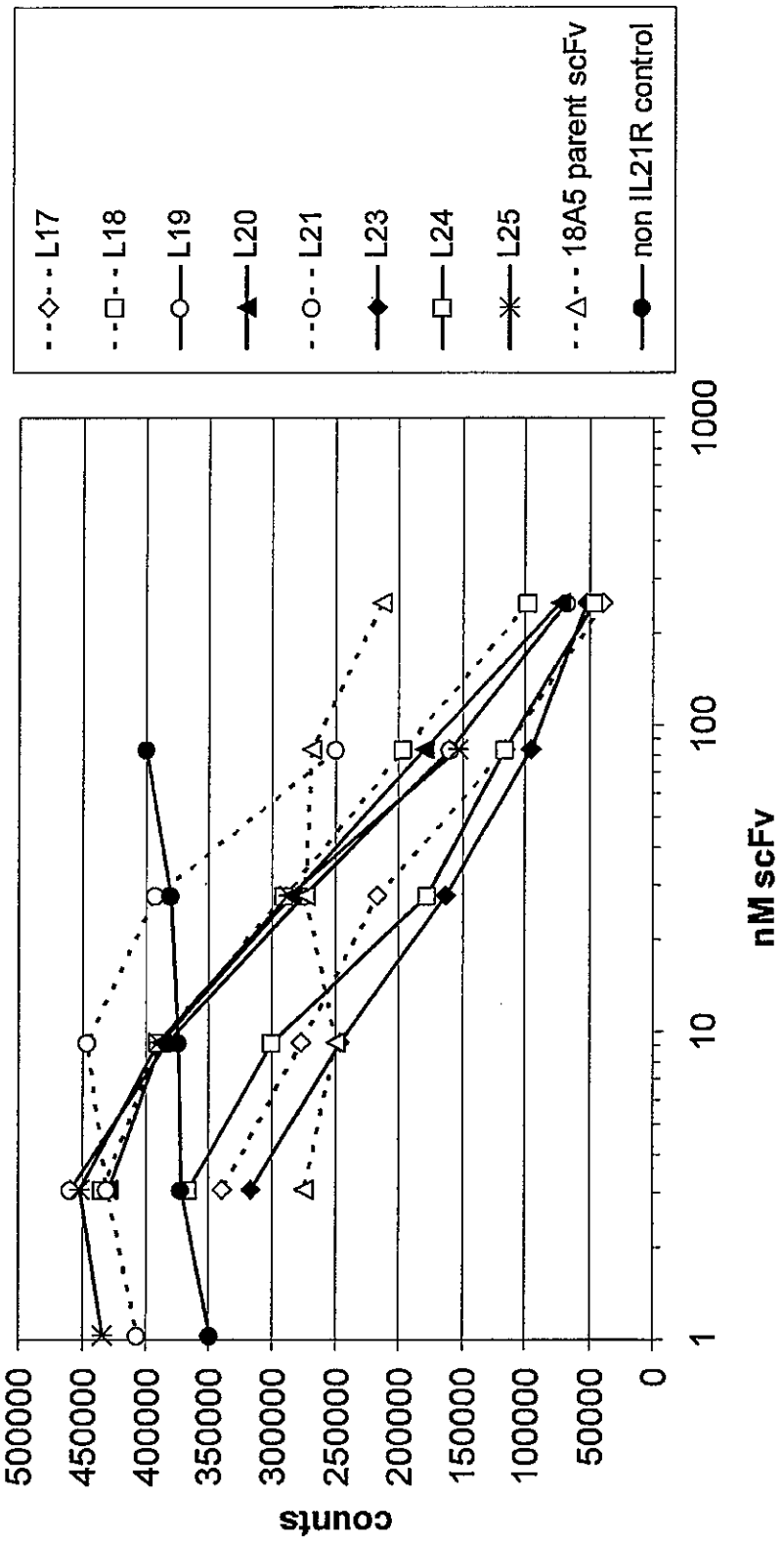

L17
L18
L19
L20
L21
L23
L24
L25
18A5 parent scFv
non IL21R control
counts
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
1
10
100
1000
nM scFv

Figure 2c

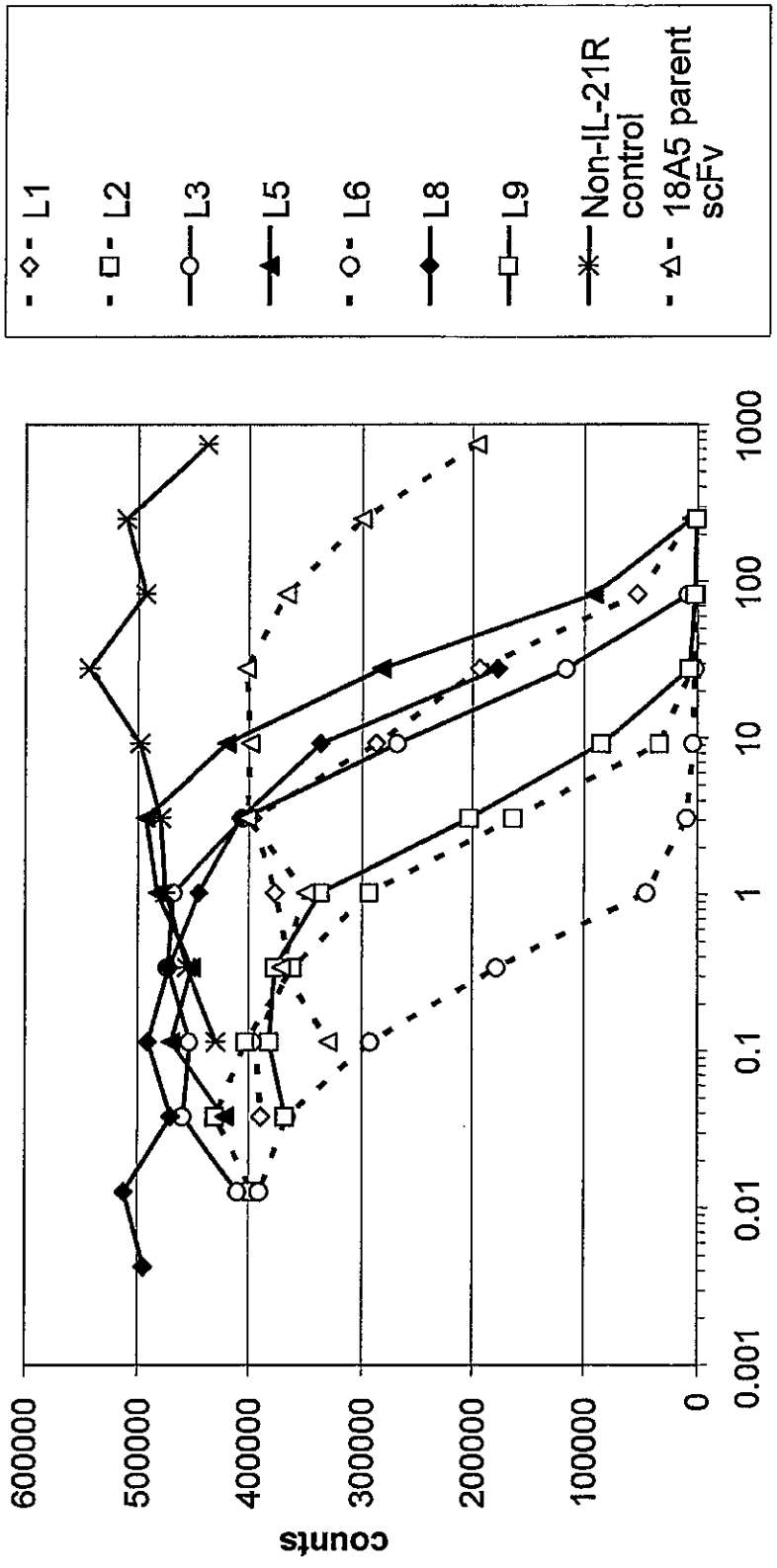

L1
L2
L3
L5
L6
L8
L9
Non-IL-21R control
18A5 parent scFv
counts
600000
500000
400000
300000
200000
100000
0
0.001
0.01
0.1
1
10
100
1000
nM scFv

Figure 3a

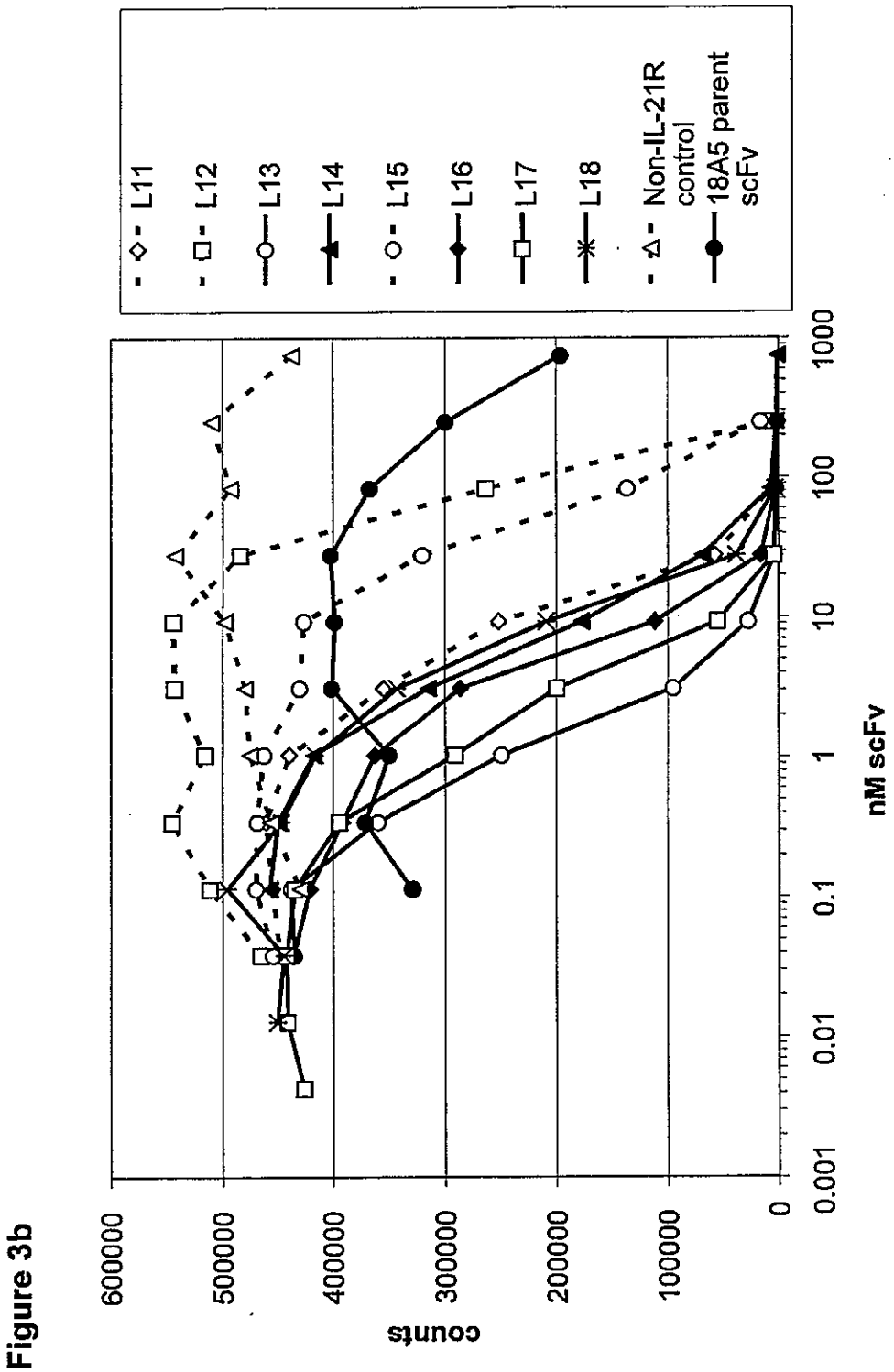

L11
L12
L13
L14
L15
L16
L17
L18
Non-IL-21R control
18A5 parent scFv
counts
600000
500000
400000
300000
200000
100000
0
0.001
0.01
0.1
1
10
100
1000
nM scFv

Figure 3b

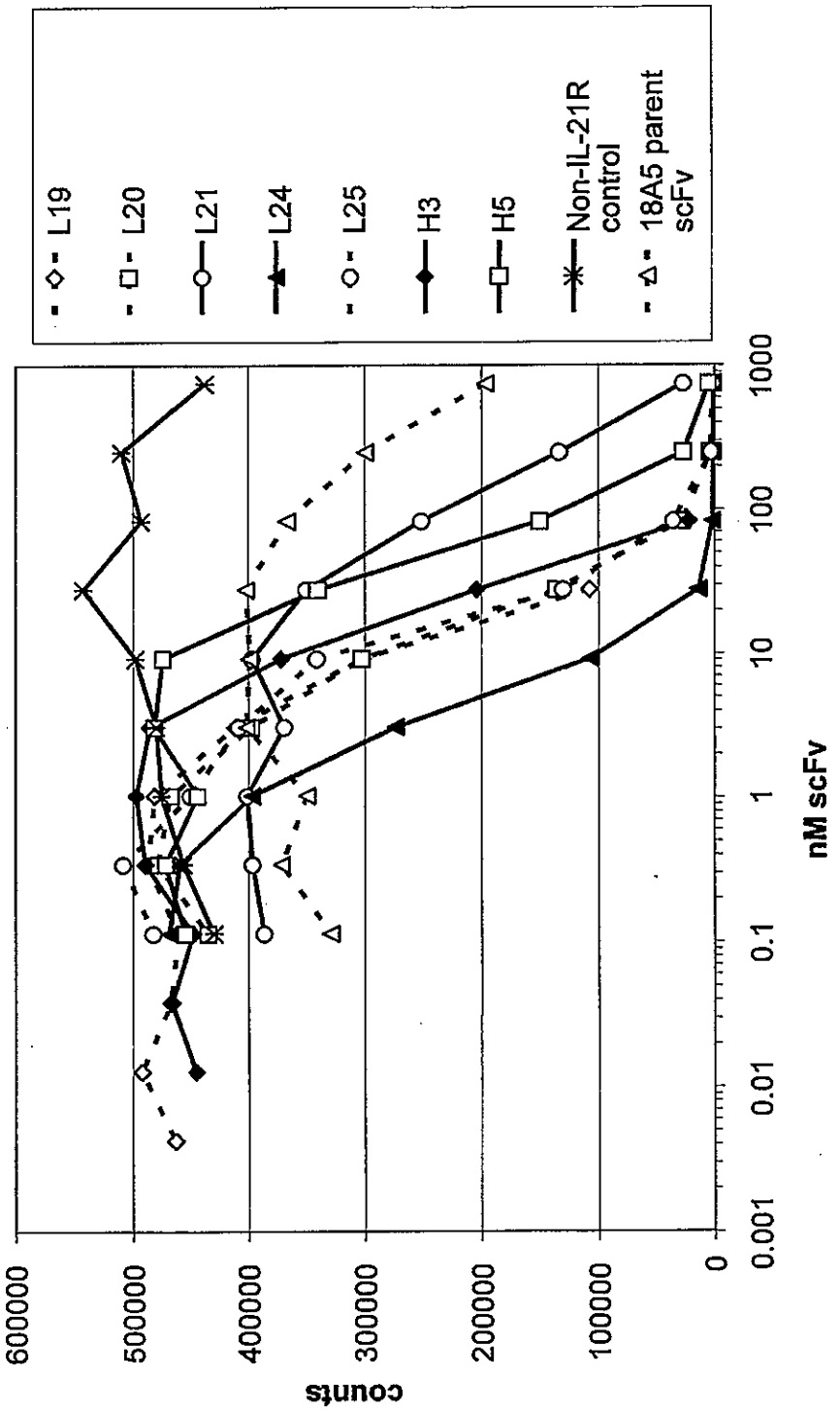

L19
L20
L21
L24
L25
H3
H5
Non-IL-21R control
18A5 parent scFv
600000
500000
400000
300000
200000
100000
0
counts
0.001
0.01
0.1
1
10
100
1000
nM scFv

Figure 3c

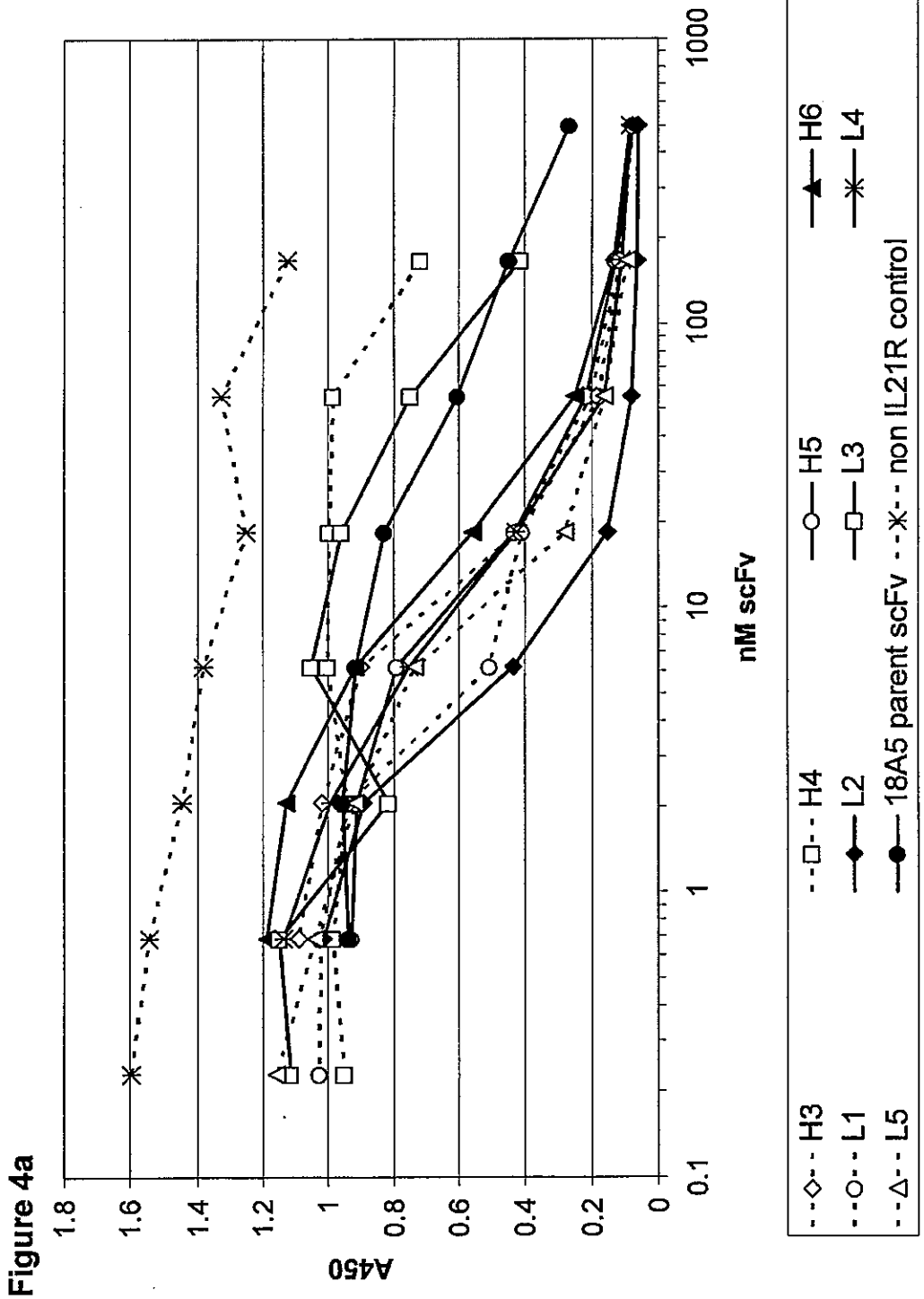

A450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.1
1
10
100
1000
nM scFv
H3
H4
H5
H6
L1
L2
L3
L4
L5
18A5 parent scFv
non IL21R control

Figure 4a

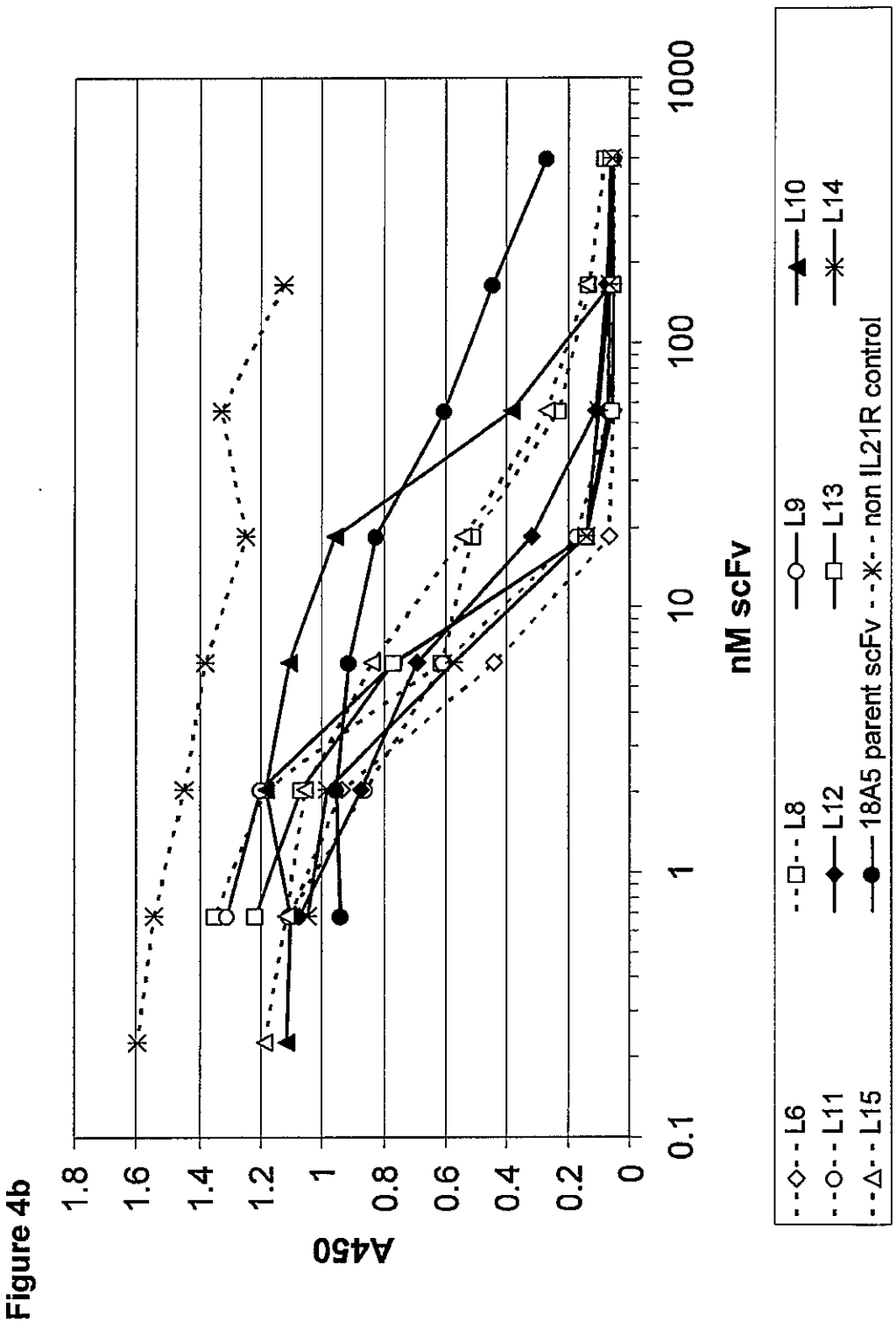

A450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.1
1
10
100
1000
nM scFv
L6
L8
L9
L10
L11
L12
L13
L14
L15
18A5 parent scFv
non IL21R control

Figure 4b

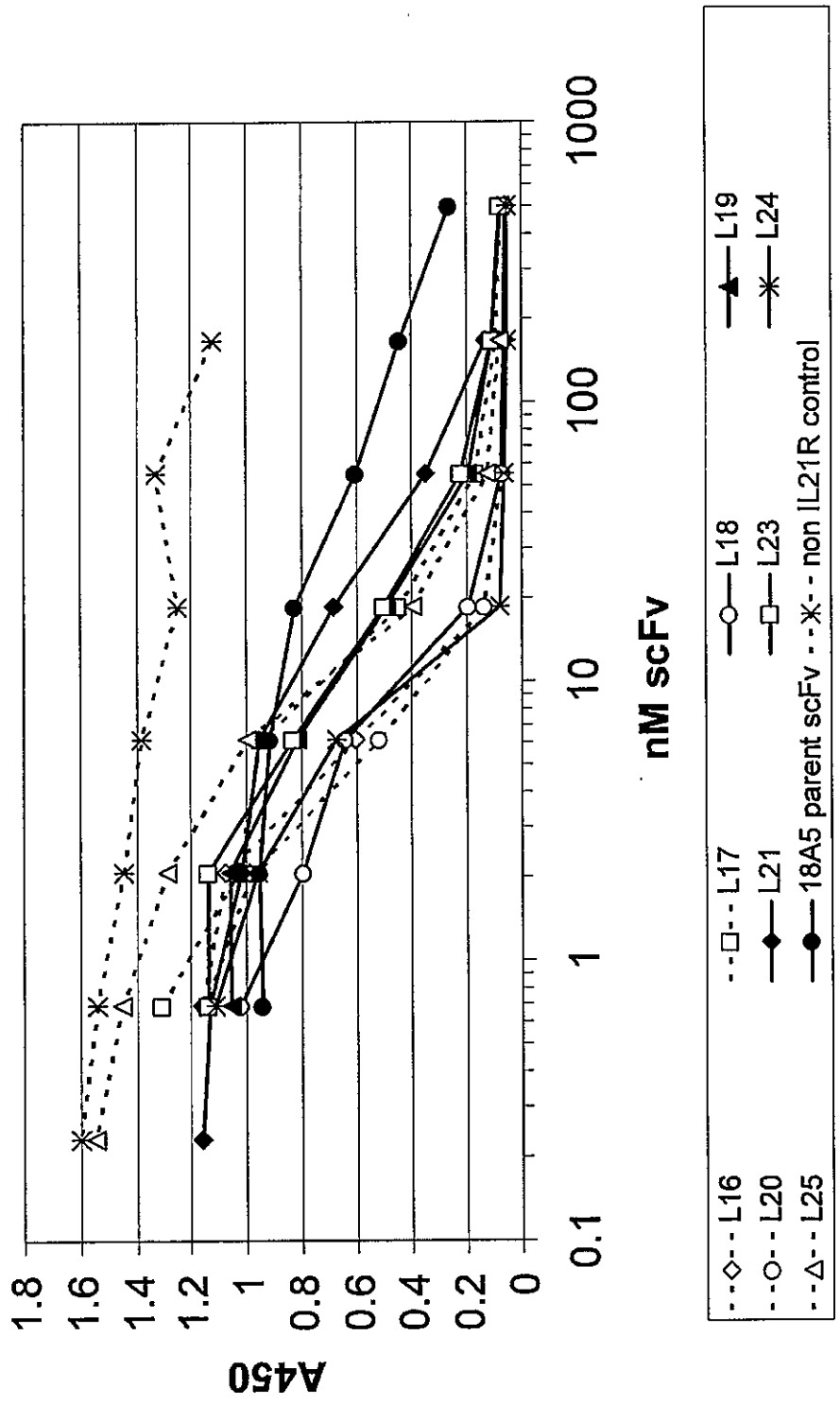

A450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.1
1
10
100
1000
nM scFv
L16
L17
L18
L19
L20
L21
L23
L24
L25
18A5 parent scFv
non IL21R control

Figure 4c

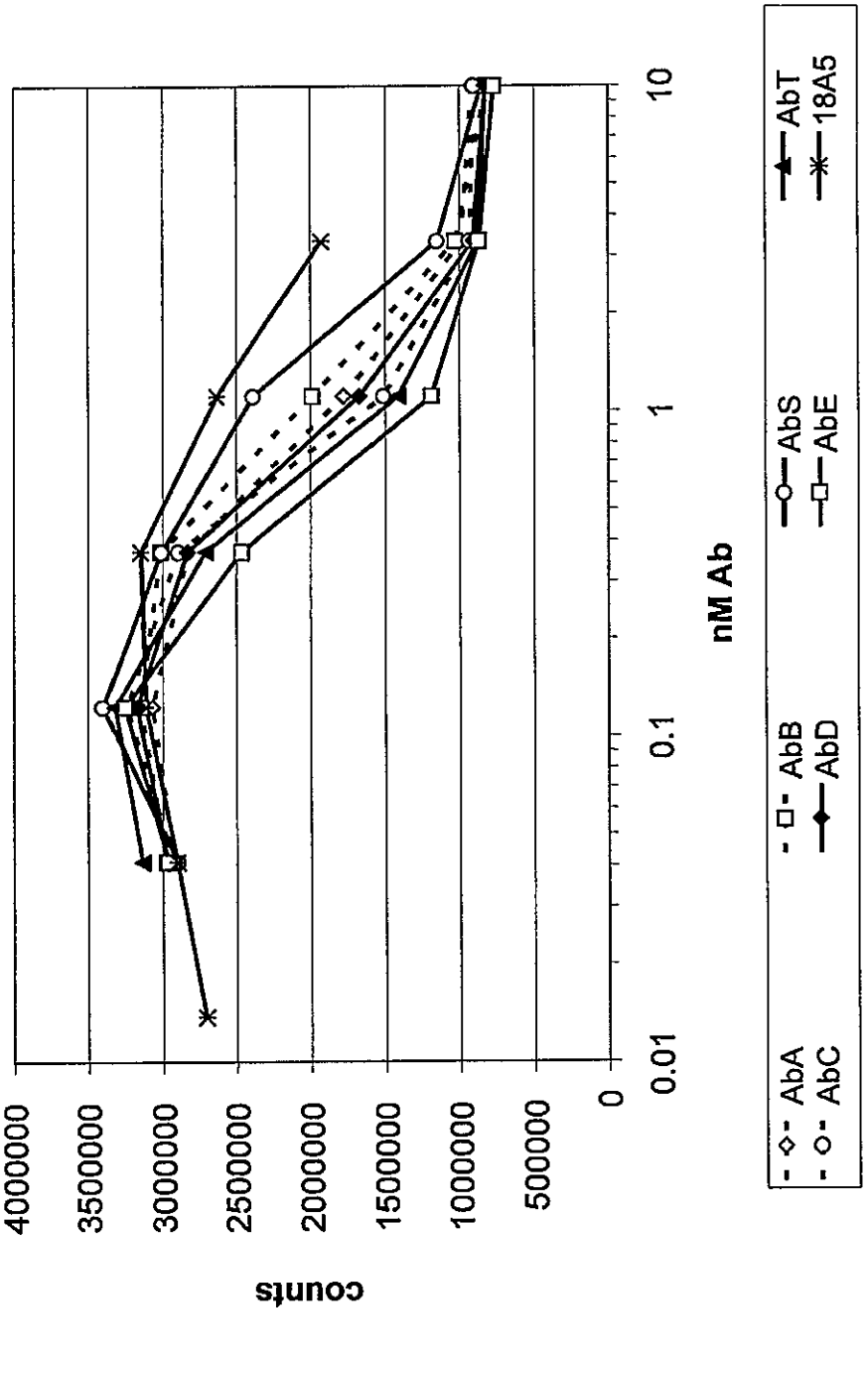

counts
4000000
3500000
3000000
2500000
2000000
1500000
1000000
500000
0
0.01
0.1
1
10
nM Ab
AbA
AbB
AbC
AbD
AbS
AbE
AbT
18A5

Figure 5a

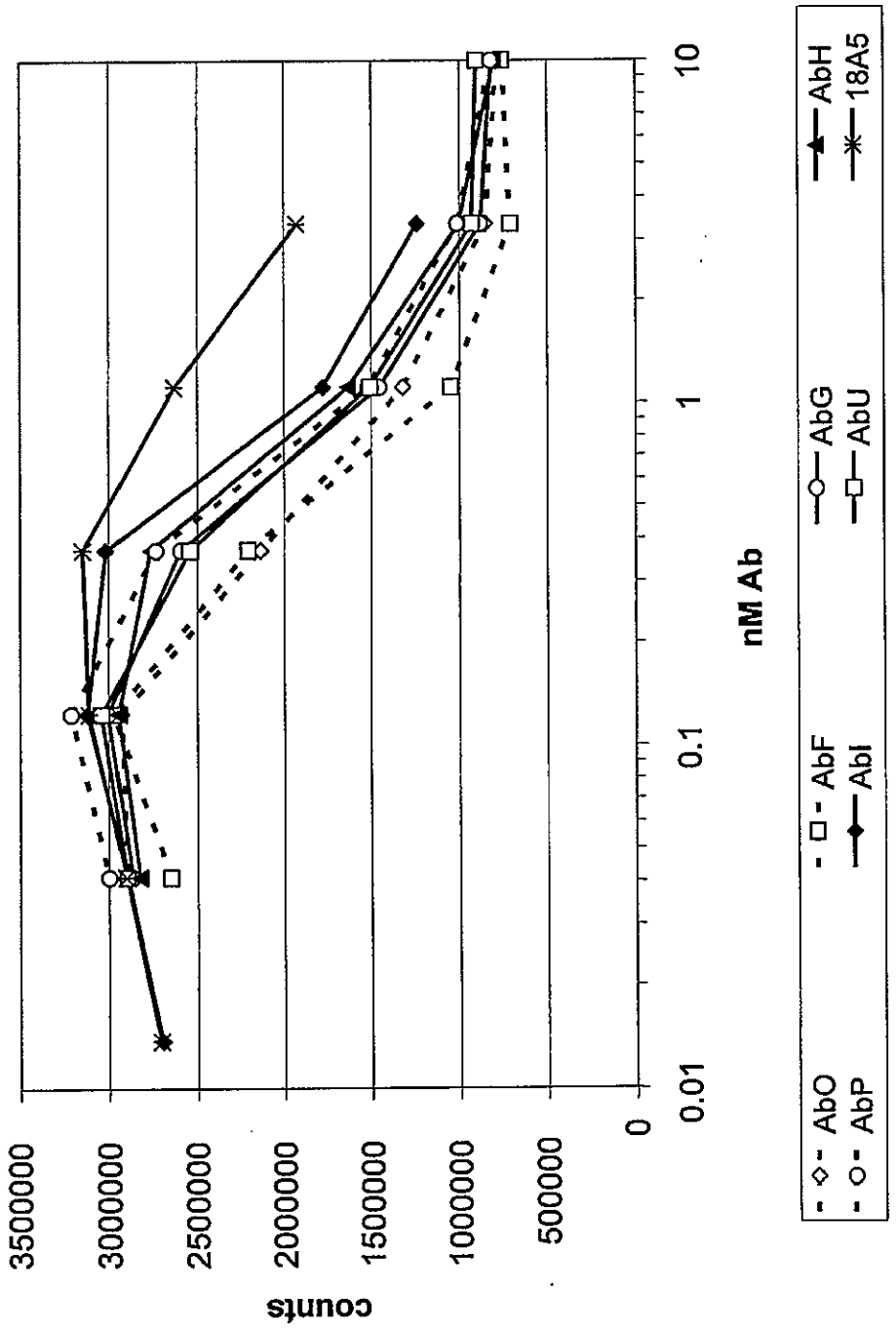

counts
3500000
3000000
2500000
2000000
1500000
1000000
500000
0
0.01
0.1
1
10
nM Ab
AbO
AbF
AbG
AbH
AbP
AbI
AbU
18A5

Figure 5b

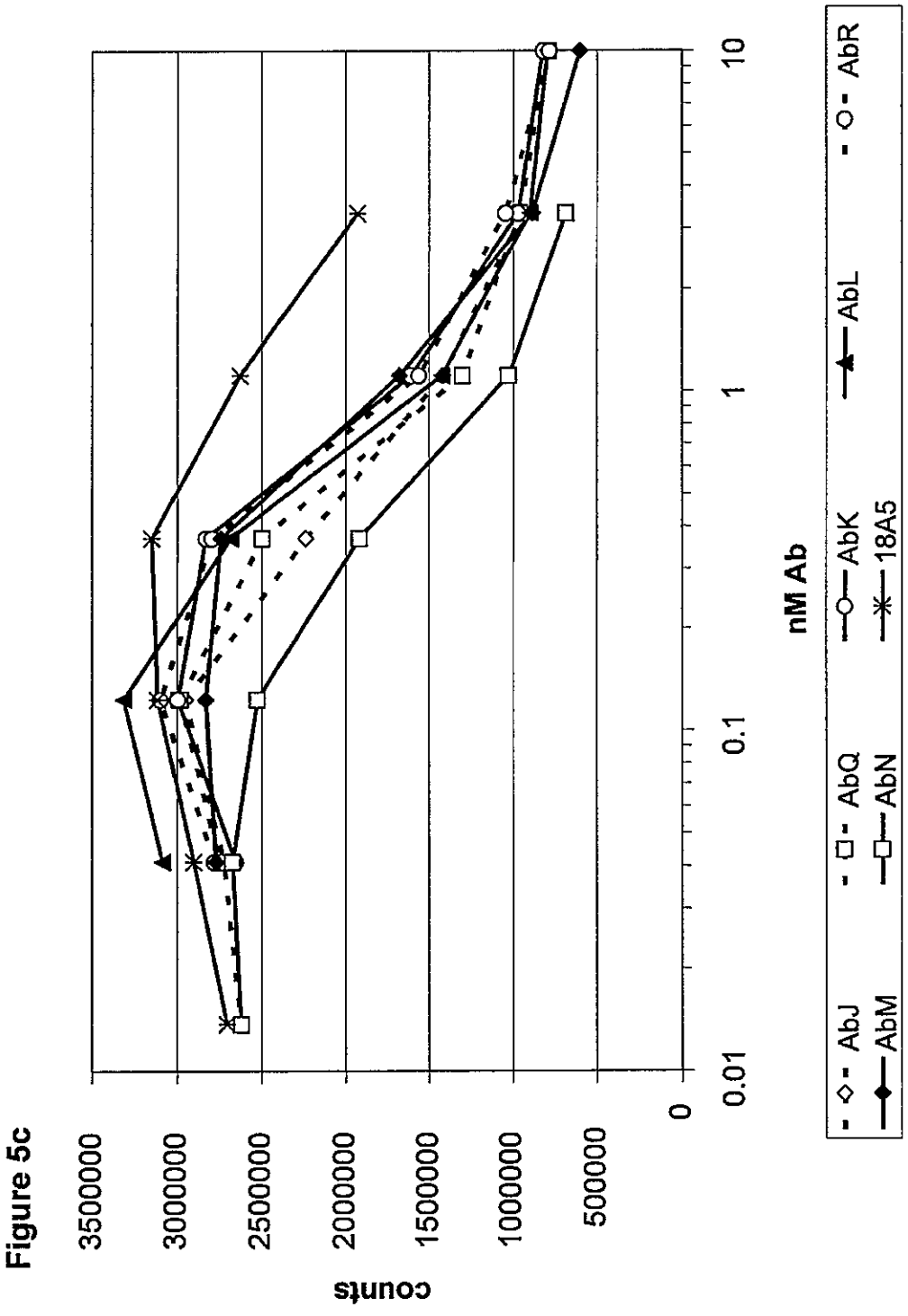

counts
3500000
3000000
2500000
2000000
1500000
1000000
500000
0
0.01
0.1
1
10
nM Ab
AbJ
AbQ
AbK
AbL
AbR
AbM
AbN
18A5

Figure 5c

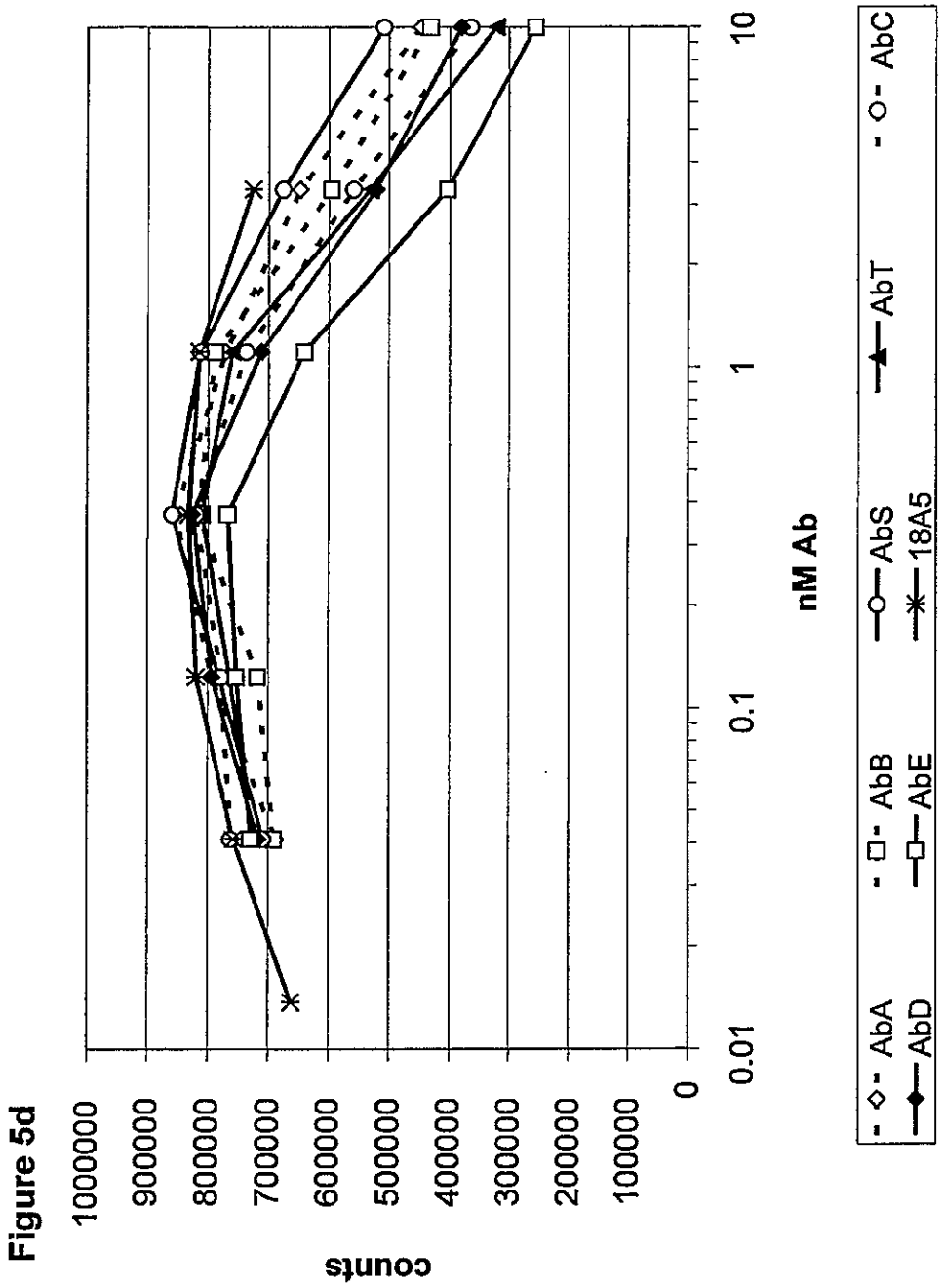

counts
1000000
900000
800000
700000
600000
500000
400000
300000
200000
100000
0
0.01
0.1
1
10
nM Ab
AbA
AbB
AbC
AbD
AbE
AbS
AbT
18A5

Figure 5d

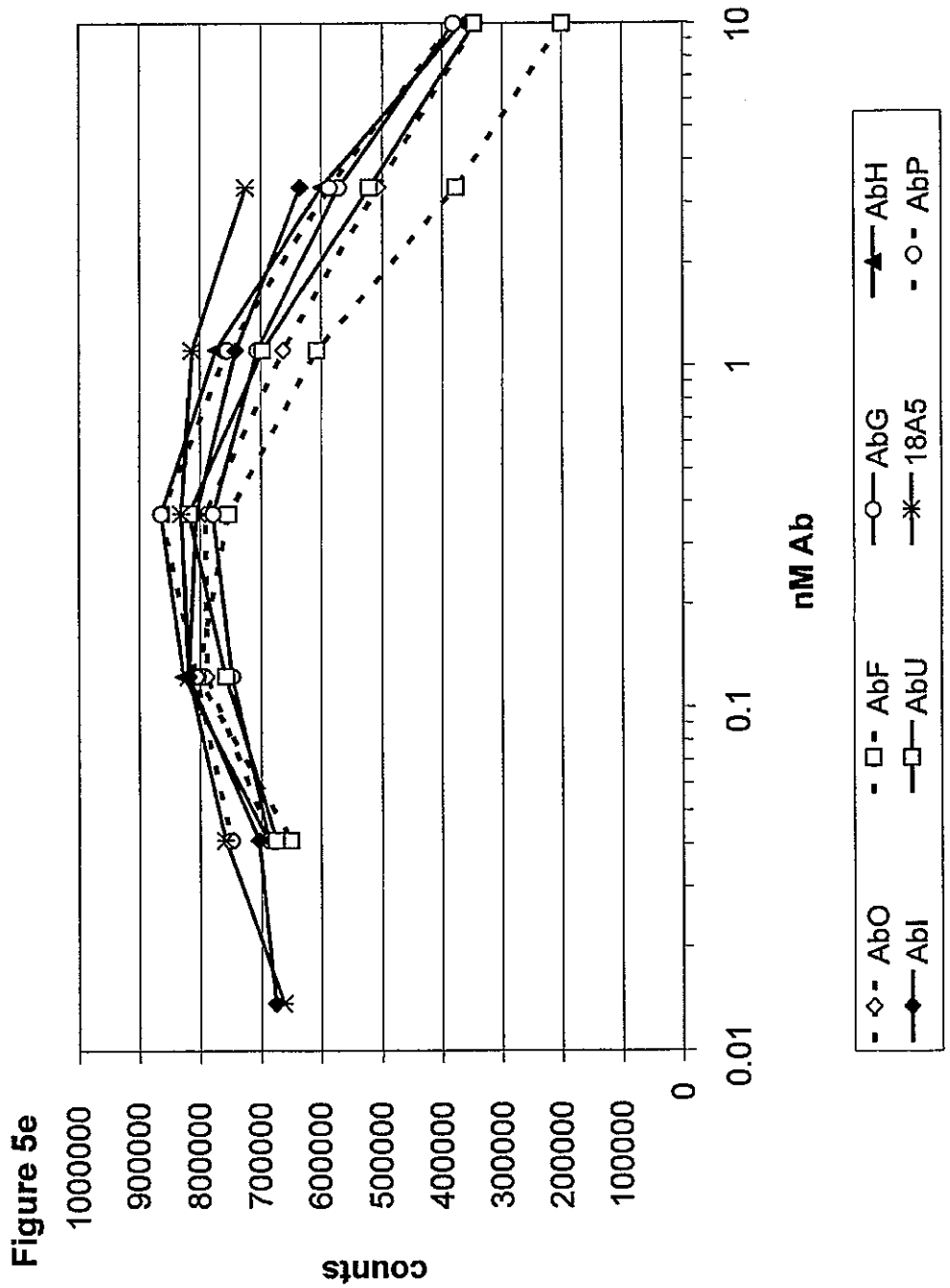

counts
1000000
900000
800000
700000
600000
500000
400000
300000
200000
100000
0
0.01
0.1
1
10
nM Ab
AbO
AbF
AbG
AbH
AbI
AbU
18A5
AbP

Figure 5e

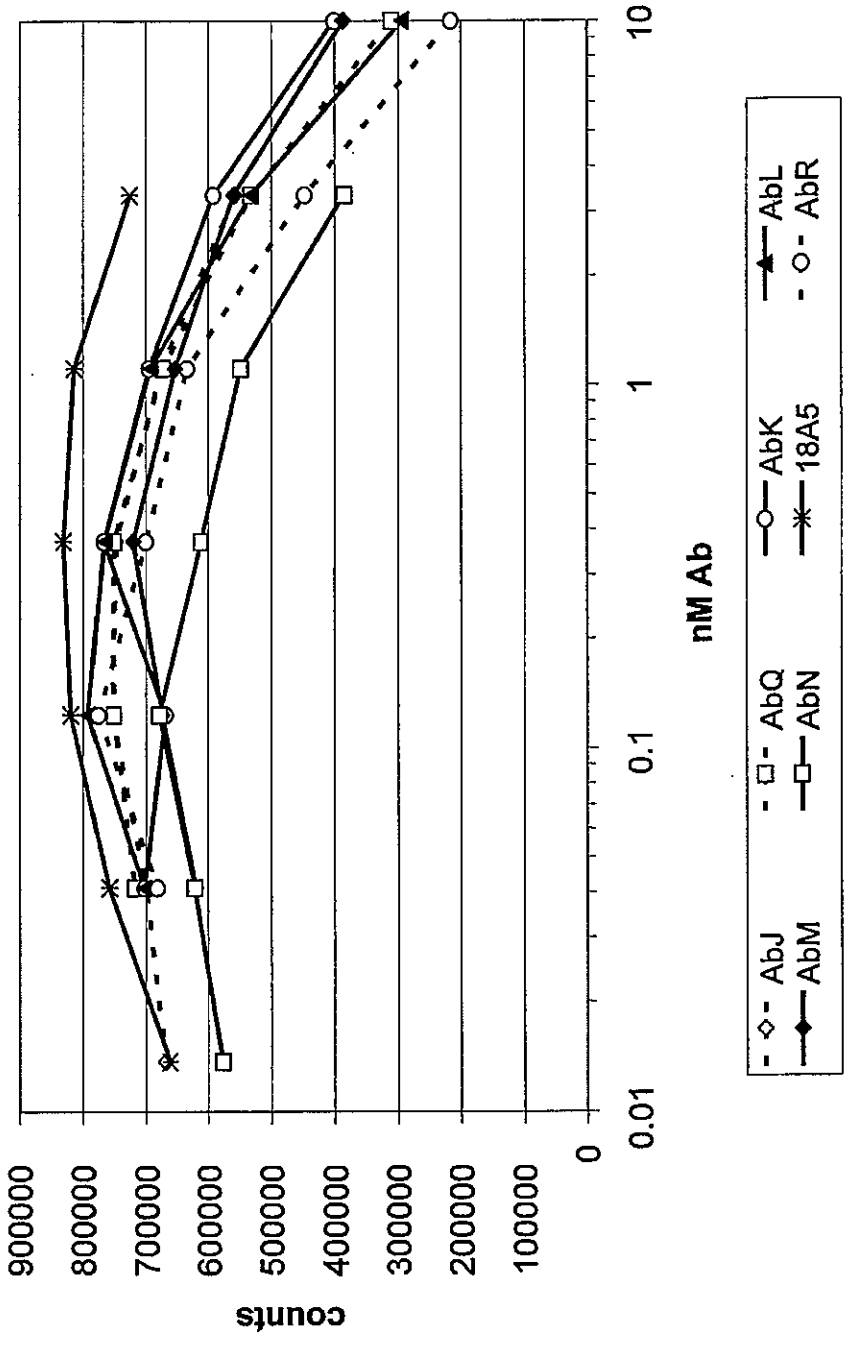

counts
900000
800000
700000
600000
500000
400000
300000
200000
100000
0
0.01
0.1
1
10
nM Ab
AbJ
AbM
AbQ
AbN
AbK
18A5
AbL
AbR

Figure 5f

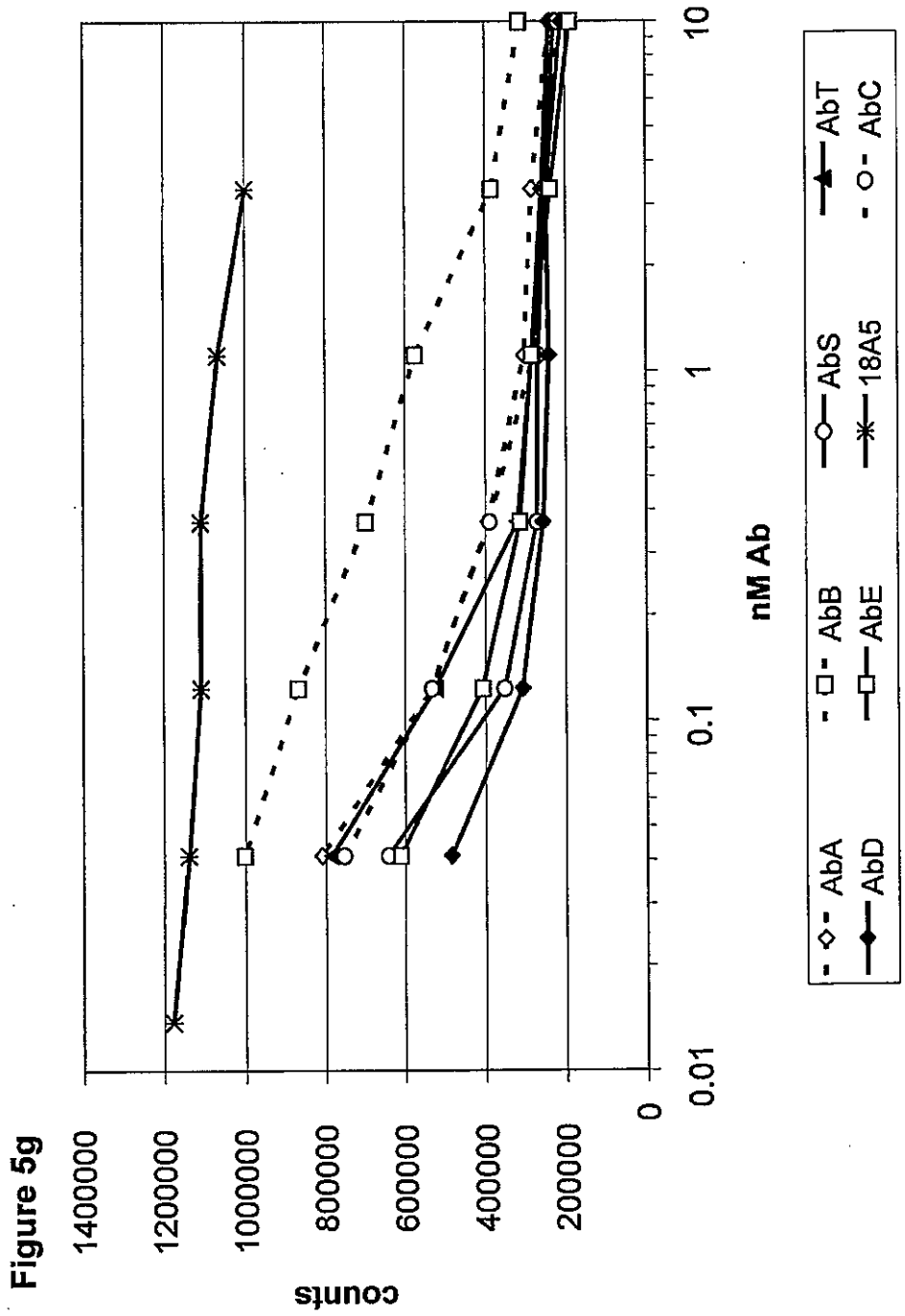

counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
nM Ab
AbA
AbB
AbS
AbT
AbC
AbD
AbE
18A5

Figure 5g

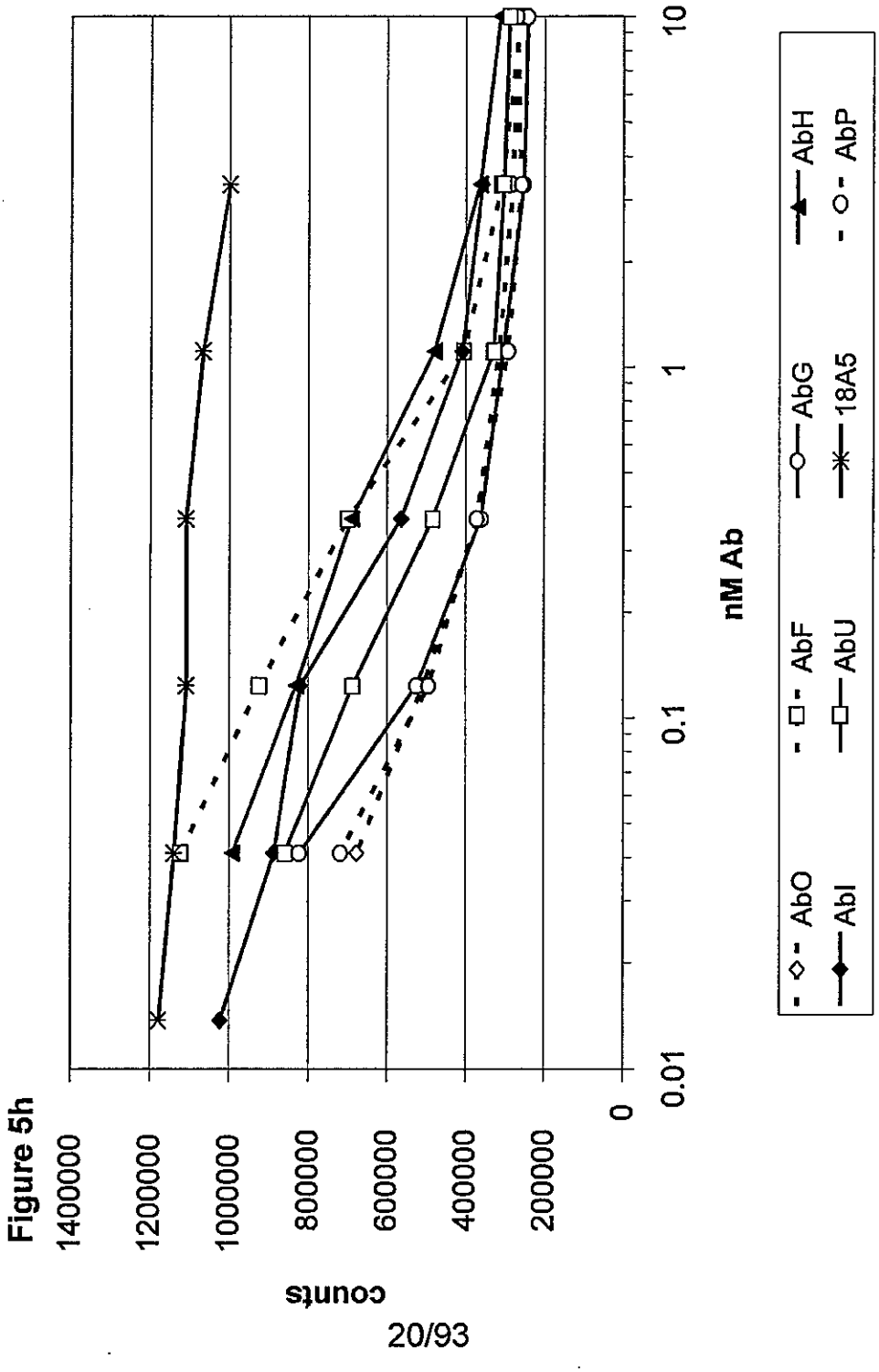

counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
nM Ab
AbO
AbF
AbG
AbH
AbI
AbU
18A5
AbP

Figure 5h

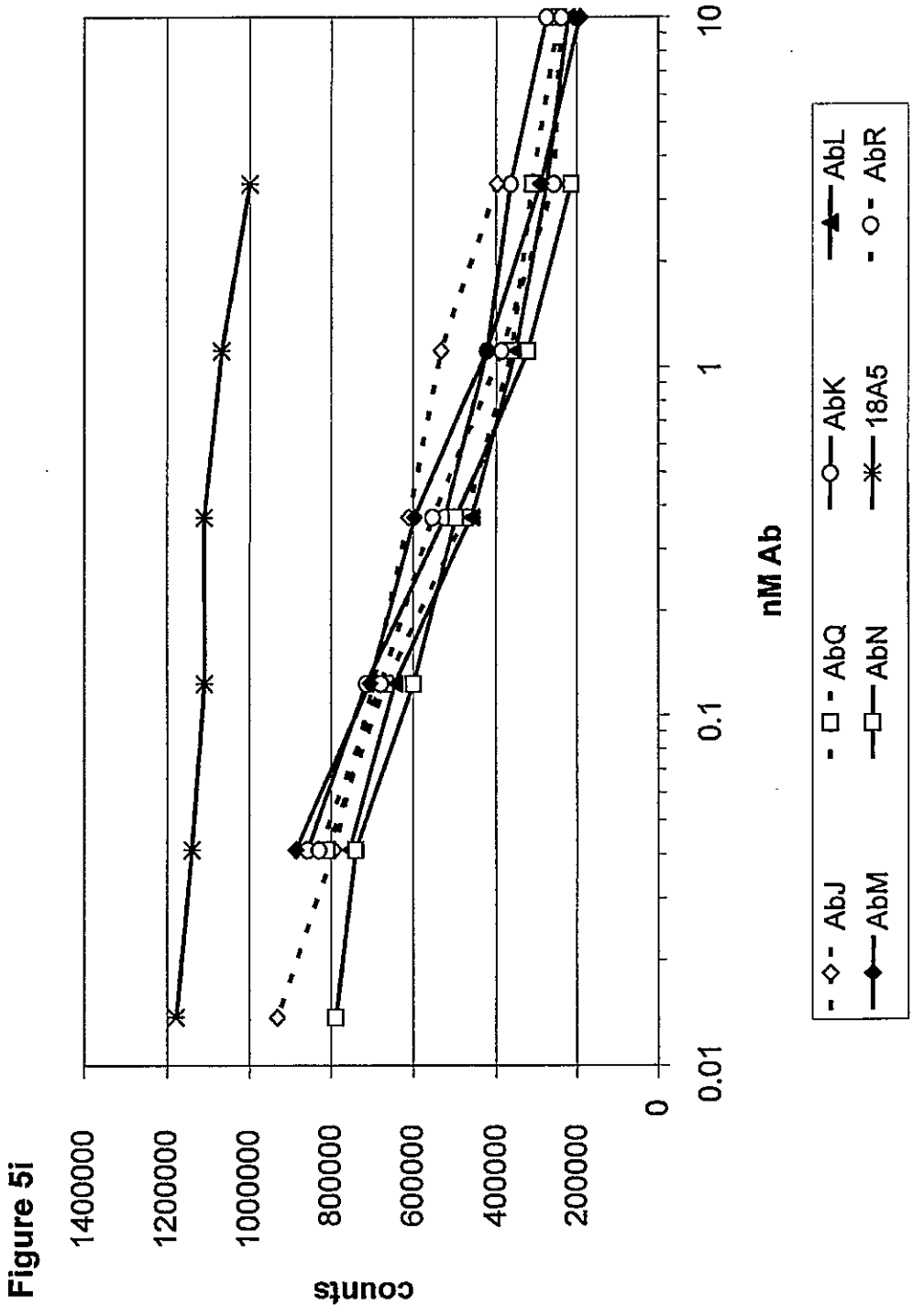

counts
1400000
1200000
1000000
800000
600000
400000
200000
0
0.01
0.1
1
10
nM Ab
AbJ
AbQ
AbK
AbL
AbM
AbN
18A5
AbR

Figure 5i

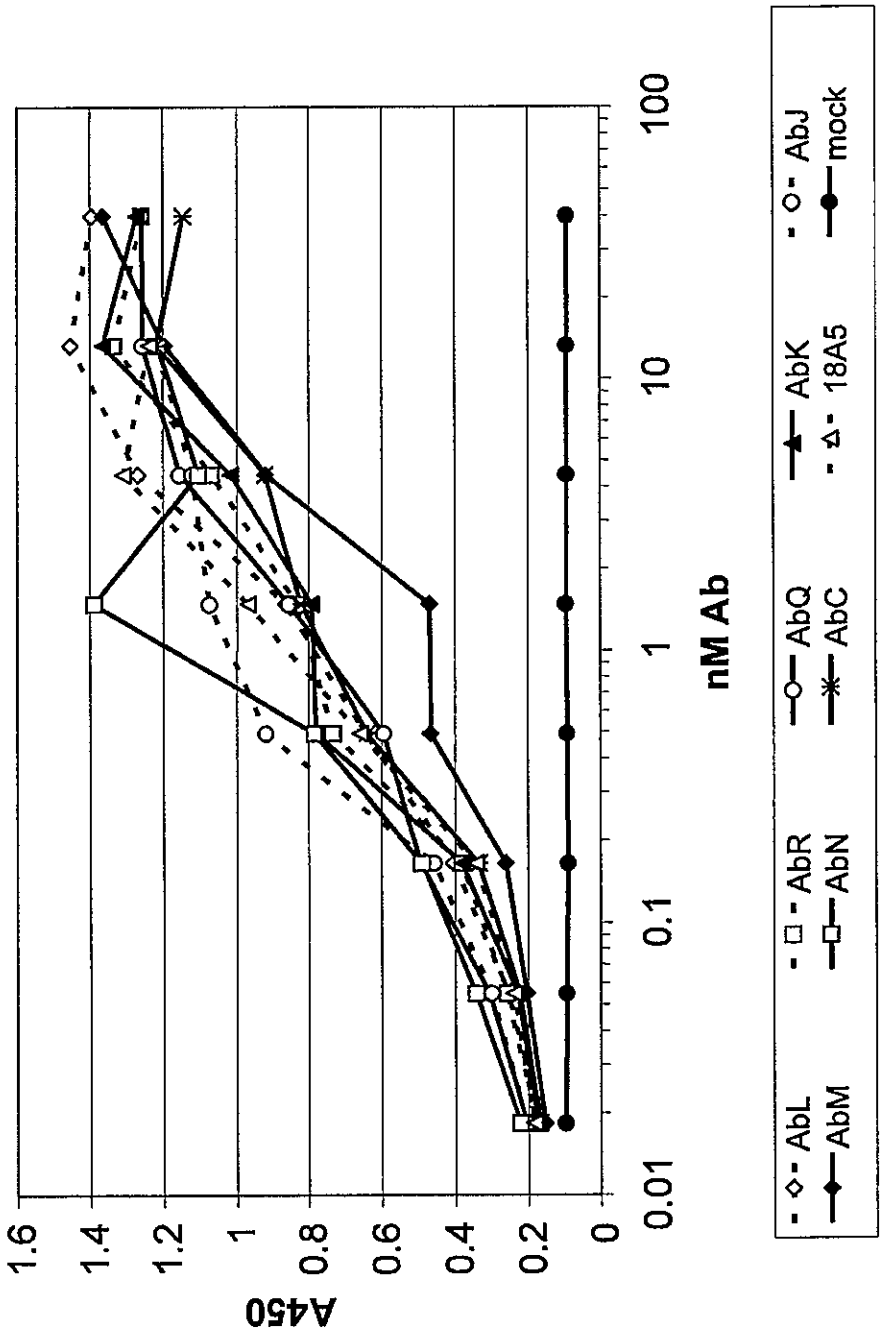

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.01
0.1
1
10
100
nM Ab
AbL
AbR
AbQ
AbK
AbJ
AbM
AbN
AbC
18A5
mock

Figure 6a

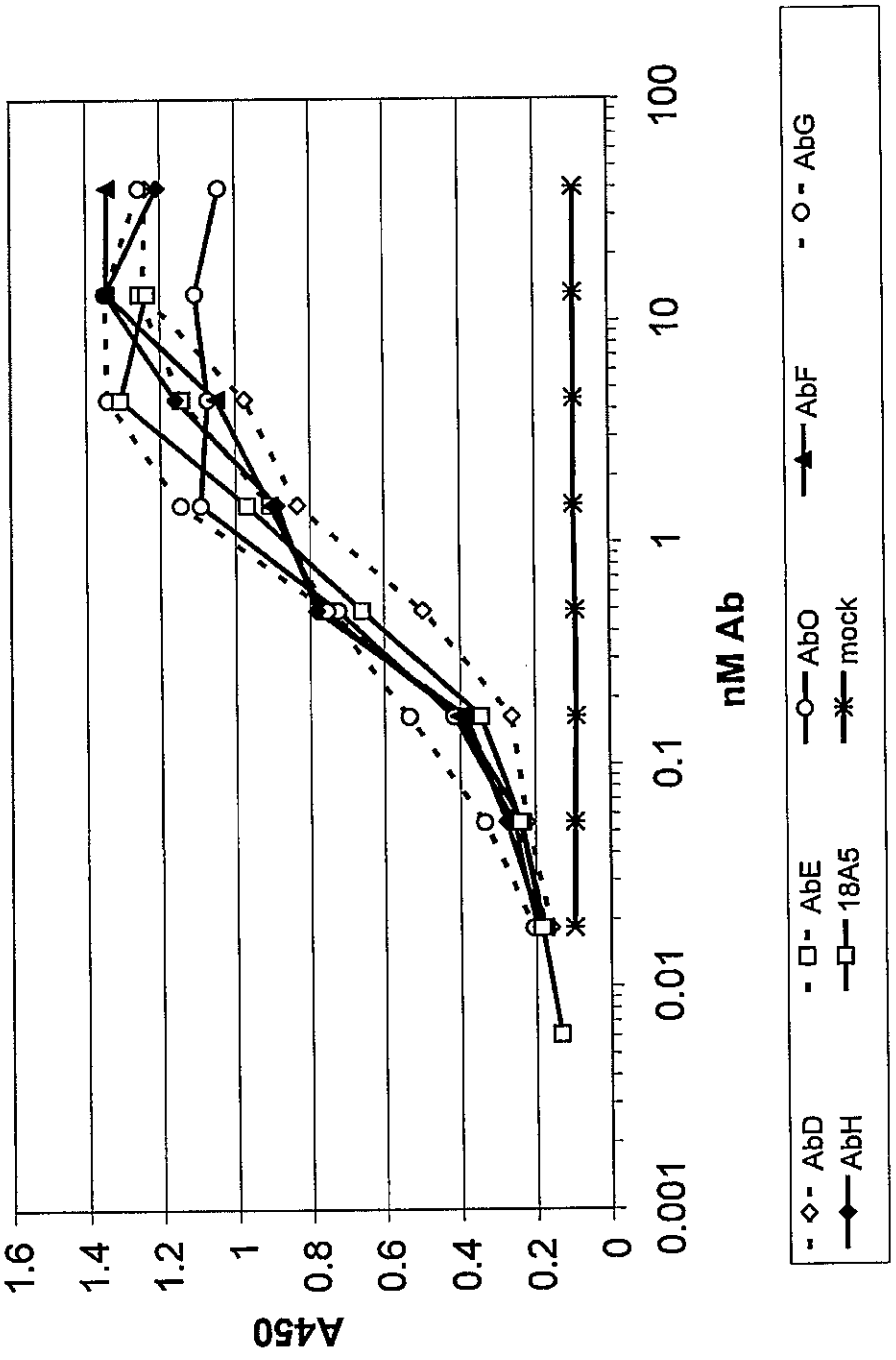

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbD
AbE
AbF
AbG
AbH
18A5
AbO
mock

Figure 6b

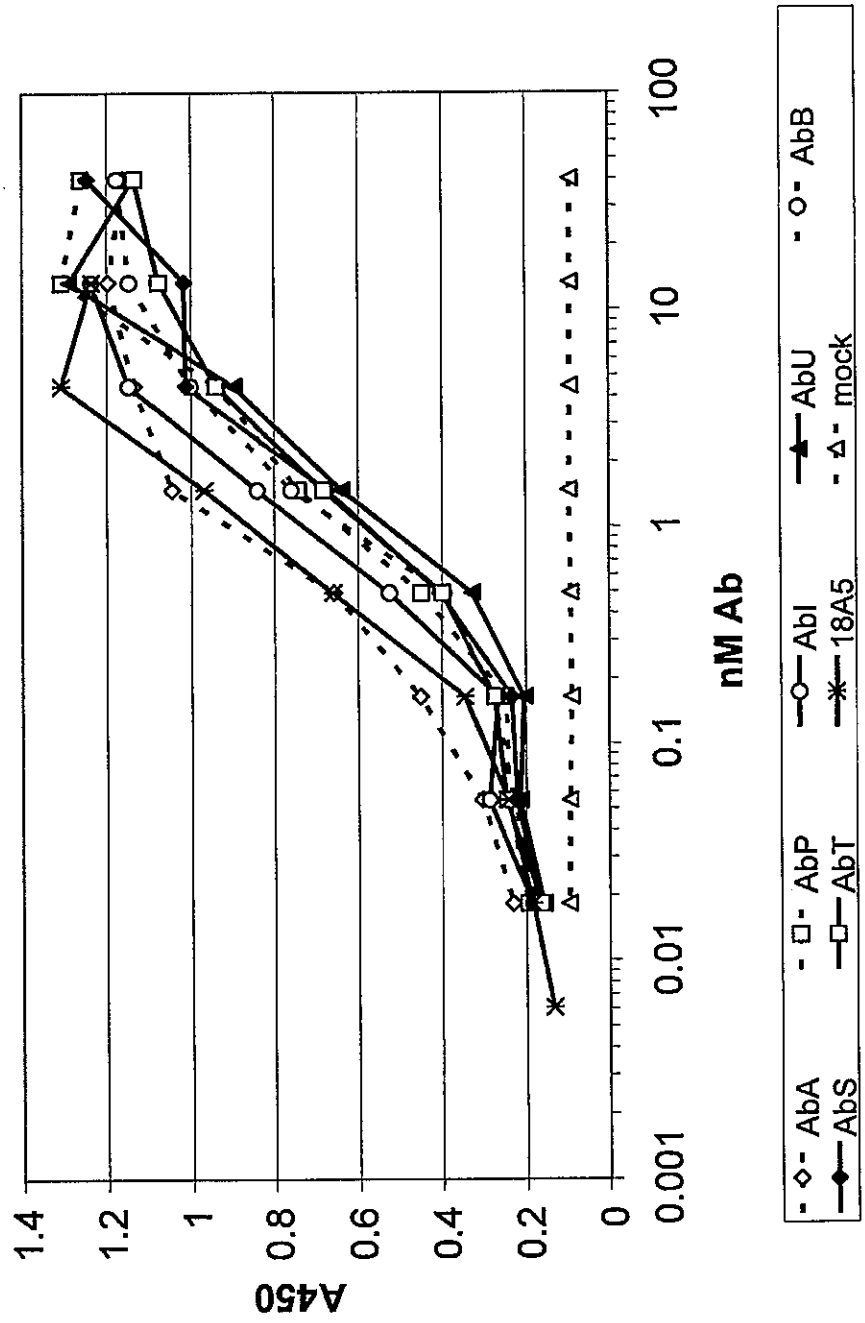

A450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbA
AbB
AbP
AbI
AbU
AbS
AbT
18A5
mock

Figure 6c

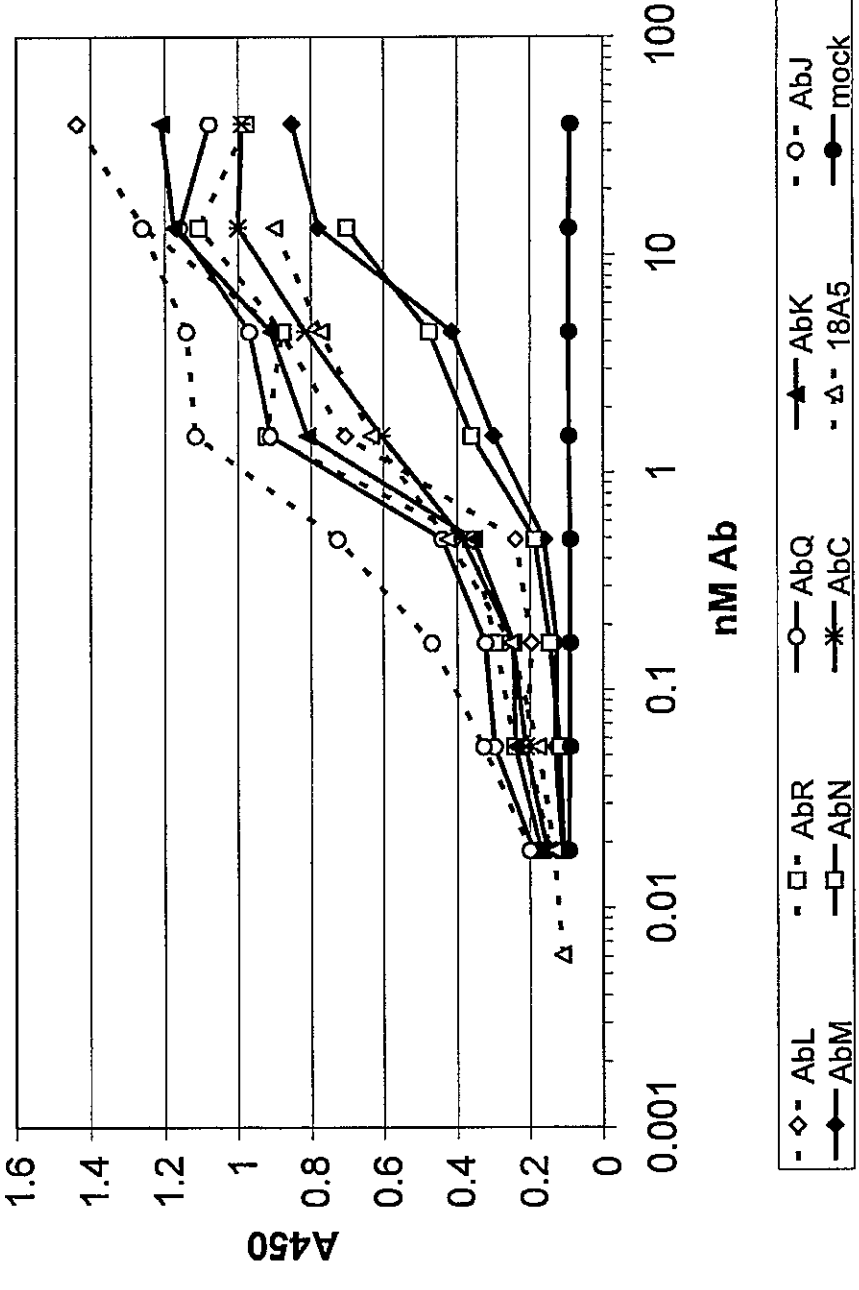

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbL
AbR
AbQ
AbK
AbJ
AbM
AbN
AbC
18A5
mock

Figure 6d

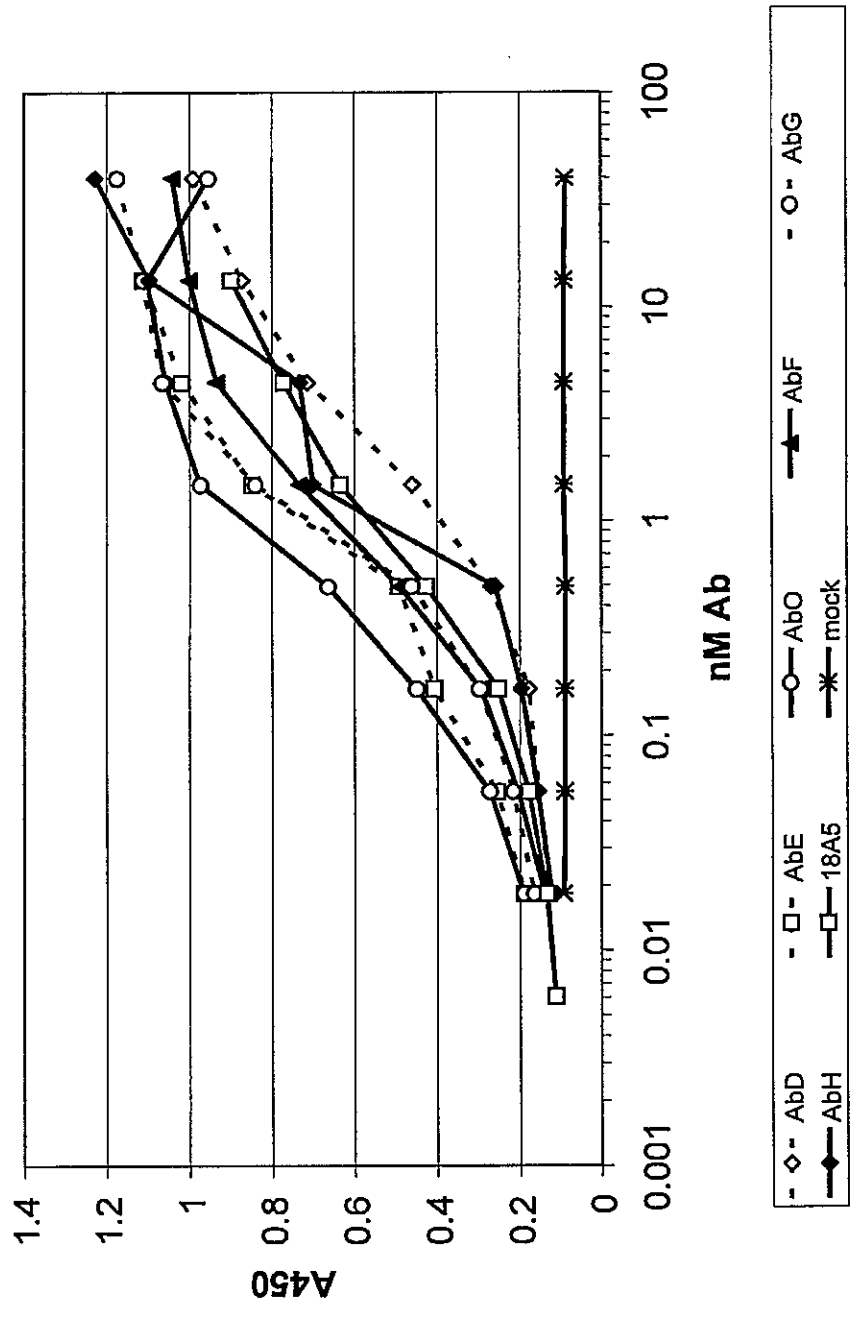

A450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbD
AbE
AbO
AbF
AbG
AbH
18A5
mock

Figure 6e

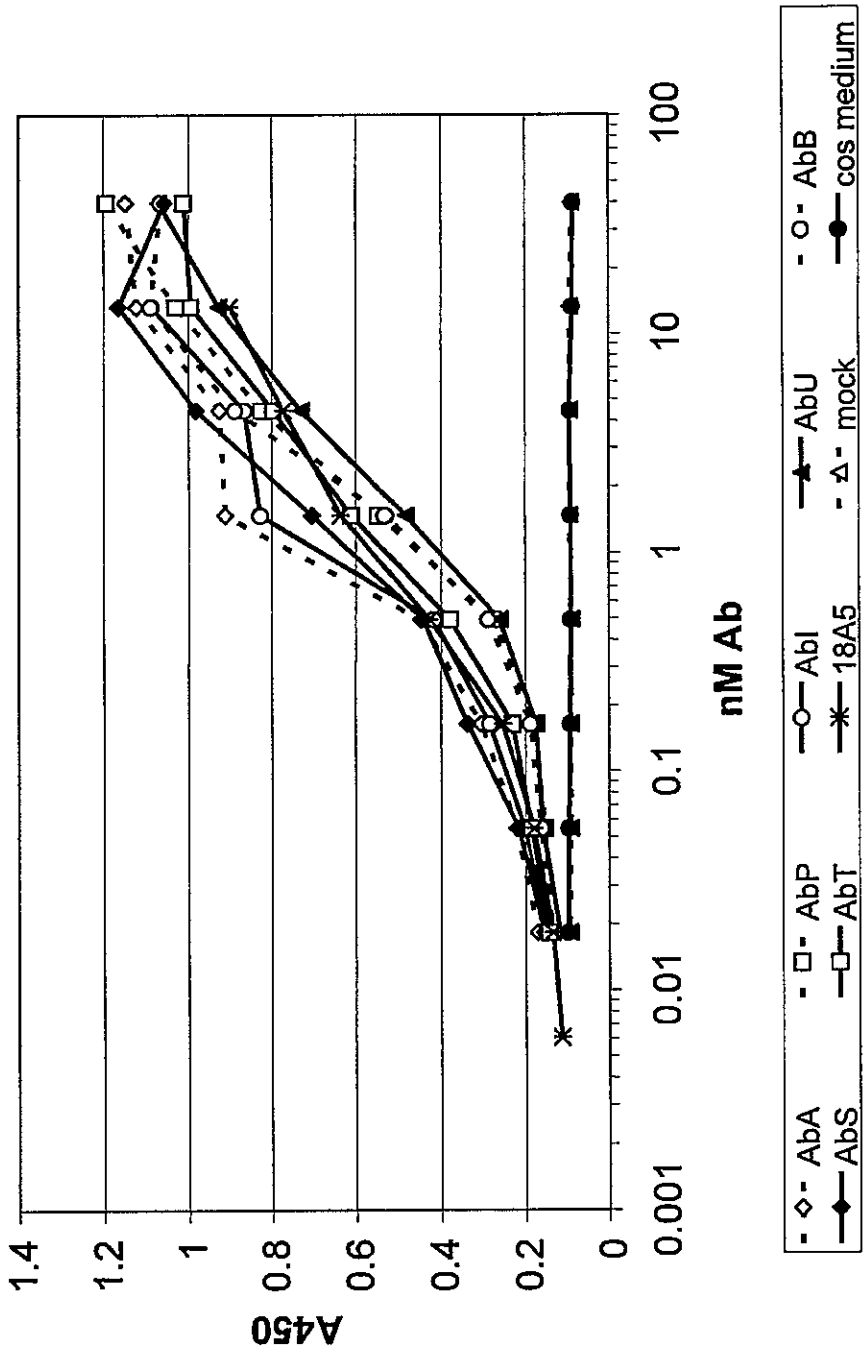

A450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbA
AbP
AbI
AbU
AbB
AbS
AbT
18A5
mock
cos medium

Figure 6f

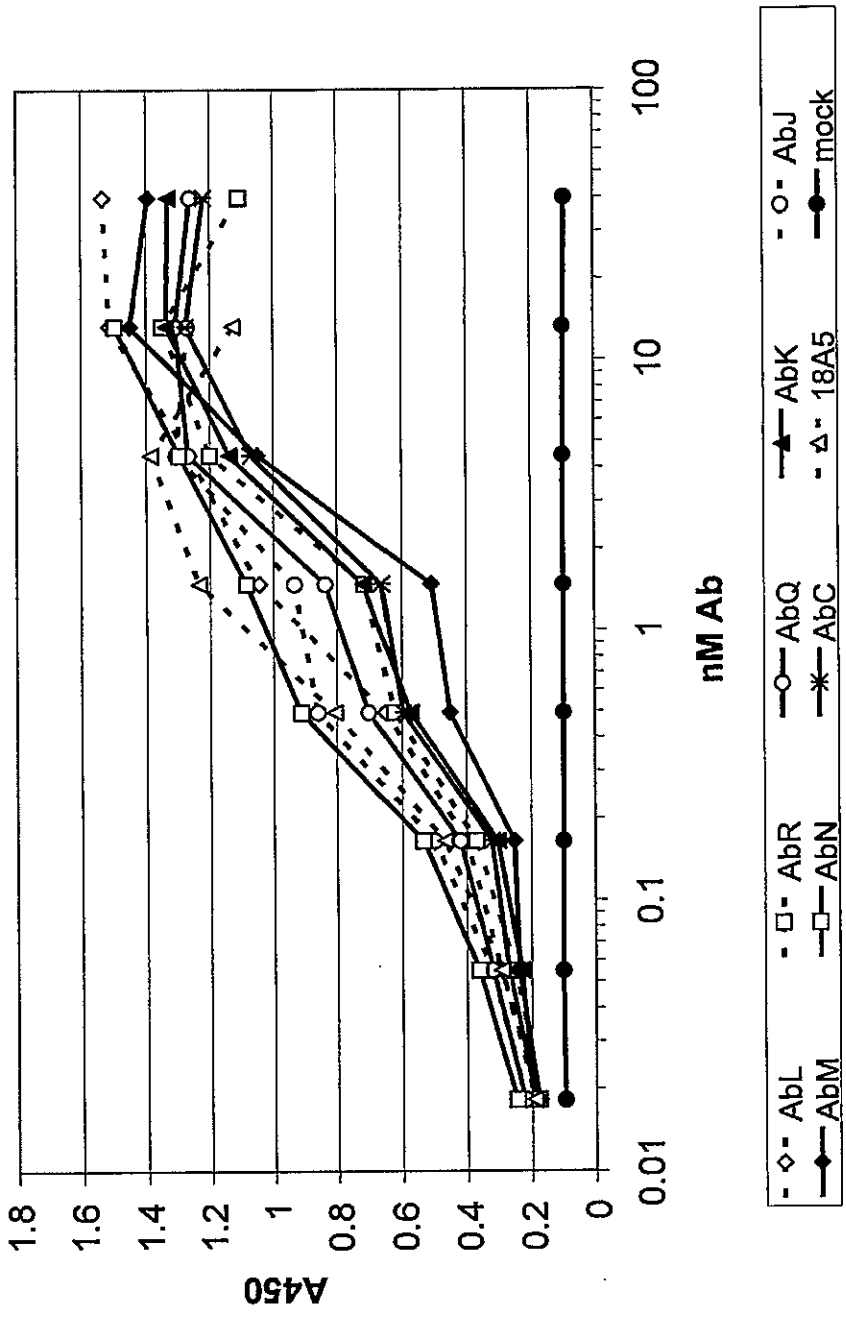

A450
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.01
0.1
1
10
100
nM Ab
AbL
AbR
AbQ
AbK
AbJ
AbM
AbN
AbC
18A5
mock

Figure 6g

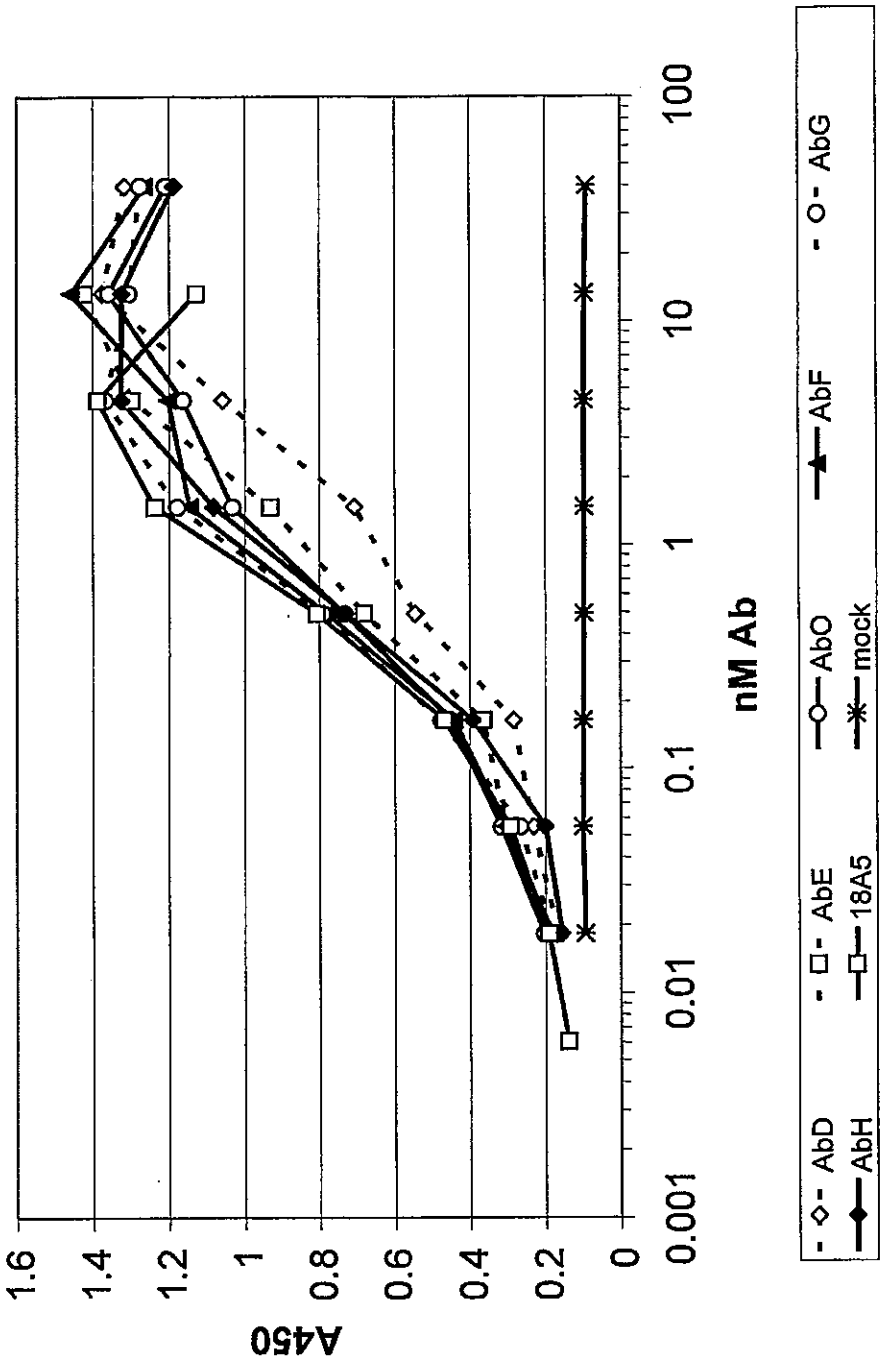

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbD
AbE
AbO
AbF
AbG
AbH
18A5
mock

Figure 6h

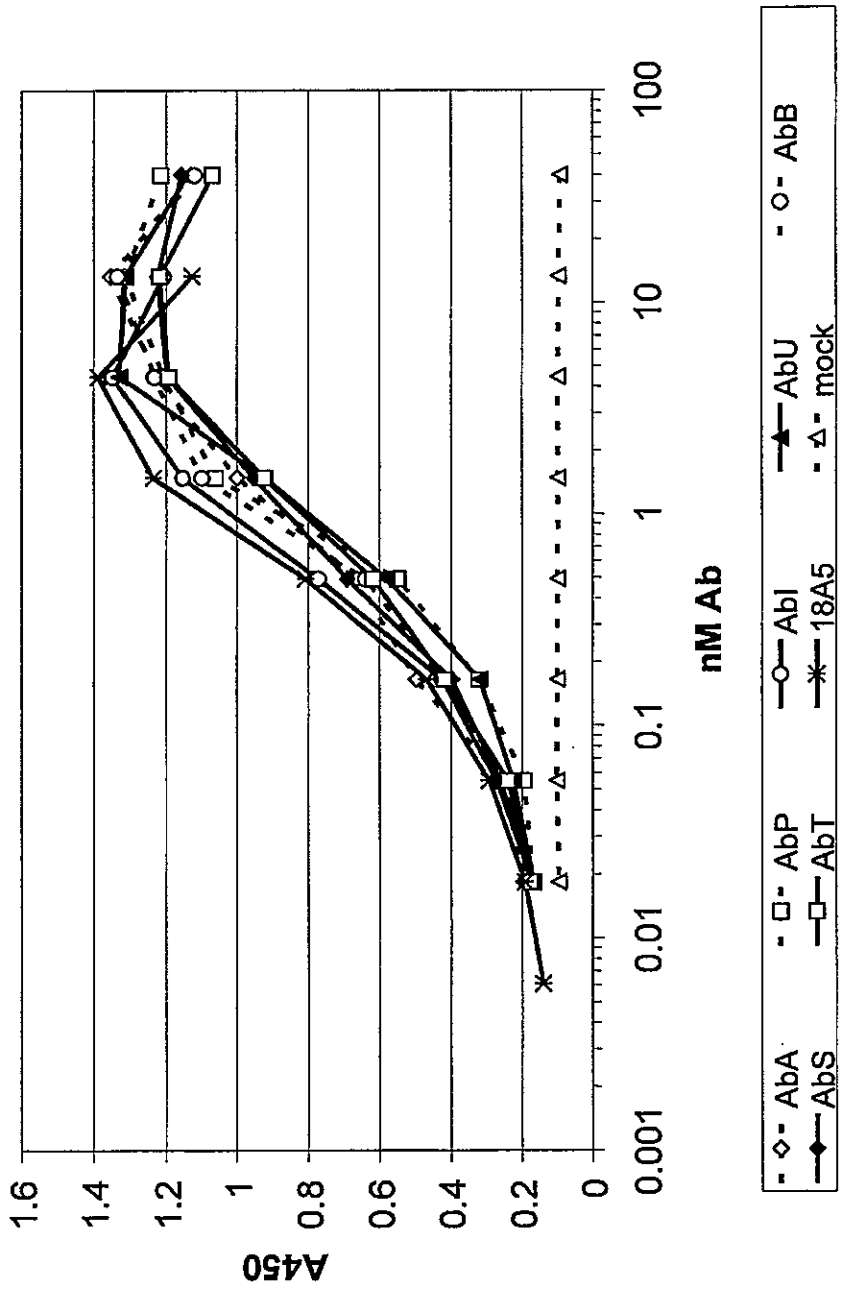

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.001
0.01
0.1
1
10
100
nM Ab
AbA
AbP
AbI
AbU
AbB
AbS
AbT
18A5
mock

Figure 6i

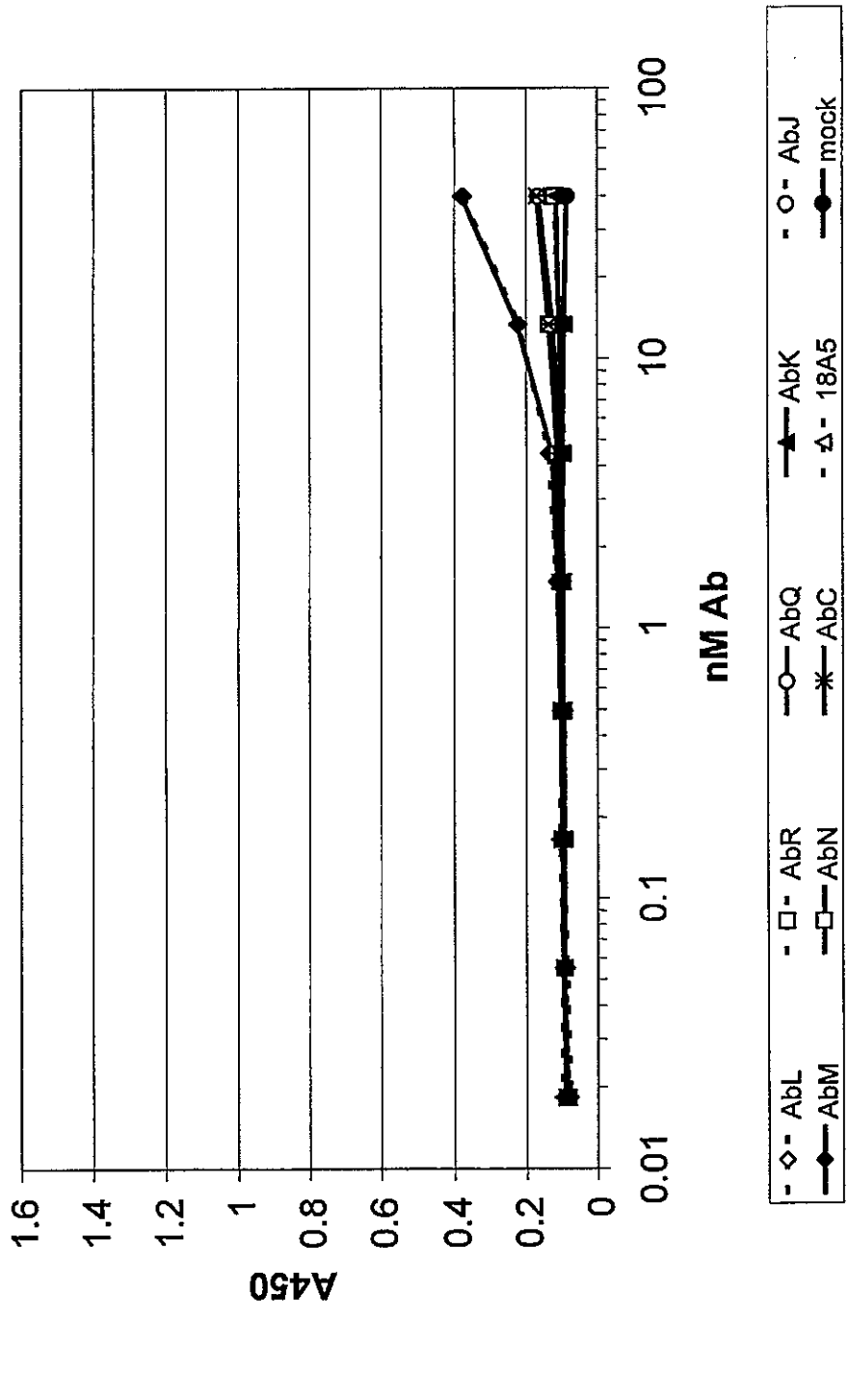

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.01
0.1
1
10
100
nM Ab
AbL
AbM
AbR
AbN
AbQ
AbC
AbK
18A5
AbJ
mock

Figure 6j

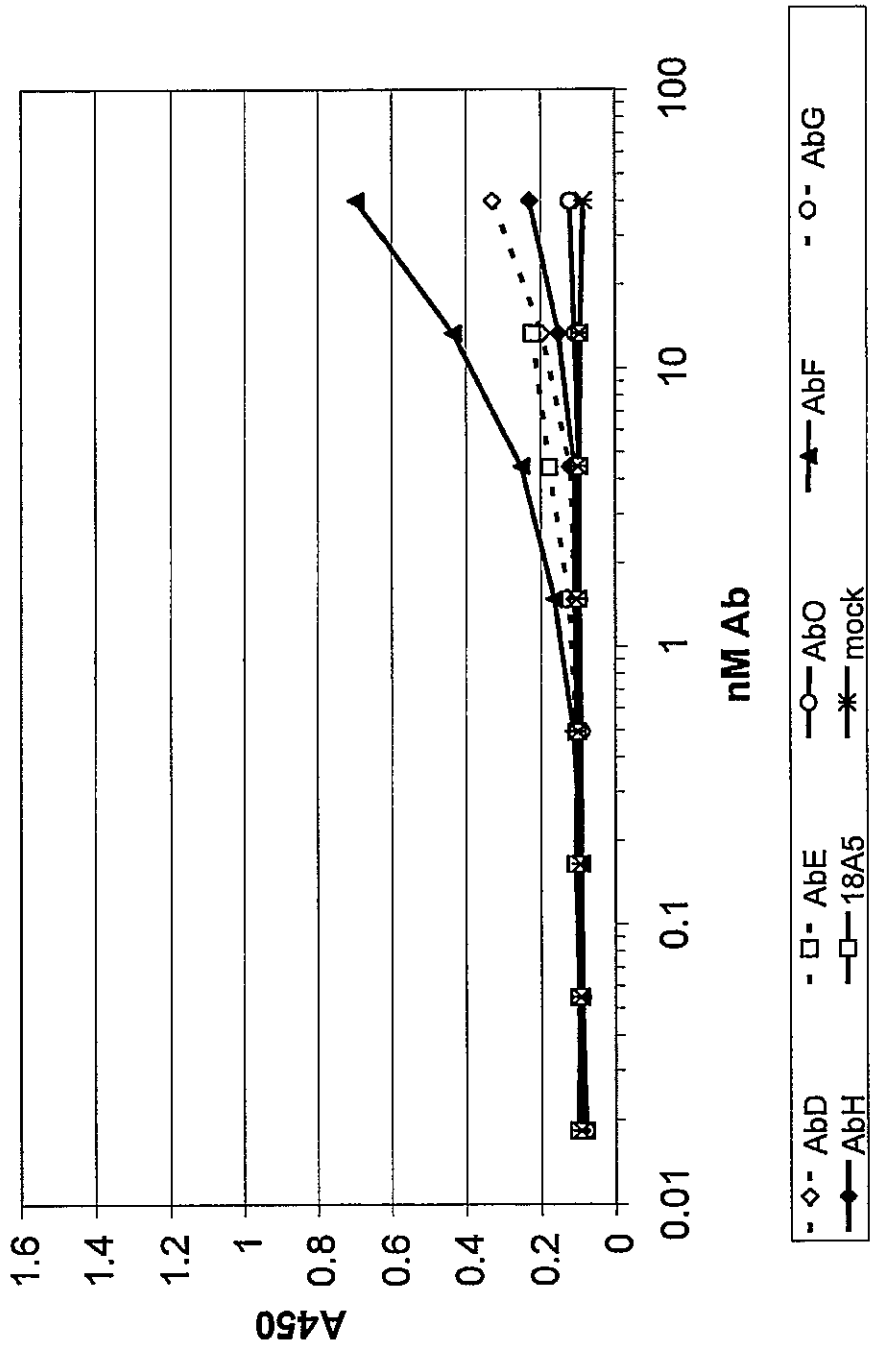

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.01
0.1
1
10
100
nM Ab
AbD
AbE
AbO
AbF
AbG
AbH
18A5
mock

Figure 6k

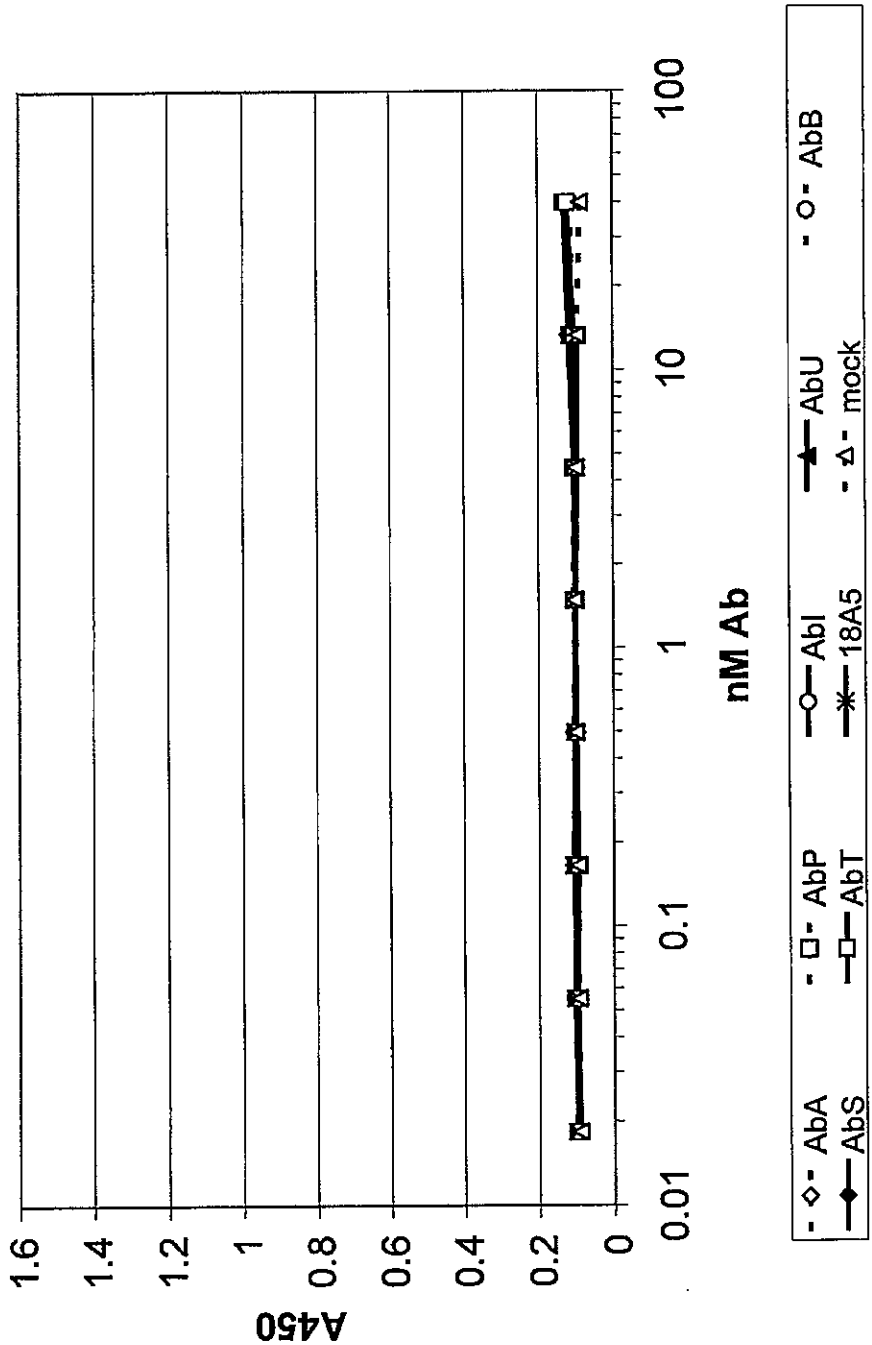

A450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.01
0.1
1
10
100
nM Ab
AbA
AbP
AbI
AbU
AbB
AbS
AbT
18A5
mock

Figure 6I

Figure 7a

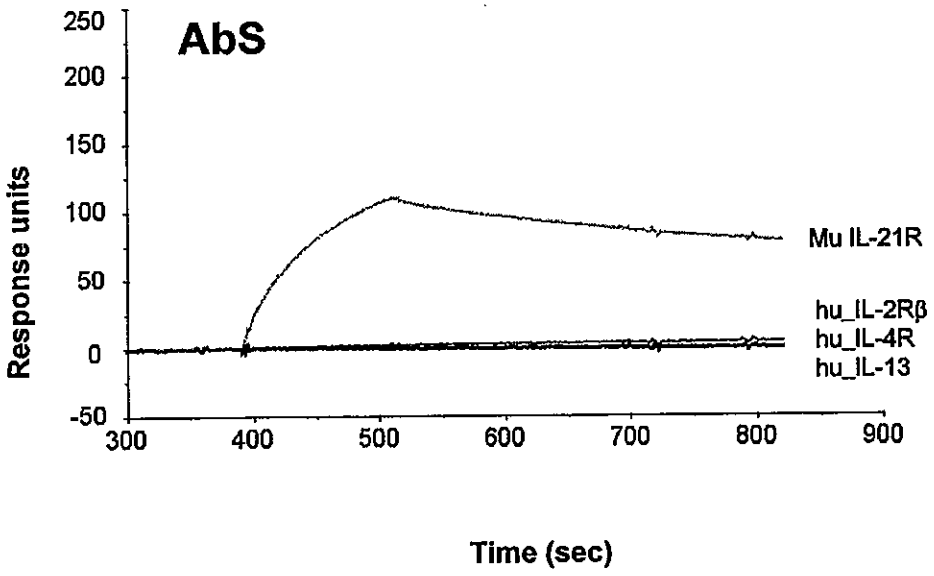

AbS
250
200
150
100
50
0
-50
Response units
300
400
500
600
700
800
900
Time (sec)
Mu IL-21R
hu_IL-2Rβ
hu_IL-4R
hu_IL-13

Figure 7b

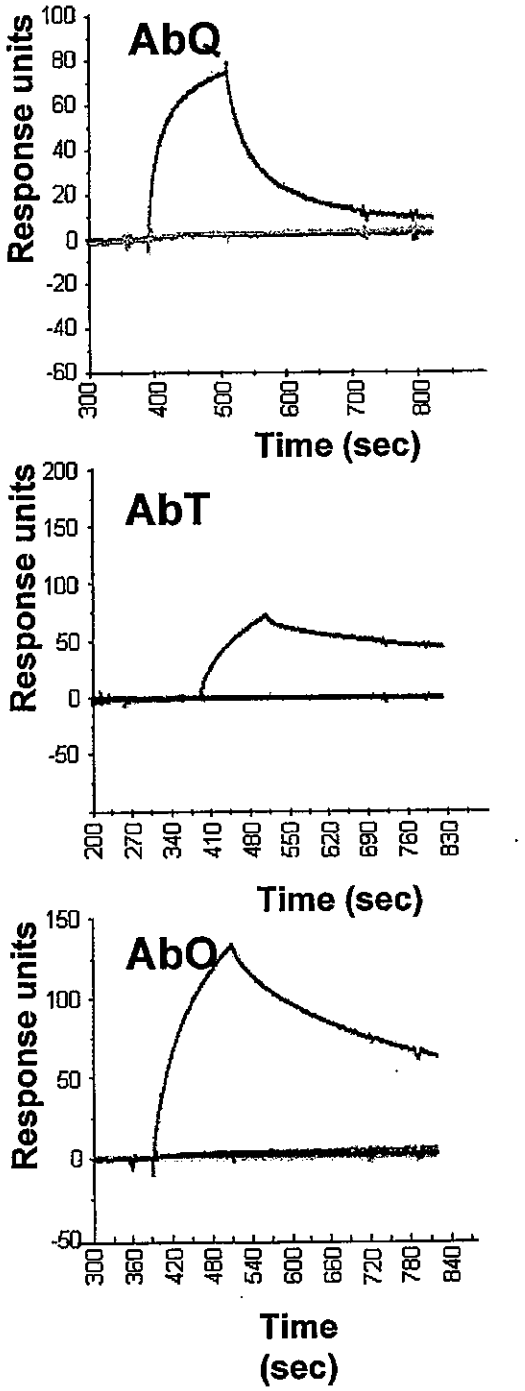
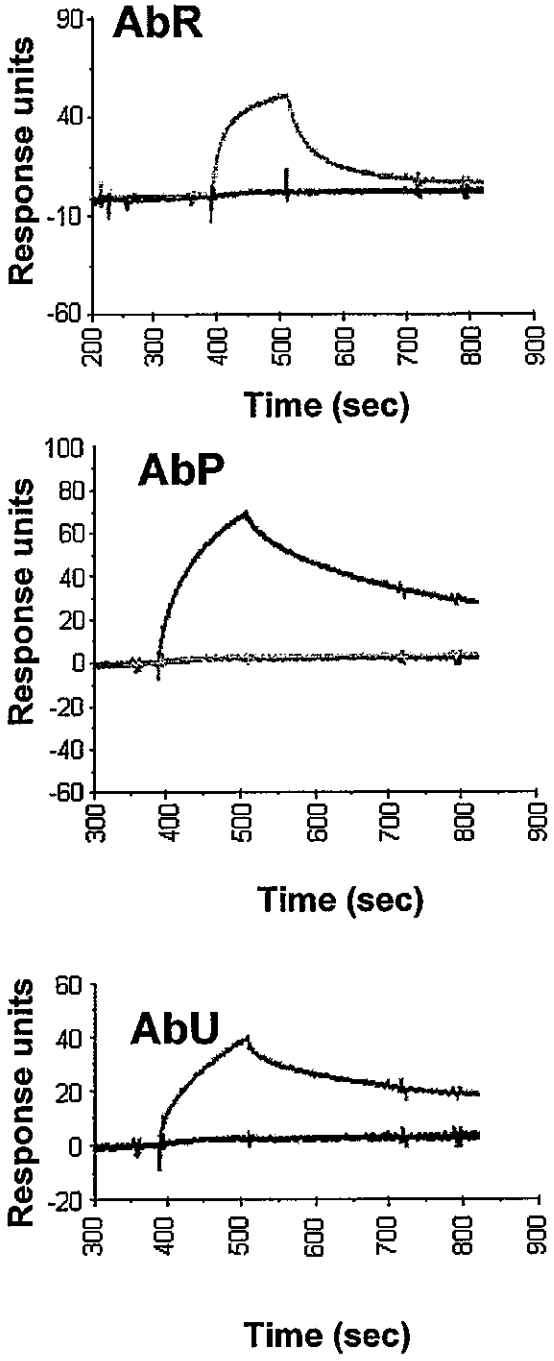

AbQ
Response units
100
80
60
40
20
0
-20
-40
-60
300
400
500
600
700
800
Time (sec)
AbT
Response units
200
150
100
50
0
-50
200
270
340
410
480
550
620
690
760
830
Time (sec)
AbQ
Response units
150
100
50
0
-50
300
360
420
480
540
600
660
720
780
840
Time
(sec)

Figure 7c


AbR
Response units
90
40
-10
-60
200
300
400
500
600
700
800
900
Time (sec)
AbP
Response units
100
80
60
40
20
0
-20
-40
-60
300
400
500
600
700
800
900
Time (sec)
AbU
Response units
60
40
20
0
-20
300
400
500
600
700
800
900
Time (sec)

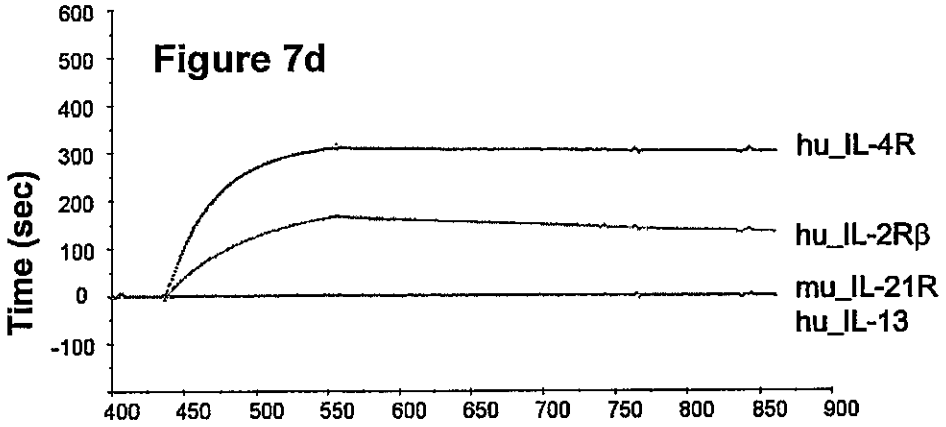

Figure 7d
600
500
400
300
200
100
0
-100
Time (sec)
400
450
500
550
600
650
700
750
800
850
900
hu_IL-4R
hu_IL-2Rβ
mu_IL-21R
hu_IL-13
Time (sec)

Figure 8a

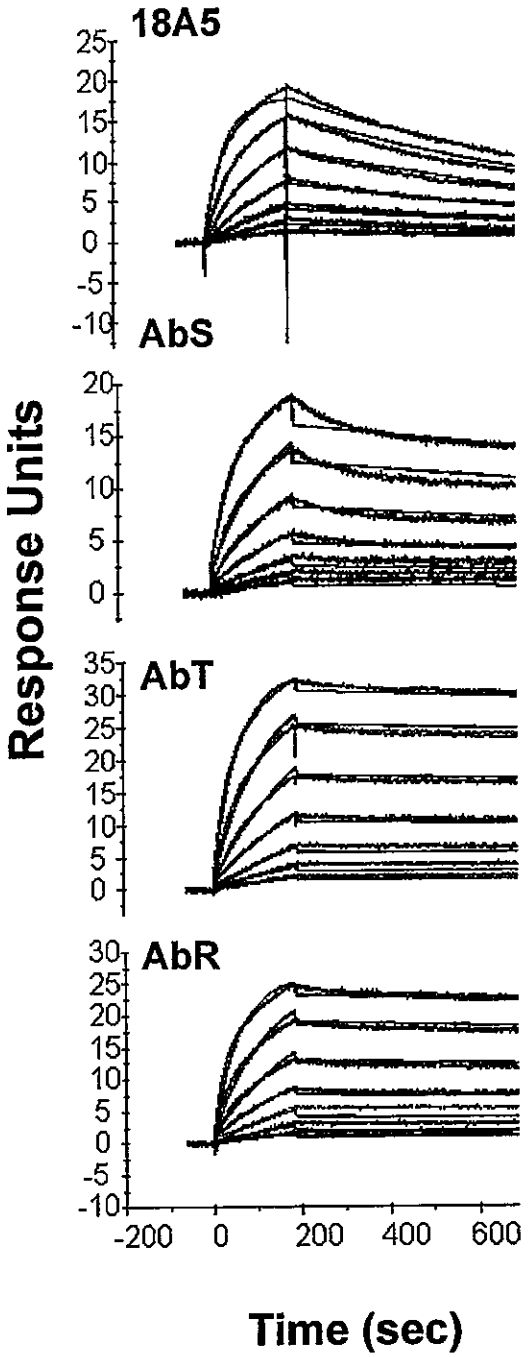

18A5
AbS
AbT
AbR
Response Units
Time (sec)
25
20
15
10
5
0
-5
-10
35
30
-200
0
200
400
600

Figure 8b

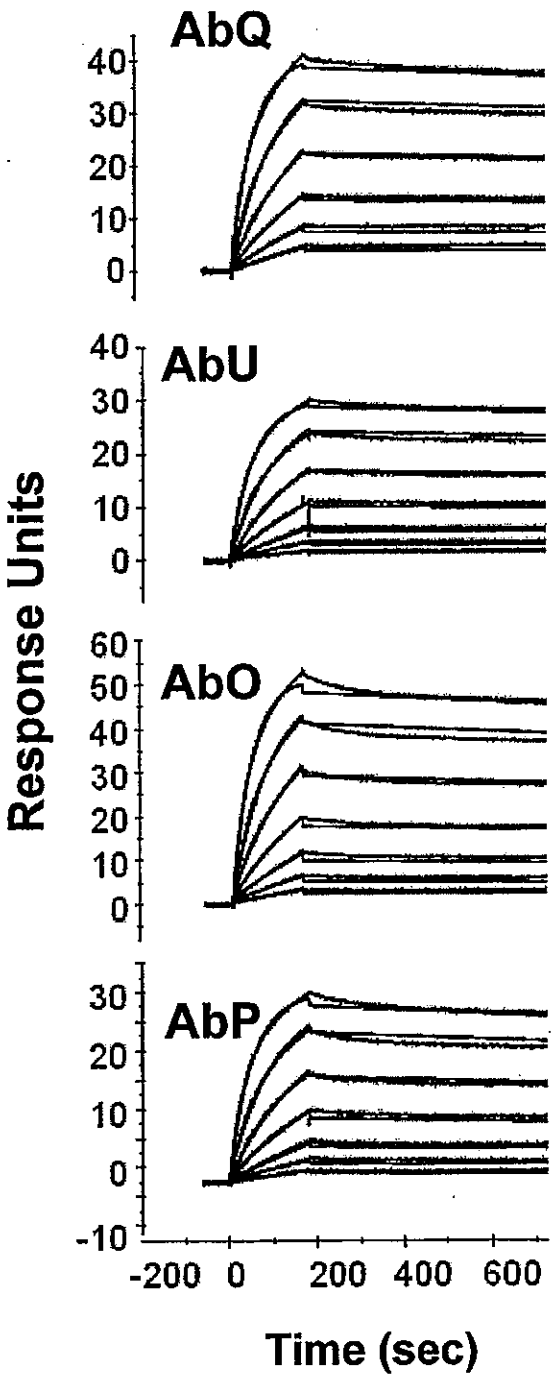

AbQ
AbU
AbO
AbP
Response Units
Time (sec)
40
30
20
10
0
60
50
-10
-200
200
400
600

Figure 8c

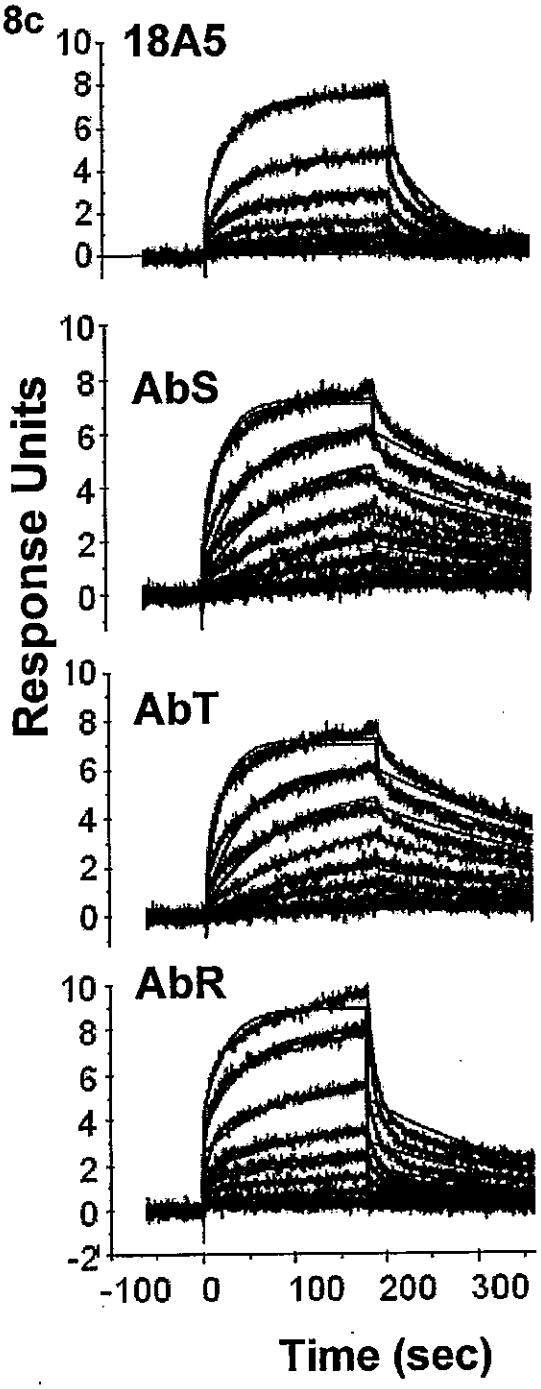
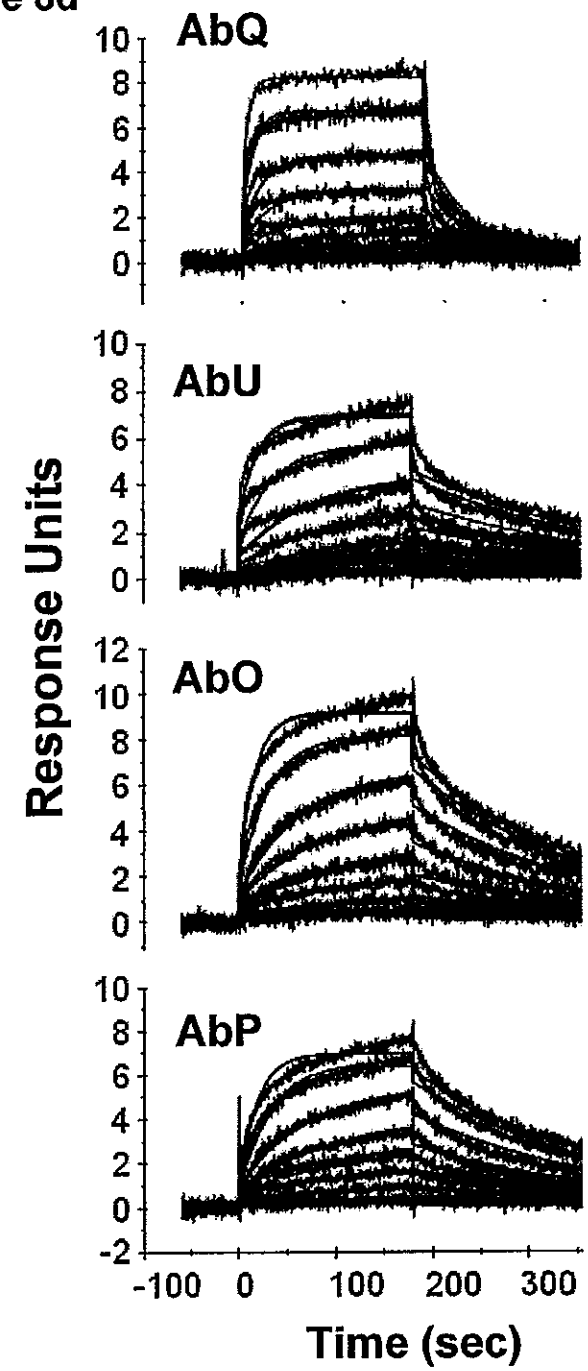

18A5
AbS
AbT
AbR
Response Units
Time (sec)
10
8
6
4
2
0
-2
-100
0
100
200
300

Figure 8d



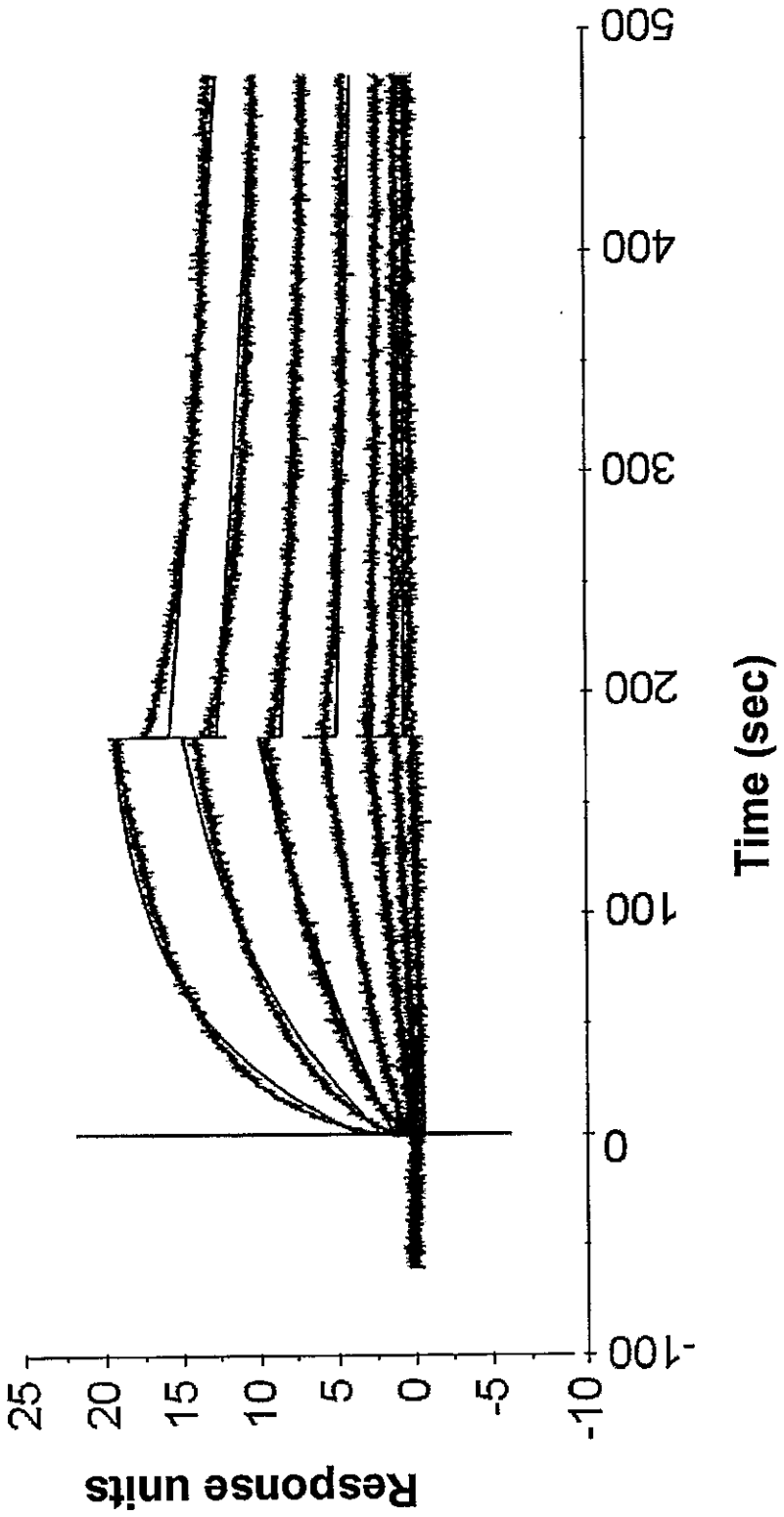

Response units
25
20
15
10
5
0
-5
-10
Time (sec)
-100
0
100
200
300
400
500

Figure 9a

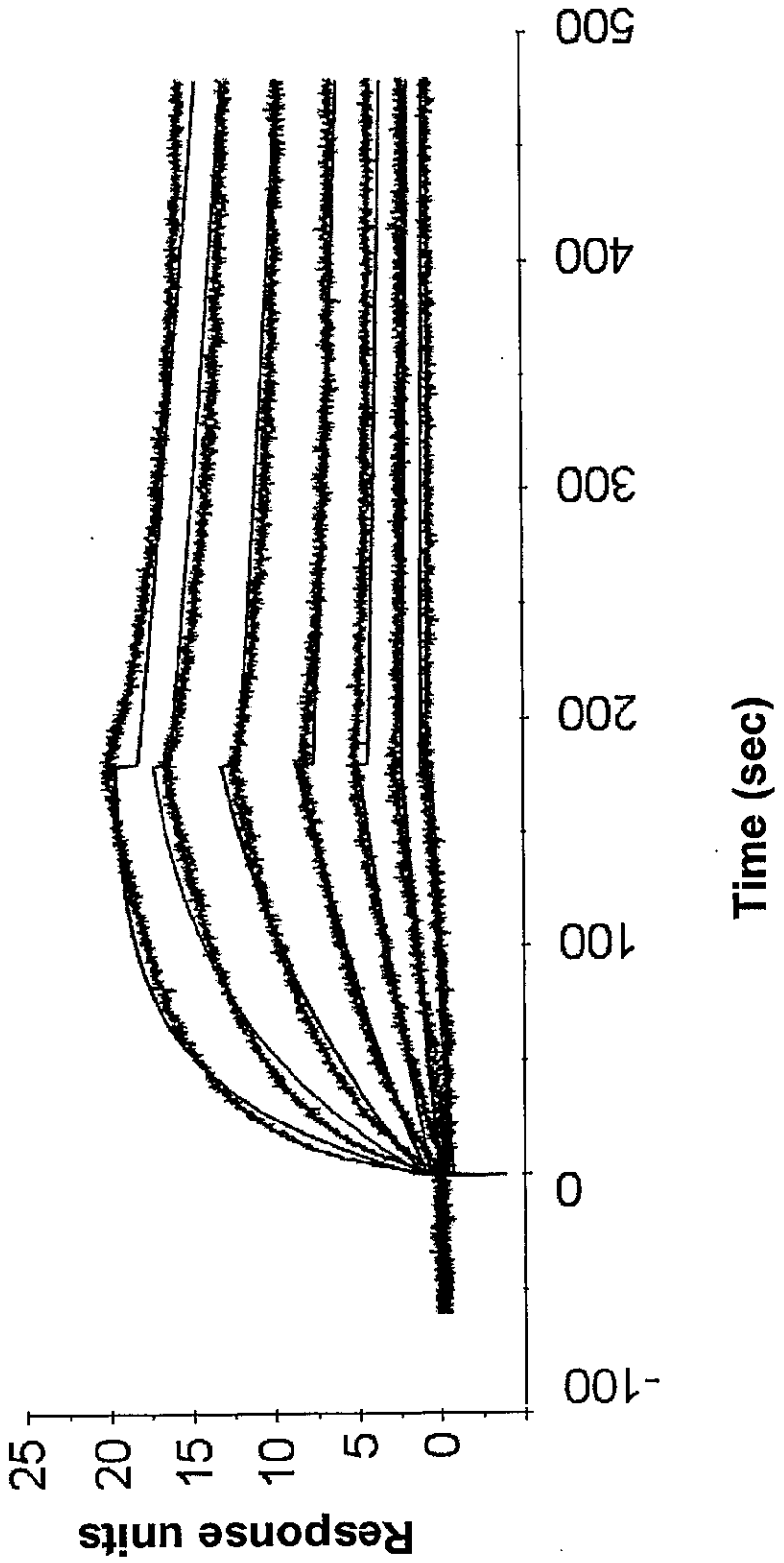


Figure 9b

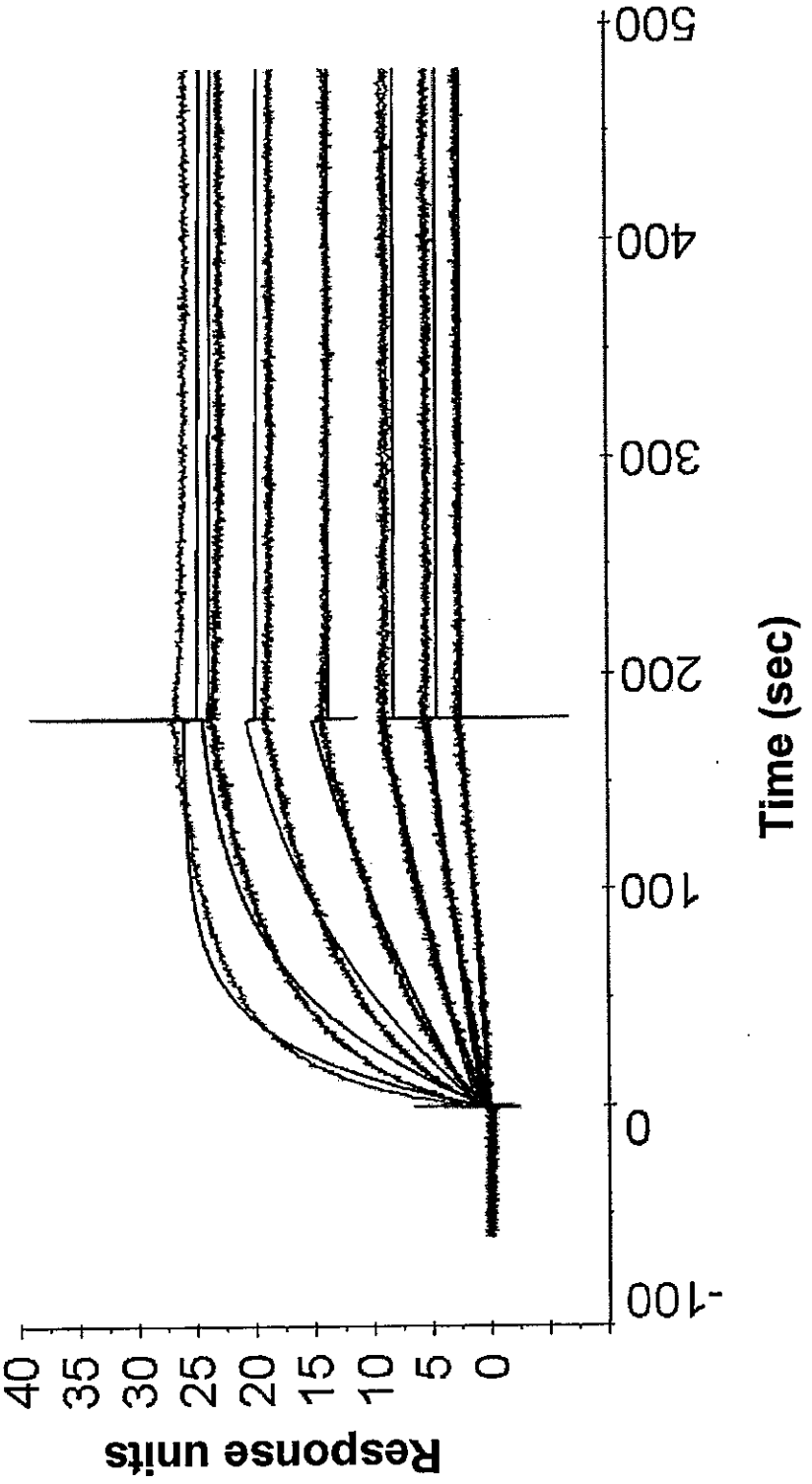

Response units
40
35
30
25
20
15
10
5
0
-100
0
100
200
300
400
500
Time (sec)

Figure 9c

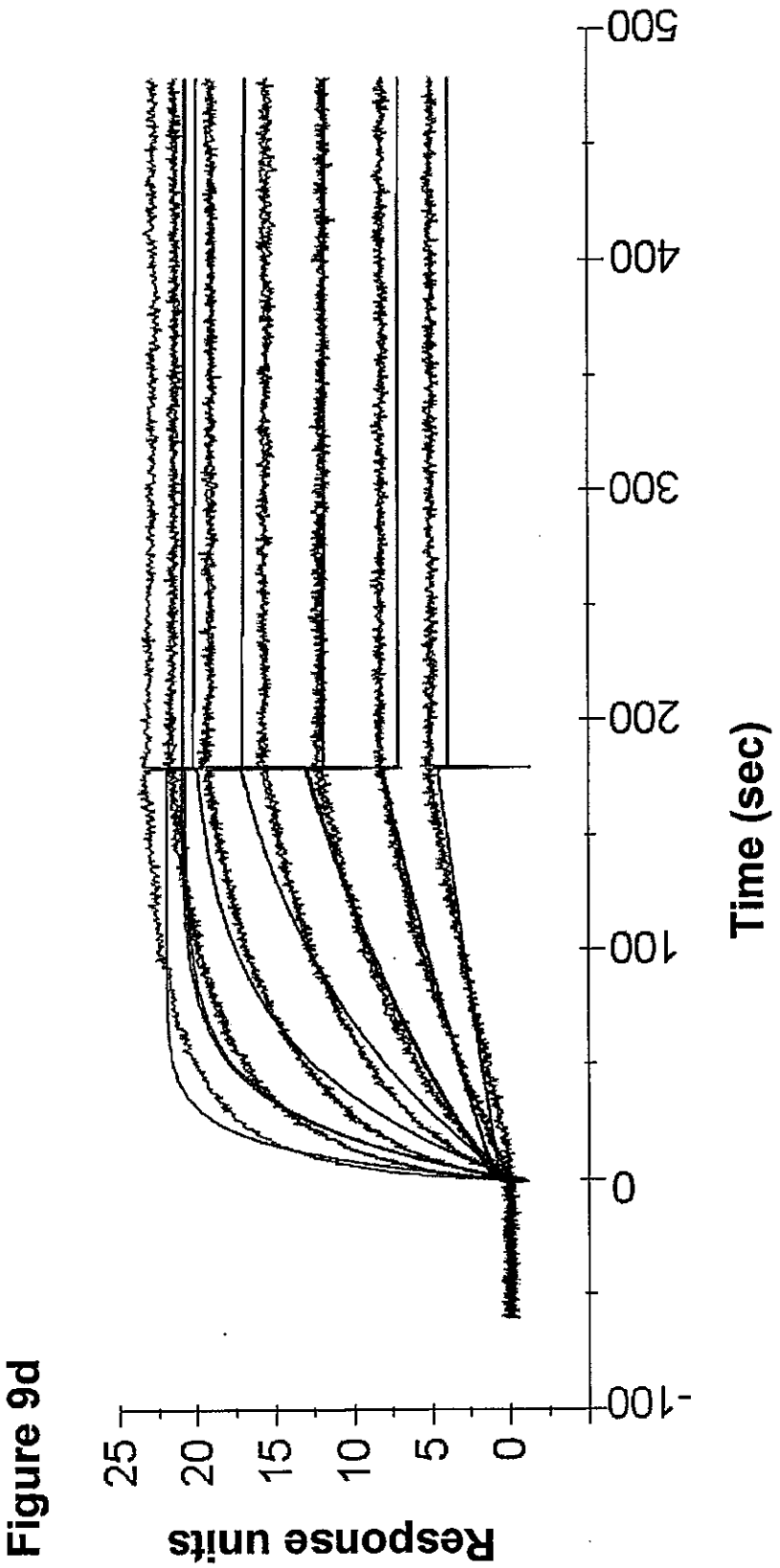


Figure 9d

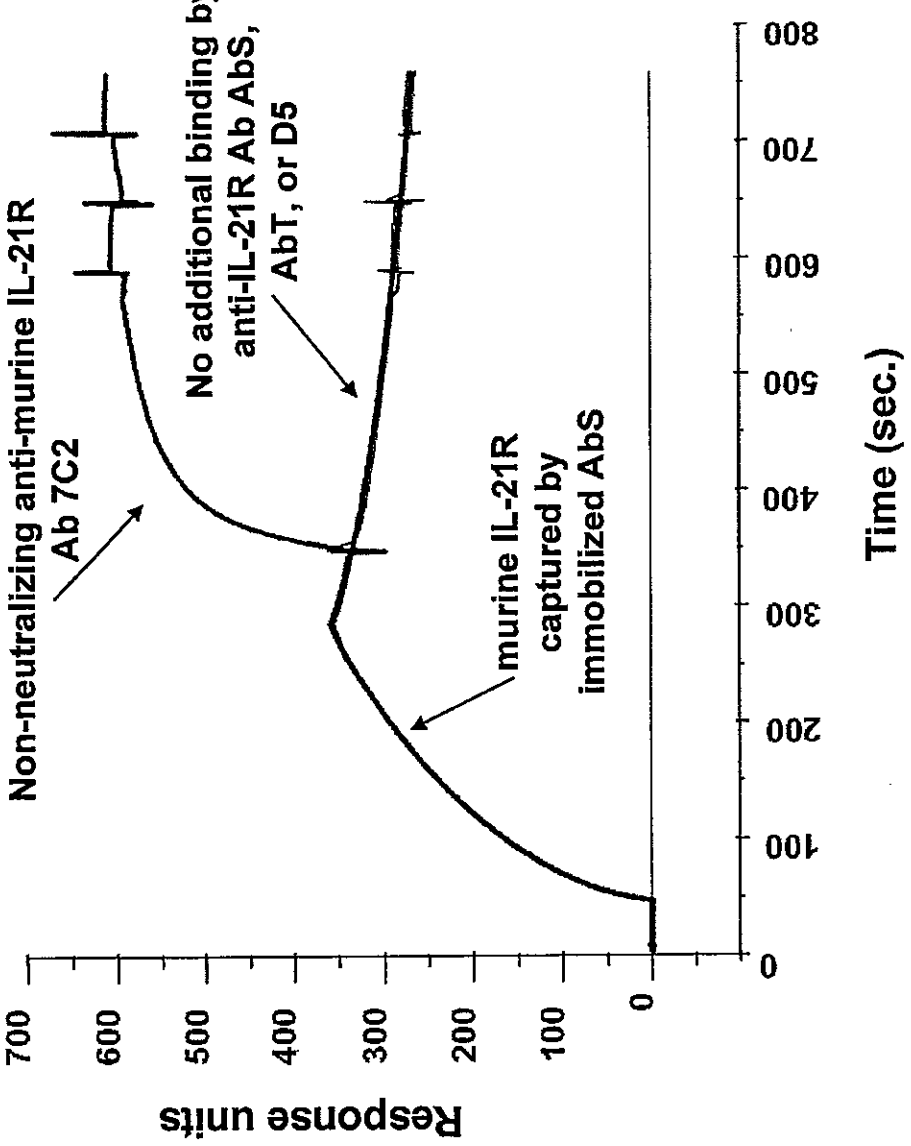

Non-neutralizing anti-murine IL-21R Ab 7C2
No additional binding by anti-IL-21R Ab AbS, AbT, or D5
murine IL-21R captured by immobilized AbS
Response units
Time (sec.)
0
100
200
300
400
500
600
700
800

Figure 10a

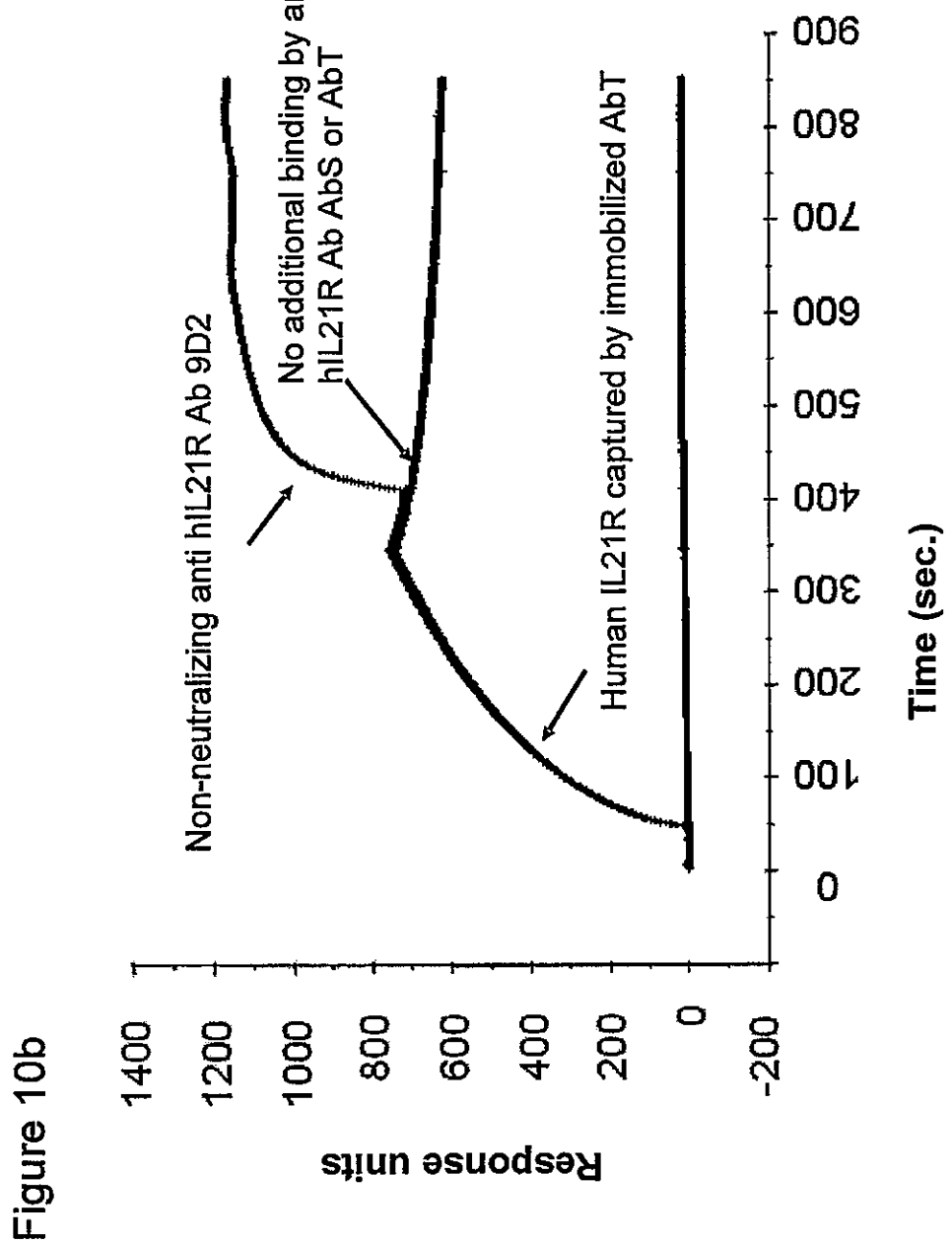

Non-neutralizing anti hIL21R Ab 9D2
No additional binding by anti-hIL21R Ab AbS or AbT
Human IL21R captured by immobilized AbT
Response units
1400
1200
1000
800
600
400
200
0
-200
0
100
200
300
400
500
600
700
800
900
Time (sec.)

Figure 10b

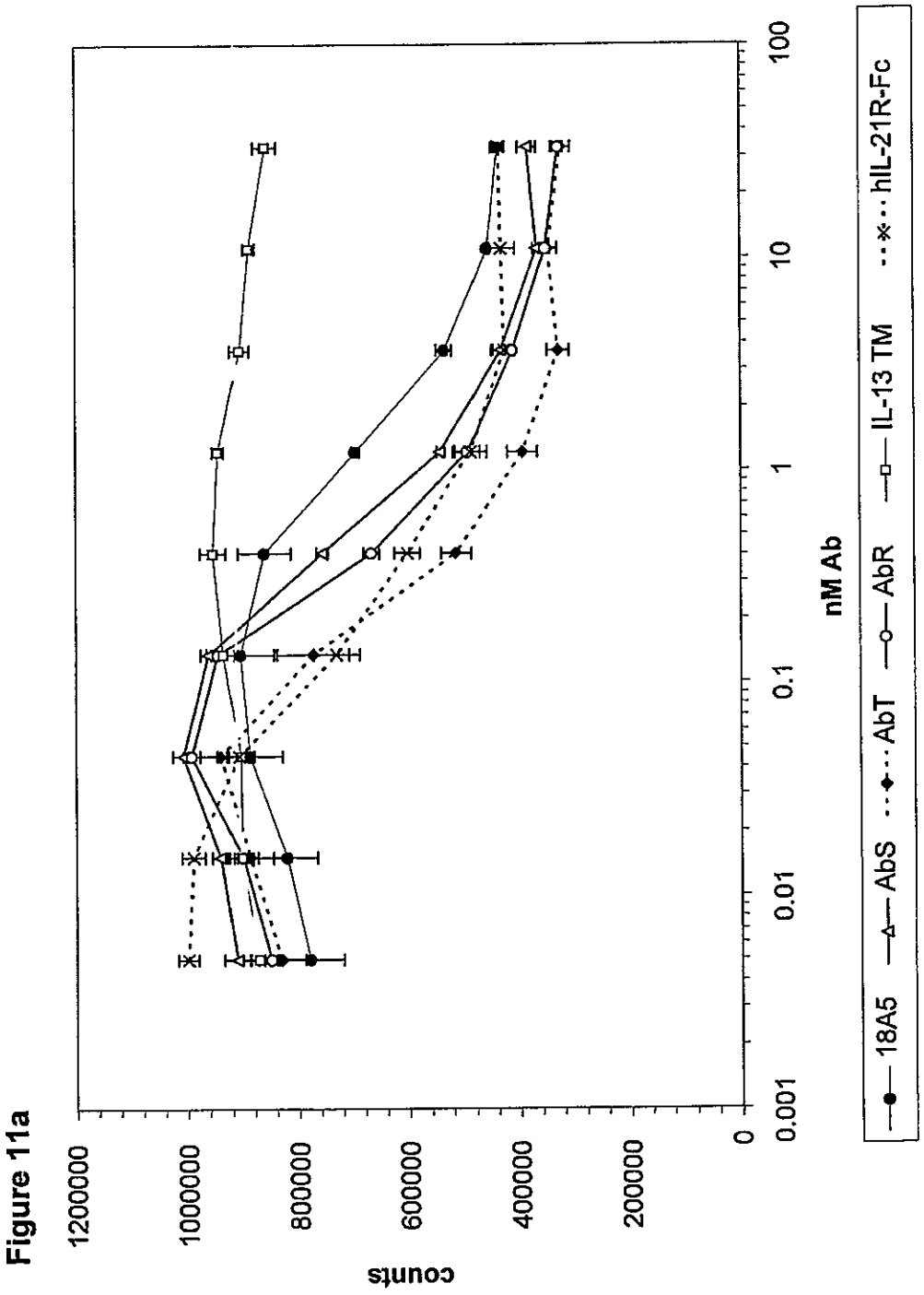

counts
1200000
1000000
800000
600000
400000
200000
0
0.001
0.01
0.1
1
10
100
nM Ab
18A5
AbS
AbT
AbR
IL-13 TM
hIL-21R-Fc

Figure 11a

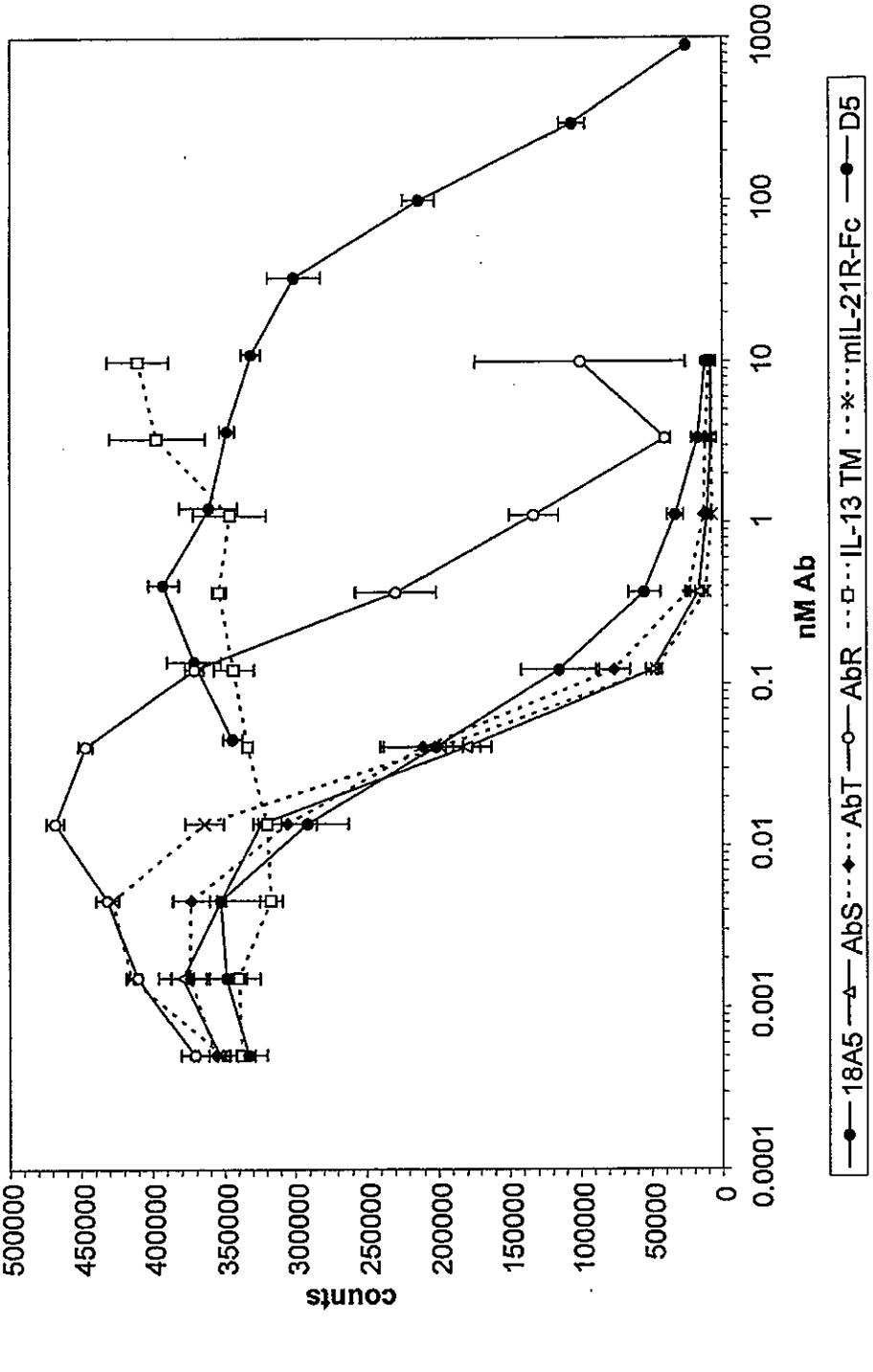

counts
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
0.0001
0.001
0.01
0.1
1
10
100
1000
nM Ab
18A5
AbS
AbT
AbR
IL-13 TM
mIL-21R-Fc
D5

Figure 11b

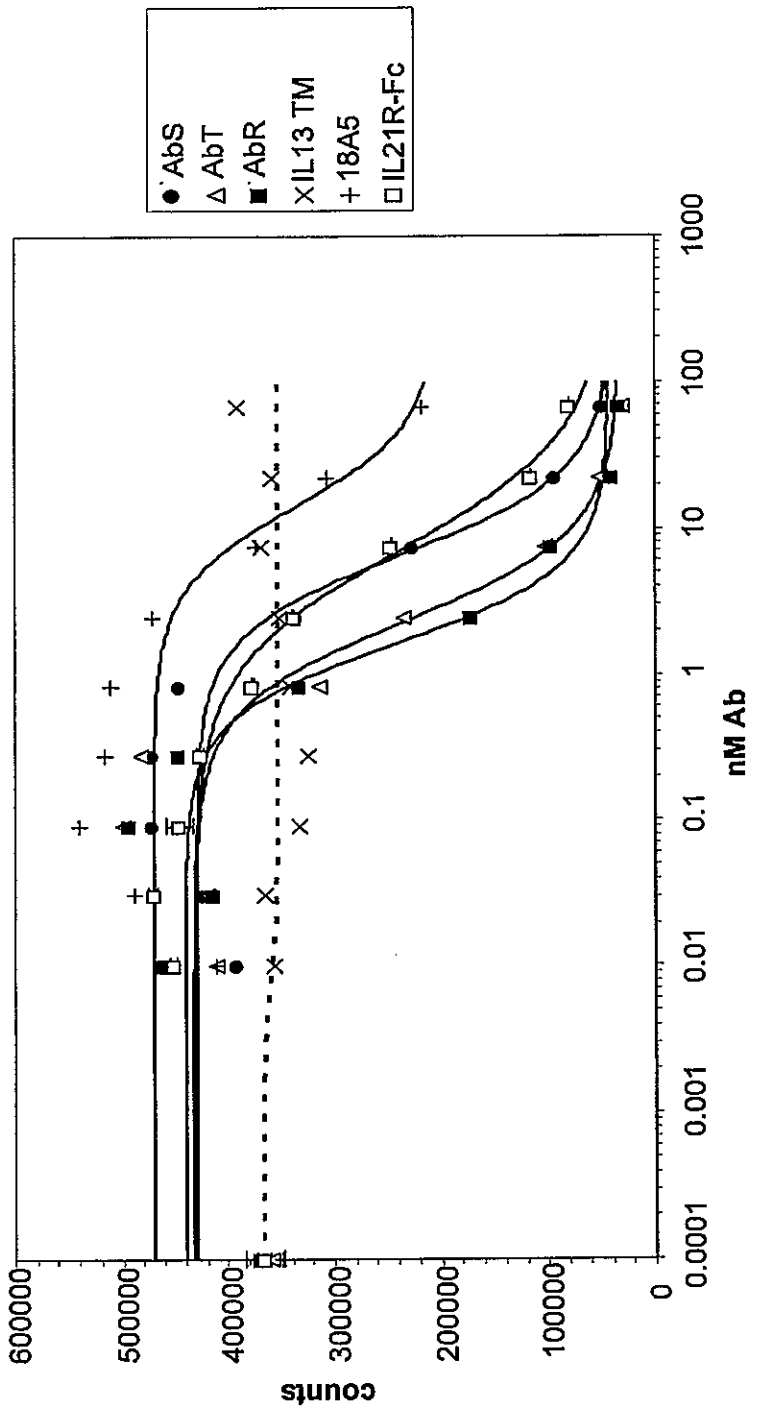

AbS
AbT
AbR
IL13 TM
18A5
IL21R-Fc
counts
600000
500000
400000
300000
200000
100000
0
0.0001
0.001
0.01
0.1
1
10
100
1000
nM Ab

Figure 11c

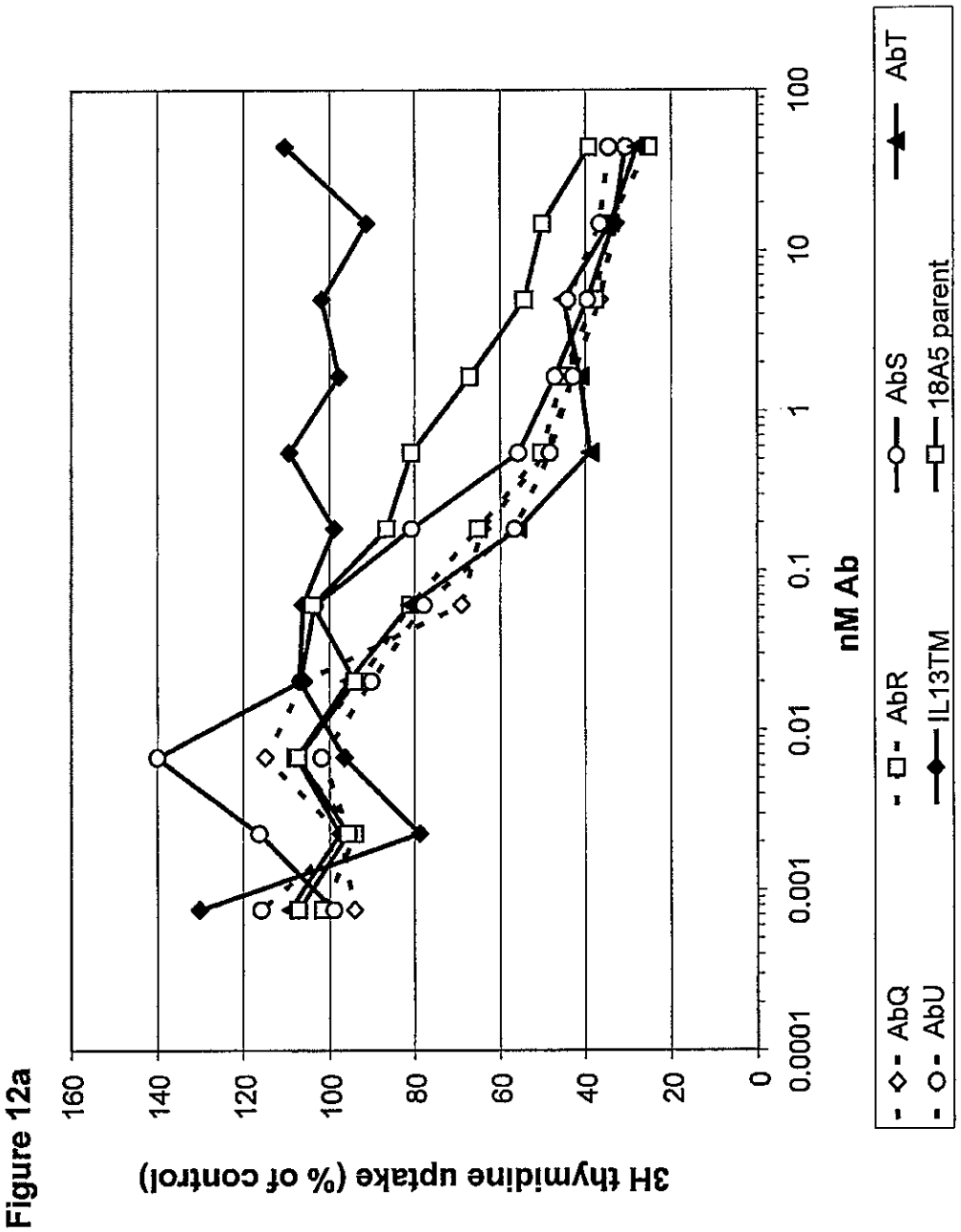

3H thymidine uptake (% of control)
160
140
120
100
80
60
40
20
0
0.0001
0.001
0.01
0.1
1
10
100
nM Ab
AbQ
AbR
AbS
AbT
AbU
IL13TM
18A5 parent

Figure 12a

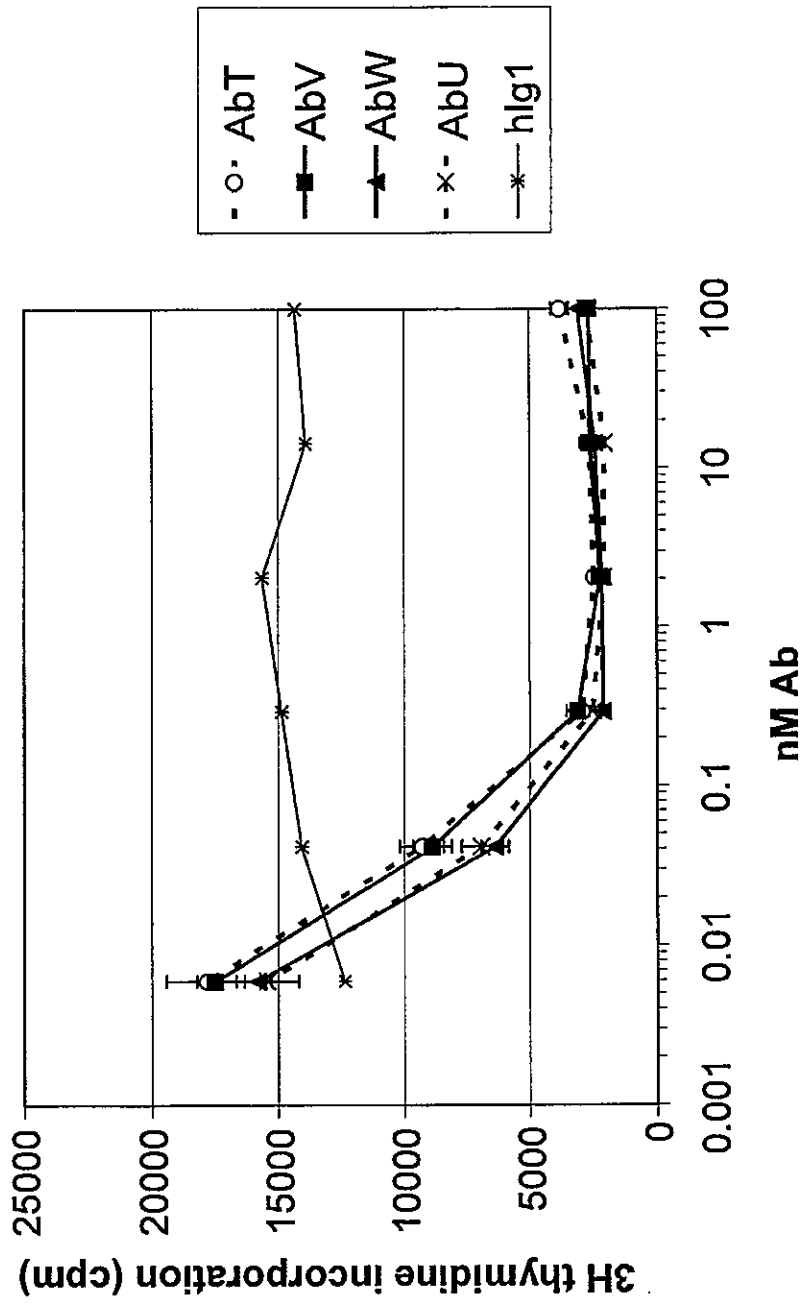

AbT
AbV
AbW
AbU
hIg1
3H thymidine incorporation (cpm)
25000
20000
15000
10000
5000
0
0.001
0.01
0.1
1
10
100
nM Ab

Figure 12b

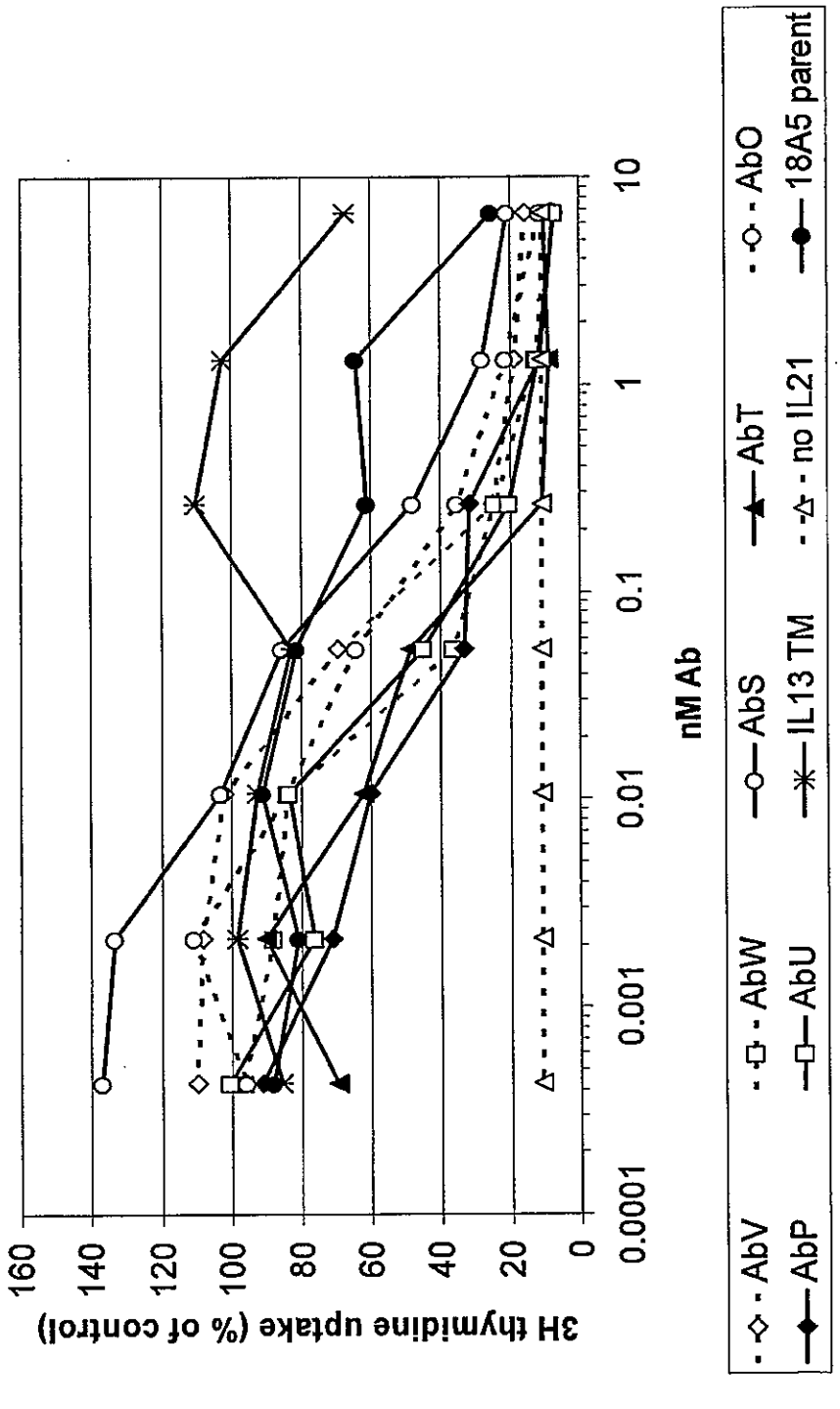

3H thymidine uptake (% of control)
160
140
120
100
80
60
40
20
0
0.0001
0.001
0.01
0.1
1
10
nM Ab
AbV
AbW
AbS
AbT
AbO
AbP
AbU
IL13 TM
no IL21
18A5 parent

Figure 13

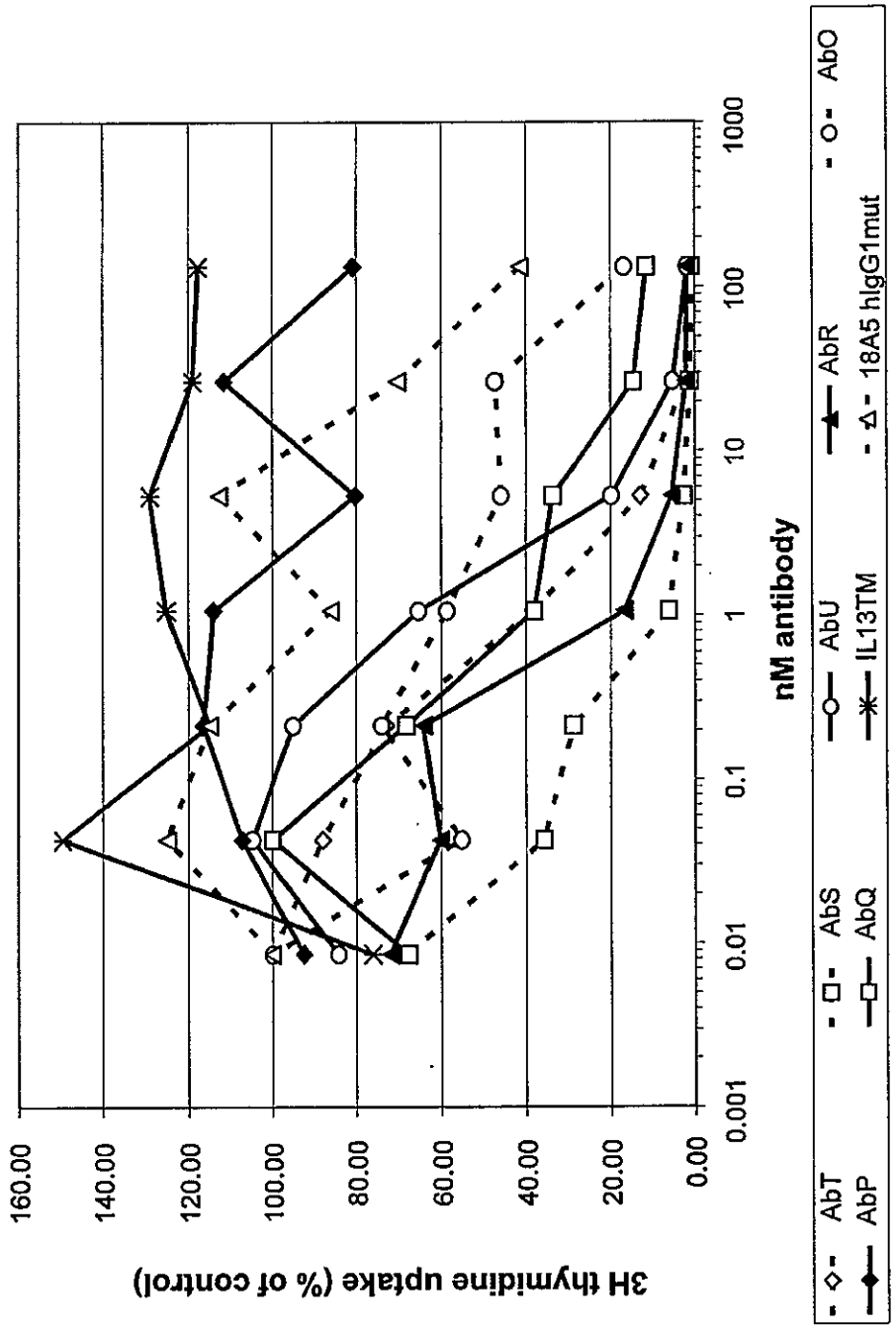

3H thymidine uptake (% of control)
160.00
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
0.001
0.01
0.1
1
10
100
1000
nM antibody
AbT
AbS
AbU
AbR
AbO
AbP
AbQ
IL13TM
18A5 hIgG1mut

Figure 14

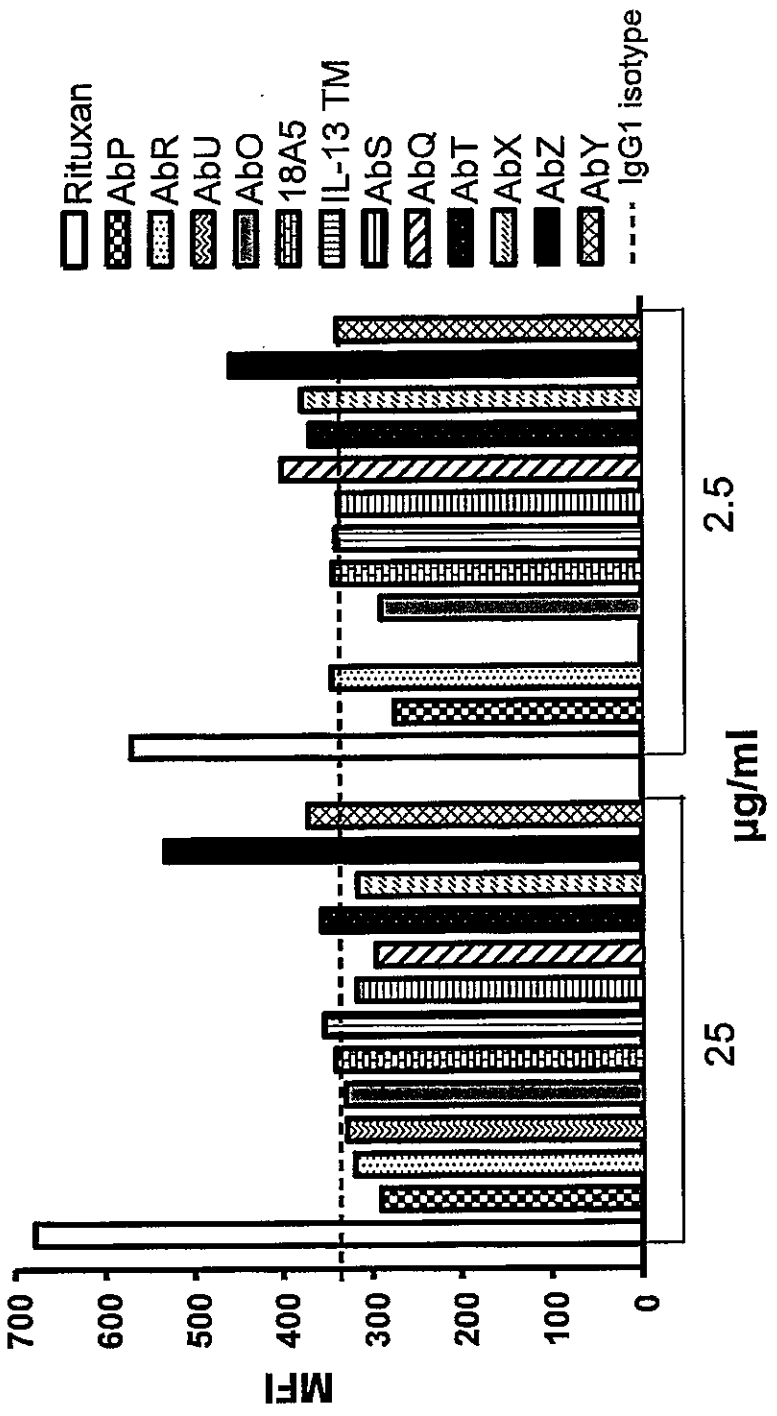

Rituxan
AbP
AbR
AbU
AbO
18A5
IL-13 TM
AbS
AbQ
AbT
AbX
AbZ
AbY
IgG1 isotype
MFI
700
600
500
400
300
200
100
0
25
2.5
µg/ml

Figure 15

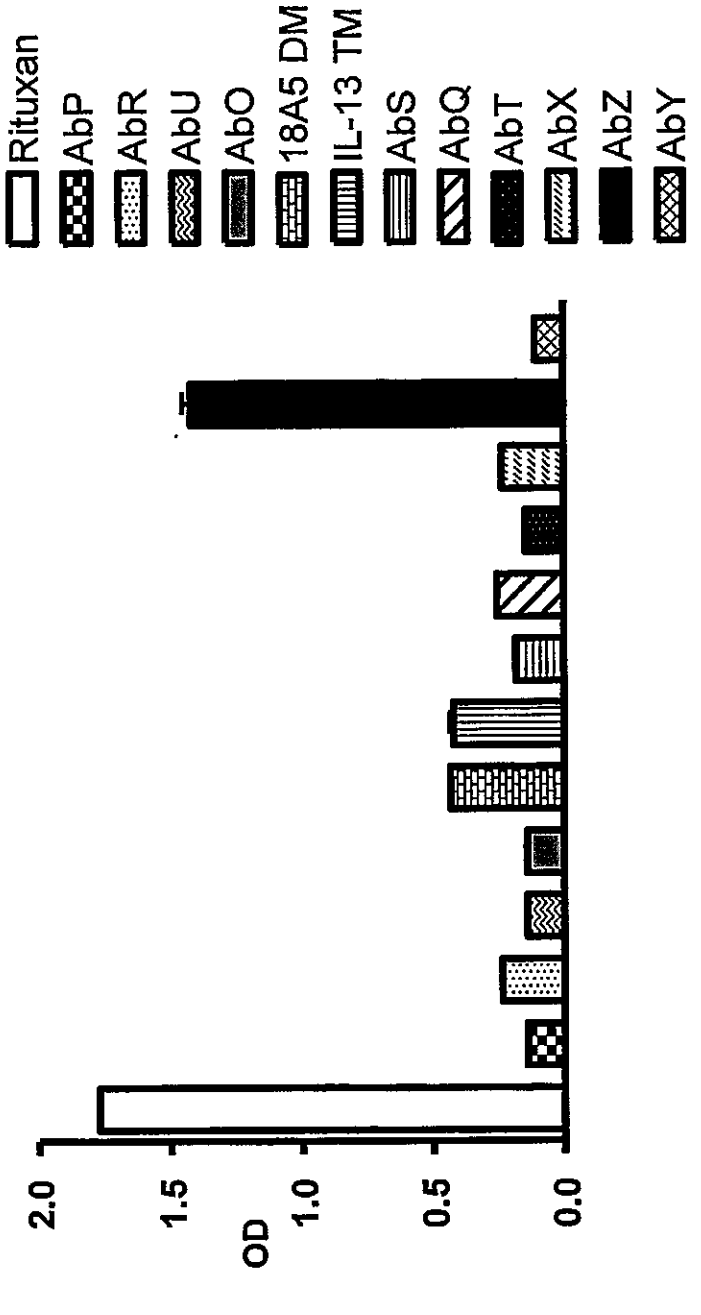

Rituxan
AbP
AbR
AbU
AbO
18A5 DM
IL-13 TM
AbS
AbQ
AbT
AbX
AbZ
AbY
OD
2.0
1.5
1.0
0.5
0.0

Figure 16

Figure 17a

AbQ:

Heavy chain for **AbQ** (SEQ ID NO:213), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 165, respectively). The heavy chain constant region is shown in lower case italics with the double mutation (L234A G237A) shown in bold lowercase underlined text (SEQ ID NO: 197).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papealgapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbQ** (SEQ ID NO: 214), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 172, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:213 is the full-length heavy chain for **AbQ:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papealgapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 17b

SEQ ID NO:14 is the V_H portion of the full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of the full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of the full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:165 is the CDR H3 portion of the V_H portion of the full-length heavy chain:

FMGFGRPEY

SEQ ID NO:197 is the heavy chain constant region with the double mutation (L234A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
*tsgvhtfpavlqssglyslssvvtvpsssl**g**tqtyicnvnhkpsnt*
*kvdkkvepkscdkthtcppcpape**a**l**g**apsvflfppkpkdtlmisr*
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:214 is the full-length light chain for **AbQ:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 17c

SEQ ID NO:215 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:172 is the CDR L3 portion of the V_L portion of the full-length light chain:

VARSVVGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 18a

AbR:

Heavy chain for **AbR** (SEQ ID NO:213), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 165, respectively). The heavy chain constant region is shown in lower case italics with the double mutation (L234A G237A) shown in bold lowercase underlined text (SEQ ID NO: 197).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papealgapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbR** (SEQ. ID NO:216), with CDRs L1, L2, and L3 underlined (SEQ. ID NOs:194, 195, and 187, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ. ID. NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:213 is the full-length heavy chain for **AbR:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papealgapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 18b

SEQ ID NO:14 is the V_H portion of the full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of the full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of the full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:165 is the CDR H3 portion of the V_H portion of the full-length heavy chain:

FMGFGRPEY

SEQ ID NO:197 is the heavy chain constant region with the double mutation (L234A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpsssl gtqtyicnvnhkpsnt
*kvdkkvepkscdkthtcppcpape**a**lg**a**psvflfppkpkdtlmisr*
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:216 is the full-length light chain for **AbR:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 18c

SEQ ID NO:217 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:187 is the CDR L3 portion of the V_L portion of the full-length light chain:

VTRSVKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 19a

AbW:

Heavy chain for **AbW** (SEQ ID NO:218), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 165, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyk ttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbW** (SEQ ID NO:216), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 187, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:218 is the full-length heavy chain for **AbW:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyk ttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 19b

SEQ ID NO:14 is the V_H portion of the full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of the full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of the full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:165 is the CDR H3 portion of the V_H portion of the full-length heavy chain:

FMGFGRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
*tsgvhtfpavlqssglyslssvvtvpsssl**g**tqtyicnvnhkpsnt*
*kvdkkvepkscdkthtcppcpape**aa**g**a**psvflfppkpkdtlmisr*
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:216 is the full-length light chain for **AbW:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 19c

SEQ ID NO:217 is V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSV
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:187 is the CDR L3 portion of the V_L portion of the full-length light chain:

VTRSVKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 20a

AbS:

Heavy chain for **AbS** (SEQ ID NO:219), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 169, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssslgtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyknttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbS** (SEQ ID NO:220), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 176, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCMSRSI
WGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:219 is the full-length heavy chain for **AbS:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssslgtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyknttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 20b

SEQ ID NO:6 is the V_H portion of the full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of the full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of the full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:169 is the CDR H3 portion of the V_H portion of the full-length heavy chain:

GGGISRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpsssl gtqtyicnvnhkpsnt
kvdkkvepkscdkthtcppcpape**aa**g**a**psvflfppkpkdtlmisr
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:220 is the full-length light chain for **AbS:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCMSRSI
WGNPHVLFGGGTQLTVLgqpkaapsvtlfppsseelqankatlvcl
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 20c

SEQ ID NO:221 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCMSRSI
WGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:176 is the CDR L3 portion of the V_L portion of the full-length light chain:

MSRSIWGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 21a

AbT:

Heavy chain for **AbT** (SEQ ID NO:219), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 169, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbT** (SEQ ID NO:222), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 178, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSN
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:219 is the full-length heavy chain for **AbT:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflysk ltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 21b

SEQ ID NO:6 is the V_H portion of full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:169 is the CDR H3 portion of the V_H portion of full-length heavy chain:

GGGISRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpsssl**aa**g**a**psvflfppkpkdtlmisr
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:222 is the full-length light chain for **AbT:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSN
KGNPHVLFGGGTQLTVLgqpkaapsvtlfppsseelqankatlvcl
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 21c

SEQ ID NO:223 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSN
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:178 is the CDR L3 portion of the V_L portion of the full-length light chain:

VARSNKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 22a

AbO:

Heavy chain for **AbO** (SEQ ID NO:219), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 169, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbO** (SEQ ID NO:224), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 185, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSA
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:219 is the full-length heavy chain for **AbO:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 22b

SEQ ID NO:6 is the V_H portion of full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:169 is the CDR H3 portion of the V_H portion of full-length heavy chain:

GGGISRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
*tsgvhtfpavlqssglyslssvvtvpsssl*gtqtyicnvnhkpsnt
*kvdkkvepkscdkthtcppcpape**aa**g**a**psvflfppkpkdtlmisr*
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:224 is the full-length light chain for **AbO:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSA
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 22c

SEQ ID NO:225 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVTRSA
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:185 is the CDR L3 portion of the V_L portion of the full-length light chain:

VTRSAKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 23a

AbP:

Heavy chain for **AbP** (SEQ ID NO:219), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 169, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapssksts g*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbP** (SEQ ID NO:226), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 189, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVSRSA
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:219 is the full-length heavy chain for **AbP:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapssksts g*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 23b

SEQ ID NO:6 is the V_H portion of full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:169 is the CDR H3 portion of the V_H portion of full-length heavy chain:

GGGISRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpssslgtqtyicnvnhkpsnt
kvdkkvepkscdkthtcppcpapeaagapsvflfppkpkdtlmisr
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:226 is the full-length light chain for **AbP:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVSRSA
KGNPHVLFGGGTQLTVLgqpkaapsvtlfppsseelqankatlvcl
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 23c

SEQ ID NO:227 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVSRSA
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:189 is the CDR L3 portion of the V_L portion of the full-length light chain:

VSRSAKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 24a

AbU:

Heavy chain for **AbU** (SEQ ID NO:219), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 169, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapssksts g*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsslgtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Light chain for **AbU** (SEQ ID NO:228), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 193, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCTTRSN
KGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:219 is the full-length heavy chain for **AbU:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS*astkgpsvfplapssksts g*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsslgtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennykttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 24b

SEQ ID NO:6 is the V_H portion of full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARGGGISRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:169 is the CDR H3 portion of the V_H portion of full-length heavy chain:

GGGISRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpsssl gtqtyicnvnhkpsnt
kvdkkvepkscdkthtcppcpape**aa**g**a**psvflfppkpkdtlmisr
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:228 is the full-length light chain for **AbU:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCTTRSN
KGNPHVLFGGGTQLTVLgqpkaapsvtlfppsseelqankatlvcl
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 24c

SEQ ID NO:229 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCTTRSN
KGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:193 is the CDR L3 portion of the V_L portion of the full-length light chain:

TTRSNKGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

Figure 25a

AbV:

Heavy chain for **AbV** (SEQ ID NO:218), with CDRs H1, H2, and H3 underlined (SEQ ID NOs:163, 164, and 165, respectively). The heavy chain constant region is shown in lower case italics with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text (SEQ ID NO:196).

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyk ttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgkk

Light chain for **AbV** (SEQ ID NO:214), with CDRs L1, L2, and L3 underlined (SEQ ID NOs:194, 195, and 172, respectively). The constant lambda light chain sequence is indicated by lower-case italics (SEQ ID NO:198).

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVL*gqpkaapsvtlfppsseelqankatlvcl*
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

SEQ ID NO:218 is the full-length heavy chain for **AbV:**

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS*astkgpsvfplapsskstsg*
gtaalgclvkdyfpepvtvswnsgaltsgvhtfpavlqssglysls
svvtvpsssl gtqtyicnvnhkpsntkvdkkvepkscdkthtcppc
papeaagapsvflfppkpkdtlmisrtpevtcvvvdvshedpevkf
nwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykc
kvsnkalpapiektiskakgqprepqvytlppsreemtknqvsltc
lvkgfypsdiavewesngqpennyk ttppvldsdgsfflyskltvd
ksrwqqgnvfscsvmhealhnhytqkslslspgk

Figure 25b

SEQ ID NO:14 is the V_H portion of the full-length heavy chain:

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGL
EWIGSISHTGNTYYNPPLKSRVTISVDTSKNQFSLKLSSVTAADTA
VYYCARFMGFGRPEYWGQGTLVTVSS

SEQ ID NO:163 is the CDR H1 portion of the V_H portion of the full-length heavy chain:

SGYYWG

SEQ ID NO:164 is the CDR H2 portion of the V_H portion of the full-length heavy chain:

SISHTGNTYYNPPLKS

SEQ ID NO:165 is the CDR H3 portion of the V_H portion of the full-length heavy chain:

FMGFGRPEY

SEQ ID NO:196 is the heavy chain constant region with the triple mutation (L234A L235A G237A) shown in bold lowercase underlined text:

astkgpsvfplapsskstsggtaalgclvkdyfpepvtvswnsgal
tsgvhtfpavlqssglyslssvvtvpsssl gtqtyicnvnhkpsnt
kvdkkvepkscdkthtcppcpape**aa**g**a**psvflfppkpkdtlmisr
tpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyr
vvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepq
vytlppsreemtknqvsltclvkgfypsdiavewesngqpennykt
tppvldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqk
slslspgk

SEQ ID NO:214 is the full-length light chain for **AbV:**

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVLgqpkaapsvtlfppsseelqankatlvcl
isdfypgavtvawkadsspvkagvetttpskqsnnkyaassylslt
peqwkshrsyscqvthegstvektvaptecs

Figure 25c

SEQ ID NO:215 is the V_L portion of the full-length light chain:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPGQAPVLV
IYGKHKRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCVARSV
VGNPHVLFGGGTQLTVL

SEQ ID NO:194 is the CDR L1 portion of the V_L portion of the full-length light chain:

QGDSLRTYYAS

SEQ ID NO:195 is the CDR L2 portion of the V_L portion of the full-length light chain:

GKHKRPS

SEQ ID NO:172 is the CDR L3 portion of the V_L portion of the full-length light chain:

VARSVVGNPHVL

SEQ ID NO:198 is the lambda light chain constant region:

gqpkaapsvtlfppsseelqankatlvclisdfypgavtvawkads
spvkagvetttpskqsnnkyaassylsltpeqwkshrsyscqvthe
gstvektvaptecs

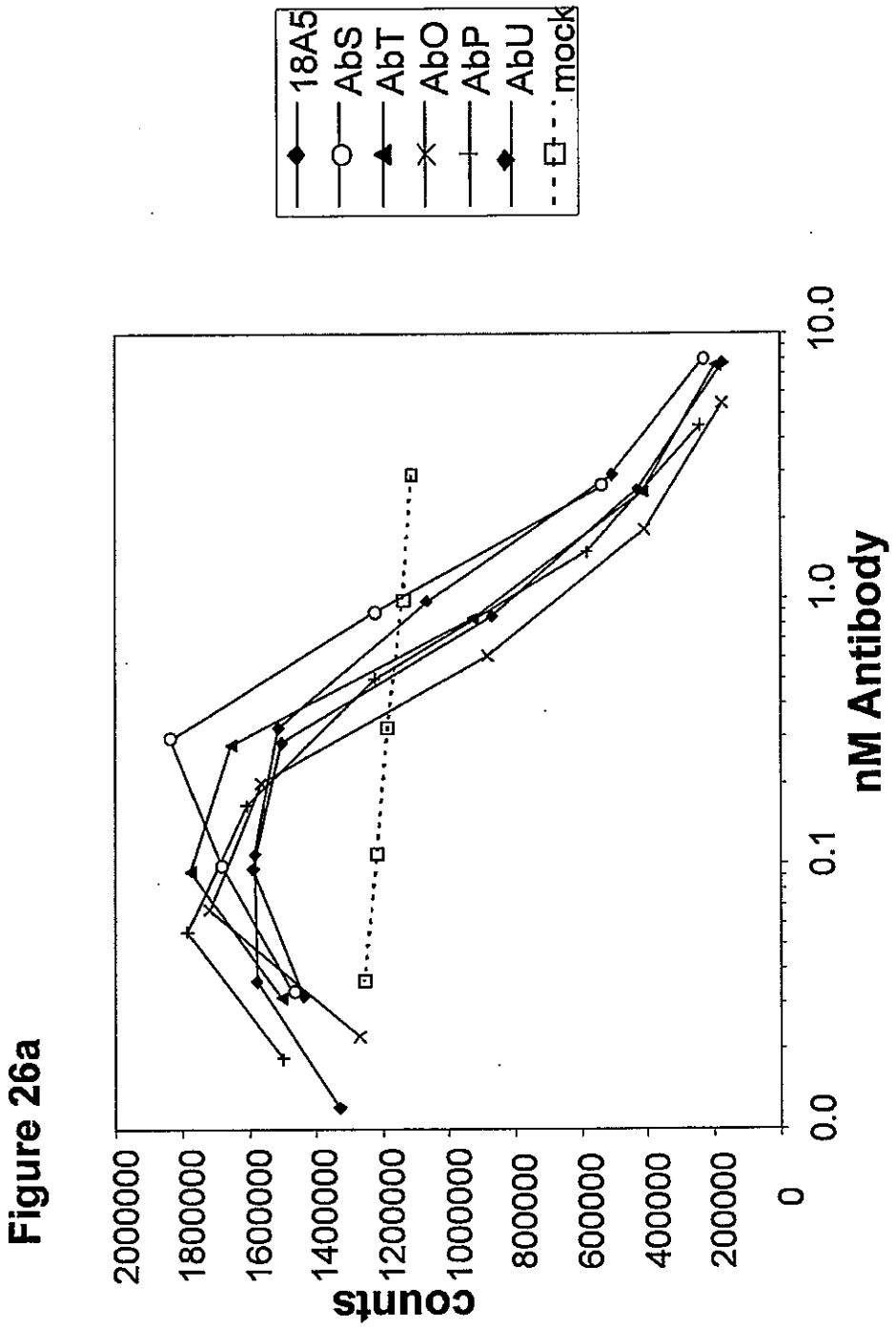

18A5
AbS
AbT
AbO
AbP
AbU
mock
counts
2000000
1800000
1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
0.0
0.1
1.0
10.0
nM Antibody

Figure 26a

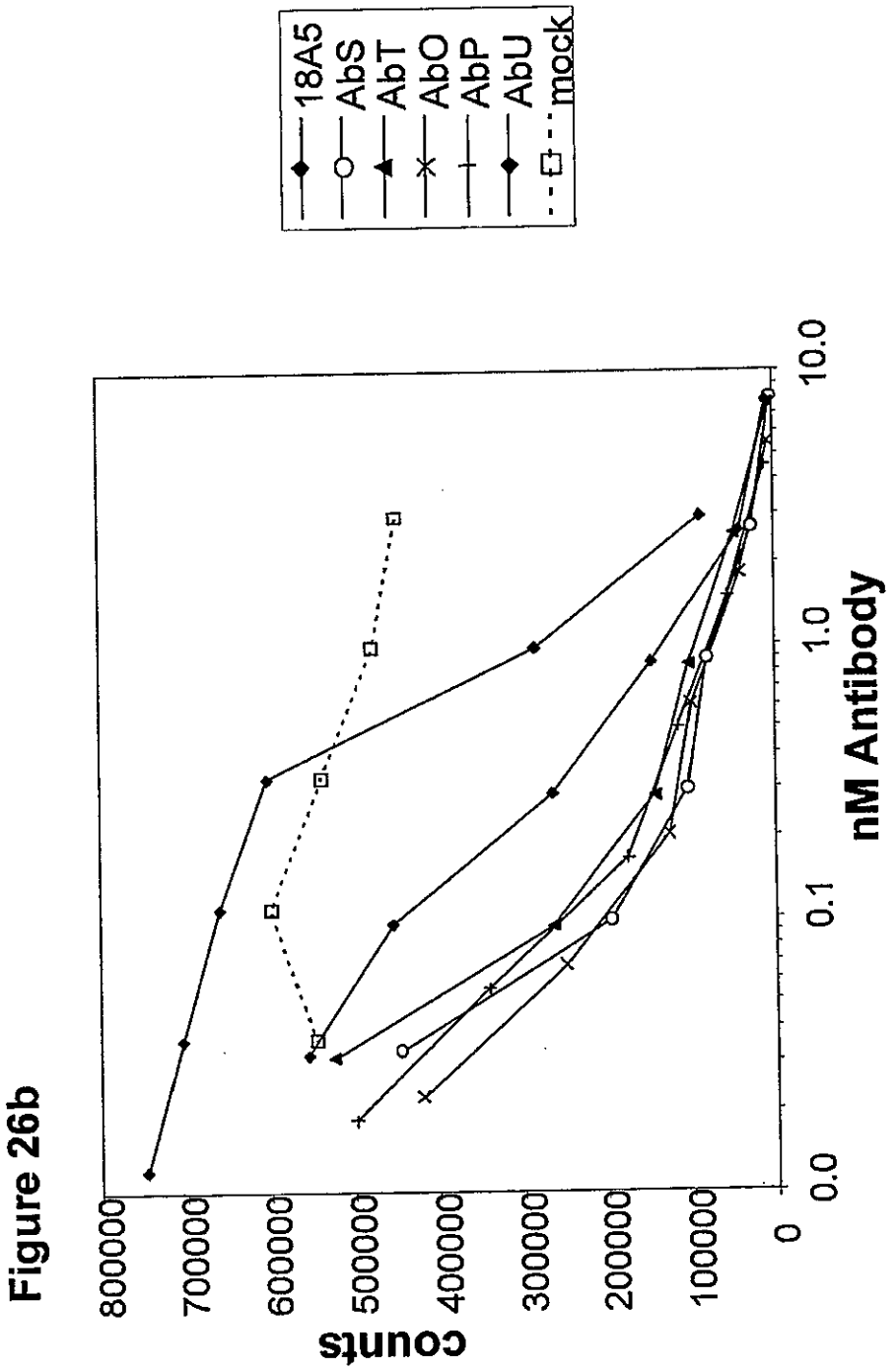

18A5
AbS
AbT
AbO
AbP
AbU
mock
counts
800000
700000
600000
500000
400000
300000
200000
100000
0
0.0
0.1
1.0
10.0
nM Antibody

Figure 26b

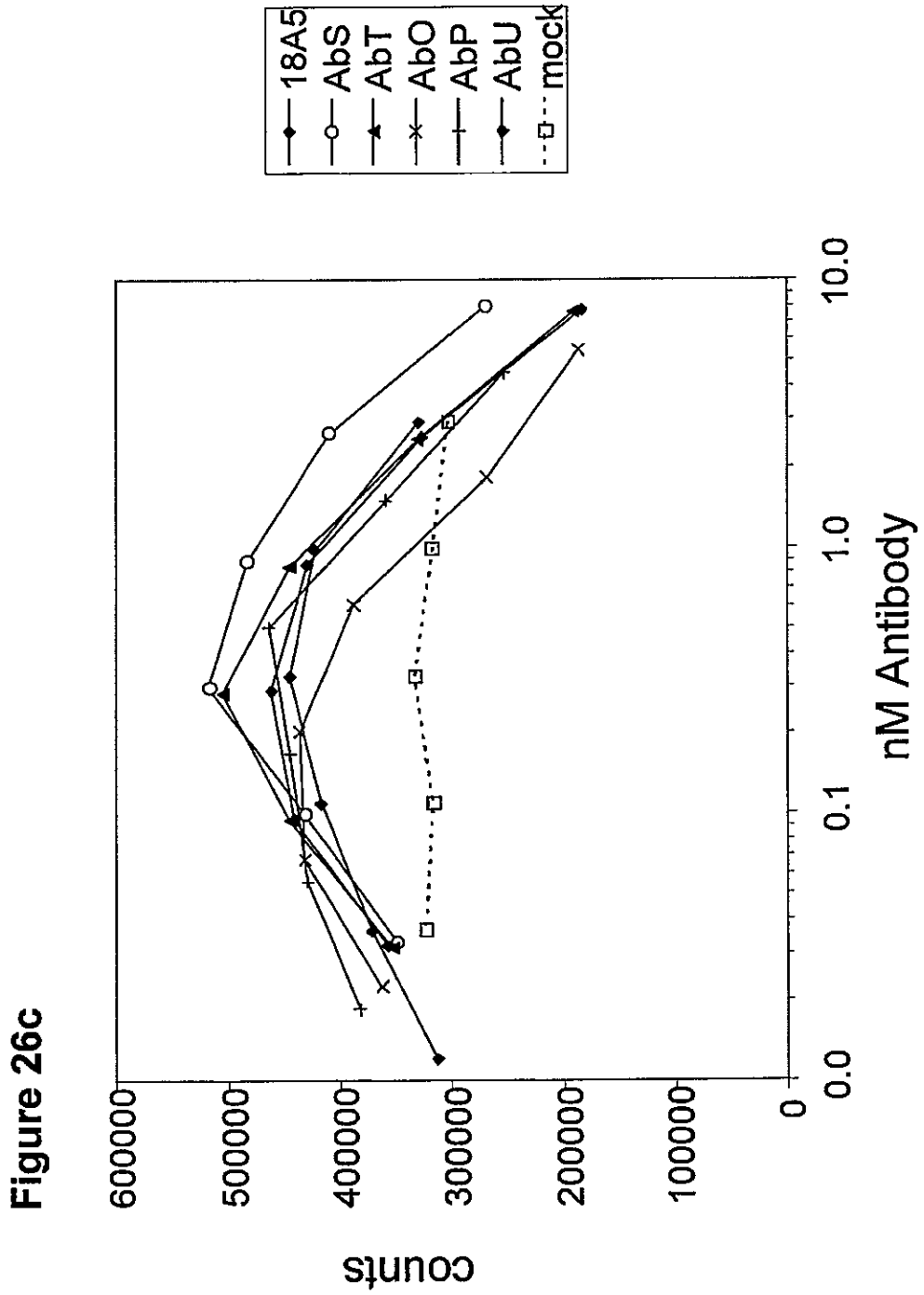
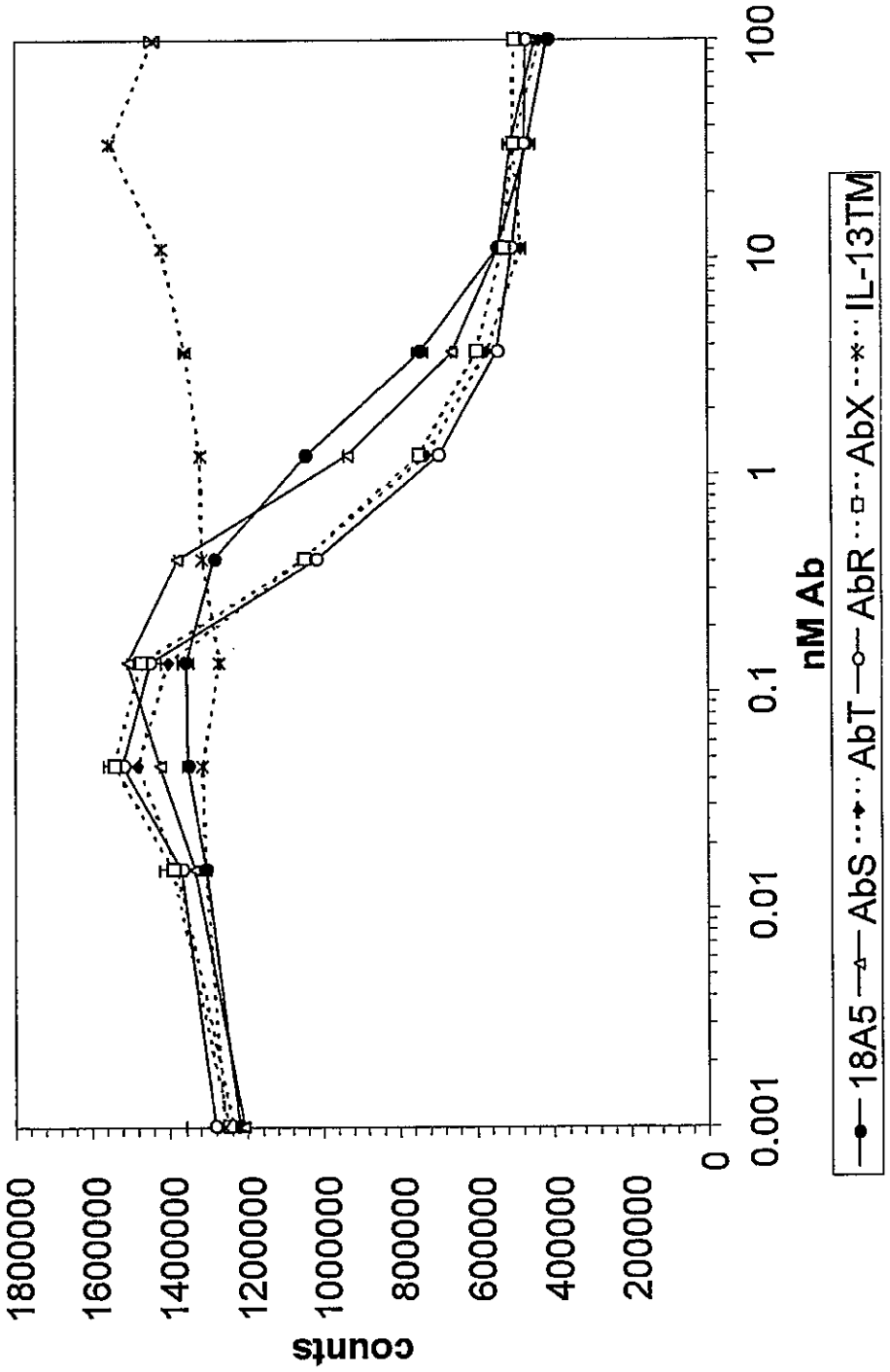

18A5
AbS
AbT
AbO
AbP
AbU
mock
counts
600000
500000
400000
300000
200000
100000
0
0.0
0.1
1.0
10.0
nM Antibody

Figure 26c

Figure 26d


counts
1800000
1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
0.001
0.01
0.1
1
10
100
nM Ab
18A5
AbS
AbT
AbR
AbX
IL-13TM

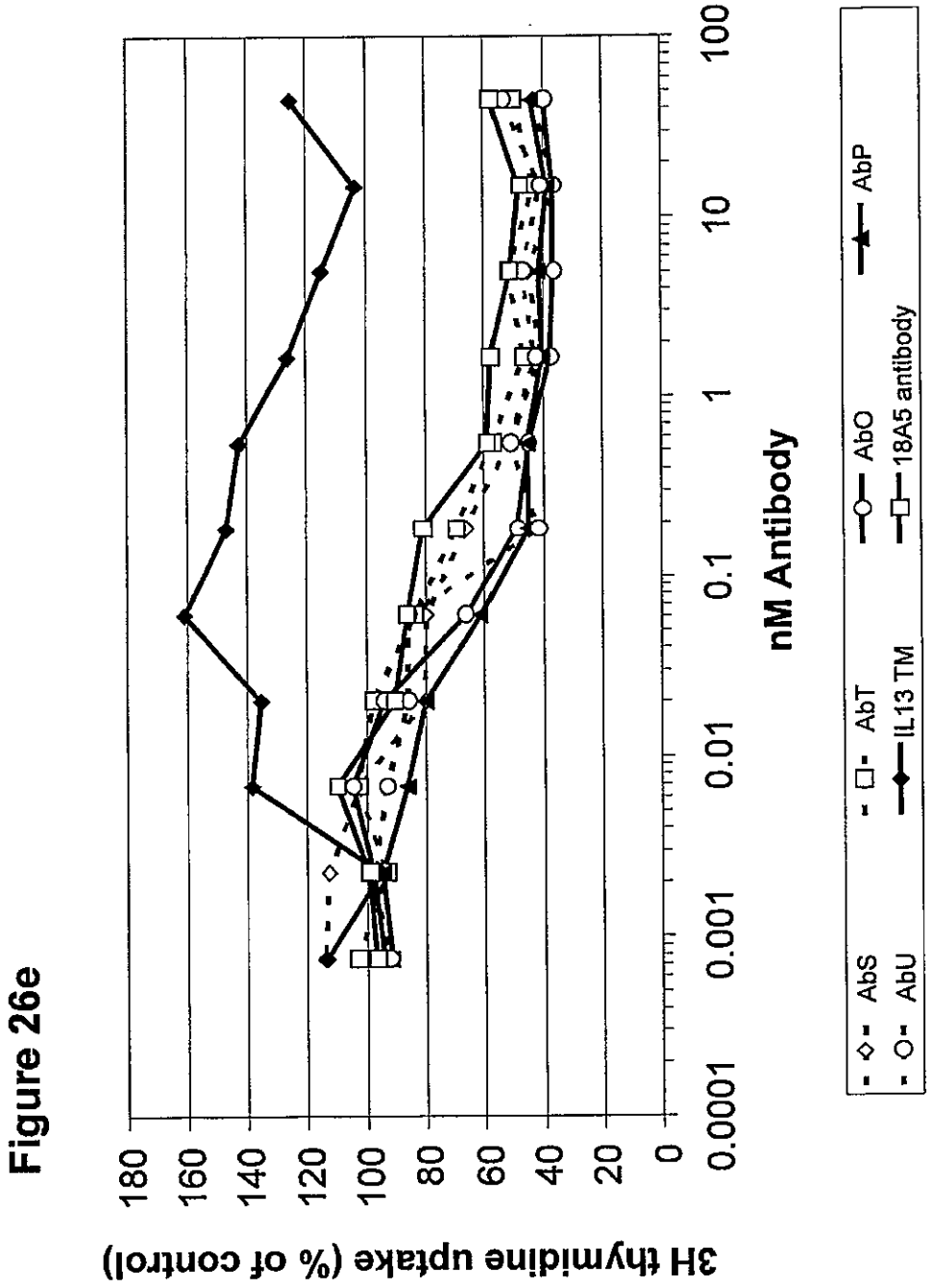

3H thymidine uptake (% of control)
180
160
140
120
100
80
60
40
20
0
0.0001
0.001
0.01
0.1
1
10
100
nM Antibody
AbS
AbT
AbO
AbP
AbU
IL13 TM
18A5 antibody

Figure 26e

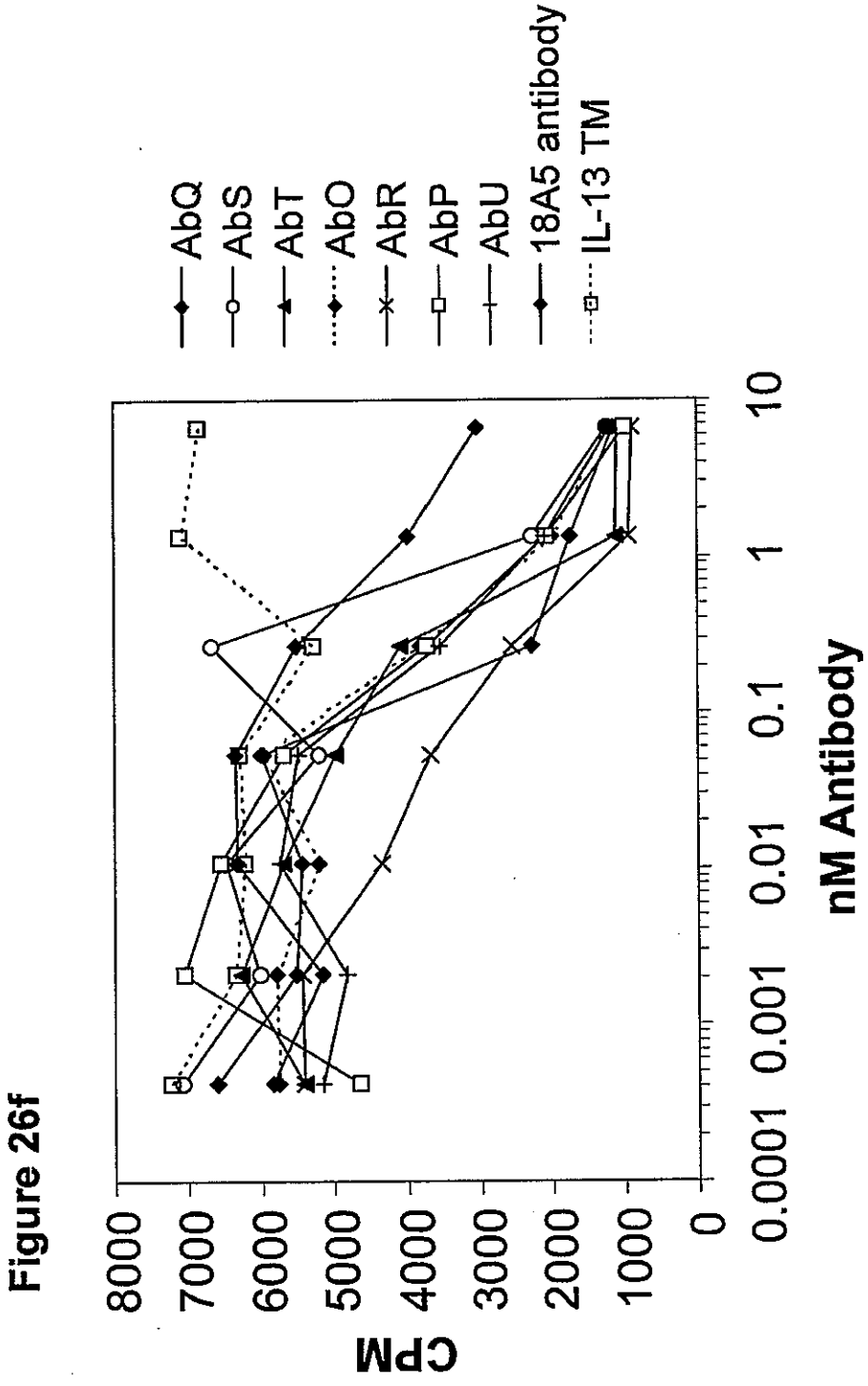

AbQ
AbS
AbT
AbO
AbR
AbP
AbU
18A5 antibody
IL-13 TM
CPM
8000
7000
6000
5000
4000
3000
2000
1000
0
0.0001
0.001
0.01
0.1
1
10
nM Antibody

Figure 26f

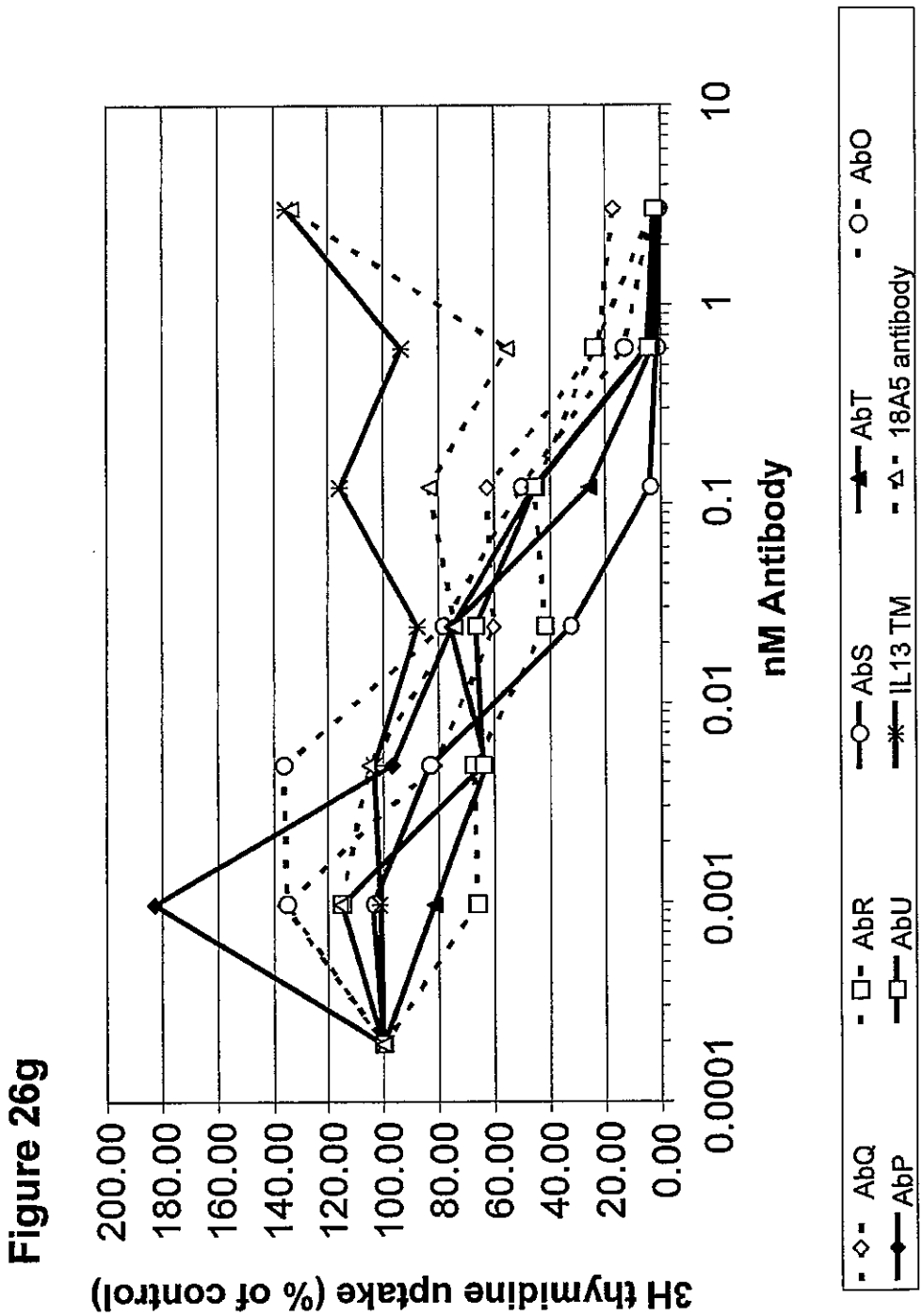

3H thymidine uptake (% of control)
200.00
180.00
160.00
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
0.0001
0.001
0.01
0.1
1
10
nM Antibody
AbQ
AbR
AbS
AbT
AbO
AbP
AbU
IL13 TM
18A5 antibody

Figure 26g

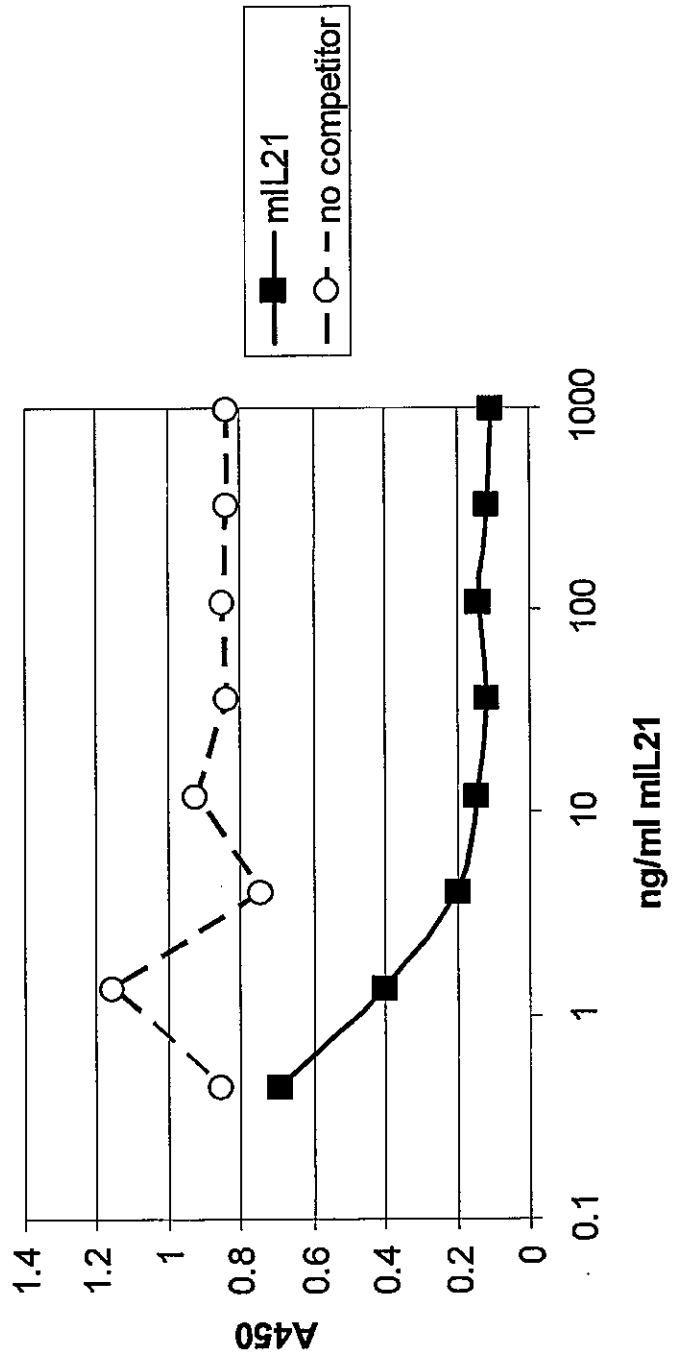

mIL21
no competitor
A450
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.1
1
10
100
1000
ng/ml mIL21

Figure 27a

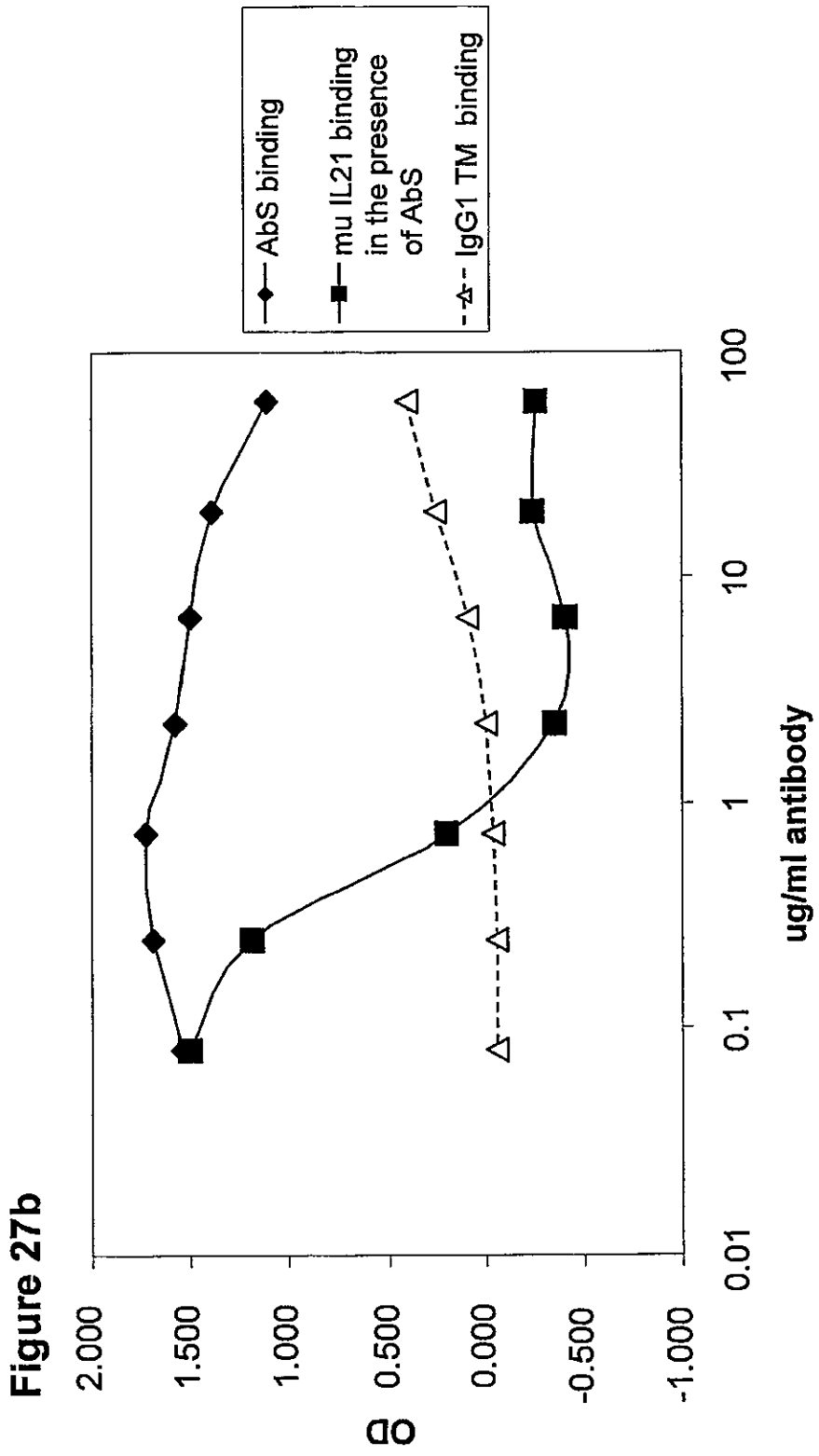

AbS binding
mu IL21 binding in the presence of AbS
IgG1 TM binding
OD
2.000
1.500
1.000
0.500
0.000
-0.500
-1.000
0.01
0.1
1
10
100
ug/ml antibody

Figure 27b

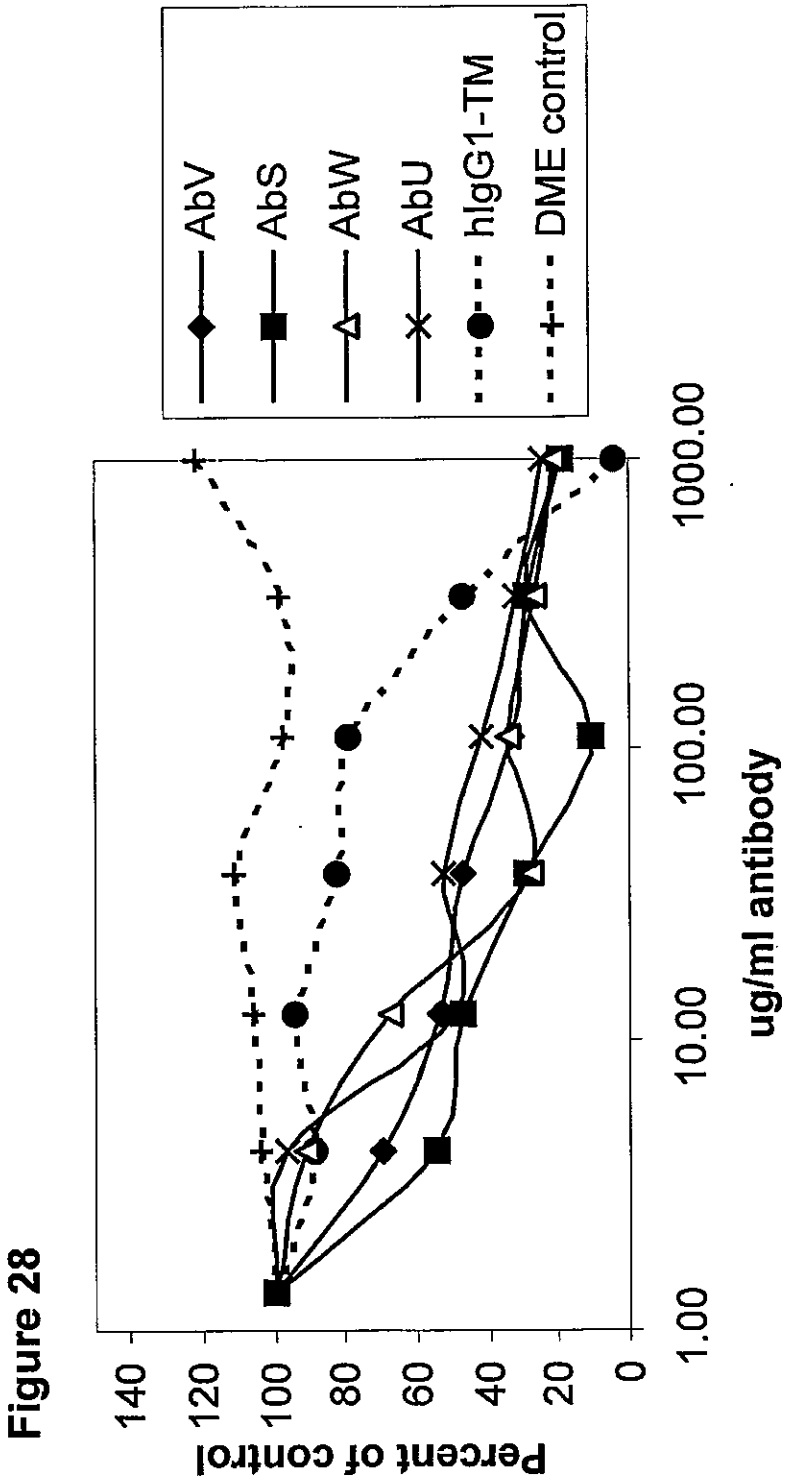

AbV
AbS
AbW
AbU
hIgG1-TM
DME control
Percent of control
140
120
100
80
60
40
20
0
1.00
10.00
100.00
1000.00
ug/ml antibody

Figure 28