FIG. 1

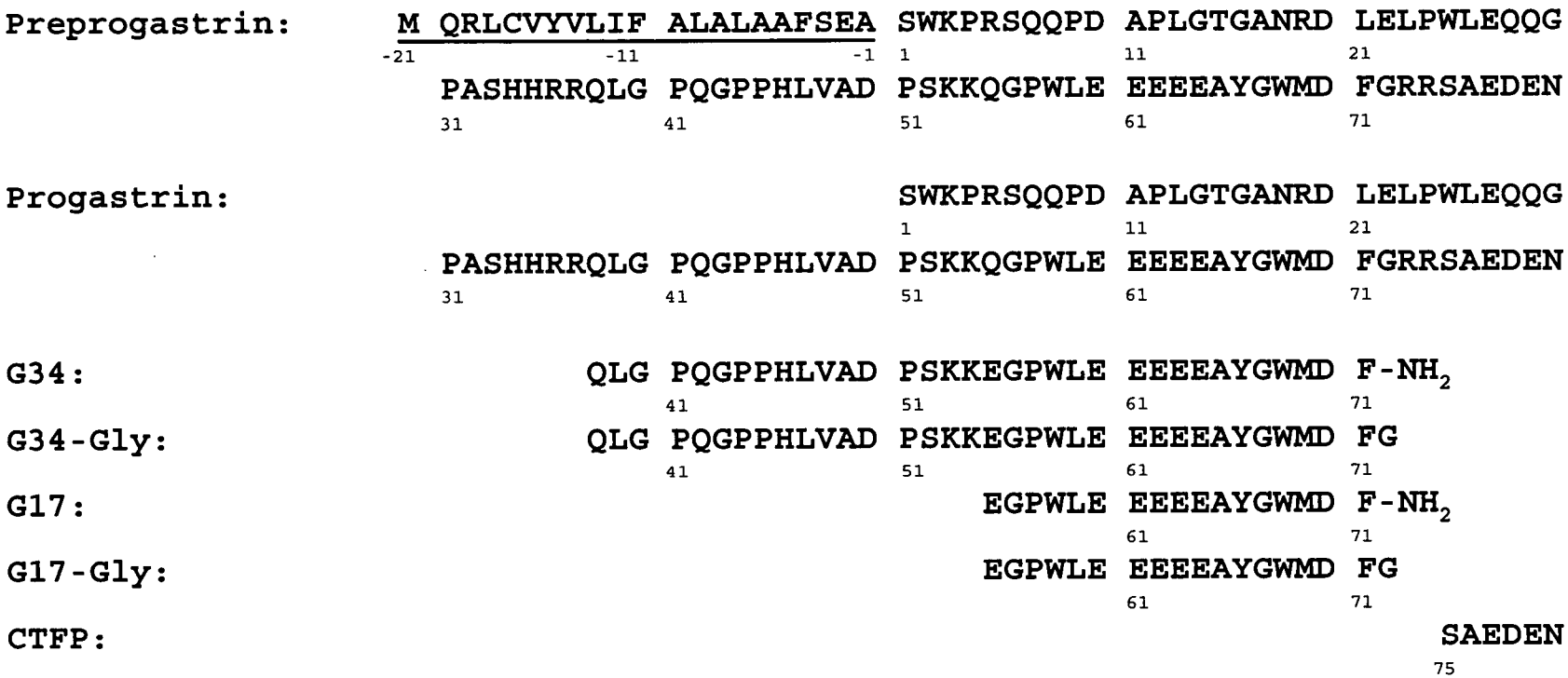

Preprogastrin:
M QRLCVYVLIF ALALAAFSEA SWKPRSQQPD APLGTGANRD LELPWLEQQG
-21 -11 -1 1 11 21
PASHHRRQLG PQGPPHLVAD PSKKQGPWLE EEEEAYGWMD FGRRSAEDEN
31 41 51 61 71
Progastrin:
SWKPRSQQPD APLGTGANRD LELPWLEQQG
1 11 21
PASHHRRQLG PQGPPHLVAD PSKKQGPWLE EEEEAYGWMD FGRRSAEDEN
31 41 51 61 71
G34:
QLG PQGPPHLVAD PSKKEGPWLE EEEEAYGWMD F-NH2
41 51 61 71
G34-Gly:
QLG PQGPPHLVAD PSKKEGPWLE EEEEAYGWMD FG
41 51 61 71
G17:
EGPWLE EEEEAYGWMD F-NH2
61 71
G17-Gly:
EGPWLE EEEEAYGWMD FG
61 71
CTFP:
SAEDEN
75

FIG. 2A

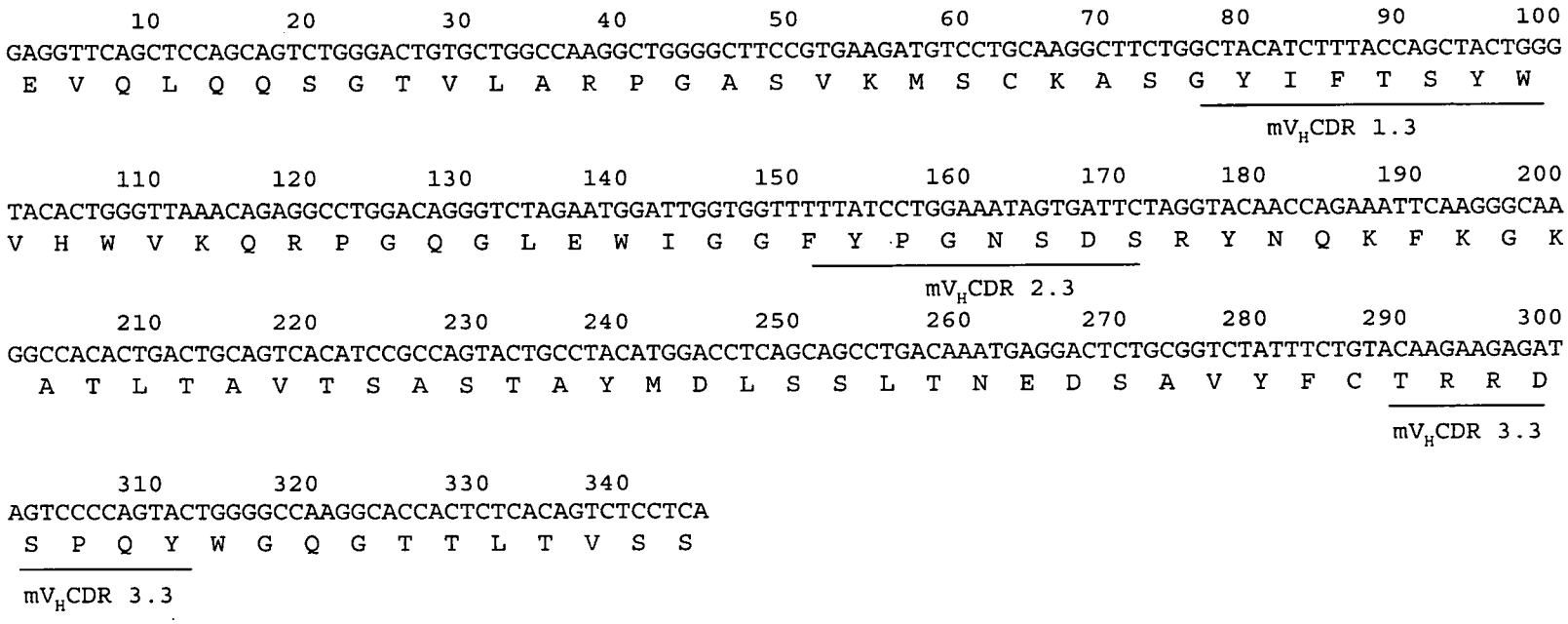

10 20 30 40 50 60 70 80 90 100
GAGGTTCAGCTCCAGCAGTCTGGGACTGTGCTGGCCAAGGCTGGGGCTTCCGTGAAGATGTCCTGCAAGGCTTCTGGCTACATCTTTACCAGCTACTGGG
E V Q L Q Q S G T V L A R P G A S V K M S C K A S G Y I F T S Y W
mV$_H$CDR 1.3
110 120 130 140 150 160 170 180 190 200
TACACTGGGTTAAACAGAGGCCTGGACAGGGTCTAGAATGGATTGGTGGTTTTTATCCTGGAAATAGTGATTCTAGGTACAACCAGAAATTCAAGGGCAA
V H W V K Q R P G Q G L E W I G G F Y P G N S D S R Y N Q K F K G K
mV$_H$CDR 2.3
210 220 230 240 250 260 270 280 290 300
GGCCACACTGACTGCAGTCACATCCGCCAGTACTGCCTACATGGACCTCAGCAGCCTGACAAATGAGGACTCTGCGGTCTATTTCTGTACAAGAAGAGAT
A T L T A V T S A S T A Y M D L S S L T N E D S A V Y F C T R R D
mV$_H$CDR 3.3
310 320 330 340
AGTCCCCAGTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
S P Q Y W G Q G T T L T V S S
mV$_H$CDR 3.3

FIG. 2B

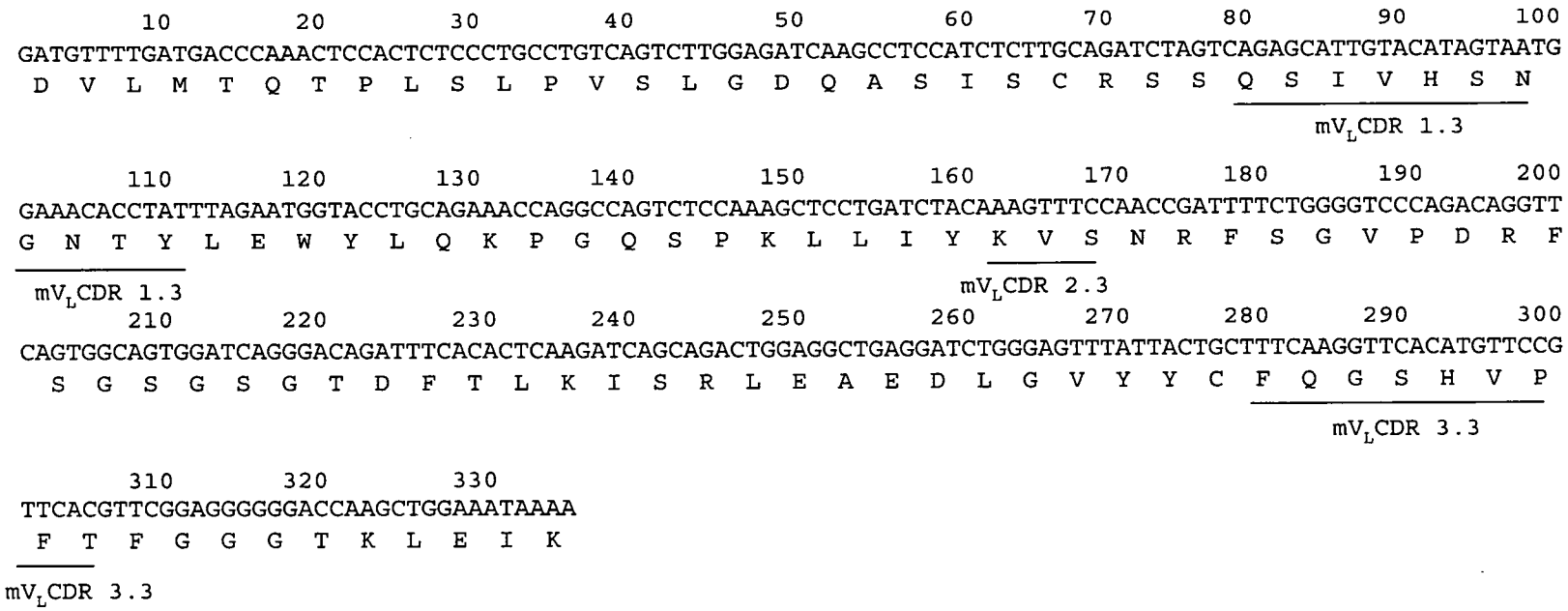

10 20 30 40 50 60 70 80 90 100
GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATG
D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q S I V H S N
mV$_L$CDR 1.3
110 120 130 140 150 160 170 180 190 200
GAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTT
G N T Y L E W Y 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
mV$_L$CDR 1.3
mV$_L$CDR 2.3
210 220 230 240 250 260 270 280 290 300
CAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGACTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCG
S G S G S G T D F T L K I S R L E A E D L G V Y Y C F Q G S H V P
mV$_L$CDR 3.3
310 320 330
TTCACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
F T F G G G T K L E I K
mV$_L$CDR 3.3

FIG. 2C

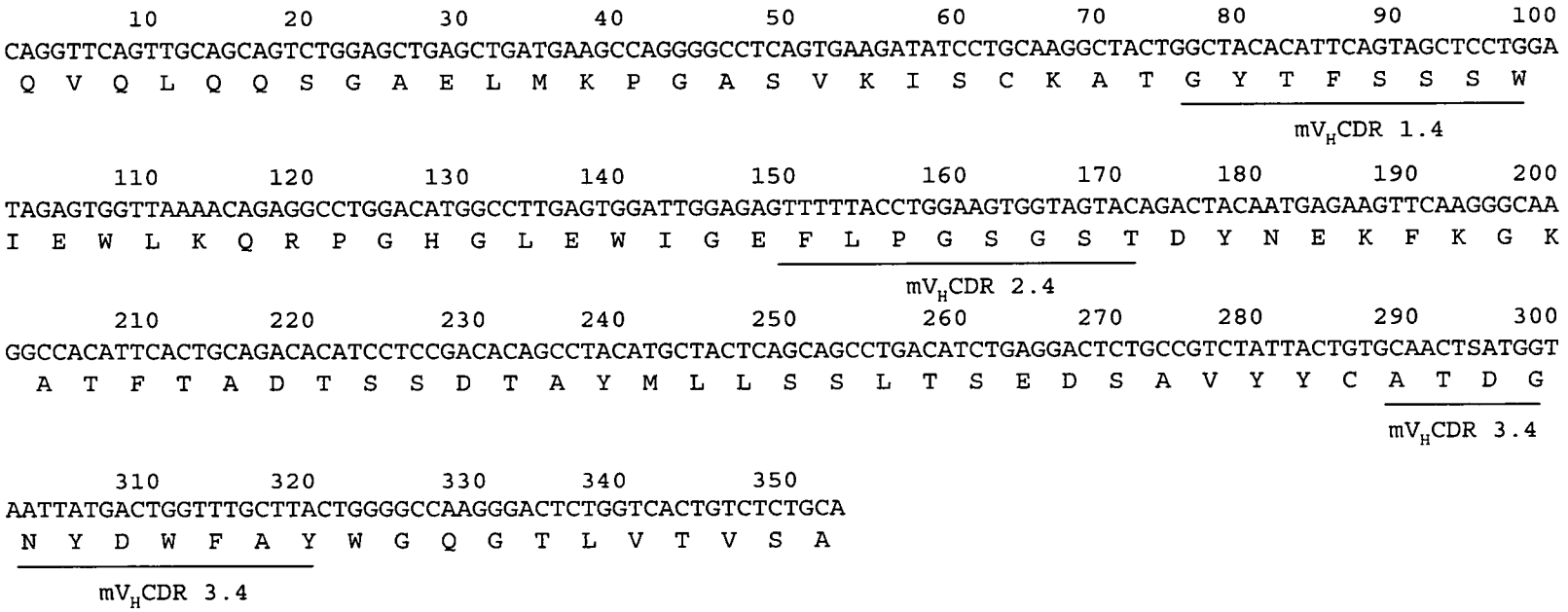

10 20 30 40 50 60 70 80 90 100
CAGGTTCAGTTGCAGCAGTCTGGAGCTGAGCTGATGAAGCCAGGGGCCTCAGTGAAGATATCCTGCAAGGCTACTGGCTACACATTCAGTAGCTCCTGGA
Q V Q L Q Q S G A E L M K P G A S V K I S C K A T G Y T F S S S W
mV$_H$CDR 1.4
110 120 130 140 150 160 170 180 190 200
TAGAGTGGTTAAAACAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGAGTTTTTACCTGGAAGTGGTAGTACAGACTACAATGAGAAGTTCAAGGGCAA
I E W L K Q R P G H G L E W I G E F L P G S G S T D Y N E K F K G K
mV$_H$CDR 2.4
210 220 230 240 250 260 270 280 290 300
GGCCACATTCACTGCAGACACATCCTCCGACACAGCCTACATGCTACTCAGCAGCCTGACATCTGAGGACTCTGCCGTCTATTACTGTGCAACTSATGGT
A T F T A D T S S D T A Y M L L S S L T S E D S A V Y Y C A T D G
mV$_H$CDR 3.4
310 320 330 340 350
AATTATGACTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
N Y D W F A Y W G Q G T L V T V S A
mV$_H$CDR 3.4

FIG. 2D

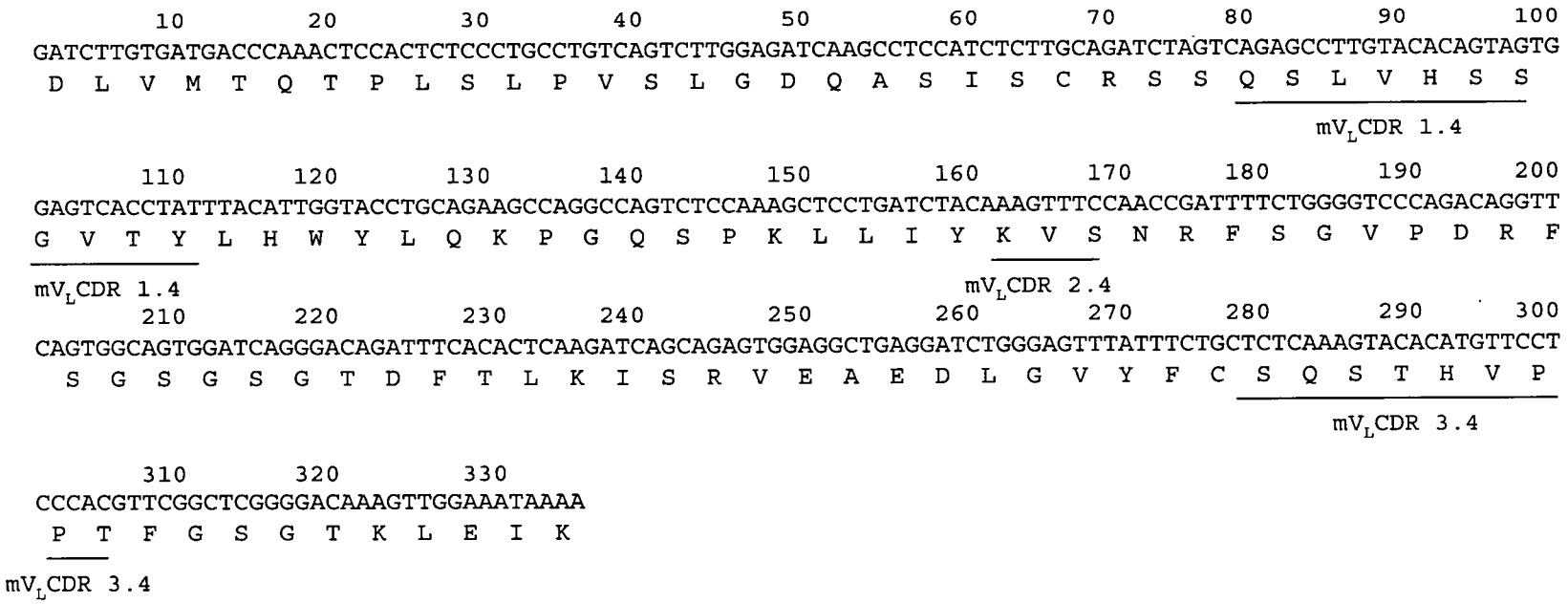

10 20 30 40 50 60 70 80 90 100
GATCTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAGTG
D L V M T Q T P L S L P V S L G D Q A S I S C R S S Q S L V H S S
mV$_L$CDR 1.4
110 120 130 140 150 160 170 180 190 200
GAGTCACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTT
G V T Y L H W Y 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
mV$_L$CDR 1.4
mV$_L$CDR 2.4
210 220 230 240 250 260 270 280 290 300
CAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCT
S G S G S G T D F T L K I S R V E A E D L G V Y F C S Q S T H V P
mV$_L$CDR 3.4
310 320 330
CCCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA
P T F G S G T K L E I K
mV$_L$CDR 3.4

FIG. 2E

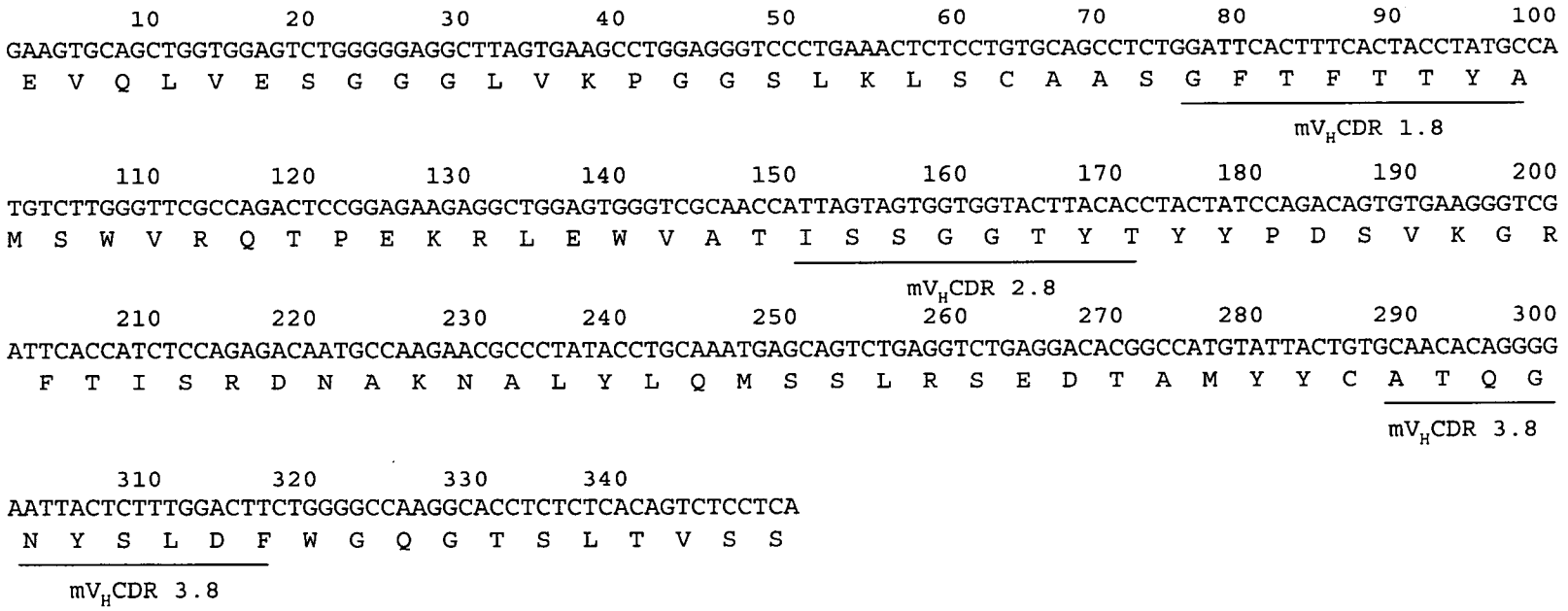

10 20 30 40 50 60 70 80 90 100
GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTTTCACTACCTATGCCA
E V Q L V E S G G G L V K P G G S L K L S C A A S G F T F T T Y A
mV$_H$CDR 1.8
110 120 130 140 150 160 170 180 190 200
TGTCTTGGGTTCGCCAGACTCCGGAGAAGAGGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGGTACTTACACCTACTATCCAGACAGTGTGAAGGGTCG
M S W V R Q T P E K R L E W V A T I S S G G T Y T Y Y P D S V K G R
mV$_H$CDR 2.8
210 220 230 240 250 260 270 280 290 300
ATTCACCATCTCCAGAGACAATGCCAAGAACGCCCTATACCTGCAAATGAGCAGTCTGAGGTCTGAGGACACGGCCATGTATTACTGTGCAACACAGGGG
F T I S R D N A K N A L Y L Q M S S L R S E D T A M Y Y C A T Q G
mV$_H$CDR 3.8
310 320 330 340
AATTACTCTTTGGACTTCTGGGGCCAAGGCACCTCTCTCACAGTCTCCTCA
N Y S L D F W G Q G T S L T V S S
mV$_H$CDR 3.8

FIG. 2F

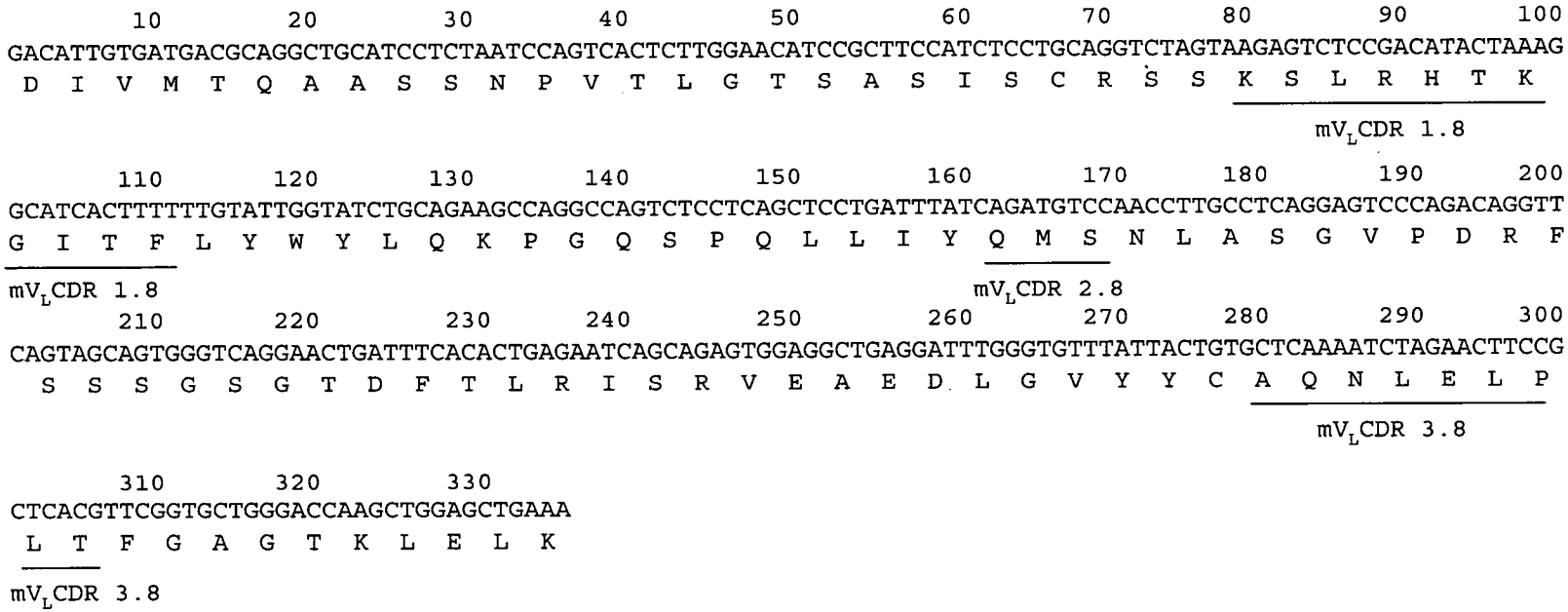

10 20 30 40 50 60 70 80 90 100
GACATTGTGATGACGCAGGCTGCATCCTCTAATCCAGTCACTCTTGGAACATCCGCTTCCATCTCCTGCAGGTCTAGTAAGAGTCTCCGACATACTAAAG
D I V M T Q A A S S N P V T L G T S A S I S C R S S K S L R H T K
mV$_L$CDR 1.8
110 120 130 140 150 160 170 180 190 200
GCATCACTTTTTTGTATTGGTATCTGCAGAAGCCAGGCCAGTCTCCTCAGCTCCTGATTTATCAGATGTCCAACCTTGCCTCAGGAGTCCCAGACAGGTT
G I T F L Y W Y L Q K P G Q S P Q L L I Y Q M S N L A S G V P D R F
mV$_L$CDR 1.8
mV$_L$CDR 2.8
210 220 230 240 250 260 270 280 290 300
CAGTAGCAGTGGGTCAGGAACTGATTTCACACTGAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGTGTTTATTACTGTGCTCAAAATCTAGAACTTCCG
S S S G S G T D F T L R I S R V E A E D L G V Y Y C A Q N L E L P
mV$_L$CDR 3.8
310 320 330
CTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA
L T F G A G T K L E L K
mV$_L$CDR 3.8

FIG. 2G

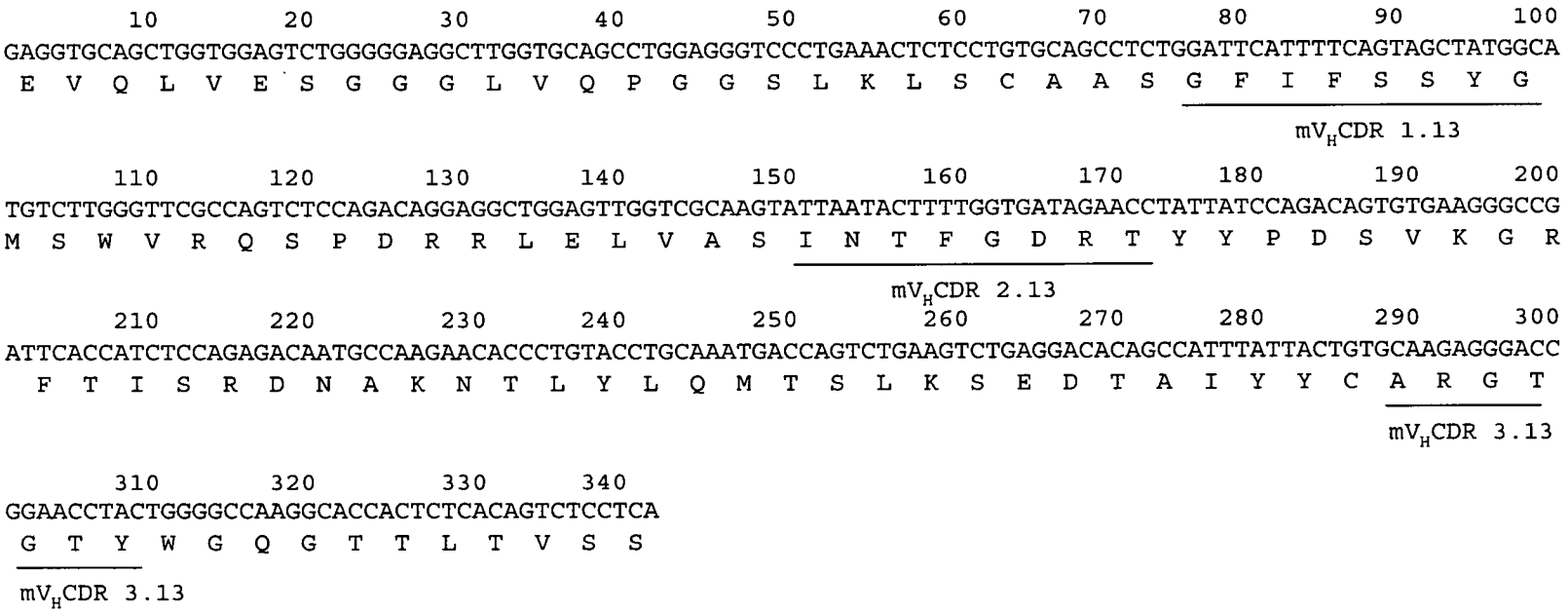

10 20 30 40 50 60 70 80 90 100
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCATTTTCAGTAGCTATGGCA
E V Q L V E S G G G L V Q P G G S L K L S C A A S G F I F S S Y G
mV$_H$CDR 1.13
110 120 130 140 150 160 170 180 190 200
TGTCTTGGGTTCGCCAGTCTCCAGACAGGAGGCTGGAGTTGGTCGCAAGTATTAATACTTTTGGTGATAGAACCTATTATCCAGACAGTGTGAAGGGCCG
M S W V R Q S P D R R L E L V A S I N T F G D R T Y Y P D S V K G R
mV$_H$CDR 2.13
210 220 230 240 250 260 270 280 290 300
ATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTGCAAATGACCAGTCTGAAGTCTGAGGACACAGCCATTTATTACTGTGCAAGAGGGACC
F T I S R D N A K N T L Y L Q M T S L K S E D T A I Y Y C A R G T
mV$_H$CDR 3.13
310 320 330 340
GGAACCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
G T Y W G Q G T T L T V S S
mV$_H$CDR 3.13

FIG. 2H

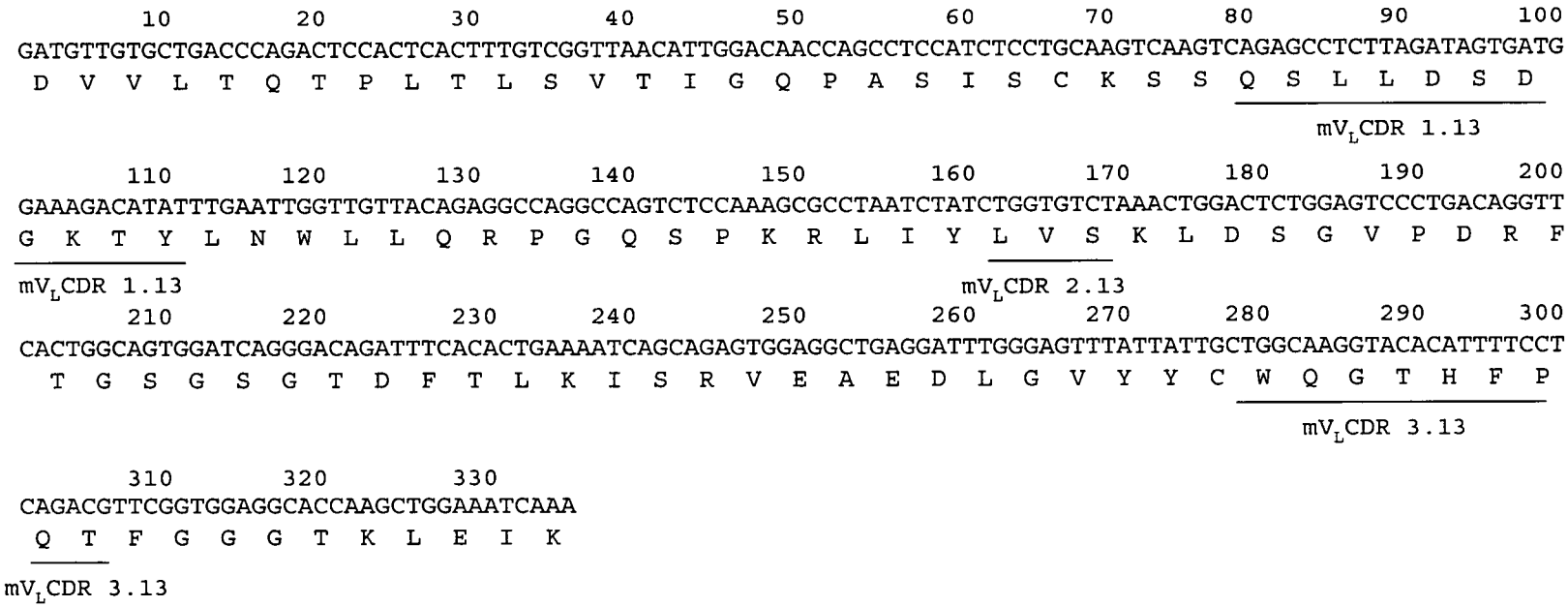

10 20 30 40 50 60 70 80 90 100
GATGTTGTGCTGACCCAGACTCCACTCACTTTGTCGGTTAACATTGGACAACCAGCCTCCATCTCCTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATG
D V V L T Q T P L T L S V T I G Q P A S I S C K S S Q S L L D S D
mV$_L$CDR 1.13
110 120 130 140 150 160 170 180 190 200
GAAAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTT
G K T Y L N W L L Q R P G Q S P K R L I Y L V S K L D S G V P D R F
mV$_L$CDR 1.13
mV$_L$CDR 2.13
210 220 230 240 250 260 270 280 290 300
CACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCAAGGTACACATTTTCCT
T G S G S G T D F T L K I S R V E A E D L G V Y Y C W Q G T H F P
mV$_L$CDR 3.13
310 320 330
CAGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA
Q T F G G G T K L E I K
mV$_L$CDR 3.13

FIG. 2I

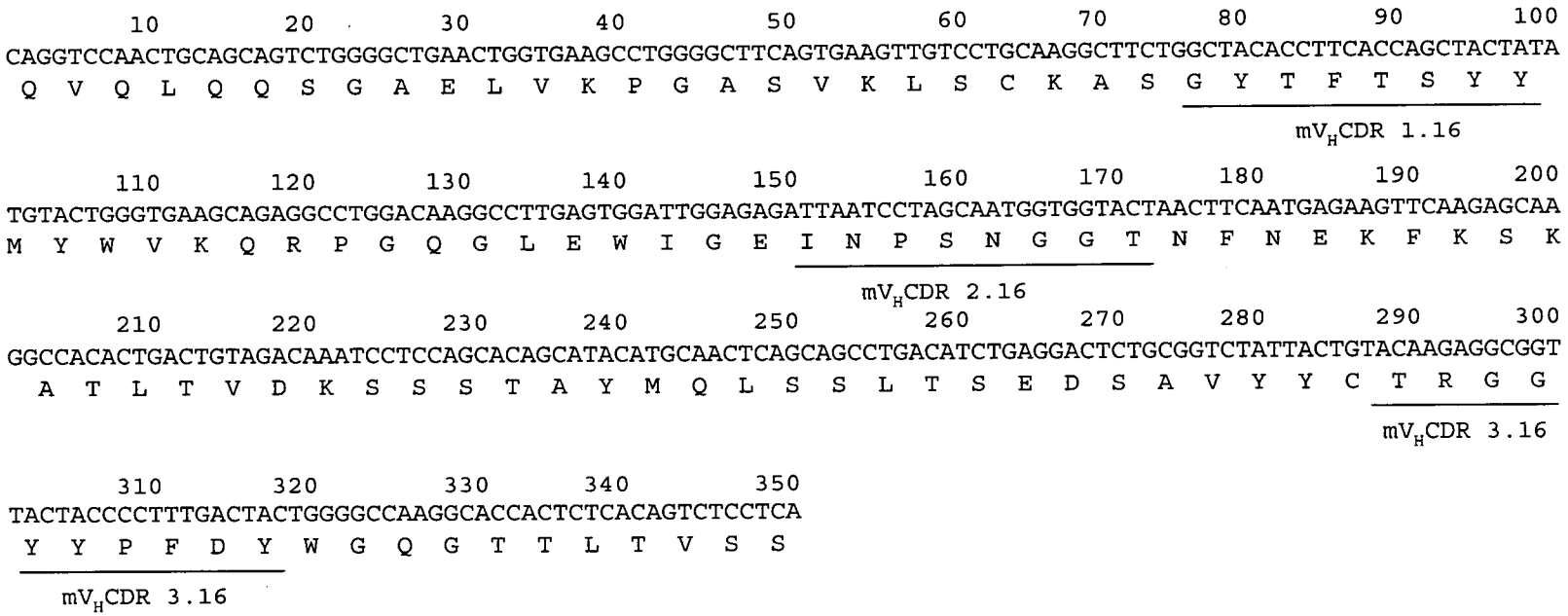

10 20 30 40 50 60 70 80 90 100
CAGGTCCAACTGCAGCAGTCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTATA
Q V Q L Q Q S G A E L V K P G A S V K L S C K A S G Y T F T S Y Y
mV$_H$CDR 1.16
110 120 130 140 150 160 170 180 190 200
TGTACTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGAGAGATTAATCCTAGCAATGGTGGTACTAACTTCAATGAGAAGTTCAAGAGCAA
M Y W V K Q R P G Q G L E W I G E I N P S N G G T N F N E K F K S K
mV$_H$CDR 2.16
210 220 230 240 250 260 270 280 290 300
GGCCACACTGACTGTAGACAAATCCTCCAGCACAGCATACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTACAAGAGGCGGT
A T L T V D K S S S T A Y M Q L S S L T S E D S A V Y Y C T R G G
mV$_H$CDR 3.16
310 320 330 340 350
TACTACCCCTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
Y Y P F D Y W G Q G T T L T V S S
mV$_H$CDR 3.16

FIG. 2J

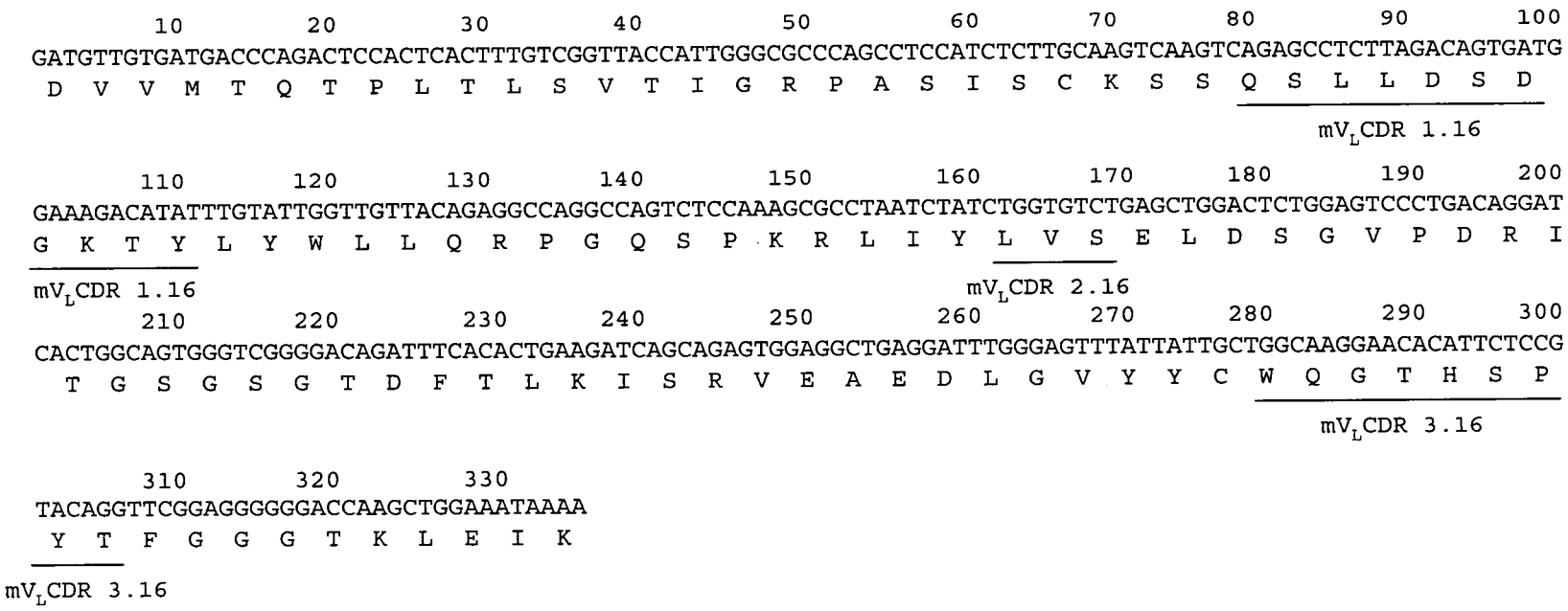

10 20 30 40 50 60 70 80 90 100
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGGCGCCCAGCCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGACAGTGATG
D V V M T Q T P L T L S V T I G R P A S I S C K S S Q S L L D S D
mV$_L$CDR 1.16
110 120 130 140 150 160 170 180 190 200
GAAAGACATATTTGTATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTGAGCTGGACTCTGGAGTCCCTGACAGGAT
G K T Y L Y W L L Q R P G Q S P K R L I Y L V S E L D S G V P D R I
mV$_L$CDR 1.16
mV$_L$CDR 2.16
210 220 230 240 250 260 270 280 290 300
CACTGGCAGTGGGTCGGGGACAGATTTCACACTGAAGATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCAAGGAACACATTCTCCG
T G S G S G T D F T L K I S R V E A E D L G V Y Y C W Q G T H S P
mV$_L$CDR 3.16
310 320 330
TACAGGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
Y T F G G G T K L E I K
mV$_L$CDR 3.16

FIG. 2K

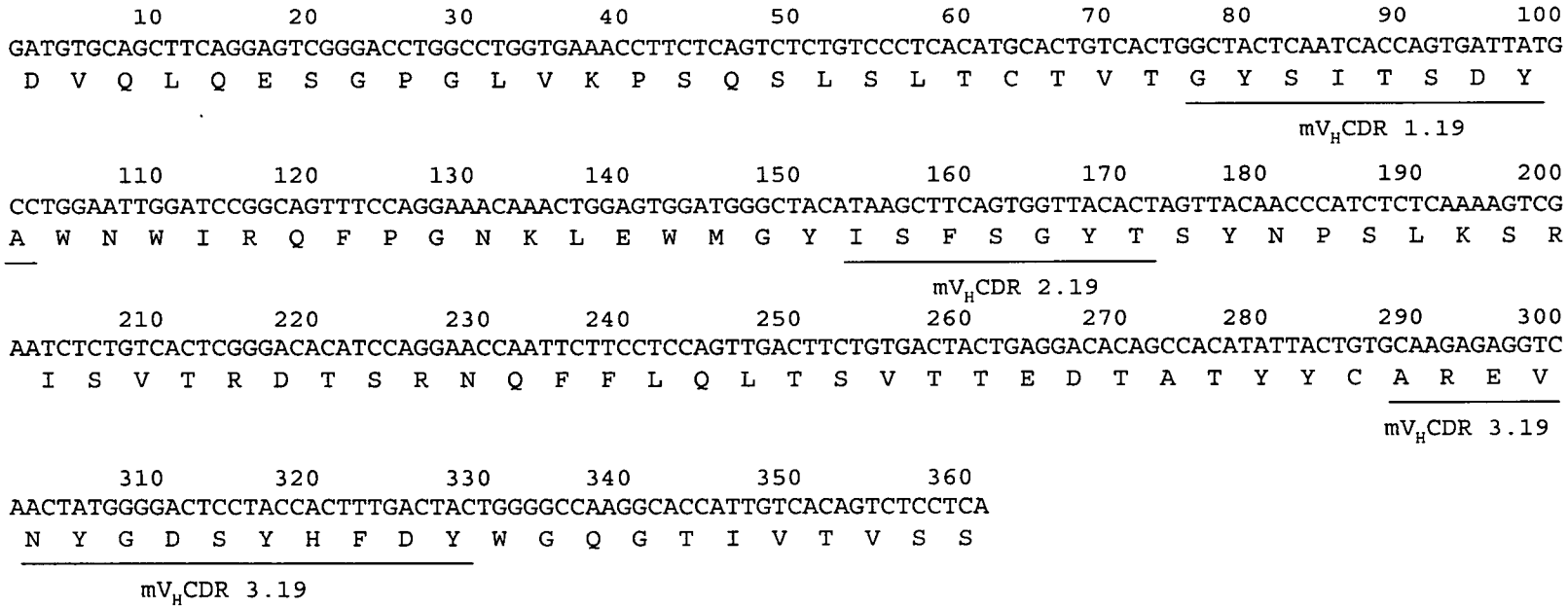

10 20 30 40 50 60 70 80 90 100
GATGTGCAGCTTCAGGAGTCGGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTGTCCCTCACATGCACTGTCACTGGCTACTCAATCACCAGTGATTATG
D V Q L Q E S G P G L V K P S Q S L S L T C T V T G Y S I T S D Y
mV$_H$CDR 1.19
110 120 130 140 150 160 170 180 190 200
CCTGGAATTGGATCCGGCAGTTTCCAGGAAACAAACTGGAGTGGATGGGCTACATAAGCTTCAGTGGTTACACTAGTTACAACCCATCTCTCAAAAGTCG
A W N W I R Q F P G N K L E W M G Y I S F S G Y T S Y N P S L K S R
mV$_H$CDR 2.19
210 220 230 240 250 260 270 280 290 300
AATCTCTGTCACTCGGGACACATCCAGGAACCAATTCTTCCTCCAGTTGACTTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGAGAGGTC
I S V T R D T S R N Q F F L Q L T S V T T E D T A T Y Y C A R E V
mV$_H$CDR 3.19
310 320 330 340 350 360
AACTATGGGGACTCCTACCACTTTGACTACTGGGGCCAAGGCACCATTGTCACAGTCTCCTCA
N Y G D S Y H F D Y W G Q G T I V T V S S
mV$_H$CDR 3.19

FIG. 2L

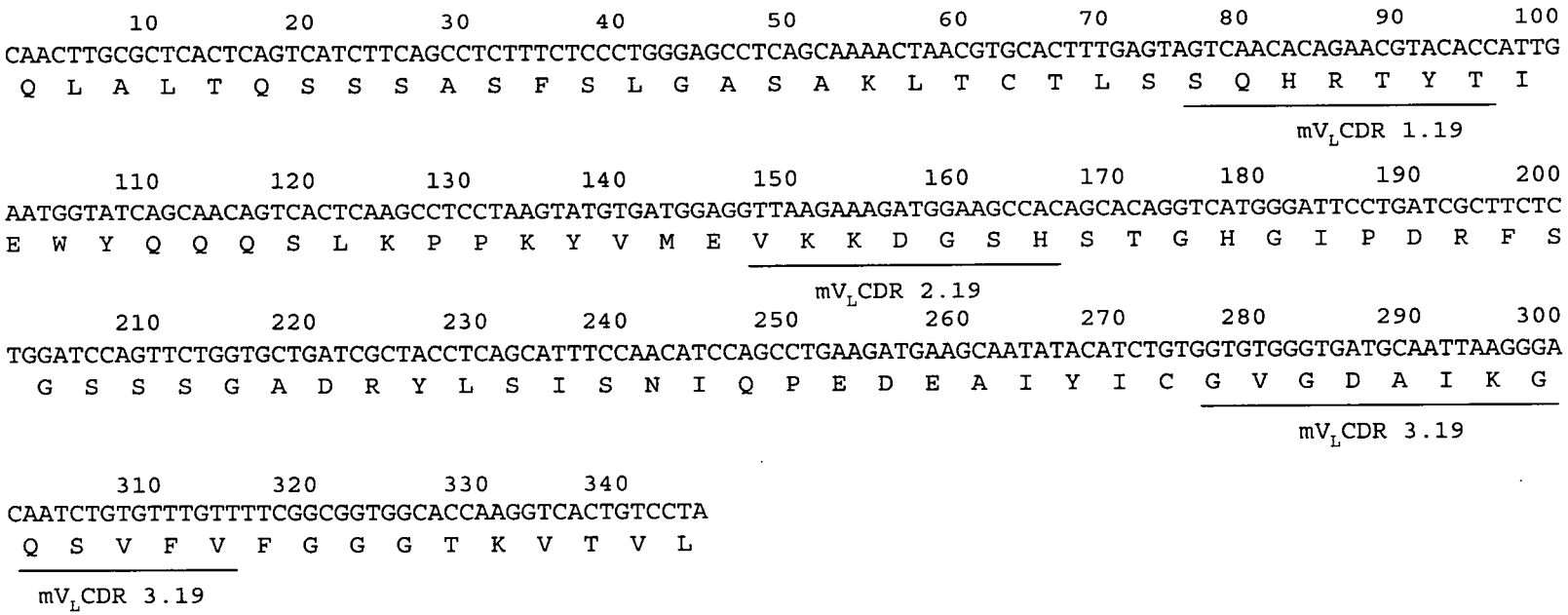

10 20 30 40 50 60 70 80 90 100
CAACTTGCGCTCACTCAGTCATCTTCAGCCTCTTTCTCCCTGGGAGCCTCAGCAAAACTAACGTGCACTTTGAGTAGTCAACACAGAACGTACACCATTG
Q L A L T Q S S S A S F S L G A S A K L T C T L S S Q H R T Y T I
mV$_L$CDR 1.19
110 120 130 140 150 160 170 180 190 200
AATGGTATCAGCAACAGTCACTCAAGCCTCCTAAGTATGTGATGGAGGTTAAGAAAGATGGAAGCCACAGCACAGGTCATGGGATTCCTGATCGCTTCTC
E W Y Q Q Q S L K P P K Y V M E V K K D G S H S T G H G I P D R F S
mV$_L$CDR 2.19
210 220 230 240 250 260 270 280 290 300
TGGATCCAGTTCTGGTGCTGATCGCTACCTCAGCATTTCCAACATCCAGCCTGAAGATGAAGCAATATACATCTGTGGTGTGGGTGATGCAATTAAGGGA
G S S S G A D R Y L S I S N I Q P E D E A I Y I C G V G D A I K G
mV$_L$CDR 3.19
310 320 330 340
CAATCTGTGTTTGTTTTCGGCGGTGGCACCAAGGTCACTGTCCTA
Q S V F V F G G G T K V T V L
mV$_L$CDR 3.19

FIG. 3A

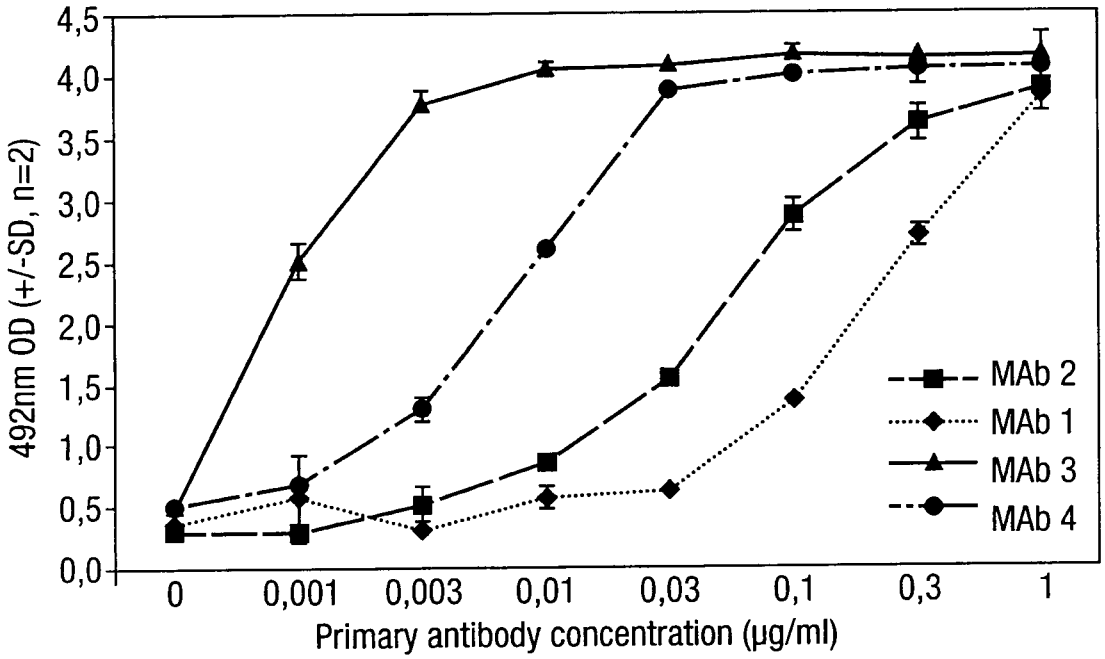

4,5
4,0
3,5
3,0
2,5
2,0
1,5
1,0
0,5
0,0
492nm OD (+/-SD, n=2)
0
0,001
0,003
0,01
0,03
0,1
0,3
1
Primary antibody concentration (µg/ml)
MAb 2
MAb 1
MAb 3
MAb 4

FIG. 3B


MAb 5
MAb 6
MAb 7
MAb 8
MAb 9
MAb 10
MAb 11
MAb 12
MAb 13
MAb 14
MAb 21
MAb 22
MAb 23
DO 492nm (+/- écart type, n=2)
6,0
5,0
4,0
3,0
2,0
1,0
0,0
mAb (ng/ml)
0
0,03
0,1
0,3
1
3
10
30

FIG. 3C

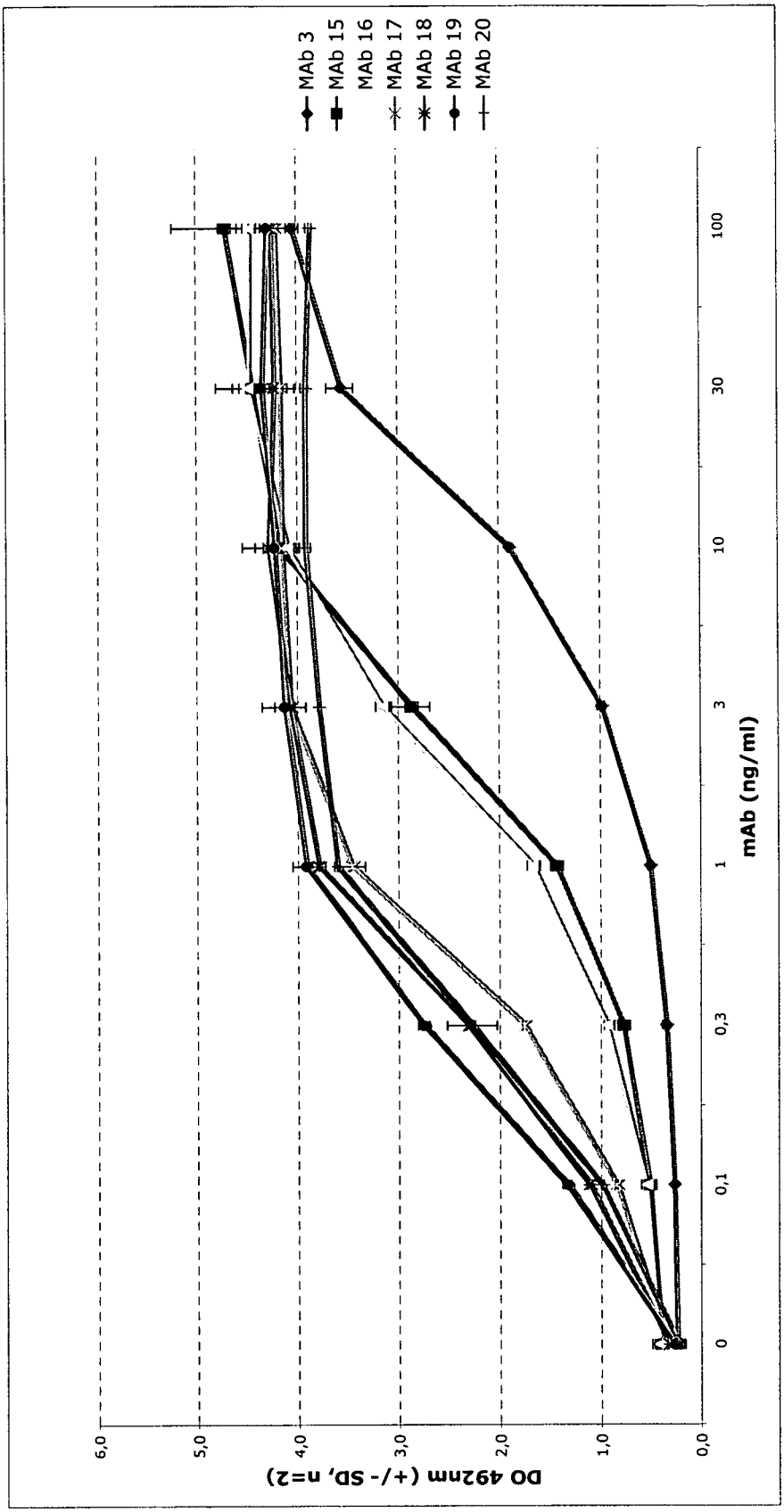

MAb 3
MAb 15
MAb 16
MAb 17
MAb 18
MAb 19
MAb 20
DO 492nm (+/- SD, n=2)
6,0
5,0
4,0
3,0
2,0
1,0
0,0
0
0,1
0,3
1
3
10
30
100
mAb (ng/ml)

FIG. 4

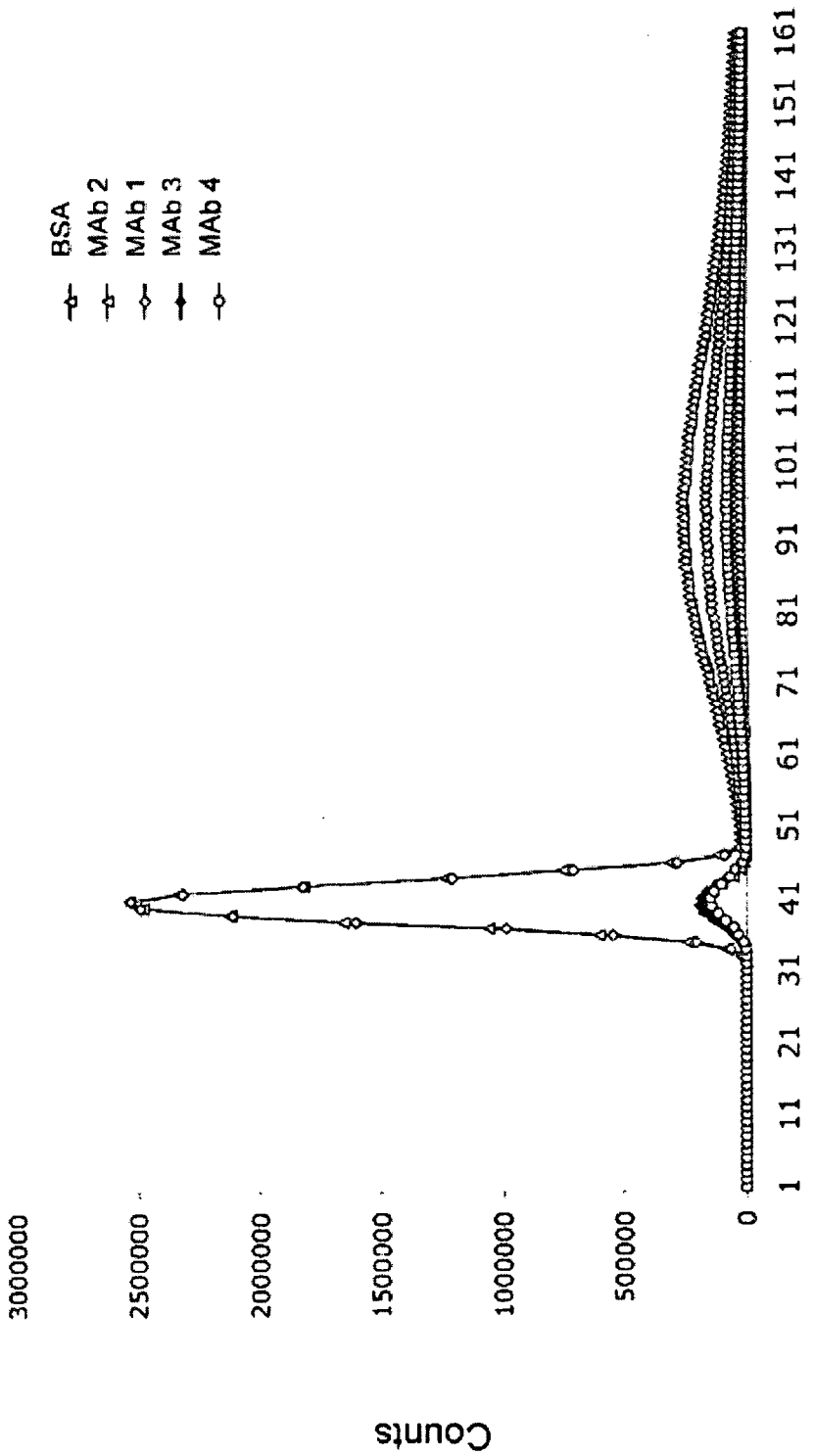

BSA
MAb 2
MAb 1
MAb 3
MAb 4
Counts
3000000
2500000
2000000
1500000
1000000
500000
0
1 11 21 31 41 51 61 71 81 91 101 111 121 131 141 151 161
Wavelength (nm)

FIG. 5A

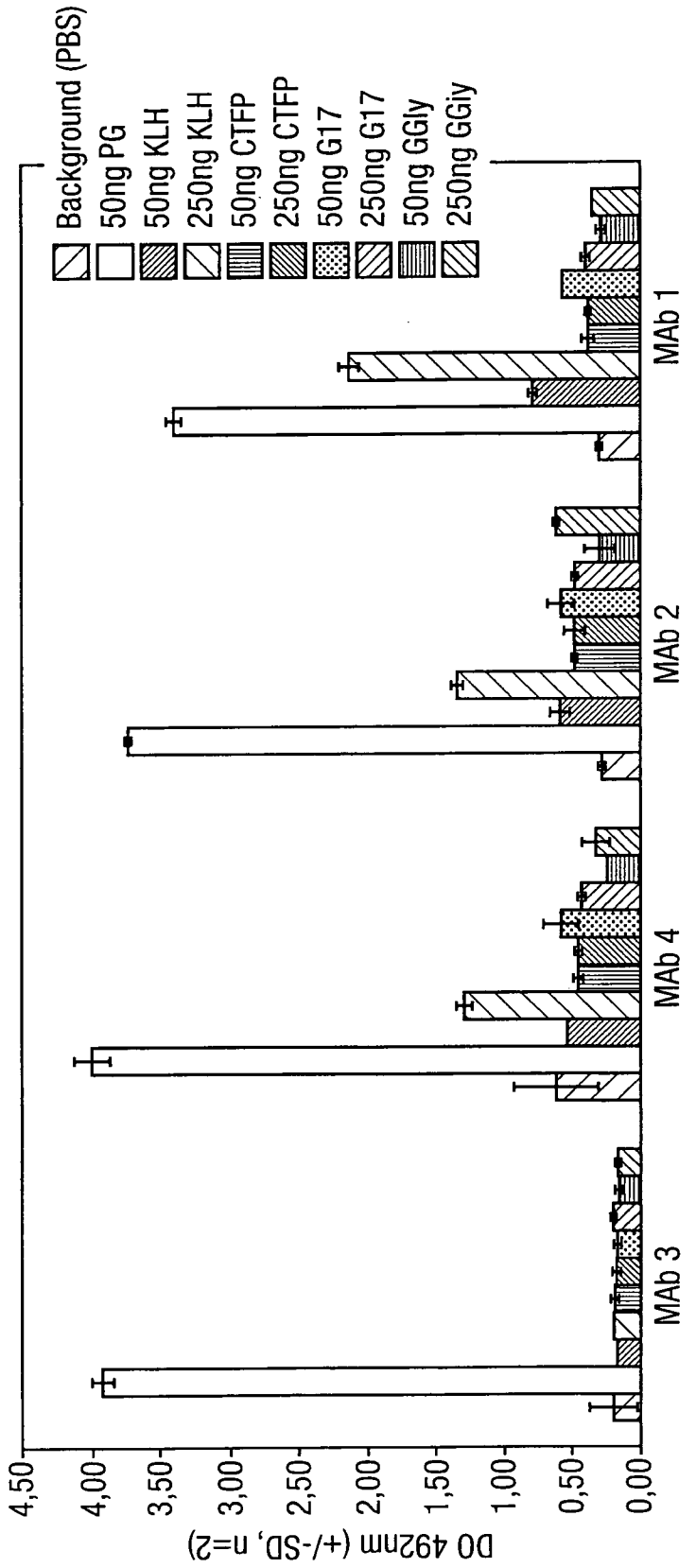

Background (PBS)
50ng PG
50ng KLH
250ng KLH
50ng CTFP
250ng CTFP
50ng G17
250ng G17
50ng GGly
250ng GGly
DO 492nm (+/-SD, n=2)
4,50
4,00
3,50
3,00
2,50
2,00
1,50
1,00
0,50
0,00
MAb 3
MAb 4
MAb 2
MAb 1

FIG. 5B

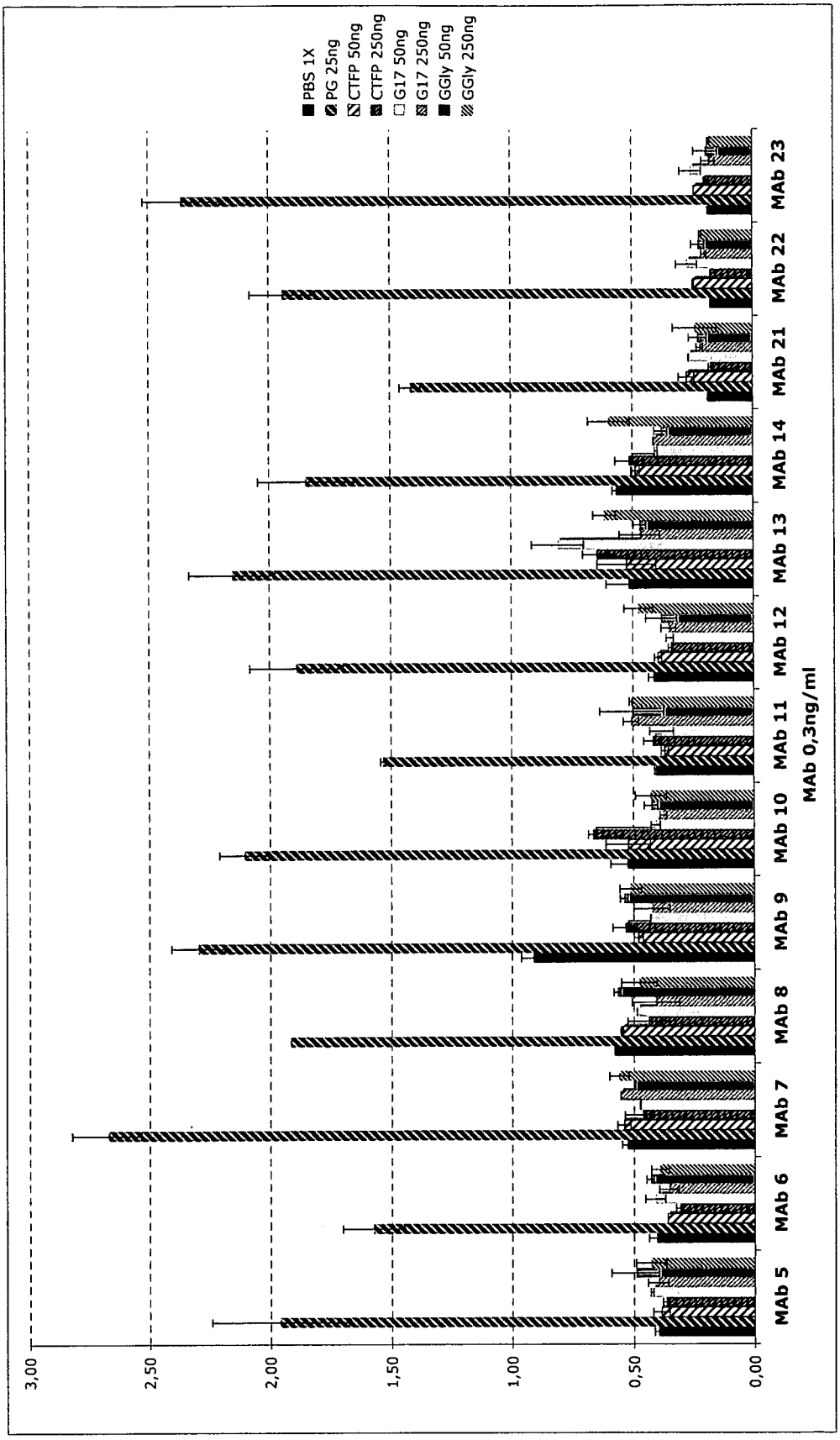

PBS 1X
PG 25ng
CTFP 50ng
CTFP 250ng
G17 50ng
G17 250ng
GGly 50ng
GGly 250ng
3,00
2,50
2,00
1,50
1,00
0,50
0,00
MAb 5
MAb 6
MAb 7
MAb 8
MAb 9
MAb 10
MAb 11
MAb 12
MAb 13
MAb 14
MAb 21
MAb 22
MAb 23
MAb 0,3ng/ml

FIG. 5C

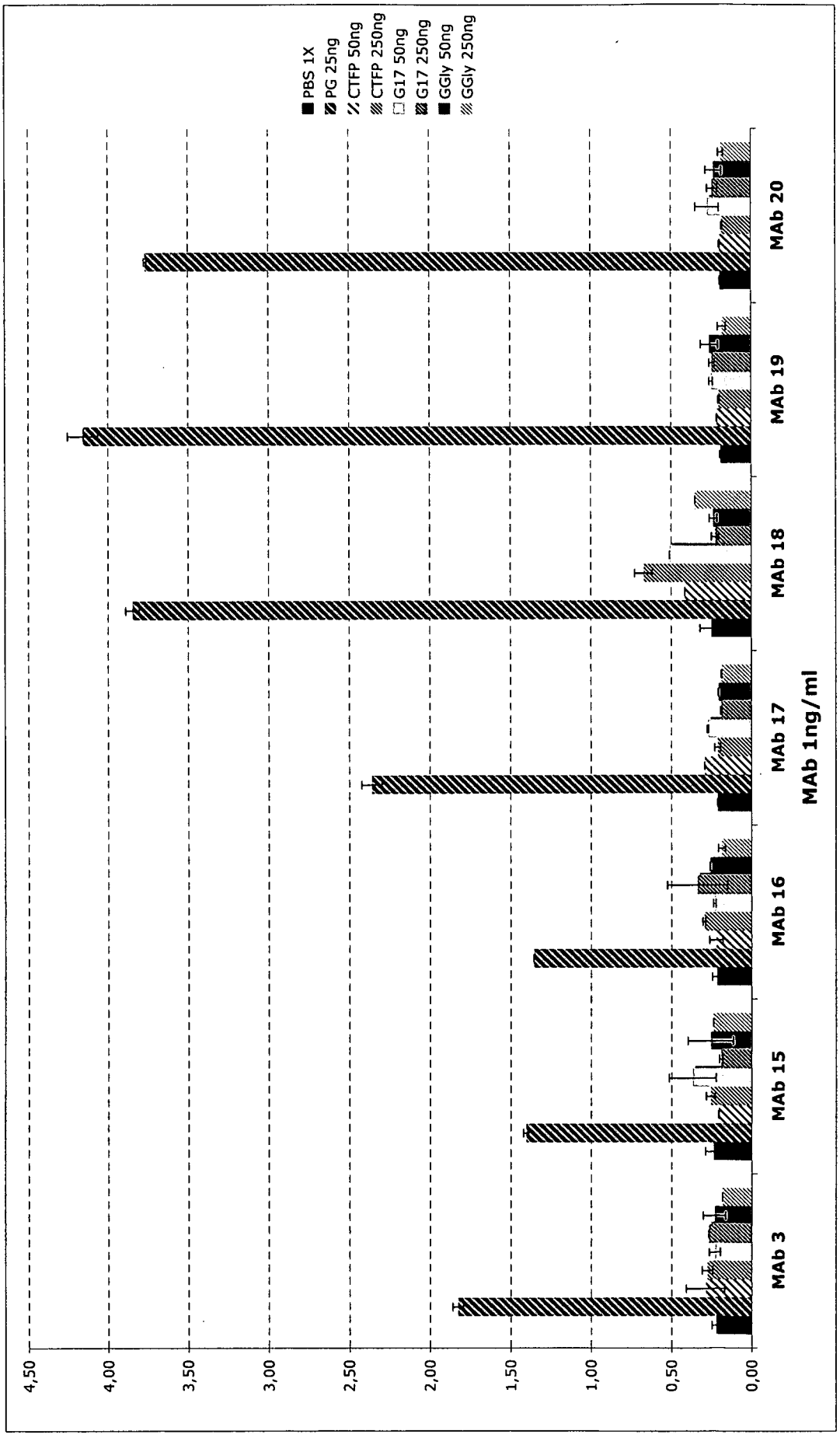

PBS 1X
PG 25ng
CTFP 50ng
CTFP 250ng
G17 50ng
G17 250ng
GGly 50ng
GGly 250ng
4,50
4,00
3,50
3,00
2,50
2,00
1,50
1,00
0,50
0,00
MAb 3
MAb 15
MAb 16
MAb 17
MAb 18
MAb 19
MAb 20
MAb 1ng/ml

FIG. 6

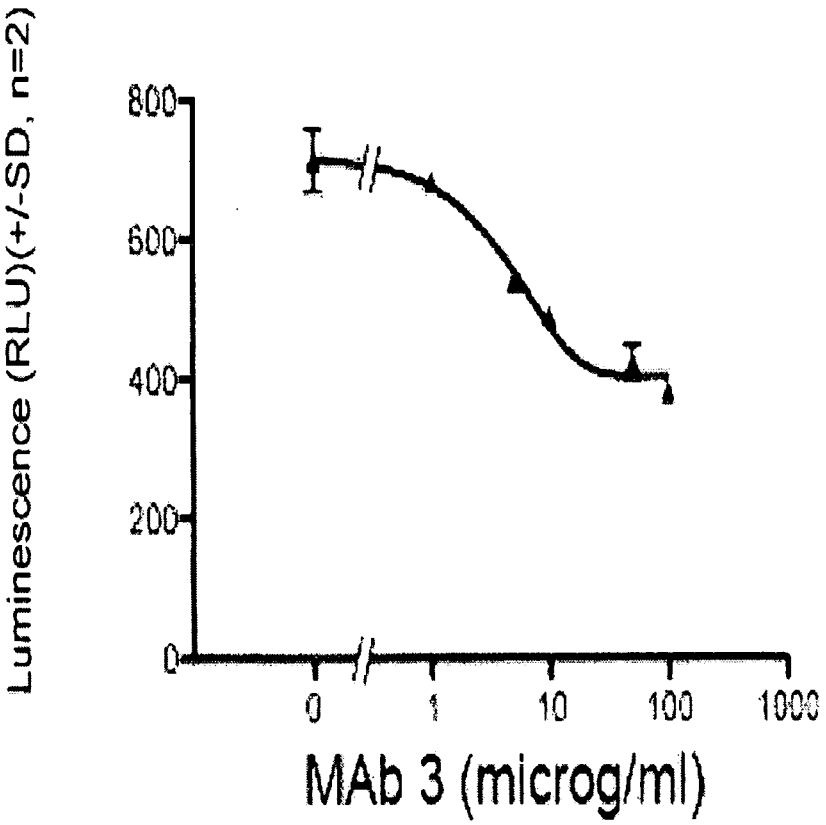

Luminescence (RLU)(+/-SD, n=2)
800
600
400
200
0
0
1
10
100
1000
MAb 3 (microg/ml)

FIG. 7A

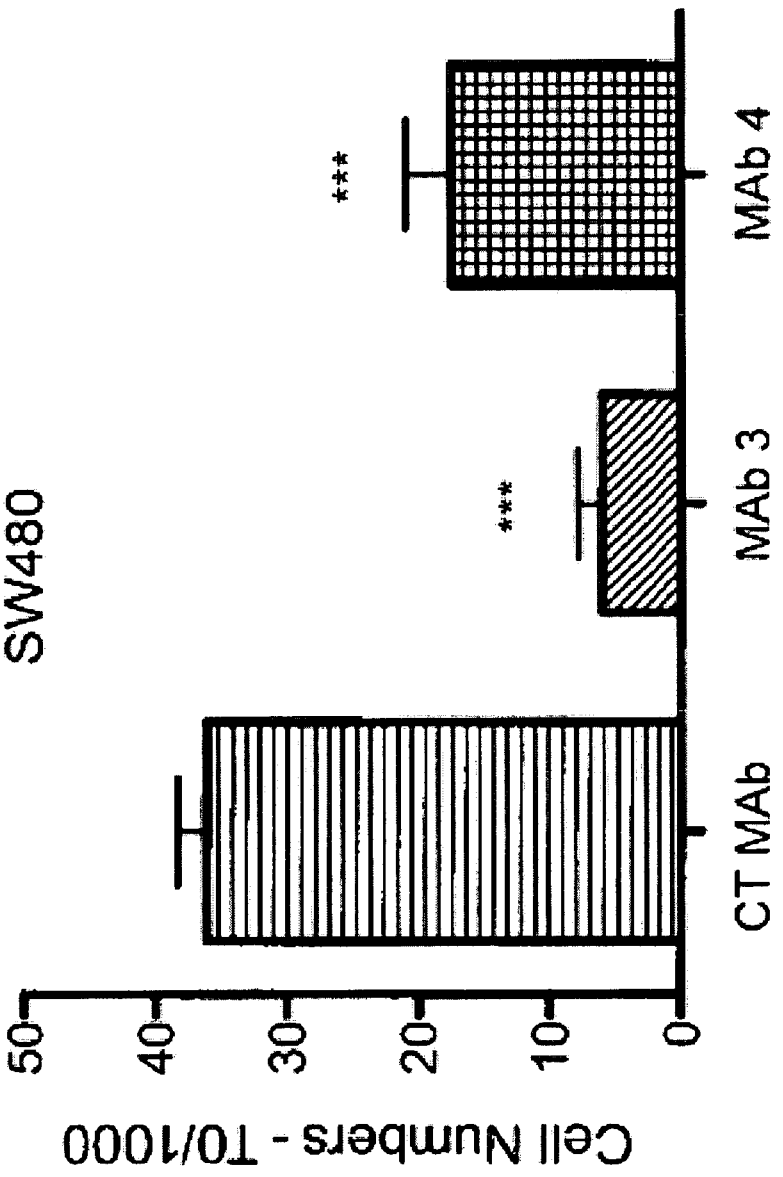


FIG. 7B

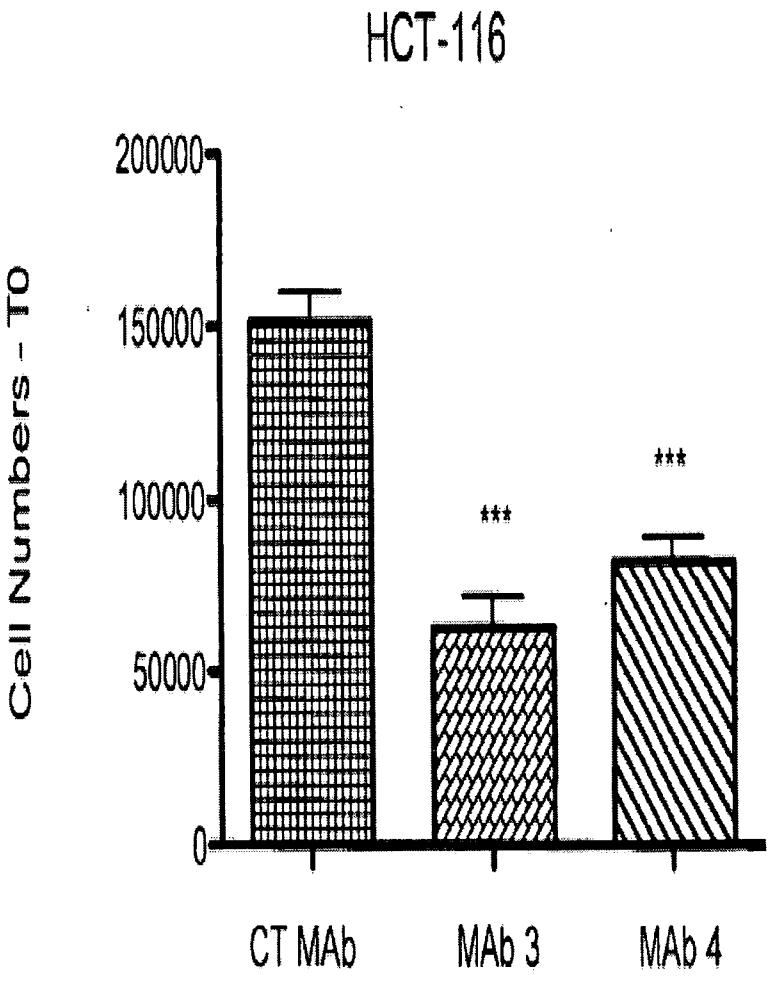

HCT-116
Cell Numbers - T0
200000
150000
100000
50000
0
***
***
CT MAb
MAb 3
MAb 4

FIG. 7C

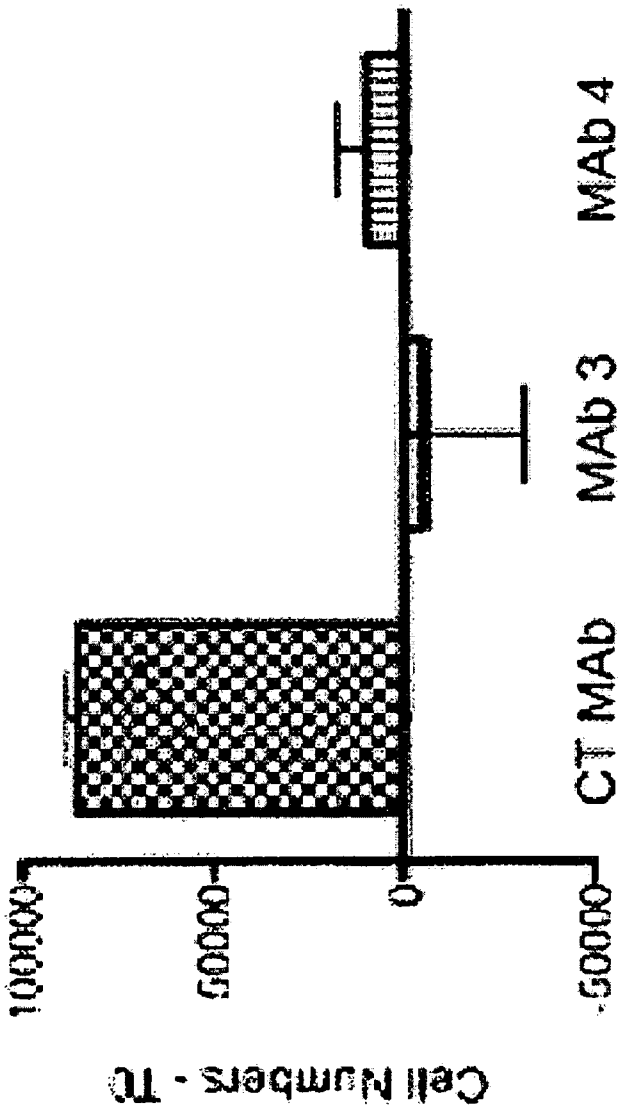


FIG. 7D

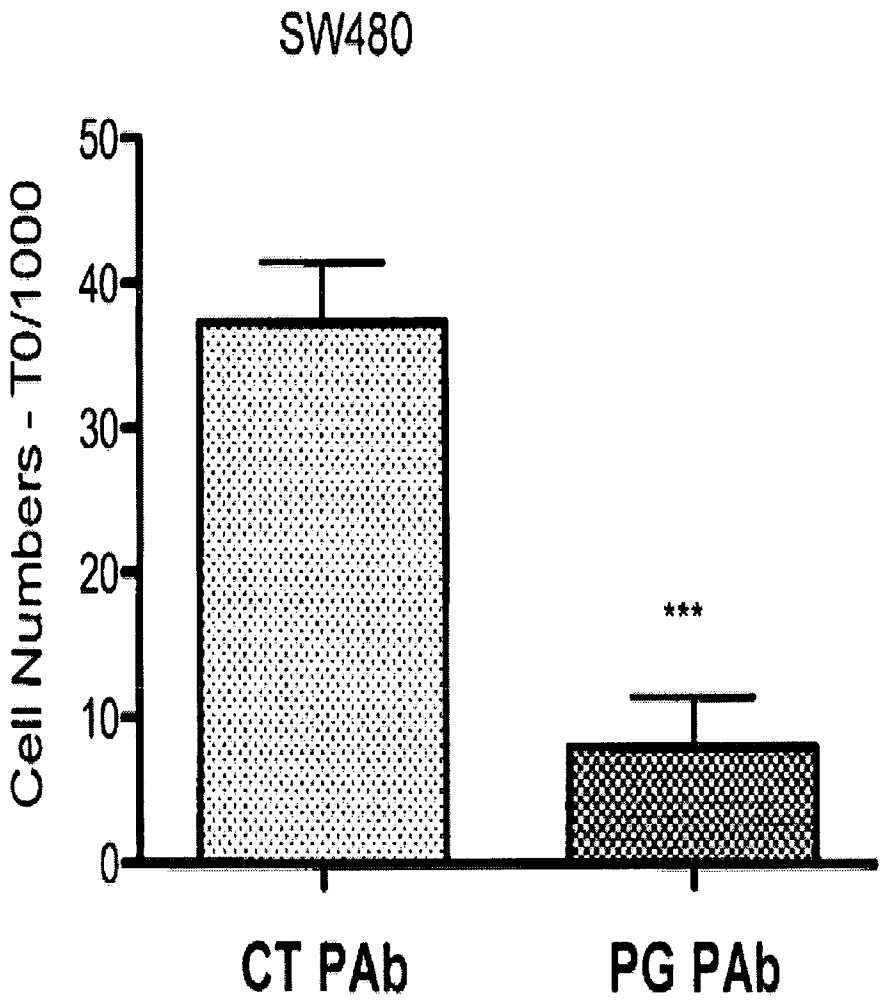


FIG. 7E

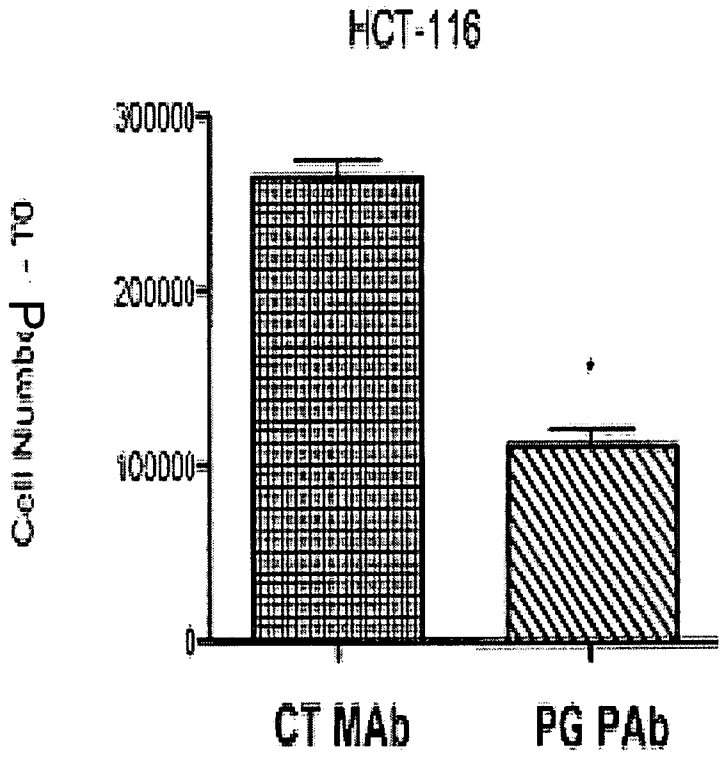


FIG. 7F

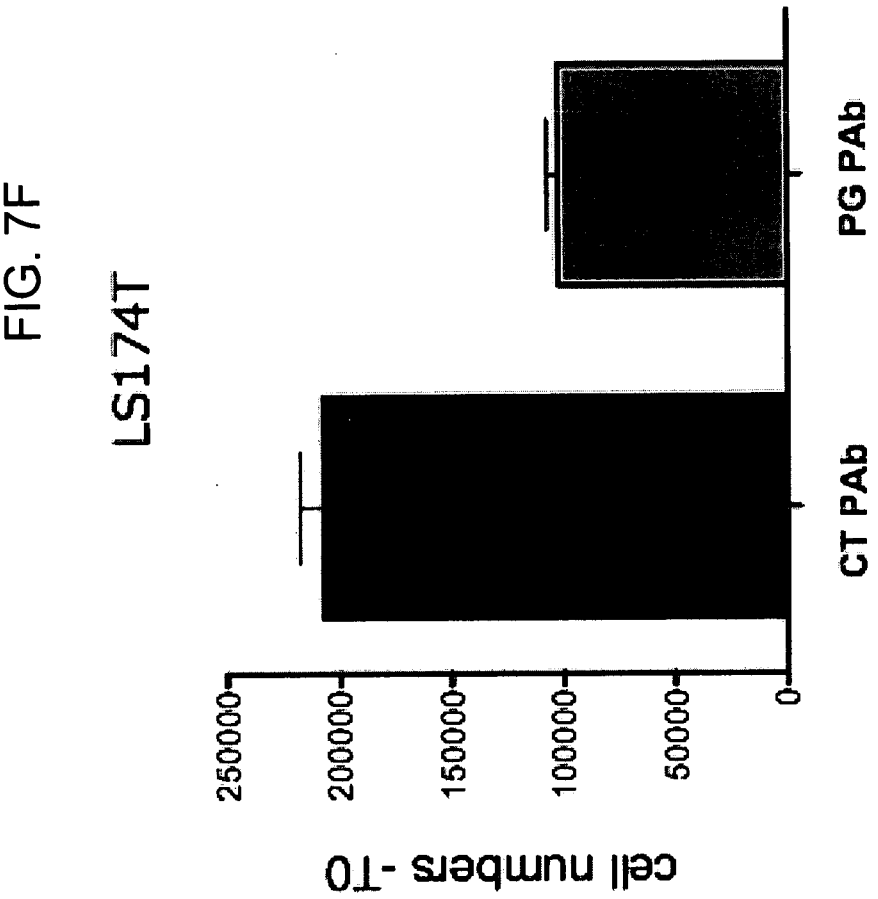

LS174T
cell numbers -T0
250000
200000
150000
100000
50000
0
CT PAb
PG PAb

FIG. 7G

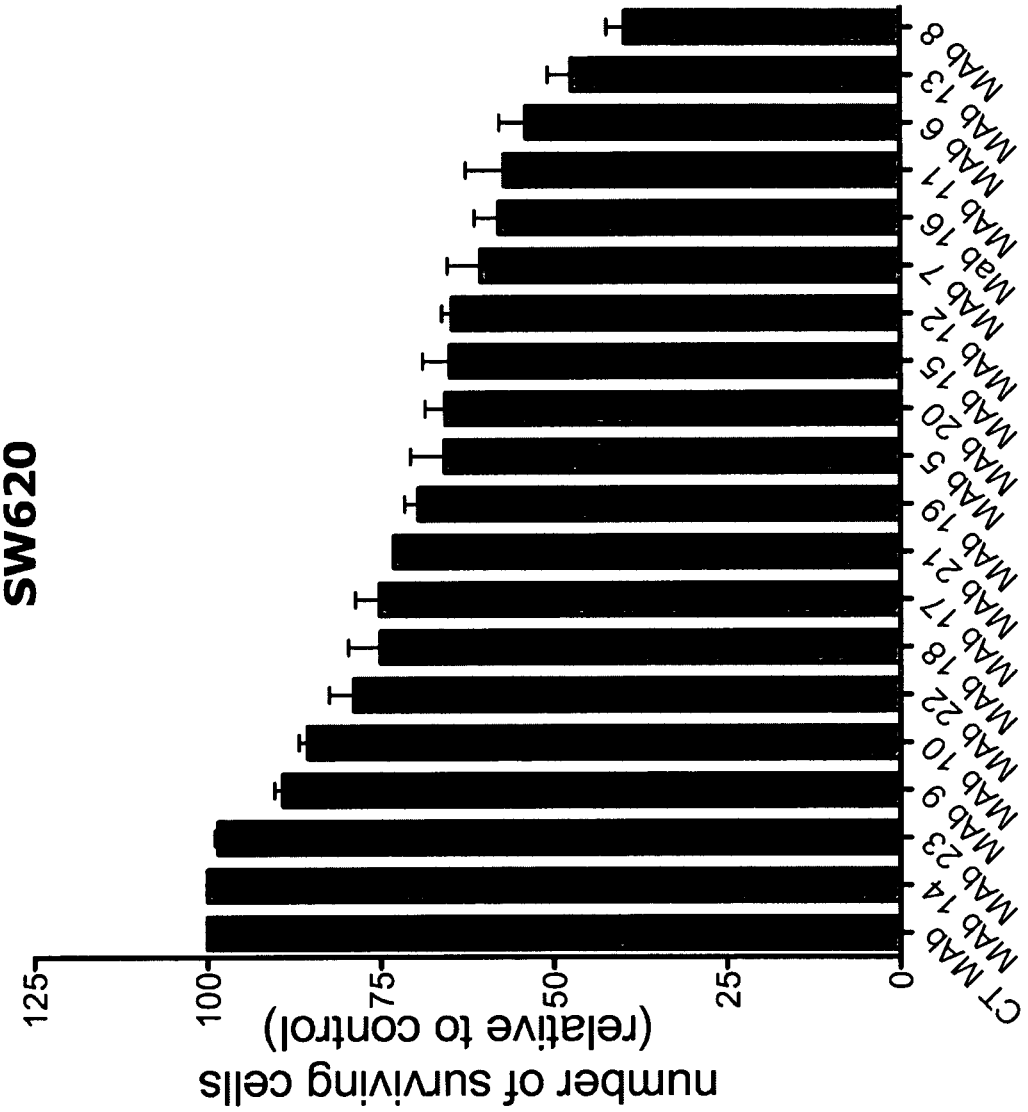

SW620
number of surviving cells
(relative to control)
125
100
75
50
25
0
CT MAb
MAb 14
MAb 23
MAb 9
MAb 10
MAb 22
MAb 18
MAb 17
MAb 21
MAb 19
MAb 5
MAb 20
MAb 15
MAb 12
Mab 7
MAb 16
MAb 11
MAb 6
MAb 13
MAb 8

FIG. 7H

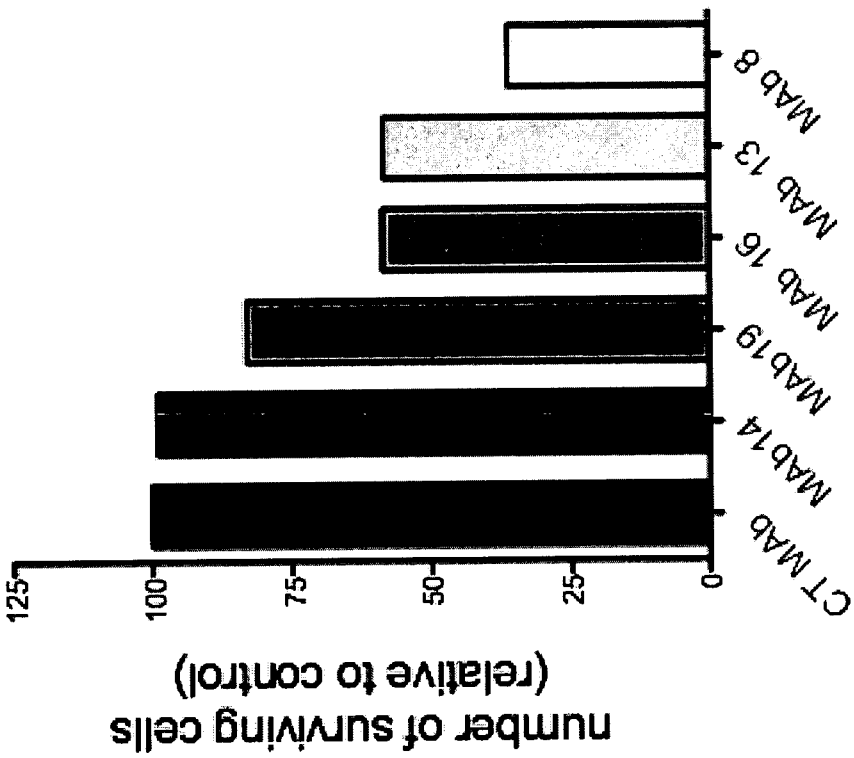

LS174T
number of surviving cells
(relative to control)
125
100
75
50
25
0
CT MAb
MAb14
MAb19
MAb 16
MAb 13
MAb 8

FIG. 7I

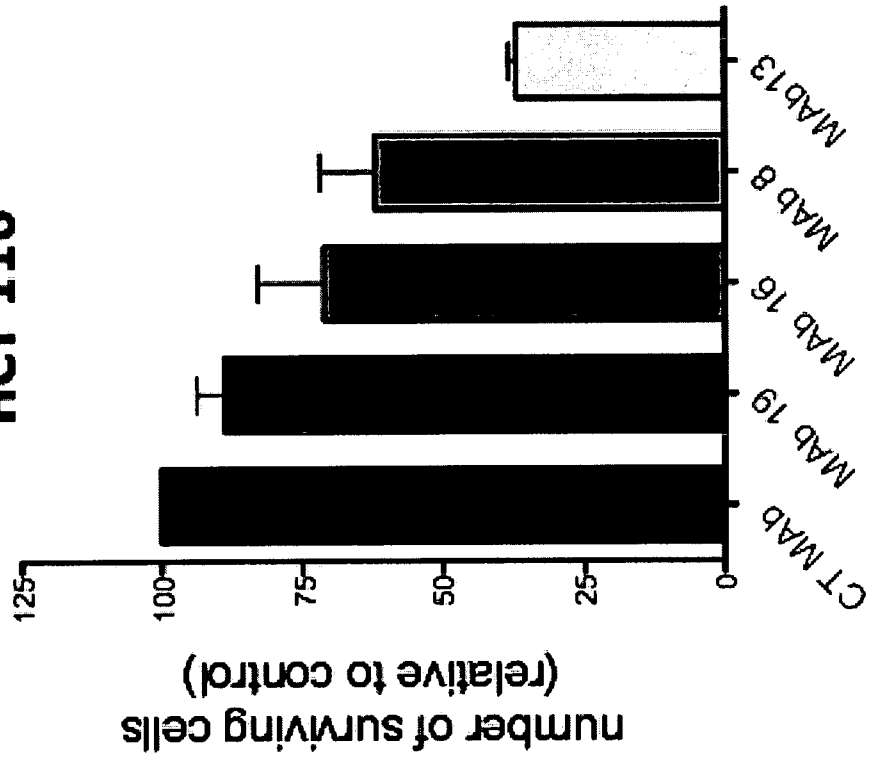

HCT 116
number of surviving cells
(relative to control)
125
100
75
50
25
0
CT MAb
MAb 19
MAb 16
MAb 8
MAb 13

FIG. 8

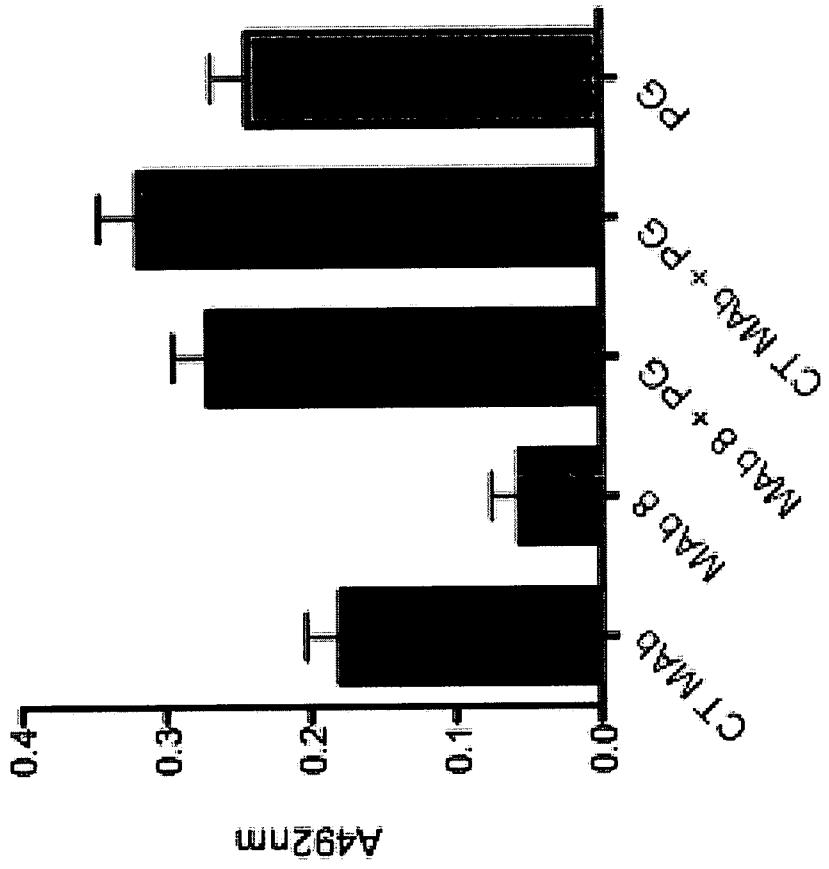


FIG. 9A

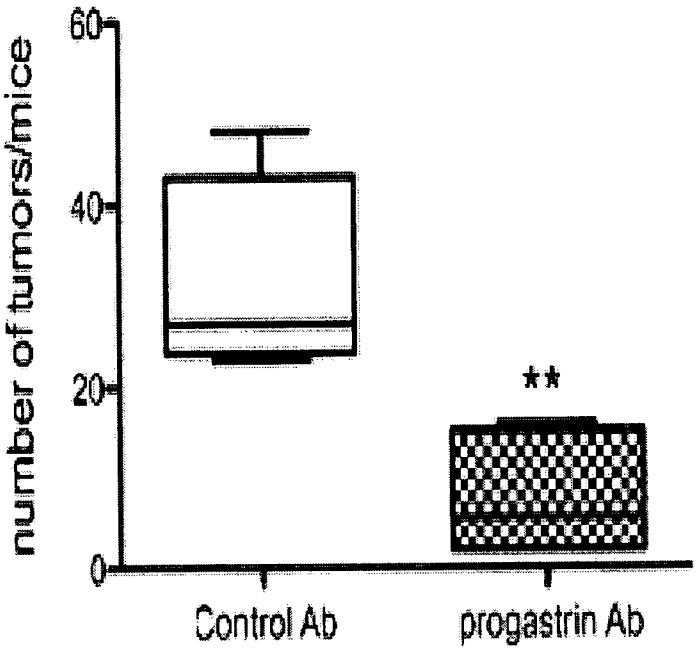
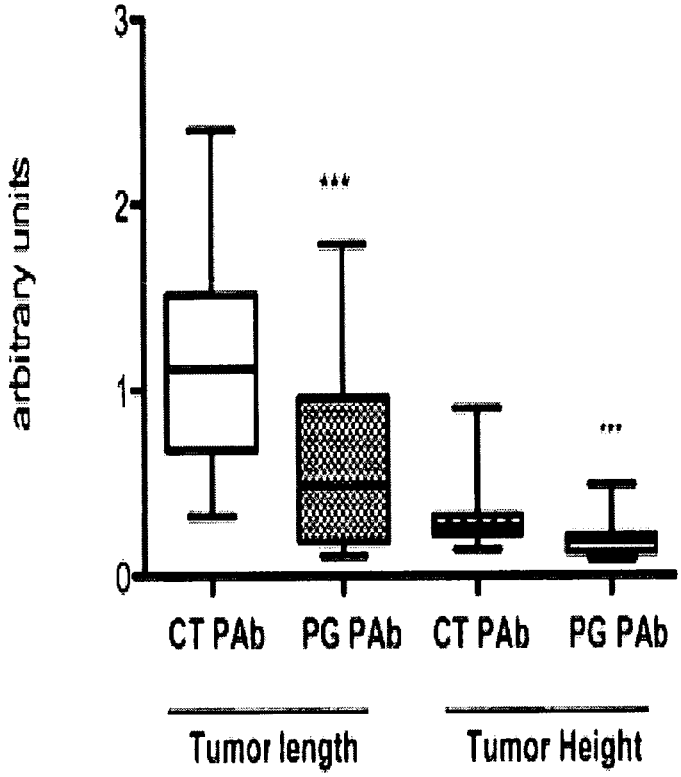


FIG. 9B


arbitrary units
3
2
1
0
***
***
CT PAb
PG PAb
CT PAb
PG PAb
Tumor length
Tumor Height