Figure 1A

Hum. anti-CD3 VL nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
CTTGCAGAGCAAGTTCAAGCGTAAGCTACATGAATTGGTATCAGCAGACACCAGGGAAAGCCCC
TAAGAGATGGATCTATGACACATCCAAAGTGGCTTCTGGGGTCCCATCAAGGTTCAGTGGCAGT
GGATCTGGGACAGATTACACTTTCACCATCAGCAGTCTGCAACCTGAAGATATTGCAACTTACT
ACTGTCAACAGTGGAGTAGTAACCCTCTCACTTTTGGCCAGGGGACCAAGCTGCAGATCACC

Hum. anti-CD3 VL AA

DIQMTQSPSSLSASVGDRVTITCRASSSVSYMNWYQQTPGKAPKRWIYDTSKVASGVPSRFSGS
GSGTDYTFTISSLQPEDIATYYCQQWSSNPLTFGQGTKLQIT

Hum. anti-CD3 VH nt

CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCT
GTAAGTCTTCTGGATACACCTTCACTAGGTATACGATGCACTGGGTCCGCCAGGCTCCAGGGAA
GGGGCTGGAGTGGATTGGATACATAAATCCTAGCCGTGGTTATACTAATTATAATCAGAAGGTG
AAGGACCGATTCACCATCTCCAGAGACAACTCCAAGAACACGGCCTTTCTGCAAATGGACAGCC
TGAGACCCGAGGACACGGGTGTGTATTTCTGTGCGAGATATTATGATGATCATTACTGCCTTGA
CTACTGGGGCCAGGGCACCCCGGTCACCGTCTCCTCA

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Figure 1A (cont.)

Hum. anti-CD3 VH AA

QVQLVQSGGGVVQPGRSLRLSCKSSGYTFTRYTMHWVRQAPGKGLEWIGYINPSRGYTNYNQKV
KDRFTISRDNSKNTAFLQMDSLRPEDTGVYFCARYYDDHYCLDYWGQGTPVTVSS

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Figure 1B

TGTACACTCCGATATCCAGCTGACCCAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCAT
CTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACCAACAGATTCCAGG
ACAGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCAGGTTTAGTGGCAG
TGGGTCTGGGACAGACTTCACCCTCAACATCCATCCTGTGGAGAAGGTGGATGCTGCAACCTATCACTGTCA
GCAAAGTACTGAGGATCCGTGGACGTTCGGTGGAGGGACCAAGCTCGAGATCAAAGGTGGTGGTGGTTCTGG
CGGCGGCGGCTCCGGTGGTGGTGGTTCTCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGG
GTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCA
GAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAACTACAATGGAAA
GTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTAGC
ATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTAT
GGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCCGGAGGTGGTGGCTCCCAGGTGCAGCTGGTGCA
GTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTAAGTCTTCTGGATACACCTTCAC
TAGGTATACGATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATTGGATACATAAATCCTAG
CCGTGGTTATACTAATTATAATCAGAAGGTGAAGGACCGATTCACCATCTCCAGAGACAACTCCAAGAACAC
GGCCTTTCTGCAAATGGACAGCCTGAGACCCGAGGACACGGGTGTGTATTTCTGTGCGAGATATTATGATGA
TCATTACTGCCTTGACTATTGGGGCCAGGGCACCCCGGTCACCGTCTCCTCAGTCGAAGGTGGAAGTGGAGG
TTCTGGTGGAAGTGGAGGTTCAGGTGGAGTGGACGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGC
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GACACCAGGGAAAGCCCCTAAGAGATGGATCTATGACACATCCAAAGTGGCTTCTGGGGTCCCATCAAGGTT
CAGTGGCAGTGGATCTGGGACAGATTACACTTTCACCATCAGCAGTCTGCAACCTGAAGATATTGCAACTTA
CTACTGTCAACAGTGGAGTAGTAACCCTCTCACTTTTGGCCAGGGGACCAAGCTGCAGATCACC

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Figure 1B (cont.)

DIQLTQSPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPRFSGSGSG
TDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIKGGGSGGGGSGGGGSQVQLQQSGAELVRPGSSV
KISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYNGKFKGKATLTADESSSTAYMQLSSLASED
SAVYFCARRETTTVGRYYYAMDYWGQGTTVTVSSGGGGSQVQLVQSGGGVVQPGRSLRLSCKSSGYTFTRYT
MHWVRQAPGKGLEWIGYINPSRGYTNYNQKVKDRFTISRDNSKNTAFLQMDSLRPEDTGVYFCARYYDDHYC
LDYWGQGTPVTVSSVEGGSGGSGGSGGSGGVDDIQMTQSPSSLSASVGDRVTITCRASSSVSYMNWYQQTPG
KAPKRWIYDTSKVASGVPSRFSGSGSGTDYTFTISSLQPEDIATYYCQQWSSNPLTFGQGTKLQIT

Figure 1C


TGTACACTCCGAGCTCGTGATGACACAGTCTCCATCCTCCCTGACTGTGACAGCAGGAGAGAAGGTCACTAT
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ACCAGGGCAGCCTCCTAAACTGTTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCAC
AGGCAGTGGATCTGGAACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTA
CTGTCAGAATGATTATAGTTATCCGCTCACGTTCGGTGCTGGGACCAAGCTTGAGATCAAAGGTGGTGGTGG
TTCTGGCGGCGGCGGCTCCGGTGGTGGTGGTTCTGAGGTGCAGCTGCTCGAGCAGTCTGGAGCTGAGCTGGT
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GGTAAAGCAGAGGCCTGGACATGGACTTGAGTGGATTGGAGATATTTTCCCTGGAAGTGGTAATATCCACTA
CAATGAGAAGTTCAAGGGCAAAGCCACACTGACTGCAGACAAATCTTCGAGCACAGCCTATATGCAGCTCAG
TAGCCTGACATTTGAGGACTCTGCTGTCTATTTCTGTGCAAGACTGAGGAACTGGGACGAGCCTATGGACTA
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TACGATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATTGGATACATAAATCCTAGCCGTGG
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AGGGAAAGCCCCTAAGAGATGGATCTATGACACATCCAAAGTGGCTTCTGGGGTCCCATCAAGGTTCAGTGG
CAGTGGATCTGGGACAGATTACACTTTCACCATCAGCAGTCTGCAACCTGAAGATATTGCAACTTACTACTG
TCAACAGTGGAGTAGTAACCCTCTCACTTTTGGCCAGGGGACCAAGCTGCAGATCACC

Figure 1C (cont.)

ELVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVPDRFTGSG
SGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEIKGGGGSGGGGSGGGGSEVQLLEQSGAELVRPG
TSVKISCKASGYAFTNYWLGWVKQRPGHGLEWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSSLT
FEDSAVYFCARLRNWDEPMDYWGQGTTVTVSSGGGGSQVQLVQSGGGVVQPGRSLRLSCKSSGYTFTRYTMH
WVRQAPGKGLEWIGYINPSRGYTNYNQKVKDRFTISRDNSKNTAFLQMDSLRPEDTGVYFCARYYDDHYCLD
YWGQGTPVTVSSVEGGSGGSGGSGGSGGVDDIQMTQSPSSLSASVGDRVTITCRASSSVSYMNWYQQTPGKA
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Figure 1D

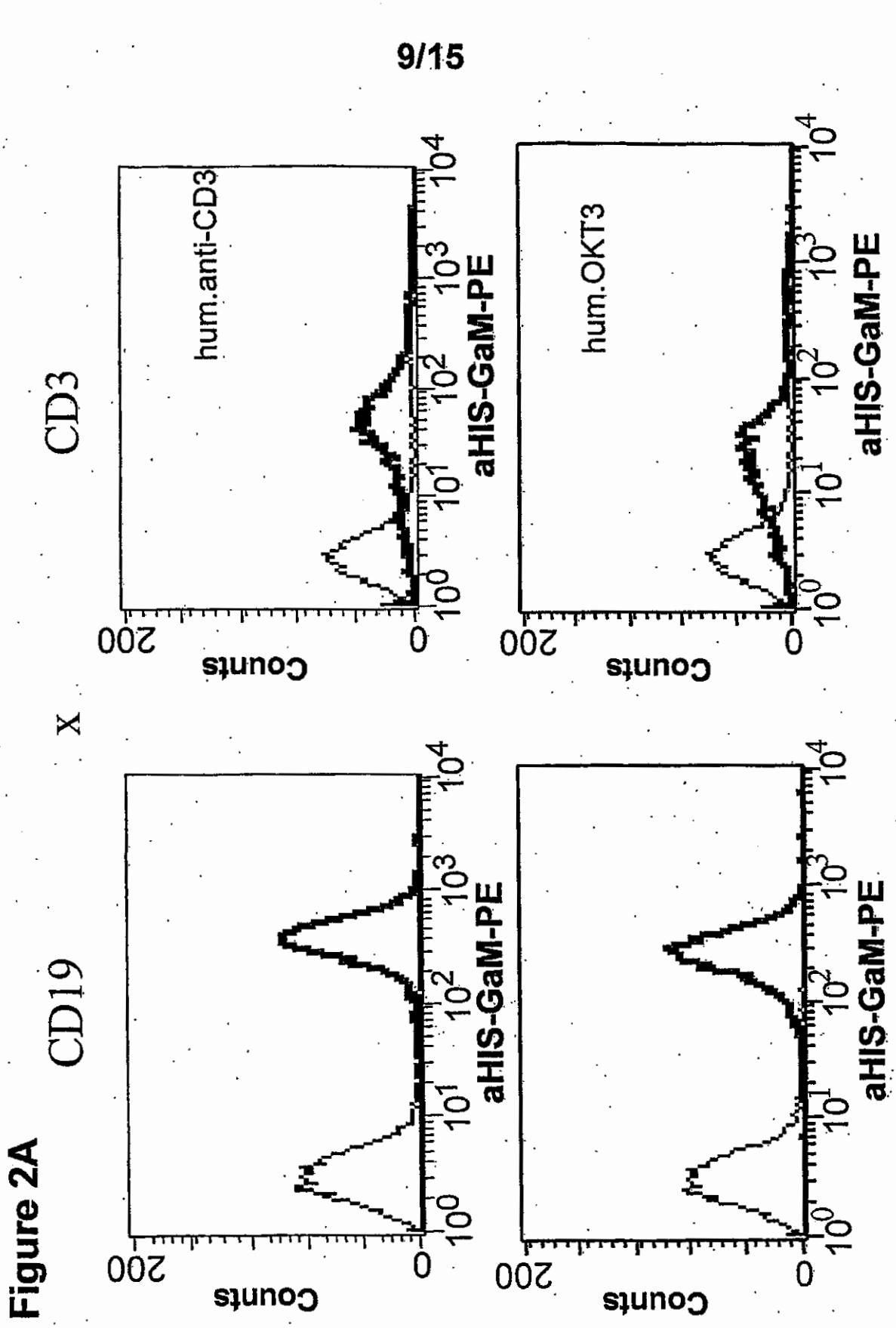
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CTGACTGCAGACAAATCCTCGAGCACAGCCTTTATGCAGCTCAGTAGCCTGACATCTGAGGACTCTGCTGTC
TATTTCTGTGCAAGATTGAGGAACTGGGACGAGGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTC
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CTGAGACTCTCCTGTAAGTCTTCTGGATACACCTTCACTAGGTATACGATGCACTGGGTCCGCCAGGCTCCA
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GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCAGA
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GACACATCCAAAGTGGCTTCTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTACACTTTC
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TTTGGCCAGGGGACCAAGCTGCAGATCACC

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Figure 1D (cont.)

ELVMTQSPSYLAASPGETITINCRASKSISKYLAWYQEKPGKTNKLLIYSGSTLQSGIPSRFSGSGSGTDFT
LTISSLEPEDFAMYYCQQHNEYPYTFGGGTKLEIKGGGGSGGGGSGGGGSEVQLLEQSGAELVKPGASVKIS
CKASGYAFTNYWLGWVKQRPGHGLEWIGDLFPGSGNTHYNERFRGKATLTADKSSSTAFMQLSSLTSEDSAV
YFCARLRNWDEAMDYWGQGTTVTVSSGGGGSQVQLVQSGGGVVQPGRSLRLSCKSSGYTFTRYTMHWVRQAP
GKGLEWIGYINPSRGYTNYNQKVKDRFTISRDNSKNTAFLQMDSLRPEDTGVYFCARYYDDHYCLDYWGQGT
PVTVSSVEGGSGGSGGSGGSGGVDDIQMTQSPSSLSASVGDRVTITCRASSVSYMNWYQQTPGKAPKRWIY
DTSKVASGVPSRFSGSGSGTDYTFTISSLQPEDIATYYCQQWSSNPLTFGQGTKLQIT

Figure 2A


CD19
x
CD3
hum.anti-CD3
hum.OKT3
Counts
aHIS-GaM-PE
0
200
10^0
10^1
10^2
10^3
10^4

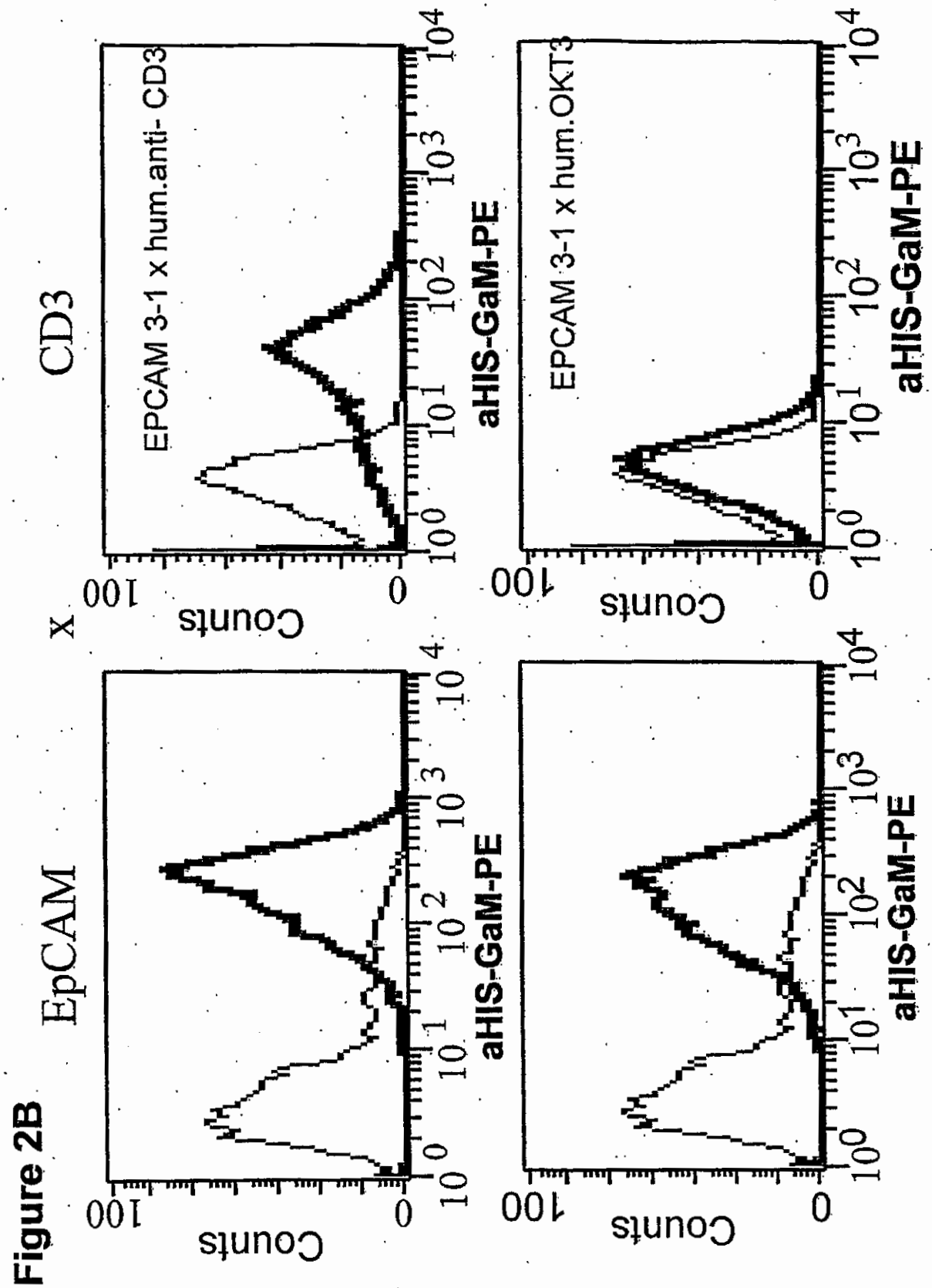

CD3
x
EpCAM
EPCAM 3-1 x hum.anti- CD3
EPCAM 3-1 x hum.OKT3
aHIS-GaM-PE
Counts
100
0
10^0
10^1
10^2
10^3
10^4

Figure 2B

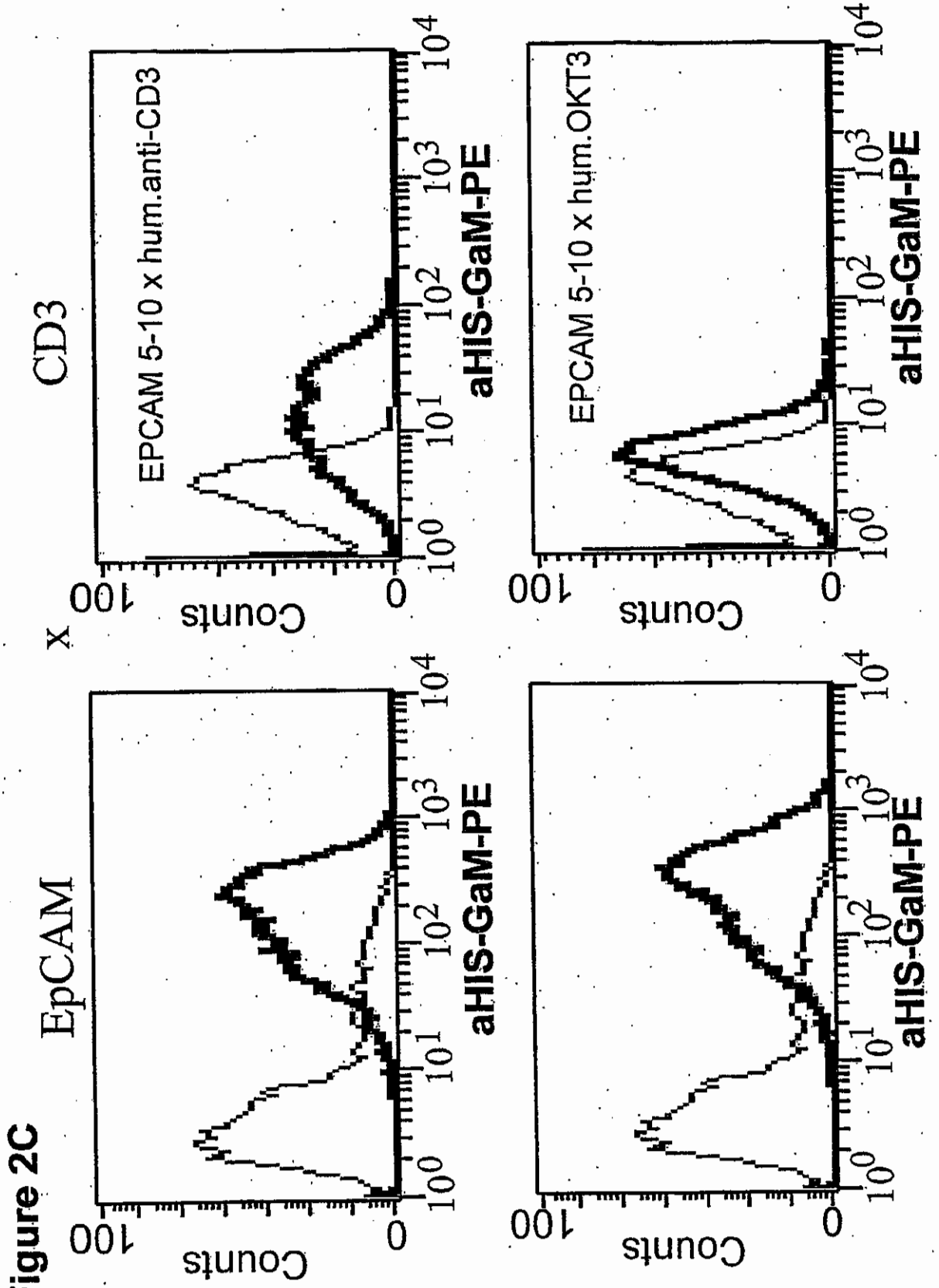

CD3
EpCAM
x
EPCAM 5-10 x hum.anti-CD3
EPCAM 5-10 x hum.OKT3
Counts
100
0
10^0
10^1
10^2
10^3
10^4
aHIS-GaM-PE

Figure 2C

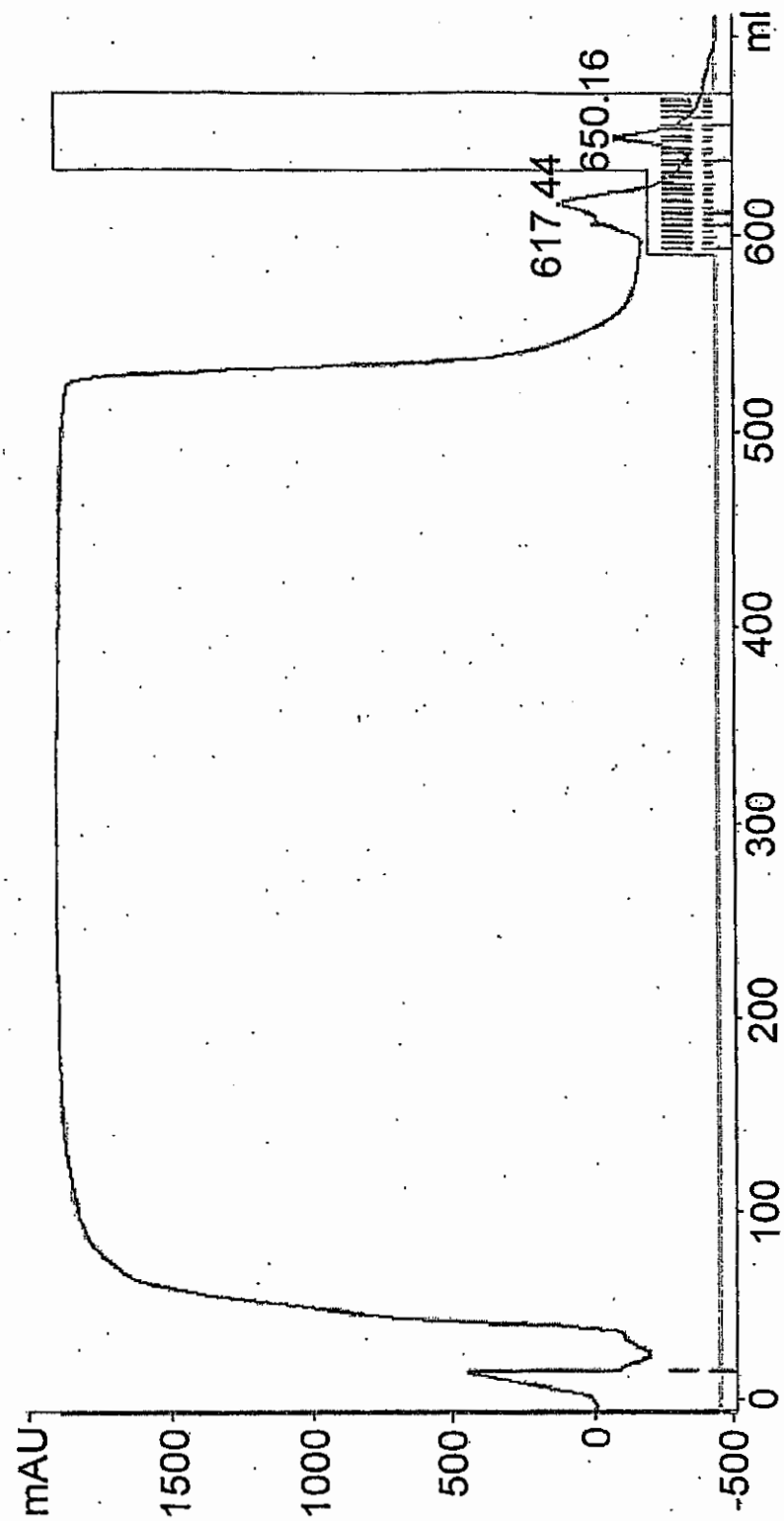


Figure 3

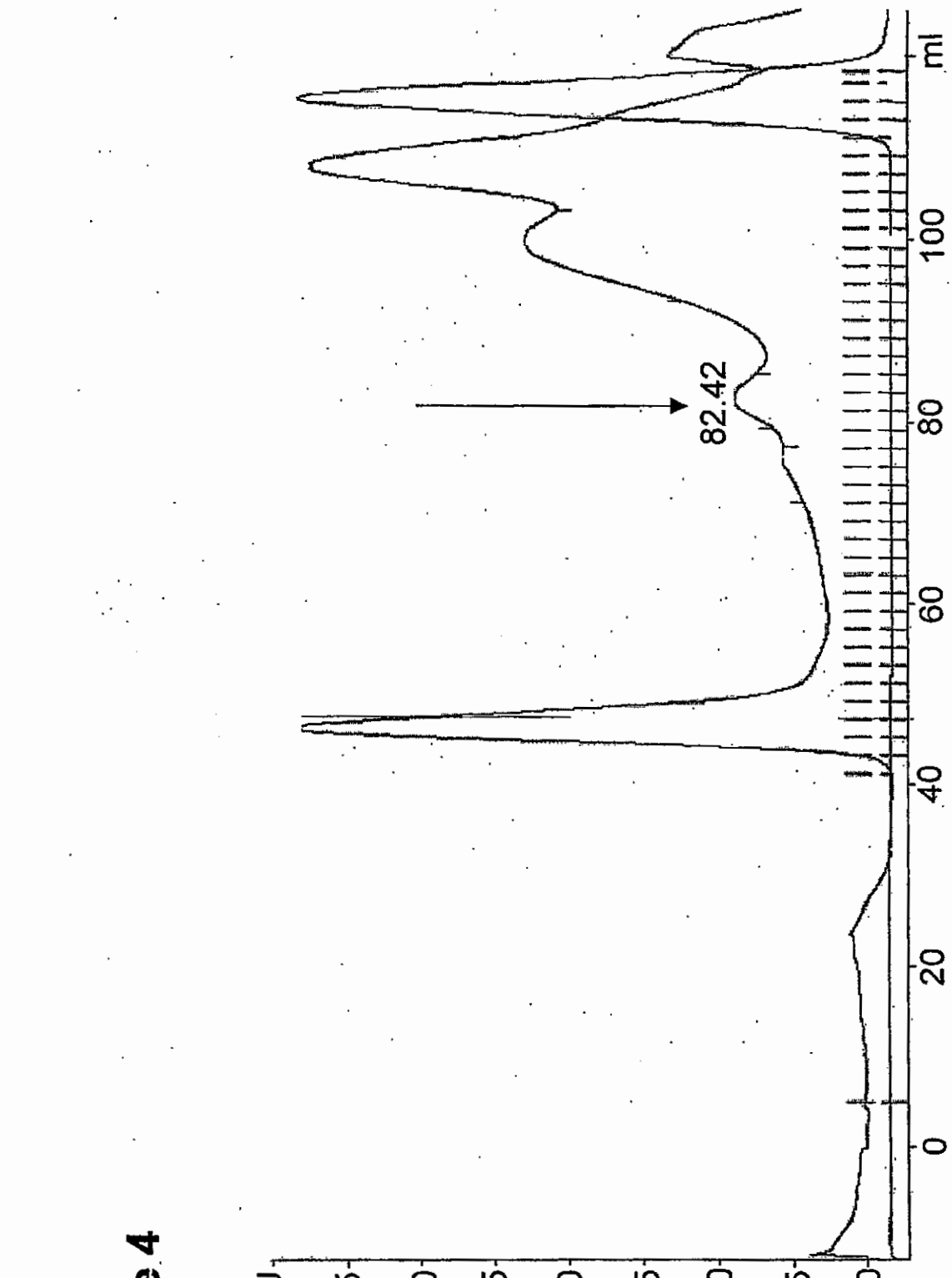
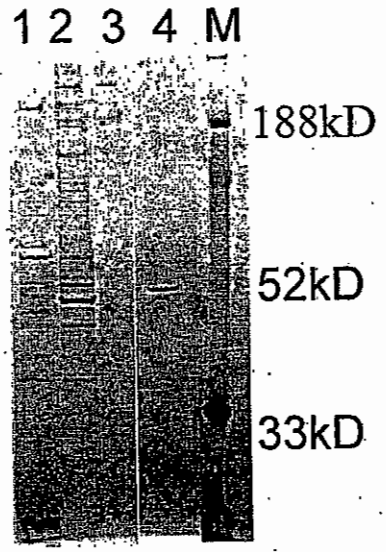


Figure 4

Figure 5



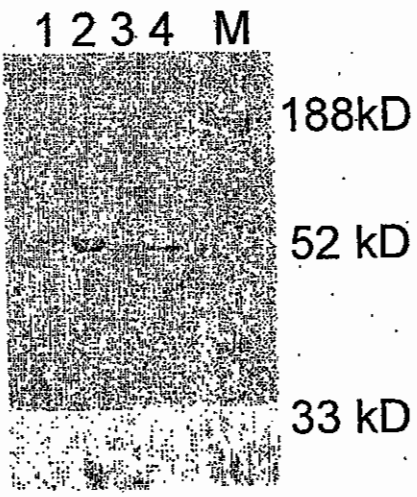
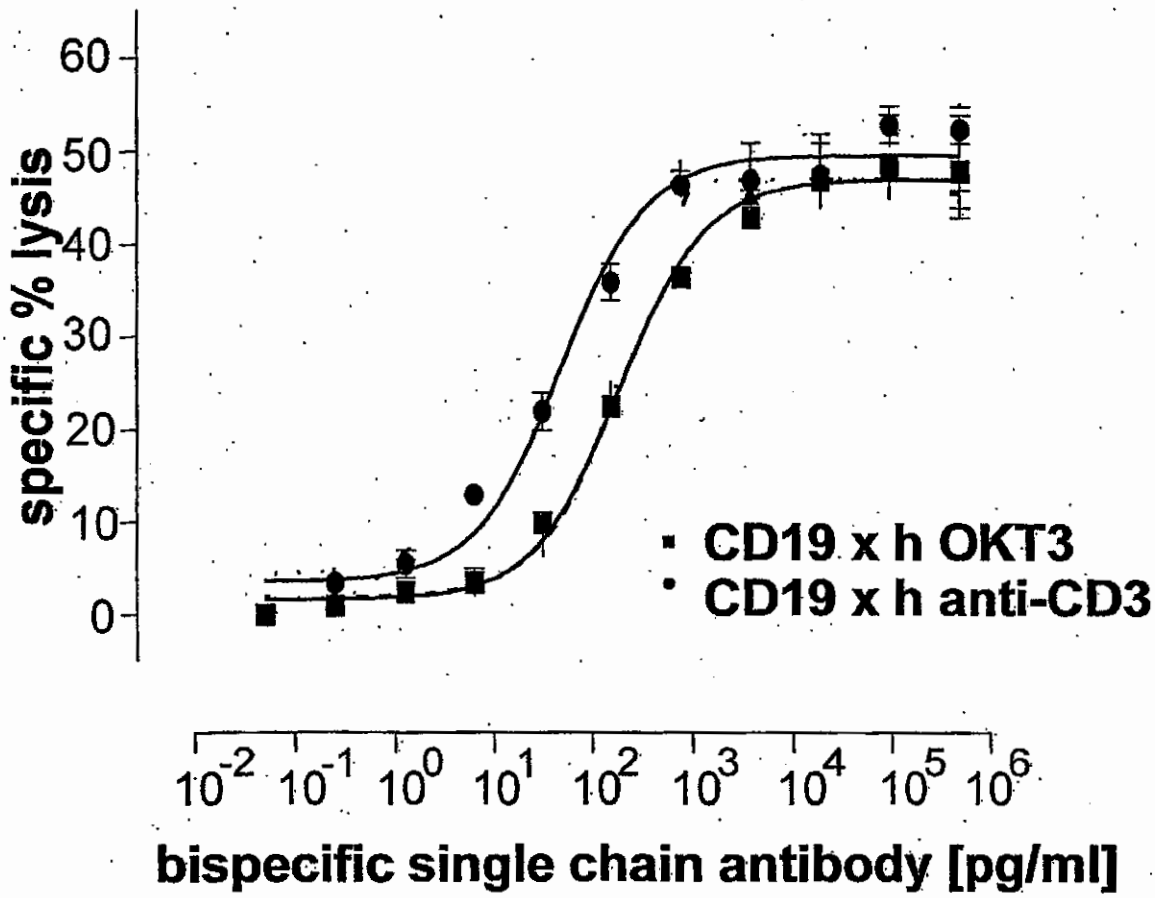


Figure 6


specific % lysis
60
50
40
30
20
10
0
CD19 x h OKT3
CD19 x h anti-CD3
10-2 10-1 100 101 102 103 104 105 106
bispecific single chain antibody [pg/ml]

SEQUENCE LISTING

<110> Micromet AG

<120> Less immunogenic binding molecules

<130> H3150 PCT

<160> 36

<170> PatentIn version 3.1

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atcacttgca gtgcaagttc aagcgtaagc tacatgaatt ggtatcagca gacaccaggg 120

aaagccccta agagatggat ctatgacaca tccaaattgg cttctggggt cccatcaagg 180

ttcagtggca gtggatctgg gacagattac actttcacca tcagcagtct gcaacctgaa 240

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accaagctgc agatcacc 318

<210> 2
<211> 106
<212> PRT
<213> artificial sequence

<220>
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105

<210> 3

<211> 30

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<210> 4

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<223> /note="Description of artificial sequence: hum. CD3 CDRL1"

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<210> 5

<211> 21

<212> DNA

<213> artificial sequence

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<210> 6

<211> 7

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1 5

<210> 7

<211> 27

<212> DNA

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<210> 8

<211> 9

<212> PRT

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1 5

<210> 9

<211> 318

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<213> artificial sequence

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aaagccccta agagatggat ctatgacaca tccaaagtgg cttctggggt cccatcaagg 180

ttcagtggca gtggatctgg gacagattac actttcacca tcagcagtct gcaacctgaa 240

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accaagctgc agatcacc 318

<210> 10

<211> 106

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

5

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
100 105

<210> 11

<211> 357

<212> DNA

<213> artificial sequence

<220>
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ccagggaagg ggctggagtg gattggatac ataaatccta gccgtggtta tactaattat 180

aatcagaagg tgaaggaccg attcaccatc tccagagaca actccaagaa cacggccttt 240

ctgcaaatgg acagcctgag acccgaggac acgggtgtgt atttctgtgc gagatattat 300

gatgatcatt actgccttga ctactggggc cagggcaccc cggtcaccgt ctcctca 357

<210> 12

<211> 119

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: hum. CD3 VH"

<400> 12

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1 5 10 15

Ser Leu Arg Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
50 55 60

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Ala Phe
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Pro Val Thr Val Ser Ser
115

<210> 13

<211> 729

<212> DNA

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<220>
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<223> /note="Description of artificial sequence: hum. CD3 VH-VL"

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ccagggaagg ggctggagtg gattggatac ataaatccta gccgtggtta tactaattat 180

aatcagaagg tgaaggaccg attcaccatc tccagagaca actccaagaa cacggccttt 240

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gaaggtggaa gtggaggttc tggtggaagt ggaggttcag gtggagtgga cgacatccag 420

atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc 480

agagcaagtt caagcgtaag ctacatgaat tggtatcagc agacaccagg gaaagcccct 540

aagagatgga tctatgacac atccaaagtg gcttctgggg tcccatcaag gttcagtggc 600

agtggatctg ggacagatta cactttcacc atcagcagtc tgcaacctga agatattgca 660

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cagatcacc 729

<210> 14

<211> 243

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: hum. CD3 VH-VL"

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1 5 10 15

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20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val
50 55 60

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Ala Phe
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Pro Val Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
115 120 125

Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145 150 155 160

Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro
165 170 175

Gly Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr
195 200 205

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys

210 215 220

Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
225 230 235 240

Gln Ile Thr

<210> 15

<211> 372

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<213> artificial sequence

<220>
<221> source

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<400> 15
caggtgcagc tgcagcagtc tggggctgag ctggtgaggc ctgggtcctc agtgaagatt 60

tcctgcaagg cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

cctggacagg gtcttgagtg gattggacag atttggcctg gagatggtga tactaactac 180

aatggaaagt tcaagggtaa agccactctg actgcagacg aatcctccag cacagcctac 240

atgcaactca gcagcctagc atctgaggac tctgcggtct atttctgtgc aagacgggag 300

actacgacgg taggccgtta ttactatgct atggactact ggggccaagg gaccacggtc 360

accgtctcct cc 372

<210> 16

<211> 124

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: CD19 VH"

<400> 16

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 17

<211> 333

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: CD19 VL"

<400> 17
gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac 120

caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct 180

gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat 240

cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg 300

acgttcggtg gagggaccaa gctcgagatc aaa 333

<210> 18

<211> 111

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: CD19 VL"

<400> 18

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly

```
1               5                  10                  15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
                85                  90                  95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 19

<211> 1494

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: anti-CD19xhum. anti-CD3"

<400> 19

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gatatccagc tgacccagtc tccagcttct ttggctgtgt ctctagggca gagggccacc     60
atctcctgca aggccagcca aagtgttgat tatgatggtg atagttattt gaactggtac    120
caacagattc caggacagcc acccaaactc ctcatctatg atgcatccaa tctagtttct    180
gggatcccac ccaggtttag tggcagtggg tctgggacag acttcaccct caacatccat    240
cctgtggaga aggtggatgc tgcaacctat cactgtcagc aaagtactga ggatccgtgg    300
acgttcggtg gagggaccaa gctcgagatc aaaggtggtg gtggttctgg cggcggcggc    360
tccggtggtg gtggttctca ggtgcagctg cagcagtctg gggctgagct ggtgaggcct    420
gggtcctcag tgaagatttc ctgcaaggct tctggctatg cattcagtag ctactggatg    480
aactgggtga agcagaggcc tggacagggt cttgagtgga ttggacagat ttggcctgga    540
gatggtgata ctaactacaa tggaaagttc aagggtaaag ccactctgac tgcagacgaa    600
tcctccagca cagcctacat gcaactcagc agcctagcat ctgaggactc tgcggtctat    660
ttctgtgcaa gacgggagac tacgacggta ggccgttatt actatgctat ggactactgg    720
ggccaaggga ccacggtcac cgtctcctcc ggaggtggtg gctcccaggt gcagctggtg    780
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cagtctgggg gaggcgtggt ccagcctggg aggtccctga gactctcctg taagtcttct 840

ggatacacct tcactaggta tacgatgcac tgggtccgcc aggctccagg gaaggggctg 900

gagtggattg gatacataaa tcctagccgt ggttatacta attataatca gaaggtgaag 960

gaccgattca ccatctccag agacaactcc aagaacacgg cctttctgca aatggacagc 1020

ctgagacccg aggacacggg tgtgtatttc tgtgcgagat attatgatga tcattactgc 1080

cttgactatt ggggccaggg caccccggtc accgtctcct cagtcgaagg tggaagtgga 1140

ggttctggtg gaagtggagg ttcaggtgga gtggacgaca tccagatgac ccagtctcca 1200

tcctccctgt ctgcatctgt aggagacaga gtcaccatca cttgcagagc aagttcaagc 1260

gtaagctaca tgaattggta tcagcagaca ccagggaaag cccctaagag atggatctat 1320

gacacatcca aagtggcttc tggggtccca tcaaggttca gtggcagtgg atctgggaca 1380

gattacactt tcaccatcag cagtctgcaa cctgaagata ttgcaactta ctactgtcaa 1440

cagtggagta gtaaccctct cacttttggc caggggacca agctgcagat cacc 1494

<210> 20

<211> 498

<212> PRT

<213> artificial sequence

<220>

<221> source

<223> /note="Description of artificial sequence: anti-CD19xhum. anti-CD3"

<400> 20

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val
        115                 120                 125

Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val
    130                 135                 140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met
145                 150                 155                 160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln
                165                 170                 175

Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly
            180                 185                 190

Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln
        195                 200                 205

Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
    210                 215                 220

Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp
225                 230                 235                 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
            260                 265                 270

Leu Arg Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Arg Tyr Thr
        275                 280                 285

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly
    290                 295                 300

Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val Lys
305                 310                 315                 320

Asp Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Ala Phe Leu
                325                 330                 335

Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala
            340                 345                 350

Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr
        355                 360                 365

Pro Val Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly
    370                 375                 380
```

Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Met Thr Gln Ser Pro
385 390 395 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
405 410 415

Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly
420 425 430

Lys Ala Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly
435 440 445

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe
450 455 460

Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
465 470 475 480

Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Gln
485 490 495

Ile Thr

<210> 21

<211> 360

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 5-10 VH"

<400> 21
gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60

atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180

tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaatcttc gagcacagcc 240

tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300

aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctcc 360

<210> 22

<211> 120

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 5-10 VH"

<400> 22

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 23

<211> 339

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 5-10 VL"

<400> 23
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

tggtaccagc agaaaccagg gcagcctcct aaactgttga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg gaacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtcagaatga ttatagttat 300

ccgctcacgt tcggtgctgg gaccaagctt gagatcaaa 339

<210> 24

<211> 113

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 5-10 VL"

<400> 24

Glu Leu Val Met Thr Gln Ser Pro Ser Ser Leu Thr Val Thr Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 25

<211> 360

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 3-1 VH"

<400> 25
gaggtgcagc tgctcgagca gtctggagct gagctggtga aacctggggc ctcagtgaag 60

atatcctgca aggcttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120

aggcctggac atggacttga gtggattgga gatcttttcc ctggaagtgg taatactcac 180

tacaatgaga ggttcagggg caaagccaca ctgactgcag acaaatcctc gagcacagcc 240

tttatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300

aggaactggg acgaggctat ggactactgg ggccaaggga ccacggtcac cgtctcctcc 360

<210> 26

<211> 120

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 3-1 VH"

<400> 26

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 27

<211> 321

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 3-1 VL"

<400> 27
gagctcgtca tgacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact 60

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 120

gggaaaacta ataagcttct tatctactct ggatccactt tgcaatctgg aattccatca 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 240

gaagattttg caatgtatta ctgtcaacag cataatgaat atccgtacac gttcggaggg 300

gggaccaagc ttgagatcaa a 321

<210> 28

<211> 107

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 3-1 VL"

<400> 28

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1 5 10 15

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 29

<211> 372

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 4-7 VH"

<400> 29
gaggtgcagc tgctcgagca gtctggagct gagctggcga ggcctggggc ttcagtgaag 60

ctgtcctgca aggcttctgg ctacaccttc acaaactatg gtttaagctg ggtgaagcag 120

aggcctggac aggtccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180

tacaatgaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcg 240

tccatggagc tccgcagcct gacctctgag gactctgcgg tctatttctg tgcaagacgg 300

ggatcctacg atactaacta cgactggtac ttcgatgtct ggggccaagg gaccacggtc 360

accgtctcct cc 372

<210> 30

<211> 124

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 4-7 VH"

<400> 30

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp
35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 31

<211> 336

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 4-7 VL"

<400> 31
gagctcgtga tgacccagac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tacctgcaga agccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300

tacacgttcg gaggggggac caagcttgag atcaaa 336

<210> 32

<211> 112

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: 4-7 VL"

<400> 32

Glu Leu Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys 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

20

65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 33

<211> 1470

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: anti-EpCAM (3-1)xhum. anti-CD3"

<400> 33
gagctcgtca tgacccagtc tccatcttat cttgctgcat ctcctggaga aaccattact 60

attaattgca gggcaagtaa gagcattagc aaatatttag cctggtatca agagaaacct 120

gggaaaacta ataagcttct tatctactct ggatccactt tgcaatctgg aattccatca 180

aggttcagtg gcagtggatc tggtacagat ttcactctca ccatcagtag cctggagcct 240

gaagattttg caatgtatta ctgtcaacag cataatgaat atccgtacac gttcggaggg 300

gggaccaagc ttgagatcaa aggtggtggt ggttctggcg gcggcggctc cggtggtggt 360

ggttctgagg tgcagctgct cgagcagtct ggagctgagc tggtgaaacc tggggcctca 420

gtgaagatat cctgcaaggc ttctggatac gccttcacta actactggct aggttgggta 480

aagcagaggc ctggacatgg acttgagtgg attggagatc ttttccctgg aagtggtaat 540

actcactaca atgagaggtt caggggcaaa gccacactga ctgcagacaa atcctcgagc 600

acagccttta tgcagctcag tagcctgaca tctgaggact ctgctgtcta tttctgtgca 660

agattgagga actgggacga ggctatggac tactggggcc aagggaccac ggtcaccgtc 720

tcctccggag gtggtggatc ccaggtgcag ctggtgcagt ctgggggagg cgtggtccag 780

cctgggaggt ccctgagact ctcctgtaag tcttctggat acaccttcac taggtatacg 840

atgcactggg tccgccaggc tccagggaag gggctggagt ggattggata cataaatcct 900

agccgtggtt atactaatta taatcagaag gtgaaggacc gattcaccat ctccagagac 960

aactccaaga acacggcctt tctgcaaatg gacagcctga gacccgagga cacgggtgtg 1020

tatttctgtg cgagatatta tgatgatcat tactgccttg actattgggg ccagggcacc 1080

ccggtcaccg tctcctcagt cgaaggtgga agtggaggtt ctggtggaag tggaggttca 1140

ggtggagtgg acgacatcca gatgacccag tctccatcct ccctgtctgc atctgtagga 1200

gacagagtca ccatcacttg cagagcaagt tcaagcgtaa gctacatgaa ttggtatcag 1260

cagacaccag ggaaagcccc taagagatgg atctatgaca catccaaagt ggcttctggg 1320

gtcccatcaa ggttcagtgg cagtggatct gggacagatt acactttcac catcagcagt 1380

ctgcaacctg aagatattgc aacttactac tgtcaacagt ggagtagtaa ccctctcact 1440

tttggccagg ggaccaagct gcagatcacc 1470

<210> 34

<211> 490

<212> PRT

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: anti-EpCAM (3-1)xhum. anti-CD3"

<400> 34

Glu Leu Val Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
1 5 10 15

Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu
115 120 125

Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser
130 135 140

Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Trp Leu Gly Trp Val
145 150 155 160

Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Leu Phe Pro

165 170 175

Gly Ser Gly Asn Thr His Tyr Asn Glu Arg Phe Arg Gly Lys Ala Thr
180 185 190

Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe Met Gln Leu Ser Ser
195 200 205

Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Leu Arg Asn
210 215 220

Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
225 230 235 240

Ser Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Gly
245 250 255

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ser Ser
260 265 270

Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Arg Gln Ala Pro
275 280 285

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr
290 295 300

Thr Asn Tyr Asn Gln Lys Val Lys Asp Arg Phe Thr Ile Ser Arg Asp
305 310 315 320

Asn Ser Lys Asn Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
325 330 335

Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys
340 345 350

Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Val Glu
355 360 365

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp
370 375 380

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
385 390 395 400

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
405 410 415

Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
420 425 430

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
435 440 445

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
450 455 460

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
465 470 475 480

Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
485 490

<210> 35

<211> 1488

<212> DNA

<213> artificial sequence

<220>
<221> source

<223> /note="Description of artificial sequence: anti-EpCAM (5-10)xhum. anti-CD3"

<400> 35
gagctcgtga tgacacagtc tccatcctcc ctgactgtga cagcaggaga gaaggtcact 60

atgagctgca agtccagtca gagtctgtta aacagtggaa atcaaaagaa ctacttgacc 120

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<223> /note="Description of artificial sequence: anti-EpCAM (5-10)xhum. anti-CD3"

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Gly Asn Gln Lys Asn Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Asn
85 90 95

Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
130 135 140

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
145 150 155 160

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
165 170 175

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gln Val Gln
245 250 255

Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
260 265 270

Leu Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His
275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile
290 295 300

Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Val Lys Asp Arg
305 310 315 320

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Ala Phe Leu Gln Met
325 330 335

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Tyr
340 345 350

Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Pro Val
355 360 365

Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
370 375 380

Gly Ser Gly Gly Val Asp Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
385 390 395 400

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
405 410 415

Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Thr Pro Gly Lys Ala
420 425 430

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Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro
        435                 440                 445

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
    450                 455                 460

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp
465                 470                 475                 480

Ser Ser Asn Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr
                485                 490                 495
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