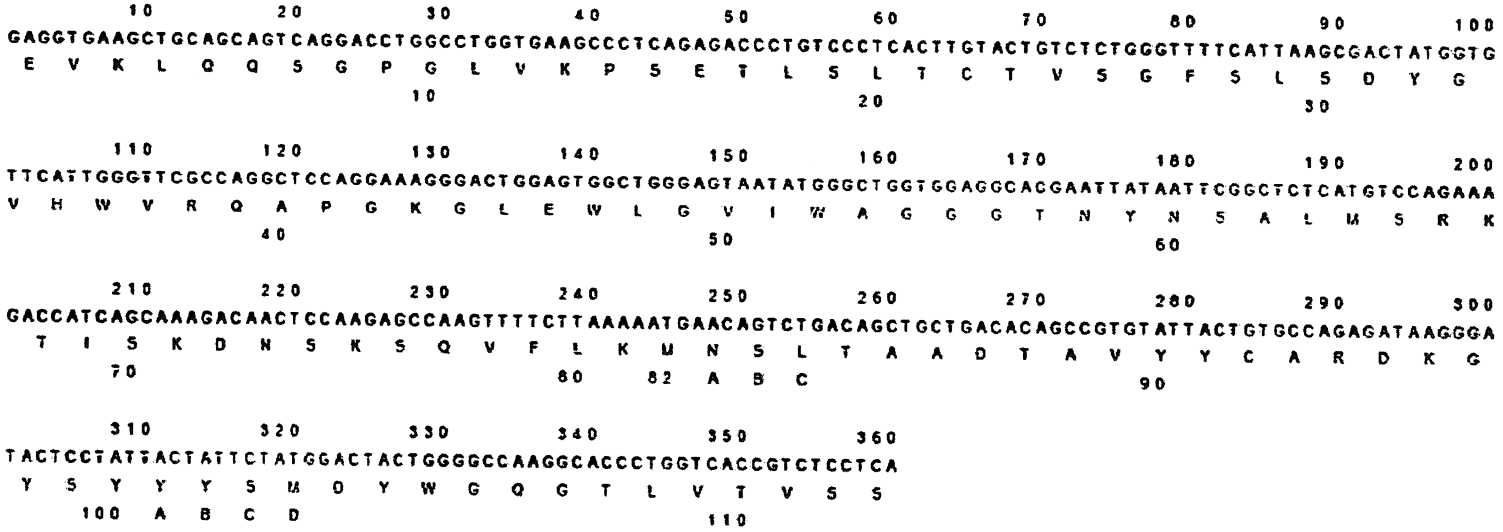
FIGURE 1

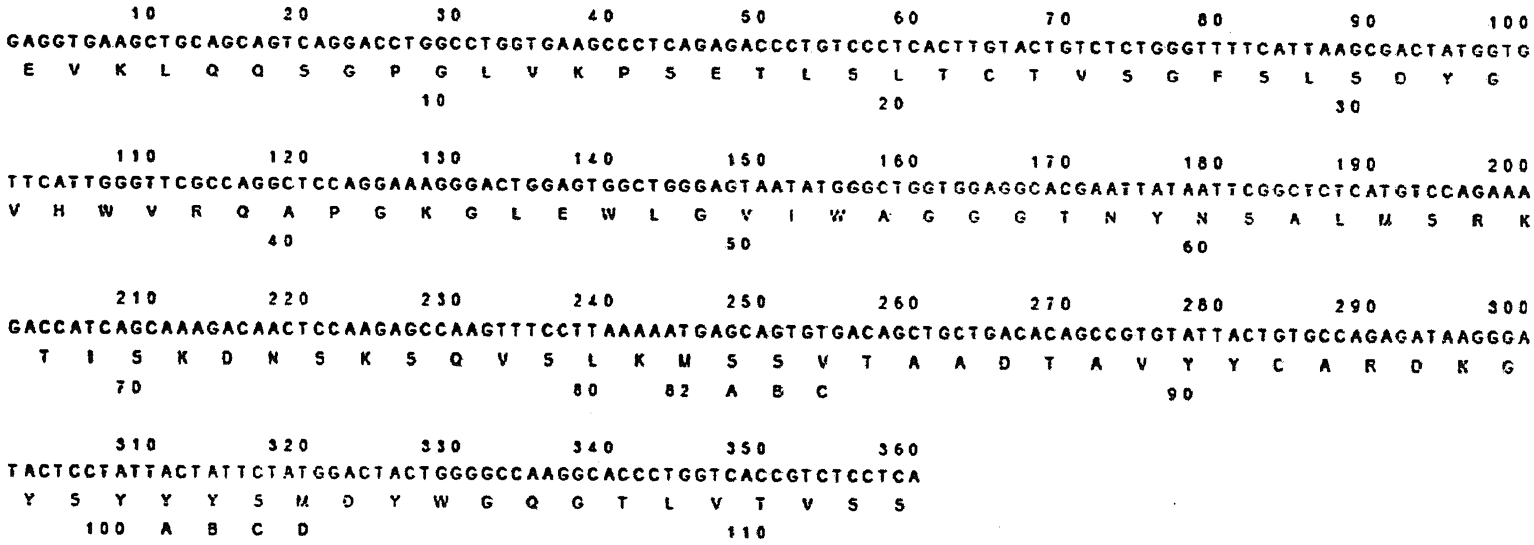
Anti-CD28 VH1 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 2

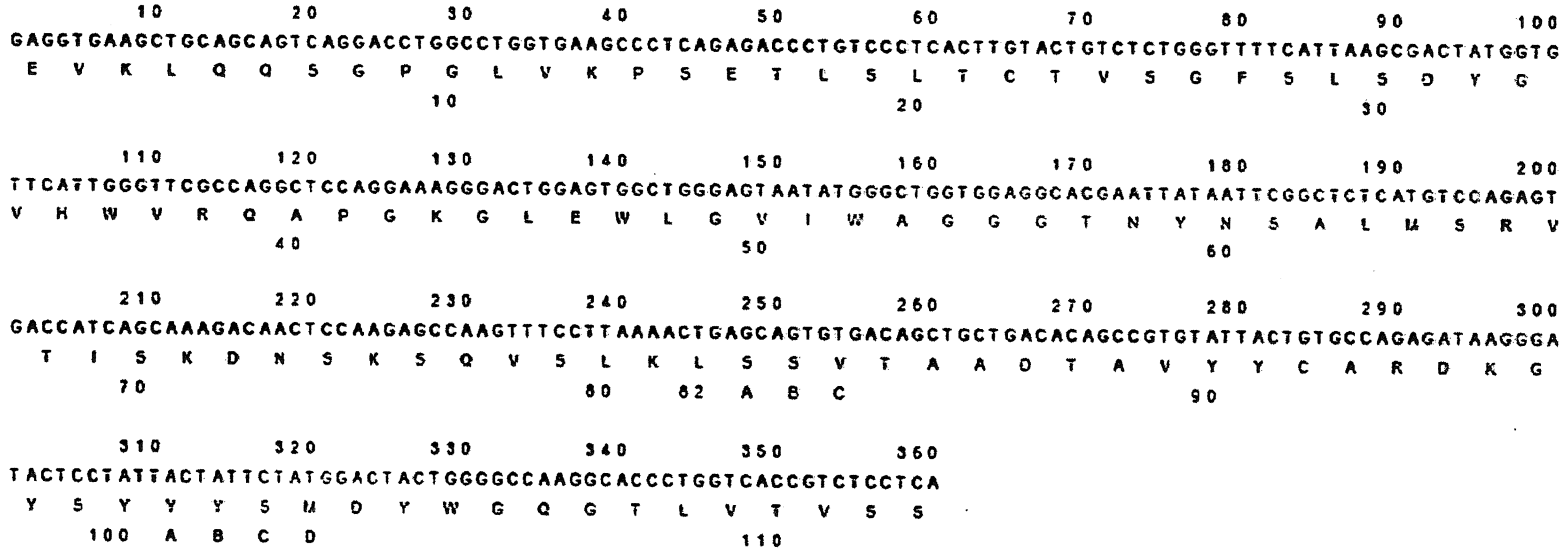
Anti-CD28 VH2 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 3

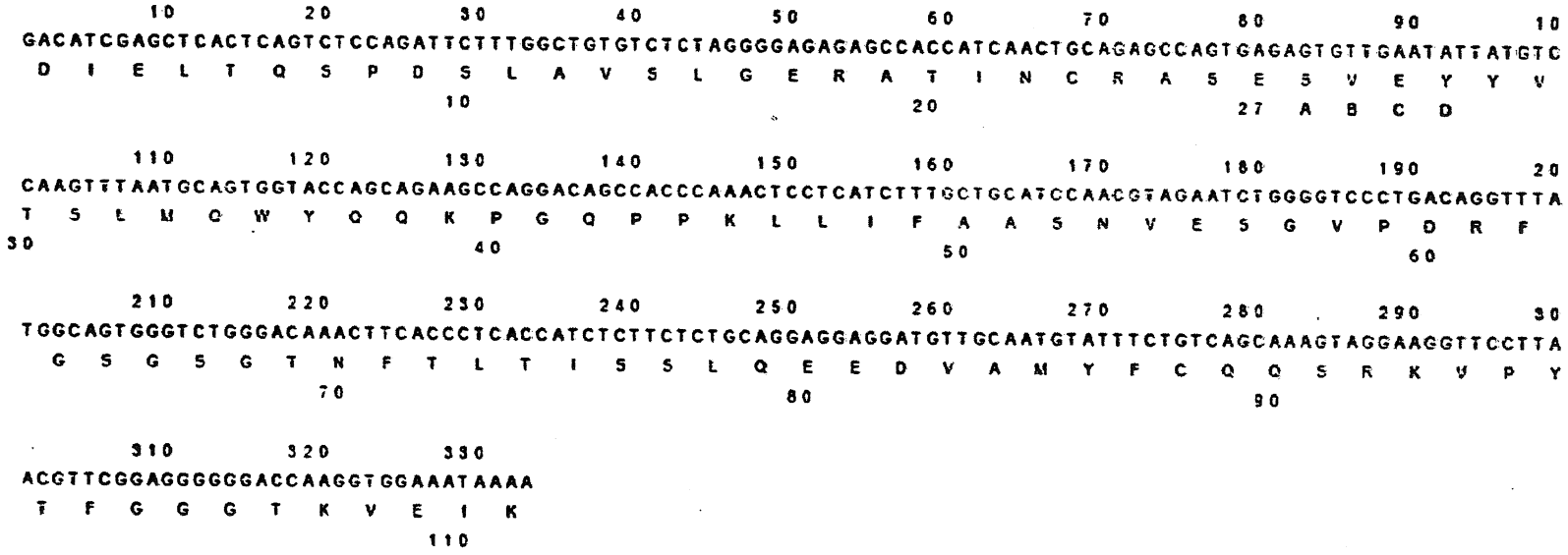
Anti-CD28 VH3 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red.

FIGURE 4

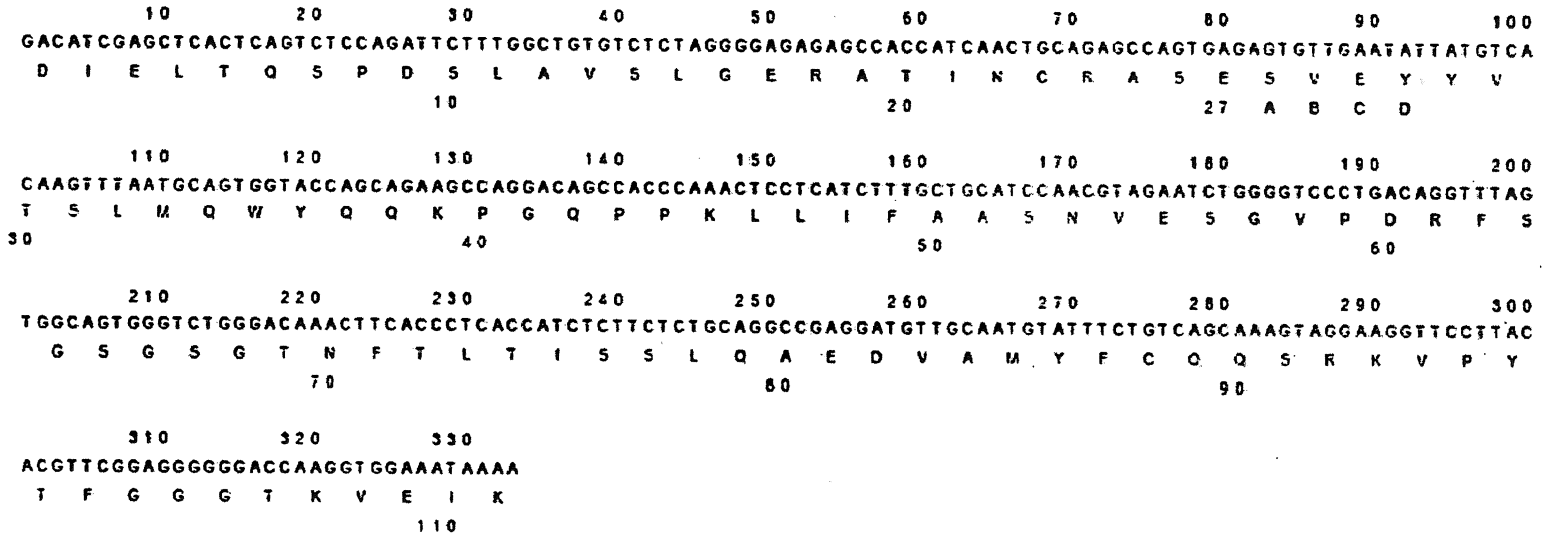
Anti-CD28 VK1 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 5

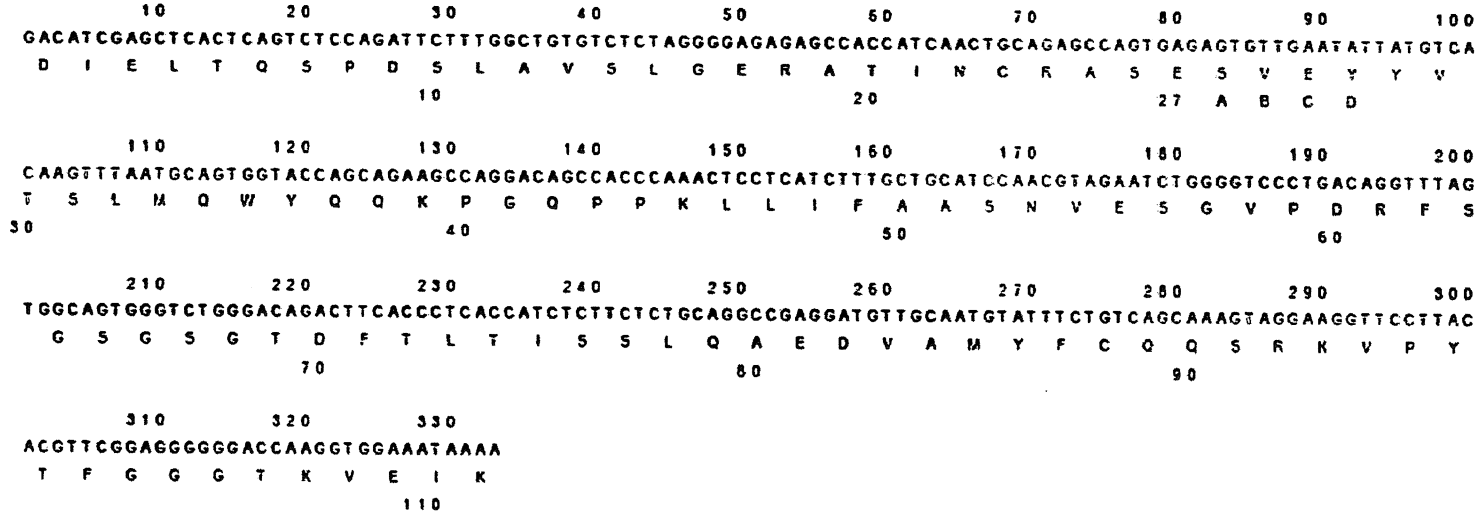
Anti-CD28 VK2 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 6

Anti-CD28 VK3 Sequences



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 7

Modified Constant Heavy:

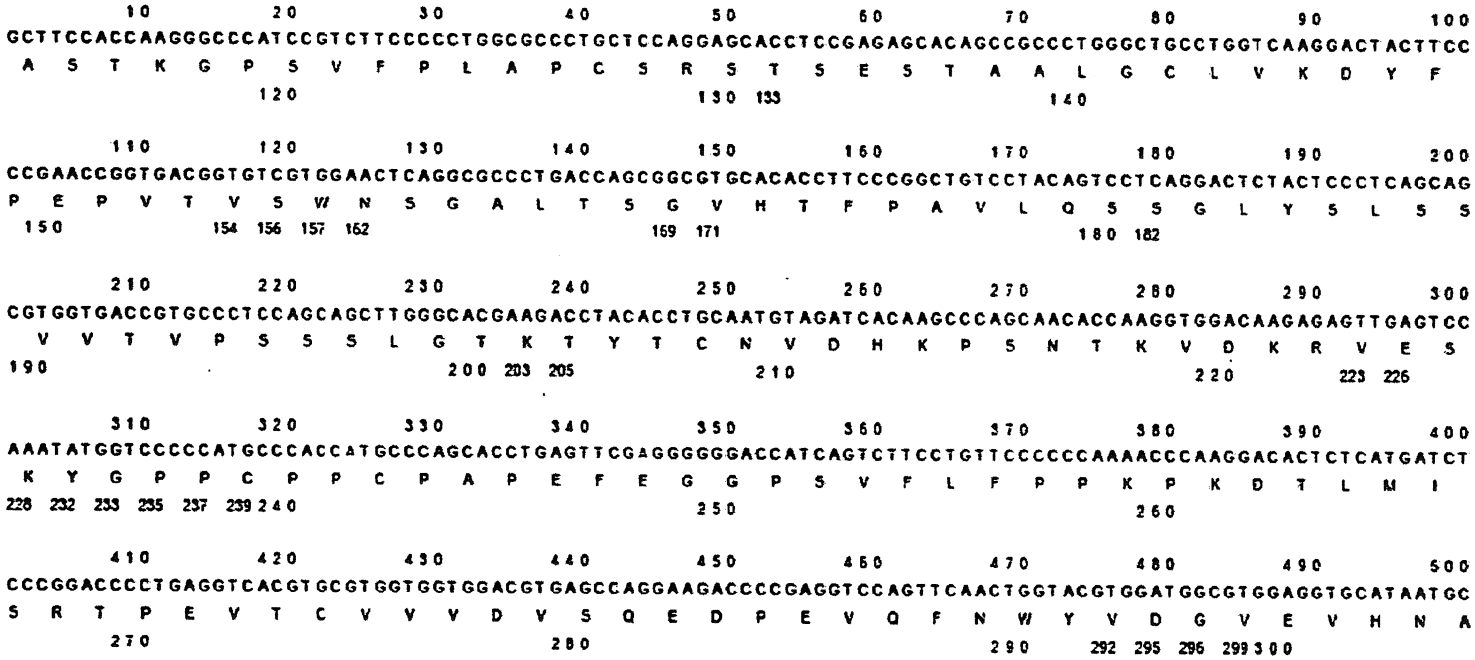
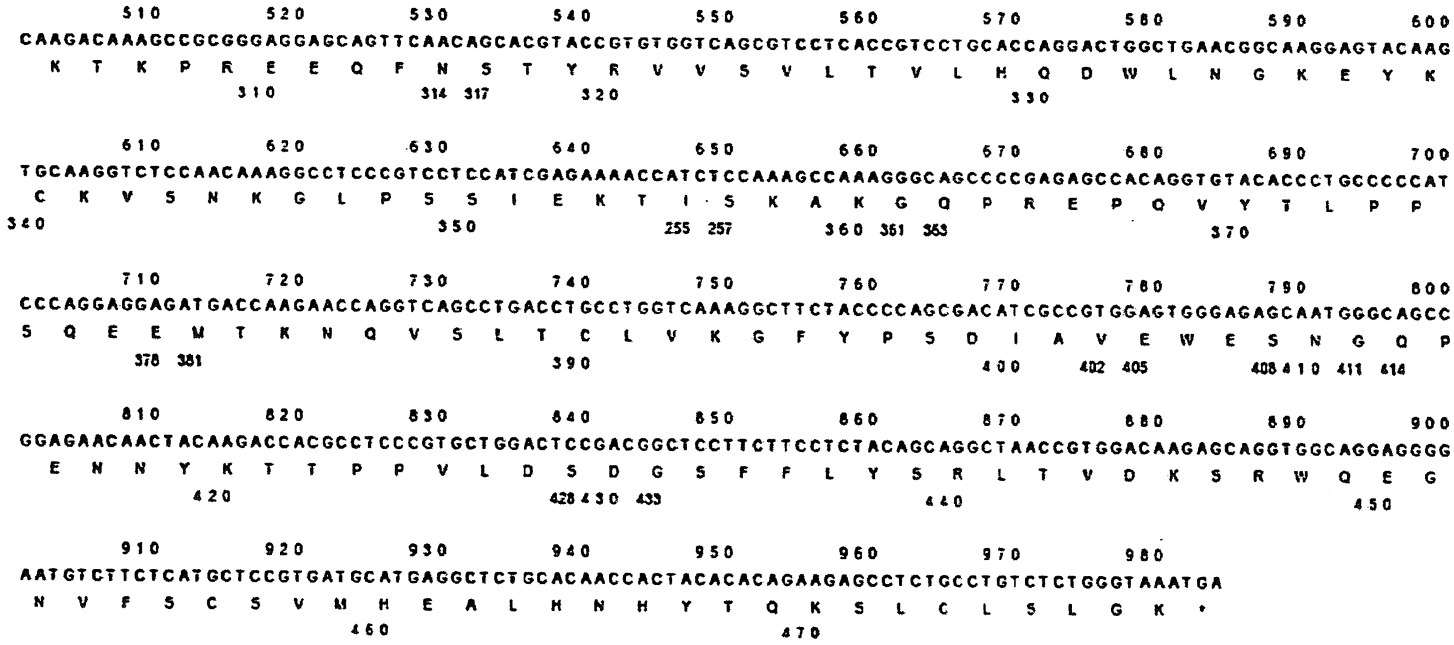


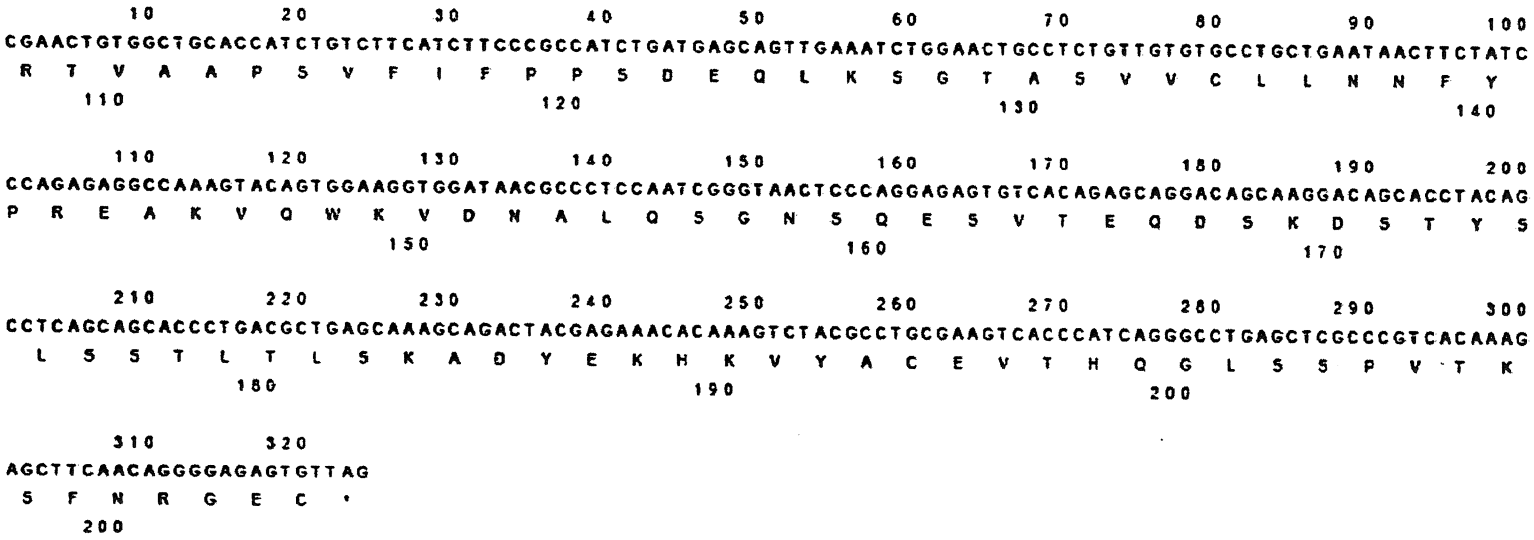
FIGURE 7 (continued)



Protein sequence numbering according to Kabat. Mutations are highlighted red.

FIGURE 8

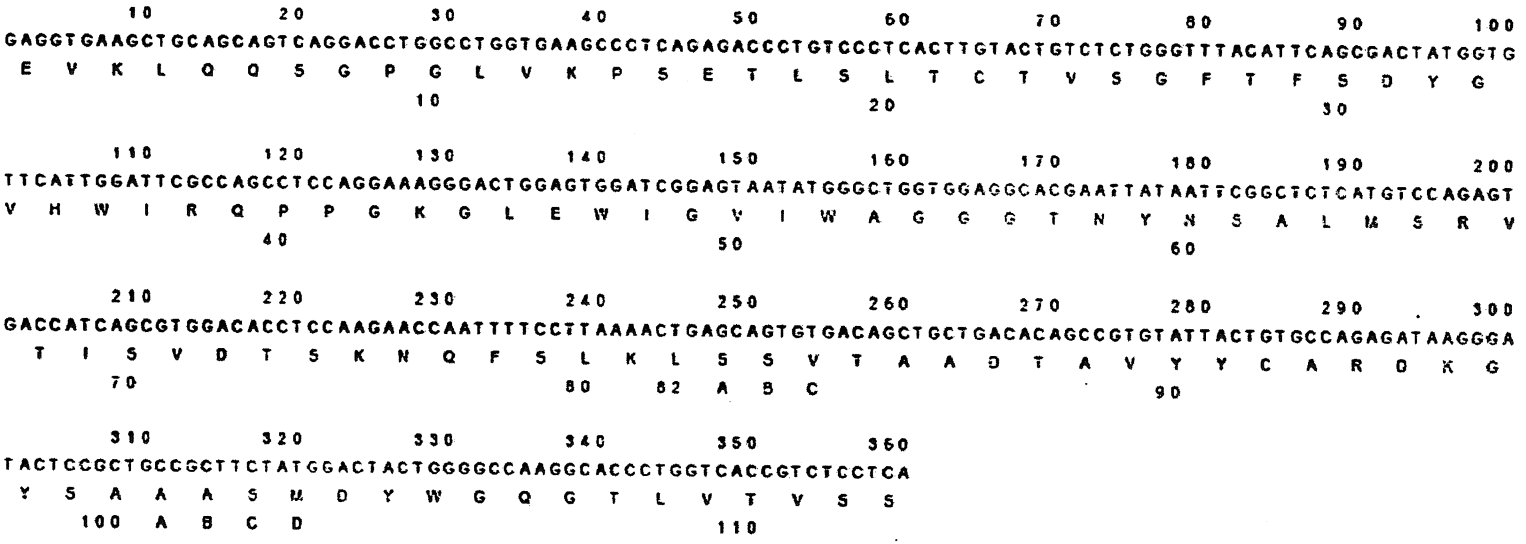
Constant κ Light:



Protein sequence numbering according to Kabat.

FIGURE 9

Potential Non-Antigen Binding Humanised Variant



CDR definitions and protein sequence numbering according to Kabat. CDR nucleotide and protein sequences are highlighted in red

FIGURE 10

```
Gln Val Gln Leu Thr Arg Glu Gly Ser Gly Ser His Ser Met Arg Tyr
1               5                  10                  15

Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile
            20                  25                  30

Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
        35                  40                  45

Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu
    50                  55                  60

Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser
65                  70                  75                  80

Gln Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln
                85                  90                  95

Ser Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val
            100                 105                 110

Gly Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp
        115                 120                 125

Gly Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala
    130                 135                 140

Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His
145                 150                 155                 160

Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp
                165                 170                 175

Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp
            180                 185                 190

Ala Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala
        195                 200                 205

Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu
    210                 215                 220
```

FIGURE 10, continued

```
Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
225                 230                 235                 240

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
                245                 250                 255

Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His
            260                 265                 270

Glu Gly Leu Pro Lys Pro Leu Thr Trp Ala Arg Glu Val Ser Glu Val
        275                 280                 285

Lys Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
    290                 295                 300

Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Ser Asp Tyr Gly Val
305                 310                 315                 320

His Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Val
                325                 330                 335

Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg
            340                 345                 350

Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
        355                 360                 365

Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp
    370                 375                 380

Lys Gly Tyr Ser Ala Ala Ala Ser Met Asp Tyr Trp Gly Gln Gly Thr
385                 390                 395                 400

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                405                 410                 415

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
            420                 425                 430

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
```

FIGURE 10, continued

```
        435                 440                 445

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    450                 455                 460

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
465                 470                 475                 480

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
                485                 490                 495

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
            500                 505                 510

Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
        515                 520                 525

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
    530                 535                 540

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
545                 550                 555                 560

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                565                 570                 575

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
            580                 585                 590

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
        595                 600                 605

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
    610                 615                 620

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
625                 630                 635                 640

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                645                 650                 655
```

FIGURE 10, continued

```
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
           660                 665                 670

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
       675                 680                 685

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
   690                 695                 700

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
705                 710                 715                 720

His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
               725                 730
```

FIGURE 11

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

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

Val Thr Ser Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

FIGURE 12

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

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

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80

Lys Met Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220
```

FIGURE 12, continued

```
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
        435                 440                 445
```

FIGURE 13

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asp Tyr
            20                  25                  30

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

Gly Val Ile Trp Ala Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Lys Thr Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Ser Leu
65                  70                  75                  80

Lys Met Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Lys Gly Tyr Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205
```

FIGURE 13, continued

```
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
    210                 215                 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
```

FIGURE 13, continued

```
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys
        435                 440                 445
```

FIGURE 14

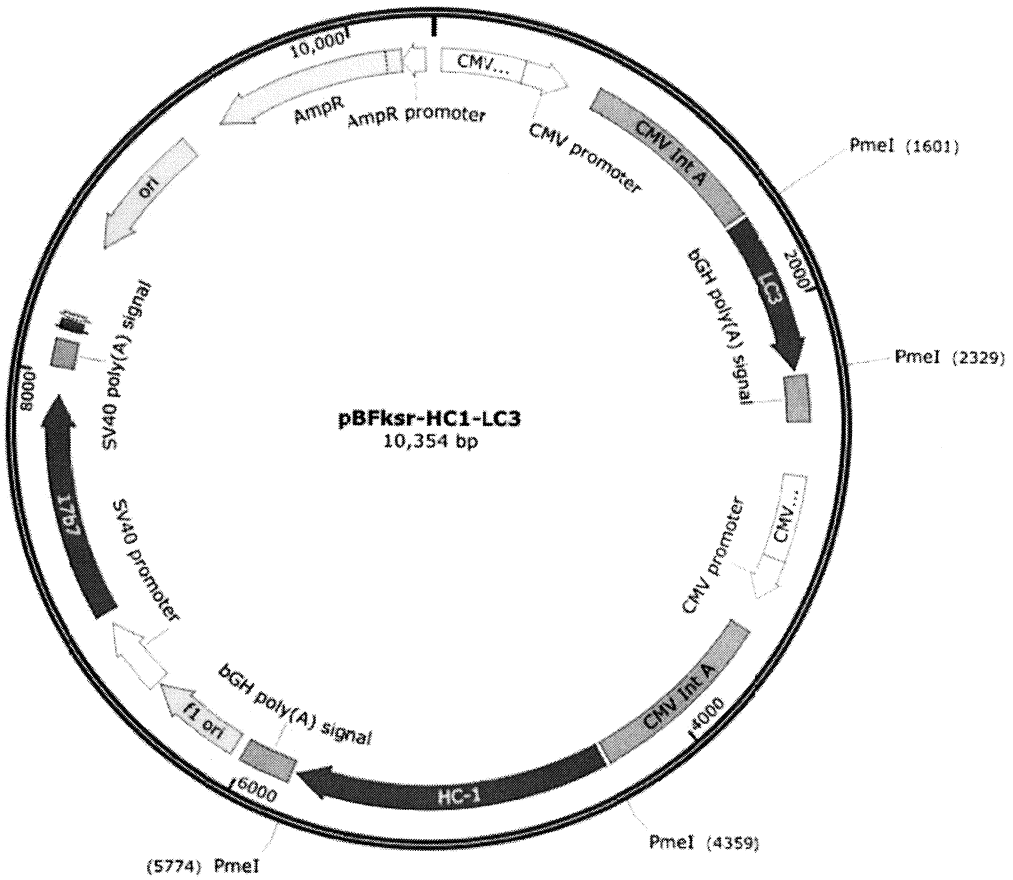

pBFksr-HC1-LC3
10,354 bp
10,000
AmpR
AmpR promoter
CMV...
CMV promoter
CMV Int A
PmeI (1601)
2000
LC3
bGH poly(A) signal
PmeI (2329)
CMV...
CMV promoter
CMV Int A
4000
HC-1
PmeI (4359)
6000
bGH poly(A) signal
f1 ori
SV40 promoter
TRZ
8000
SV40 poly(A) signal
ori
(5774) PmeI

FIGURE 15

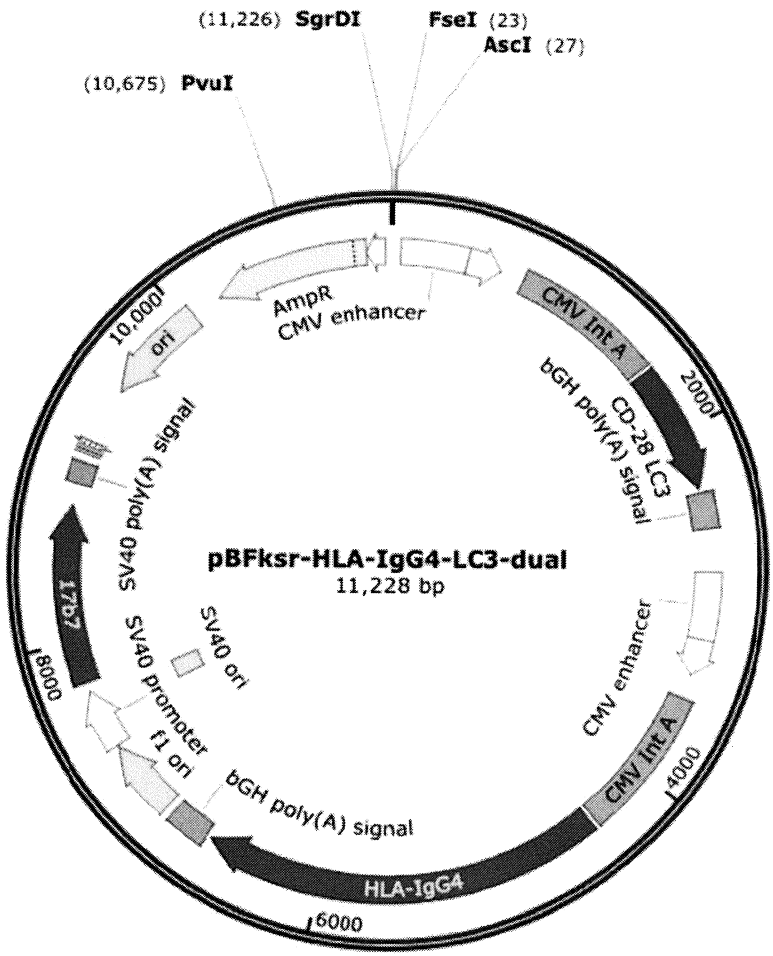

(11,226) SgrDI
FseI (23)
AscI (27)
(10,675) PvuI
AmpR
CMV enhancer
CMV Int A
bGH poly(A) signal
CD-28 LC3
2000
pBFksr-HLA-IgG4-LC3-dual
11,228 bp
CMV enhancer
CMV Int A
4000
HLA-IgG4
6000
bGH poly(A) signal
f1 ori
SV40 promoter
SV40 ori
8000
LTR7
SV40 poly(A) signal
ori
10,000

FIGURE 16

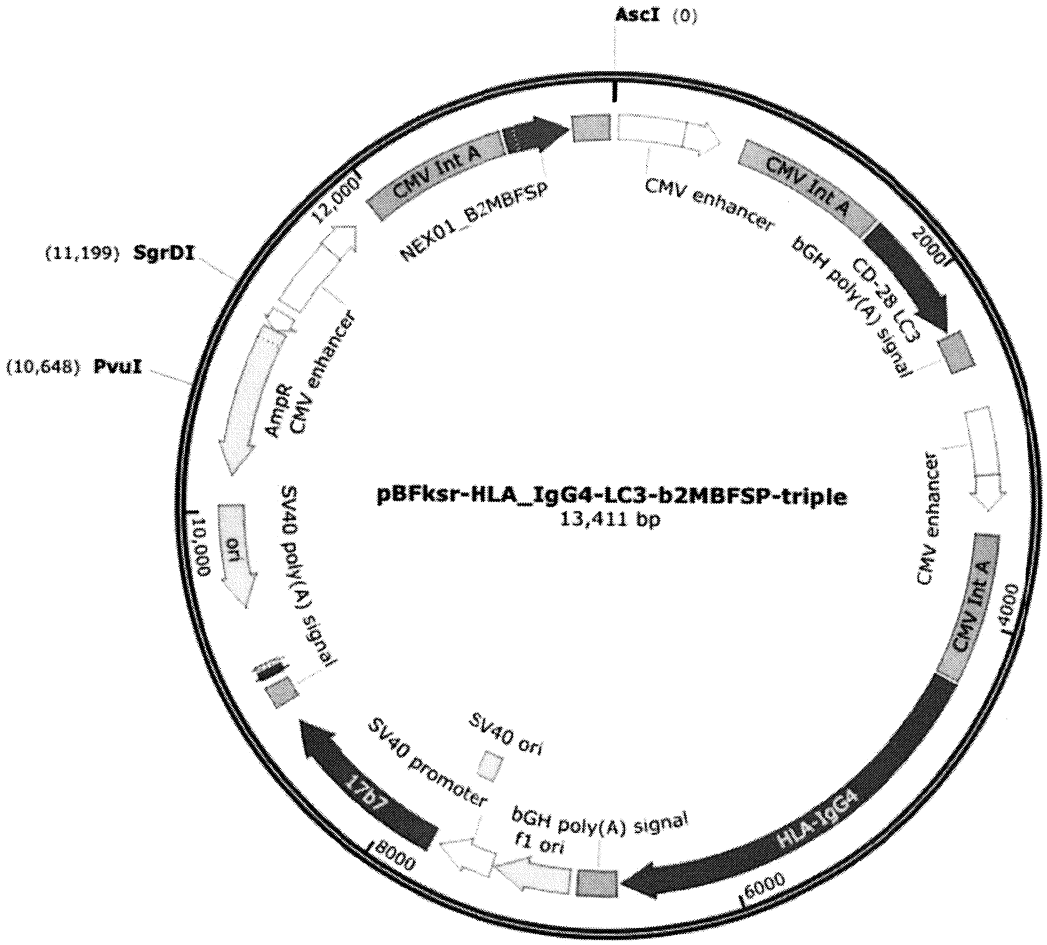

AscI (0)
CMV Int A
NEX01_B2MBFSP
CMV enhancer
CMV Int A
bGH poly(A) signal
CD-28 LC3
2000
CMV enhancer
CMV Int A
4000
HLA-IgG4
6000
bGH poly(A) signal
f1 ori
SV40 ori
SV40 promoter
1767
8000
SV40 poly(A) signal
ori
10,000
AmpR
CMV enhancer
12,000
(11,199) SgrDI
(10,648) PvuI
pBFksr-HLA_IgG4-LC3-b2MBFSP-triple
13,411 bp

FIGURE 17

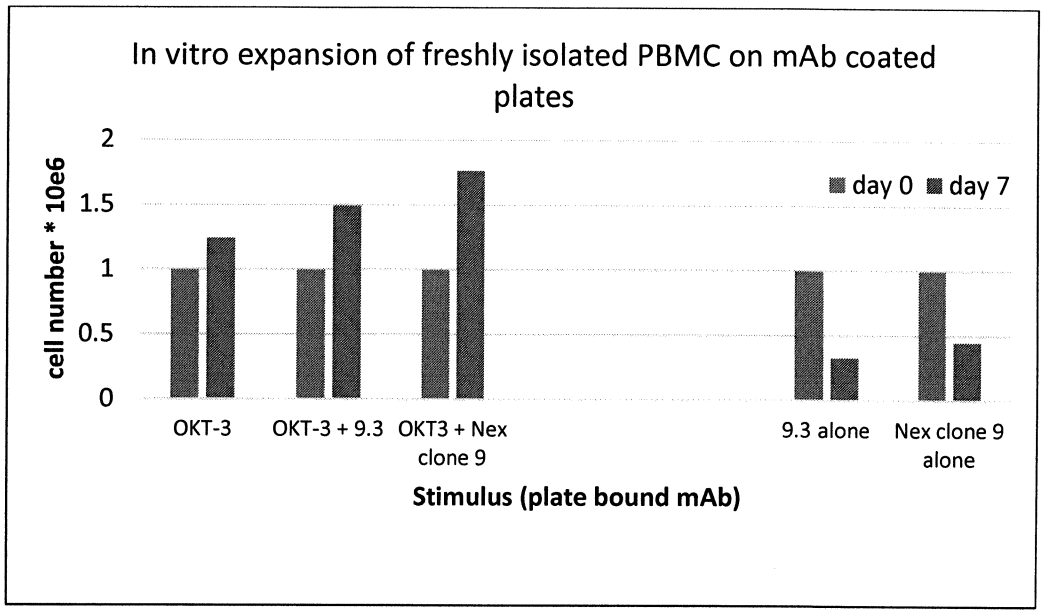
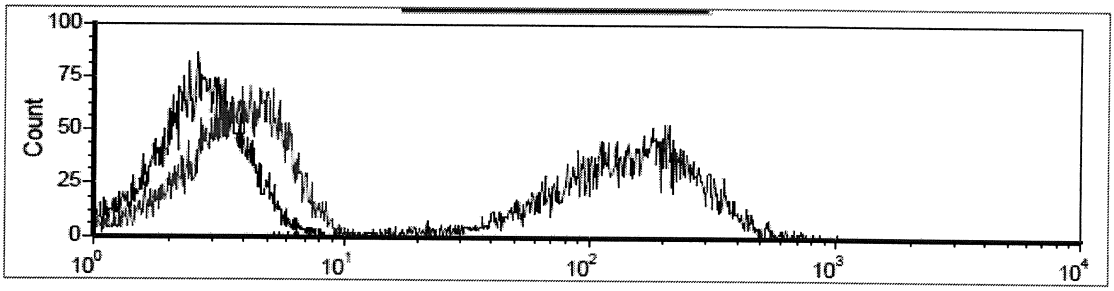

In vitro expansion of freshly isolated PBMC on mAb coated plates
cell number * 10e6
2
1.5
1
0.5
0
day 0
day 7
OKT-3
OKT-3 + 9.3
OKT3 + Nex clone 9
9.3 alone
Nex clone 9 alone
Stimulus (plate bound mAb)

FIGURE 18

A


100
75
50
25
0
Count
10^0
10^1
10^2
10^3
10^4

B

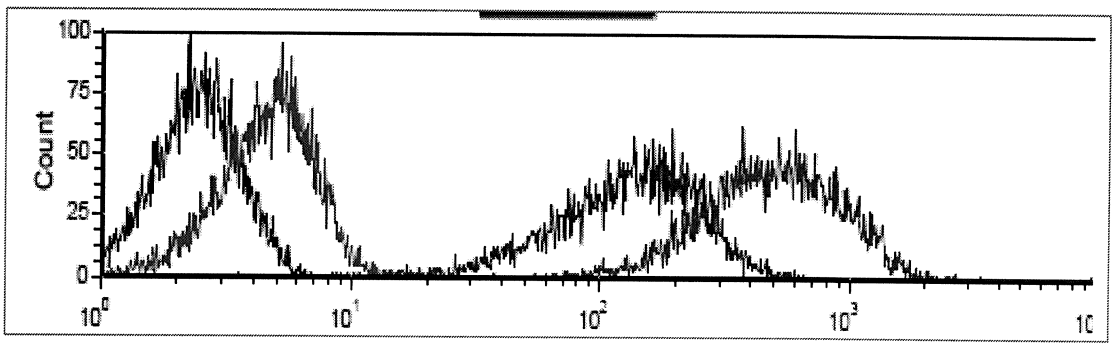

100
75
50
25
0
Count
10^0
10^1
10^2
10^3
10

FIGURE 19

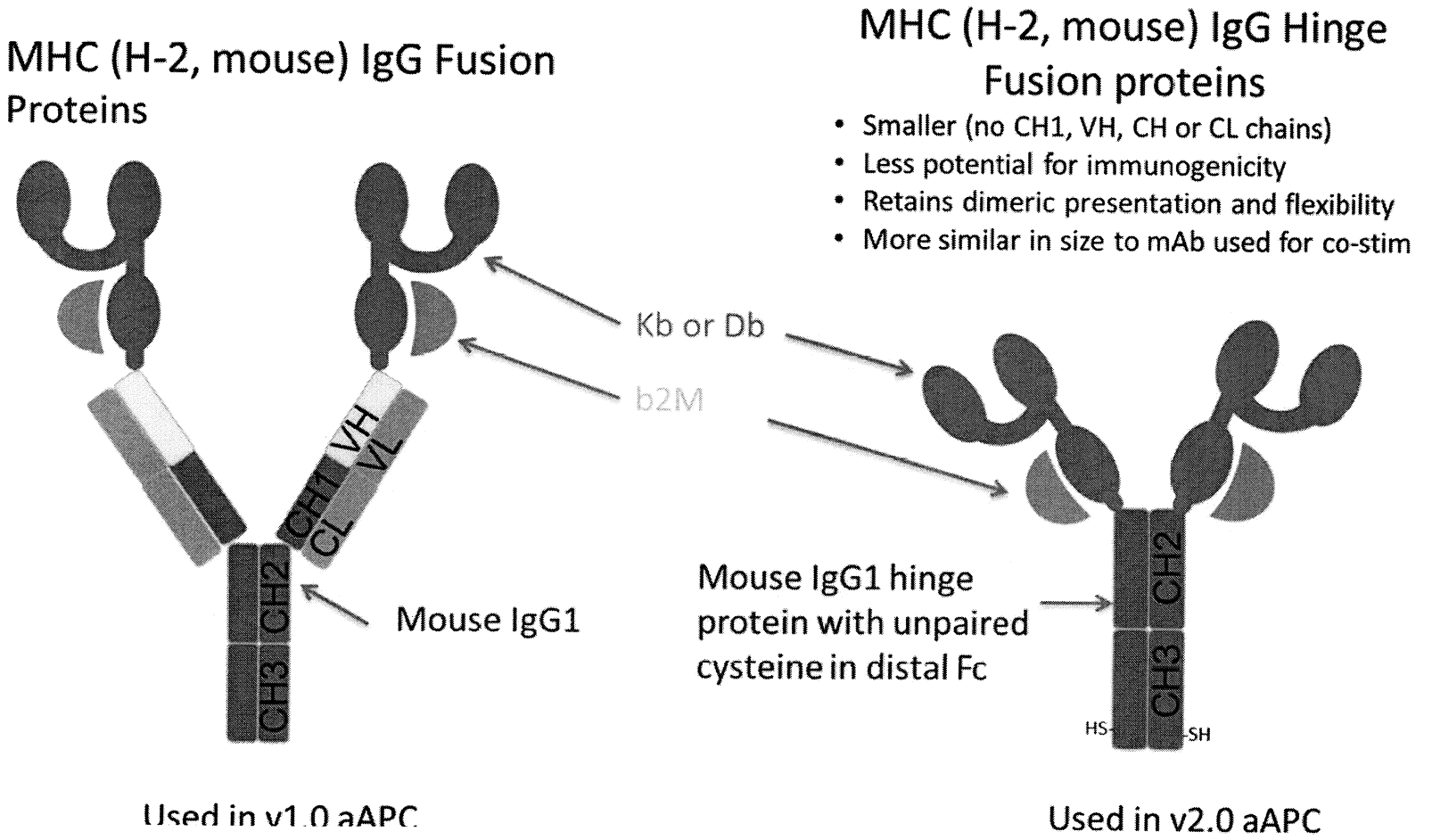
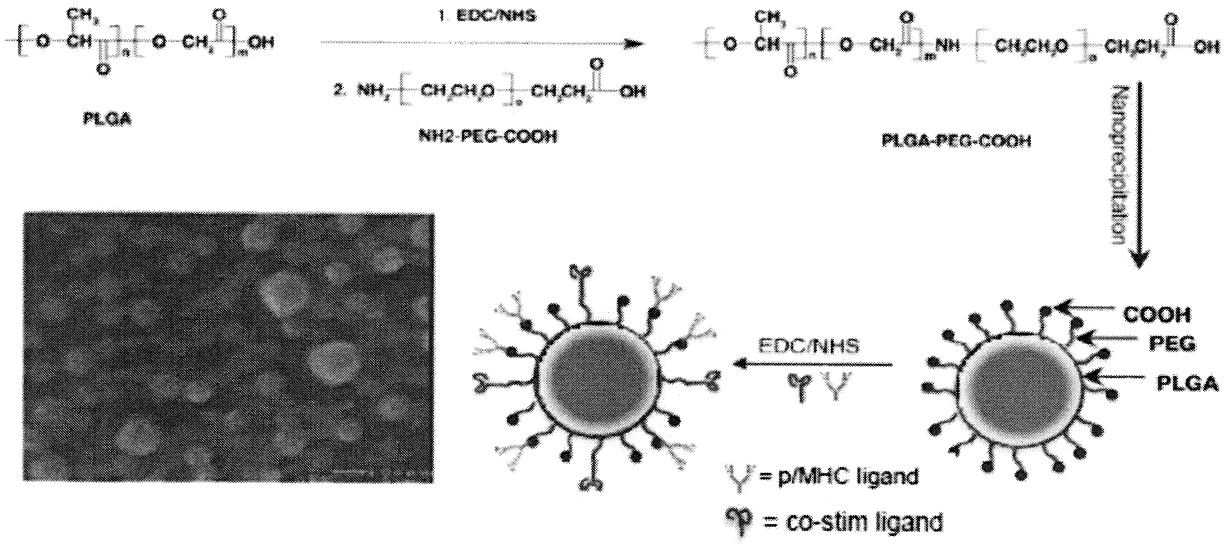

MHC (H-2, mouse) IgG Fusion Proteins
MHC (H-2, mouse) IgG Hinge Fusion proteins
• Smaller (no CH1, VH, CH or CL chains)
• Less potential for immunogenicity
• Retains dimeric presentation and flexibility
• More similar in size to mAb used for co-stim
Kb or Db
b2M
VH
VL
CH1
CL
CH2
CH3
Mouse IgG1
Mouse IgG1 hinge protein with unpaired cysteine in distal Fc
HS
SH
Used in v1.0 aAPC
Used in v2.0 aAPC

FIGURE 20



Batch	Composition	Ratio	Size	ζ (mV)	% Ligand	Active	Stable
PLGA	PLGA 40K	1.0	200 nm	-30 mV	H2-Ig 20% α-CD28 20%	+	N
63A	PLGA-PEG-COOH 40K/3K PLGA-mPEG 17K/3K	0.2 0.8	115 nm	-5 mV	H2-Ig > 50% α-CD28 > 50%	++	Y

- PLGA-PEG is biocompatible and recognized by FDA as safe for use in humans
- PEG provides "stealth" layer to prevent removal from circulation by phagocytic cells for better PK/PD
- Nano-size (<200 nm) allows distribution to target tissues (lymph nodes, spleen, tumor sites)
- Polymer composition provides long elimination half-life and infrequent dosing

FIGURE 21

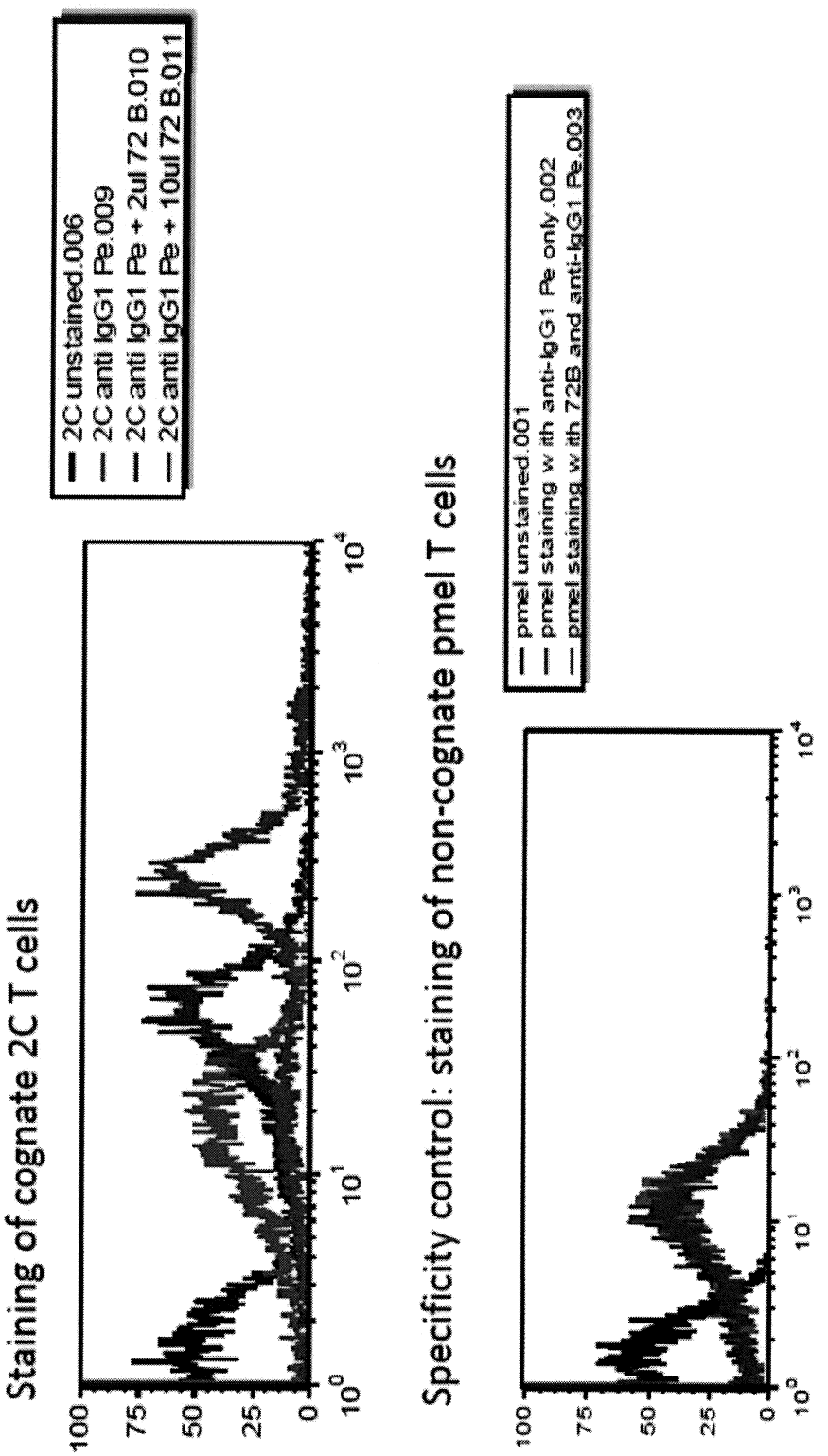

Staining of cognate 2C T cells
2C unstained.006
2C anti IgG1 Pe.009
2C anti IgG1 Pe + 2ul 72 B.010
2C anti IgG1 Pe + 10ul 72 B.011
100
75
50
25
0
10^0
10^1
10^2
10^3
10^4
Specificity control: staining of non-cognate pmel T cells
pmel unstained.001
pmel staining with anti-IgG1 Pe only.002
pmel staining with 72B and anti-IgG1 Pe.003
100
75
50
25
0
10^0
10^1
10^2
10^3
10^4

FIGURE 22

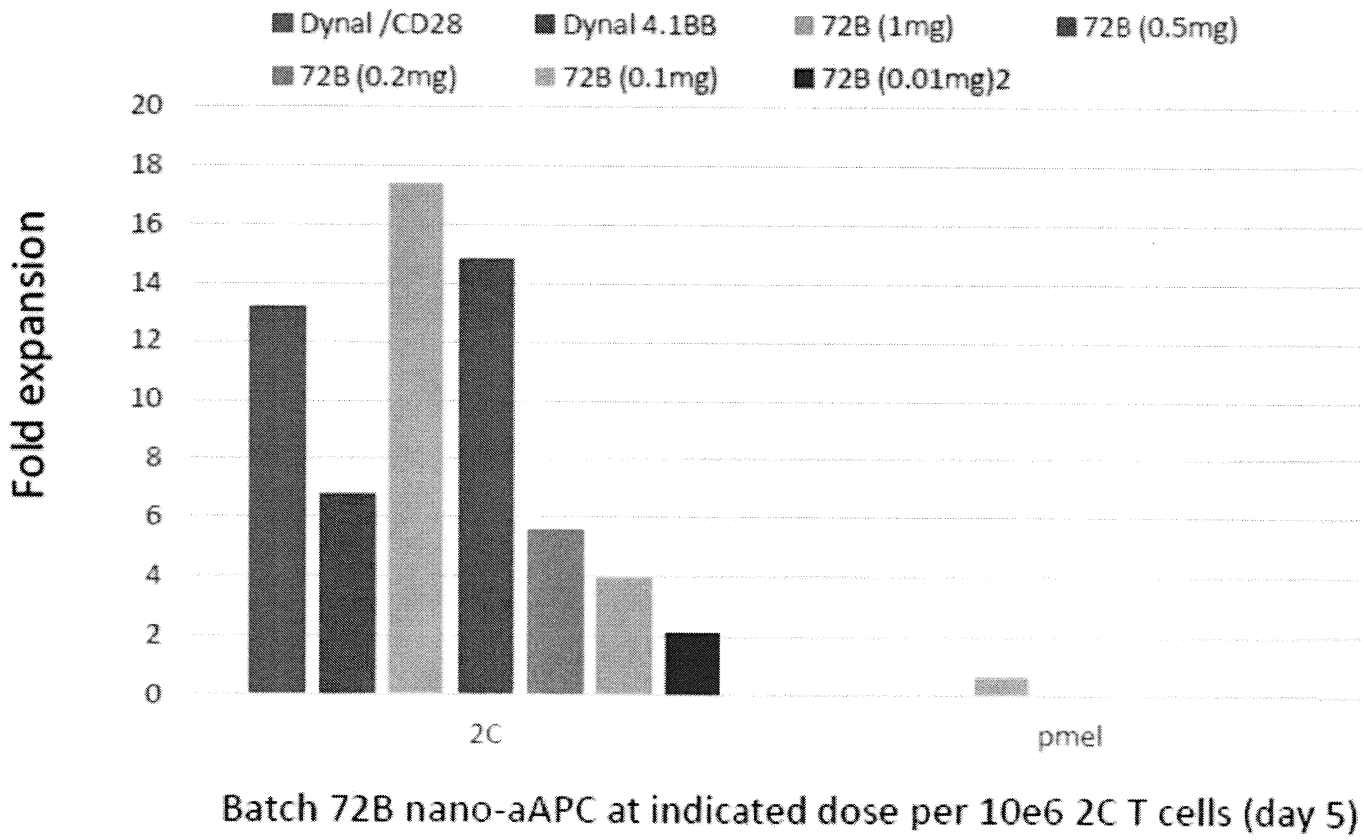

Dynal /CD28
Dynal 4.1BB
72B (1mg)
72B (0.5mg)
72B (0.2mg)
72B (0.1mg)
72B (0.01mg)2
Fold expansion
20
18
16
14
12
10
8
6
4
2
0
2C
pmel
Batch 72B nano-aAPC at indicated dose per 10e6 2C T cells (day 5)

FIGURE 23

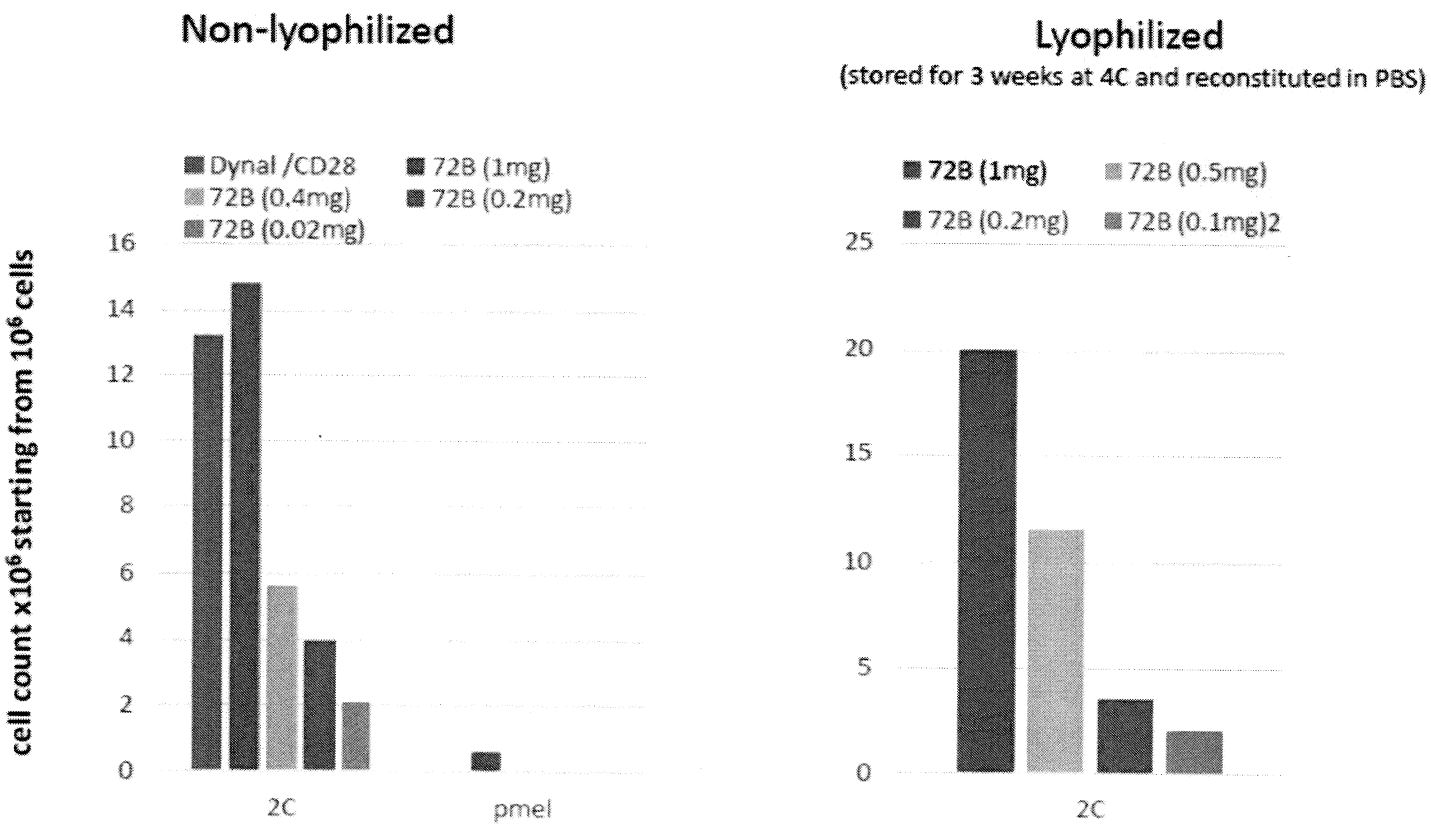
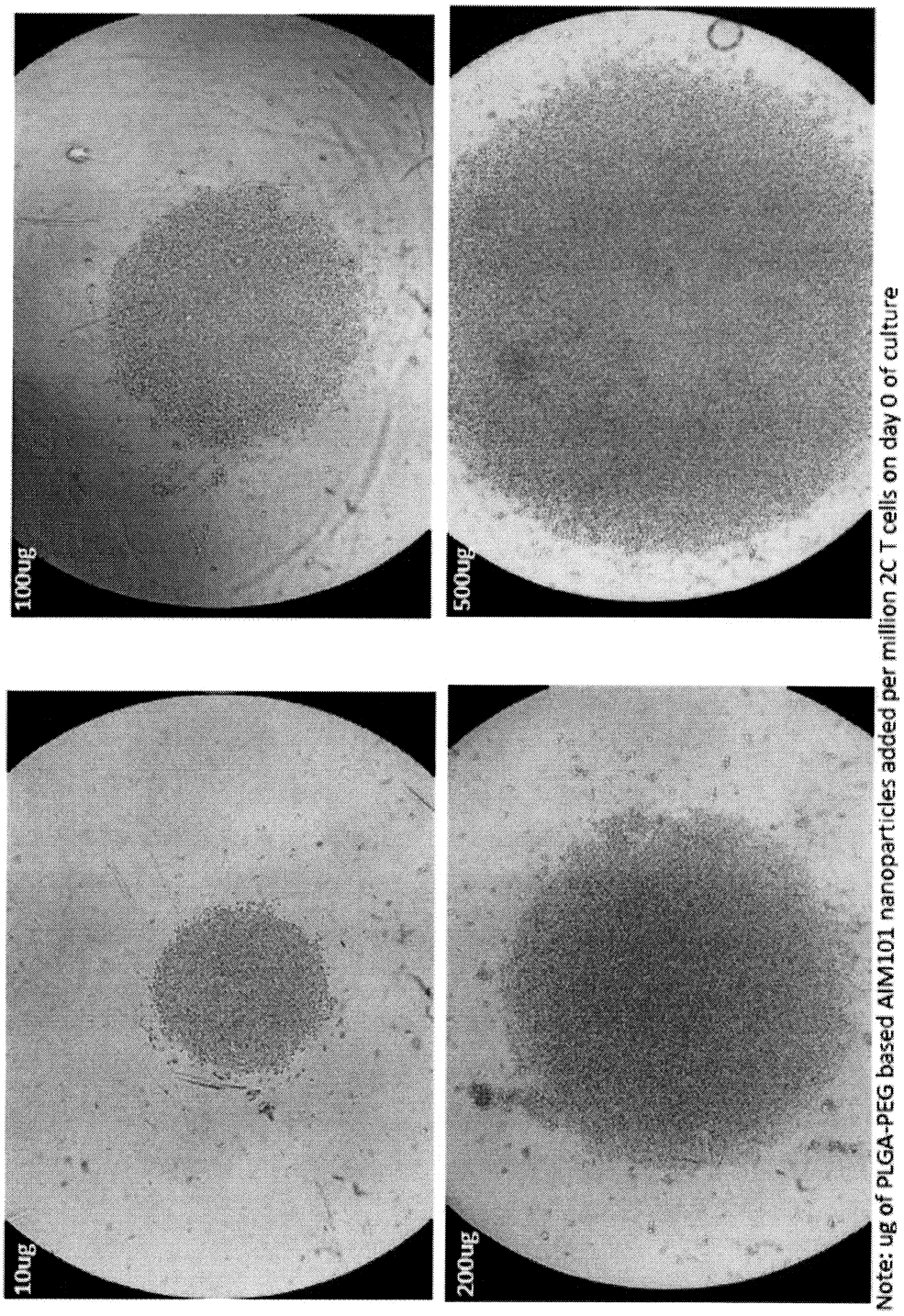

Non-lyophilized
Dynal /CD28
72B (1mg)
72B (0.4mg)
72B (0.2mg)
72B (0.02mg)
cell count x10^6 starting from 10^6 cells
16
14
12
10
8
6
4
2
0
2C
pmel
Lyophilized
(stored for 3 weeks at 4C and reconstituted in PBS)
72B (1mg)
72B (0.5mg)
72B (0.2mg)
72B (0.1mg)2
25
20
15
10
5
0
2C

FIGURE 24


10ug
100ug
200ug
500ug
Note: ug of PLGA-PEG based AIM101 nanoparticles added per million 2C T cells on day 0 of culture

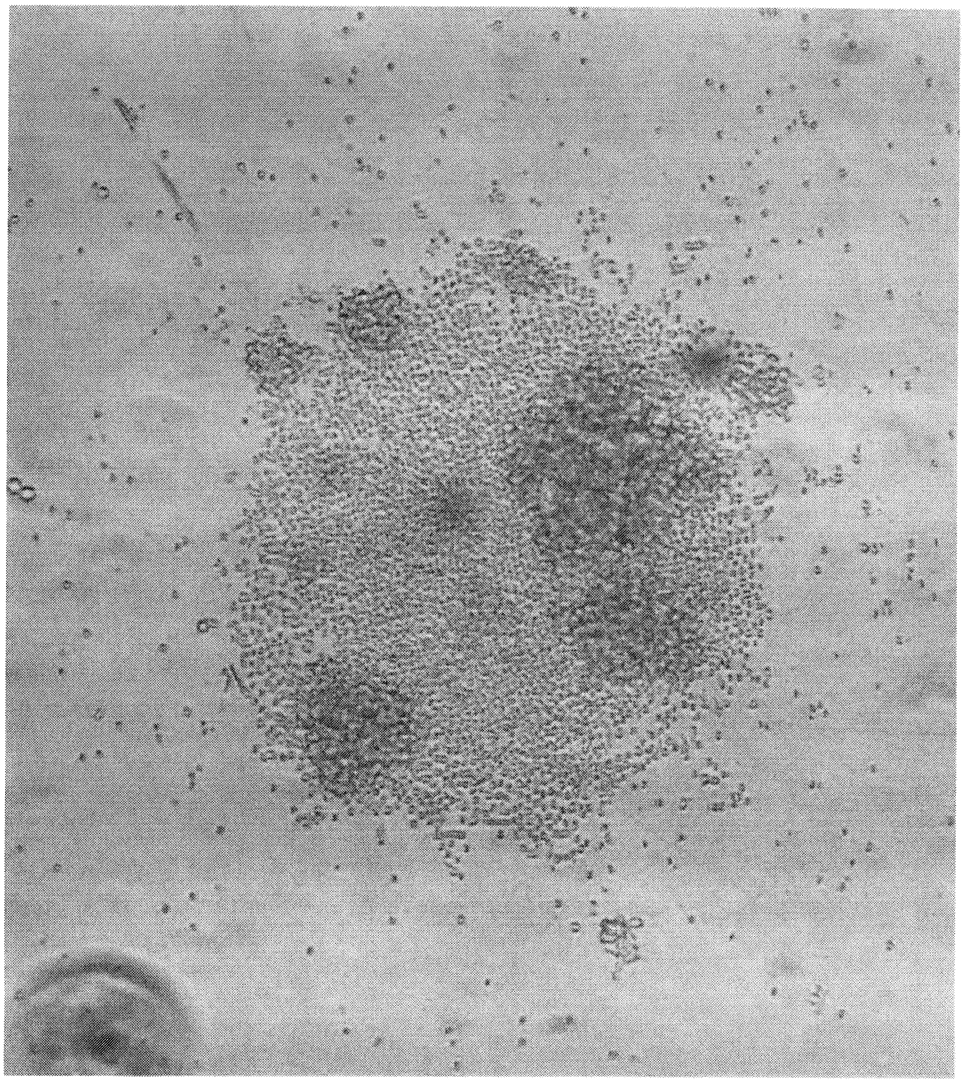
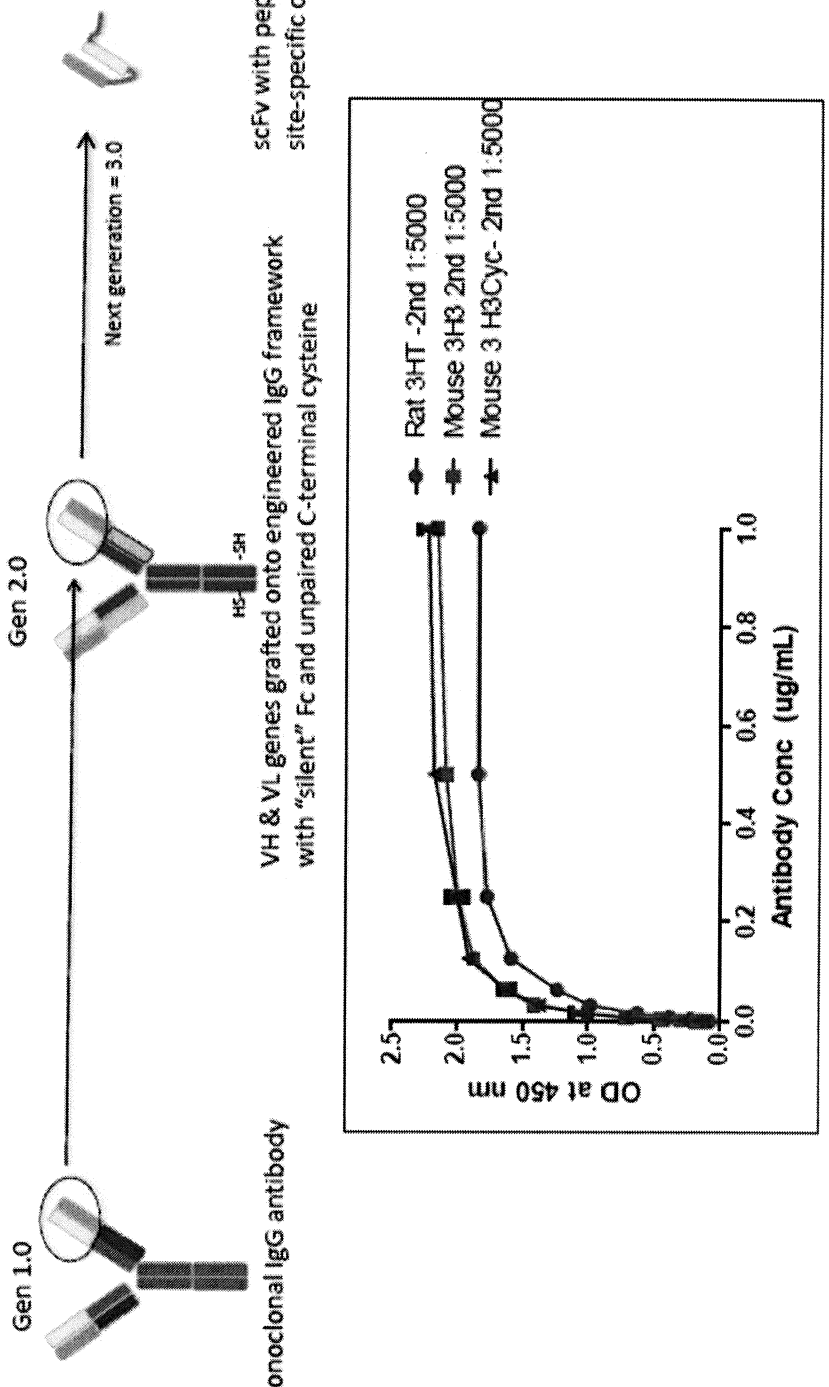


FIGURE 25

FIGURE 26


Gen 1.0
Monoclonal IgG antibody
Gen 2.0
VH & VL genes grafted onto engineered IgG framework
with "silent" Fc and unpaired C-terminal cysteine
Next generation = 3.0
scFv with peptide tether
site-specific conjugation
Rat 3HT -2nd 1:5000
Mouse 3H3 2nd 1:5000
Mouse 3 H3Cyc- 2nd 1:5000
OD at 450 nm
Antibody Conc (ug/mL)

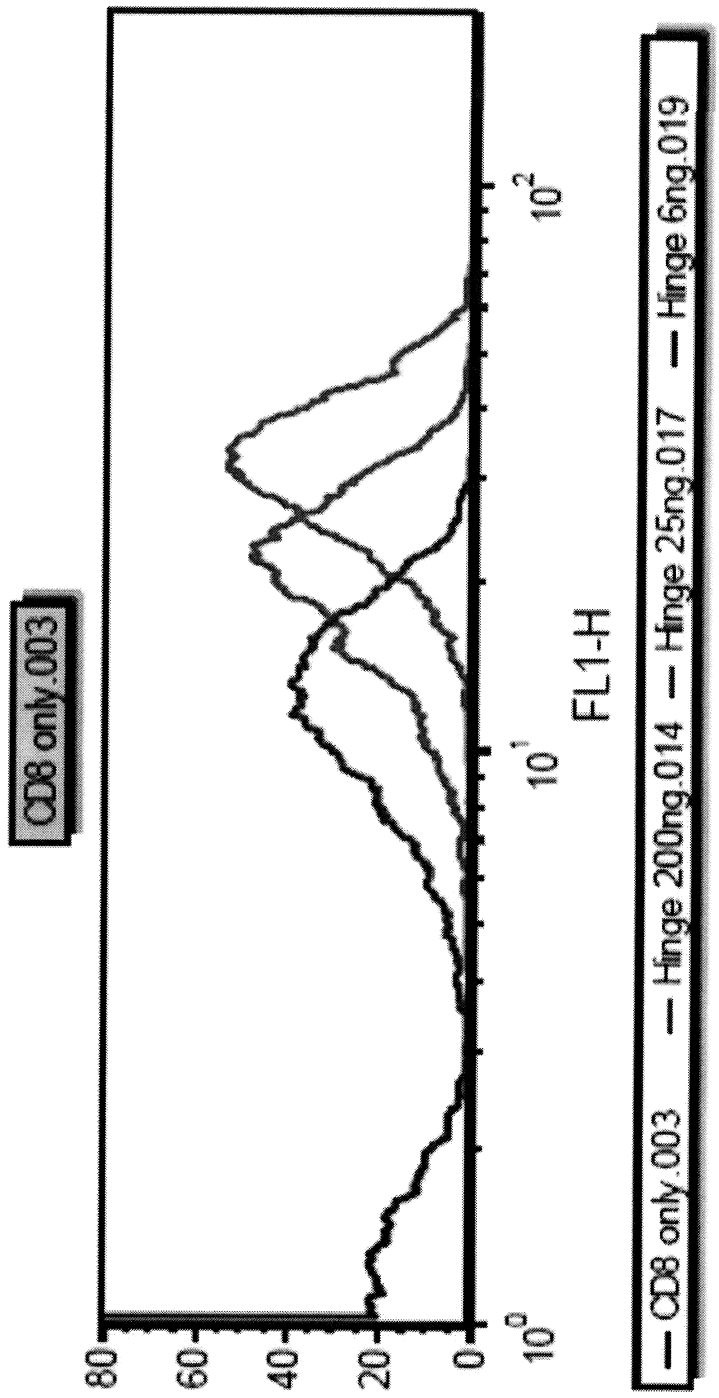
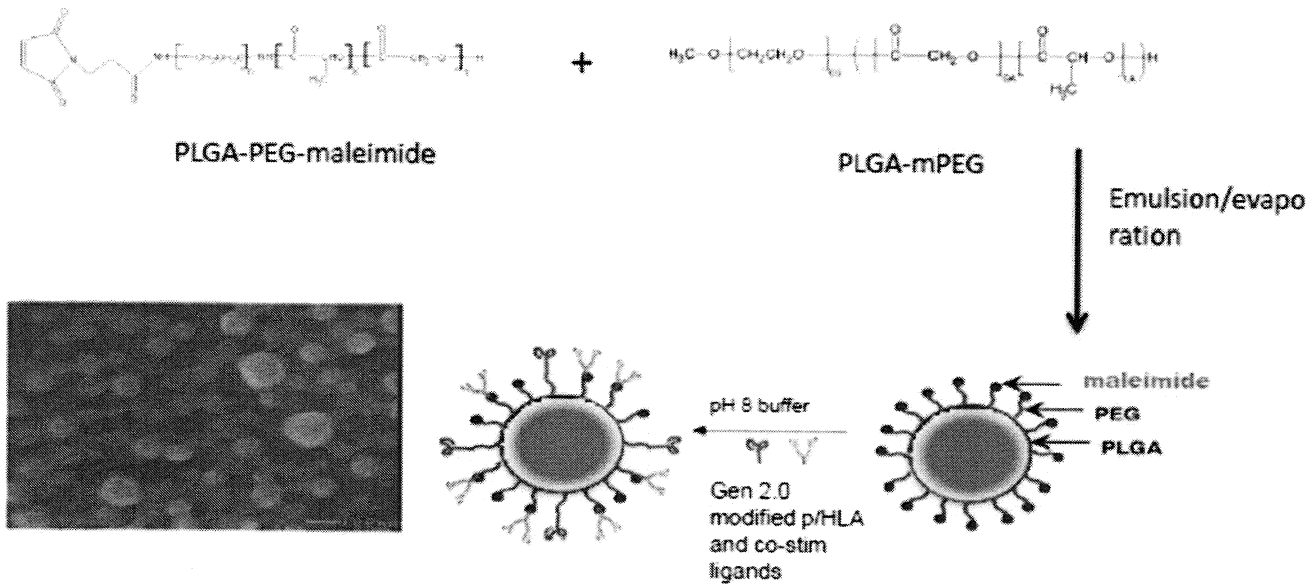

CD8 only.003
80
60
40
20
0
10^0
10^1
10^2
FL1-H
CD8 only.003
Hinge 200ng.014
Hinge 25ng.017
Hinge 6ng.019

FIGURE 27

FIGURE 28



Batch	Composition	Ratio	Size	ζ (mV)	% Ligand Bound	Active	Stable
72B	PLGA-PEG-COOH (20K:5K) PLGA-mPEG (20K:5K) PLGA (35K)	**0.25** 0.25 0.50	162 nm	-8.4 mV	H2-Ig 50% α-CD28 50%	++	Y
77B	PLGA-PEG-mal (20K:5K) PLGA-mPEG 20K/5K PLGA (35K)	**0.05** 0.45 0.50	145 nm	-4.1 mV	H2-Ig > 50% α-CD28 > 50%	++	Y

FIGURE 29

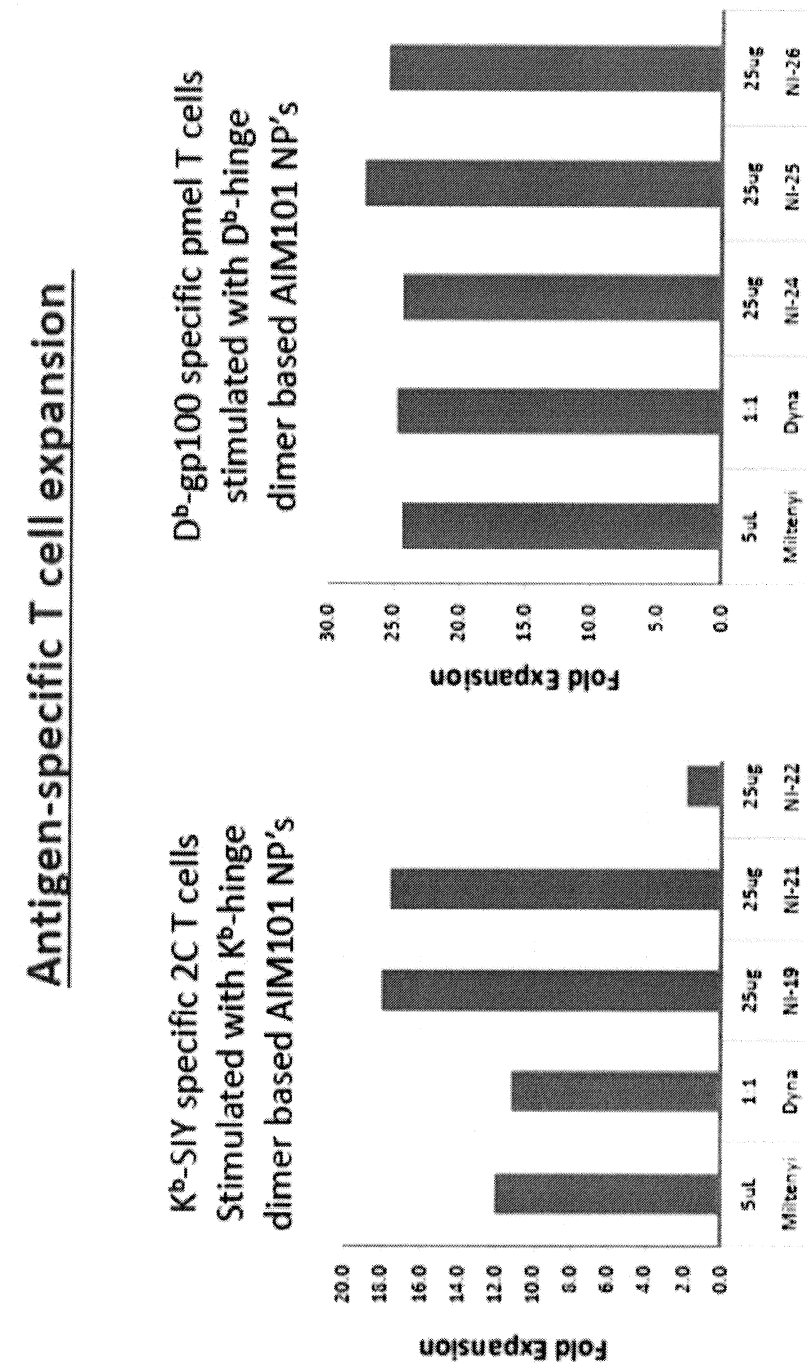

Antigen-specific T cell expansion
Kb-SIY specific 2C T cells
Stimulated with Kb-hinge
dimer based AIM101 NP's
Fold Expansion
20.0
18.0
16.0
14.0
12.0
10.0
8.0
6.0
4.0
2.0
0.0
Sol.
Miltenyi
1:1
Dyna
25ug
NI-19
25ug
NI-21
25ug
NI-22
Db-gp100 specific pmel T cells
stimulated with Db-hinge
dimer based AIM101 NP's
Fold Expansion
30.0
25.0
20.0
15.0
10.0
5.0
0.0
Sol.
Miltenyi
1:1
Dyna
25ug
NI-24
25ug
NI-25
25ug
NI-26
Stimulus per 10e6 T cells

FIGURE 30

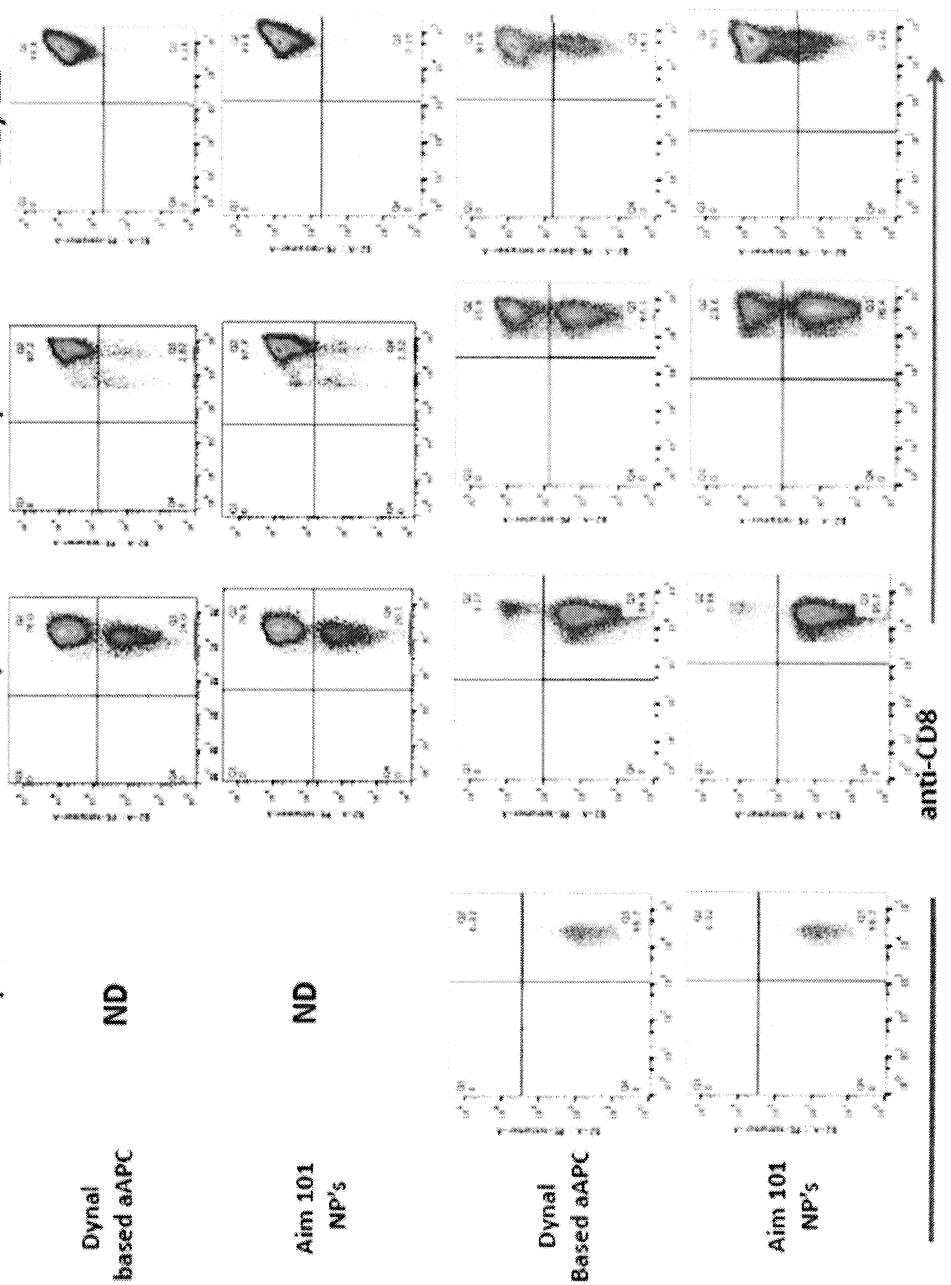
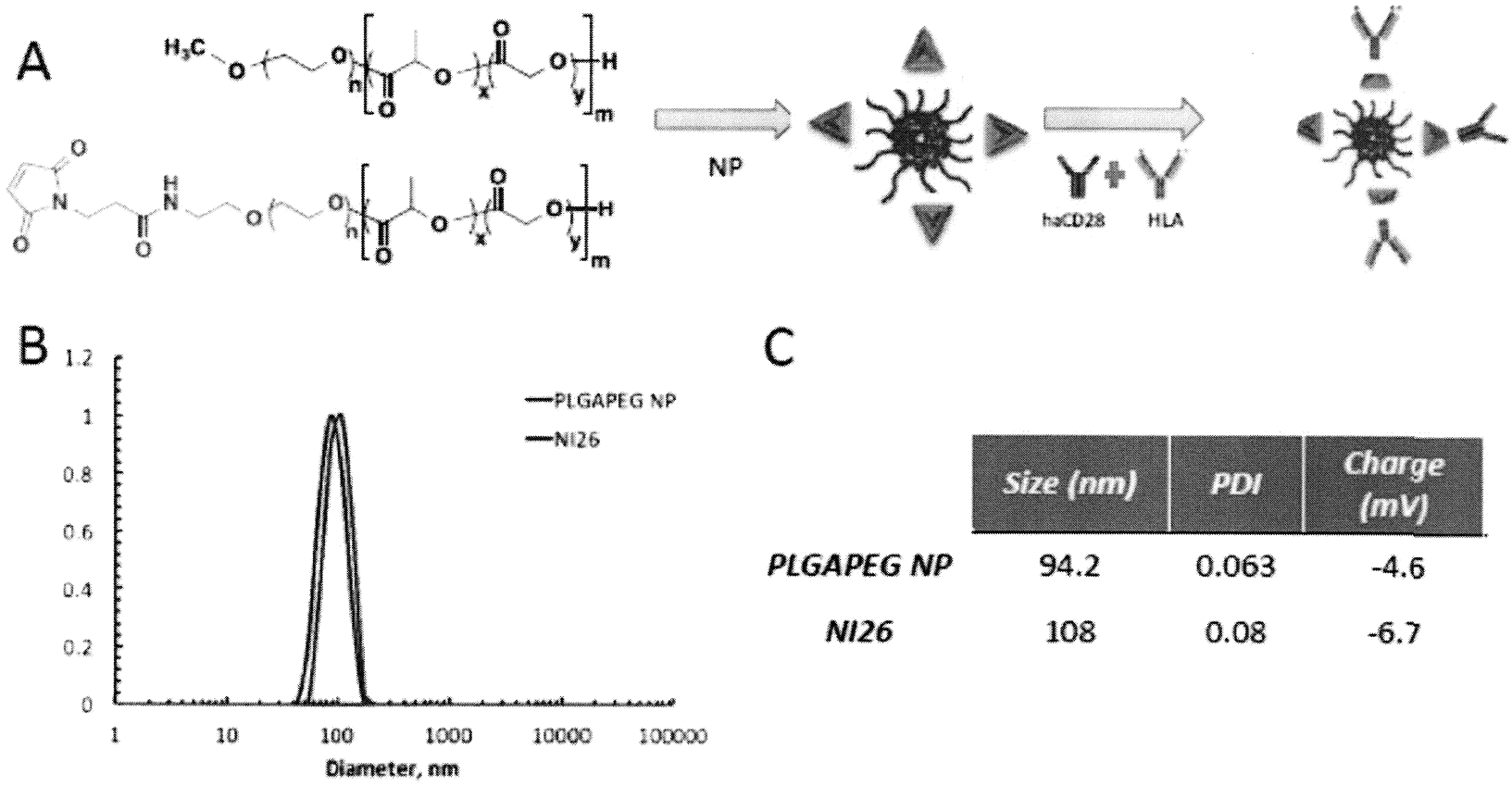

aAPC based expansion of human CMV or Mart-1 specific T cells
Day 0
Day 7
Day 14
Day 21
ND
ND
Dynal based aAPC
Aim 101 NP's
CMV - tetramer
Dynal Based aAPC
Aim 101 NP's
Mart-1 tetramer
anti-CD8

FIGURE 31



	Size (nm)	PDI	Charge (mV)
PLGAPEG NP	94.2	0.063	-4.6
NI26	108	0.08	-6.7

FIGURE 32

Batch	*Maleimide content (%w/w)*	*Average size (nm)*	*ξ (mV)*	*µg Prot input/mg NP*	*Coupling efficiency, %*	*# ligands/NP*
NI19	5	91.8	-8.7	51.5	41.6	45.8
NI20	25	95.9	-4.9	51.5	95.8	120.2
NI21	55	98	-3.1	51.5	93.5	125.2
NI22	55	102	-8.6	51.5	79.1	119
NI23*	0	68	-9.2	51.5	------	-------
NI24	1	80.9	-2.5	51.5	22.9	17.3
NI25	10	92.9	-5.8	51.5	67.2	76.8
NI26	10	108	-6.7	51.5	59.6	106.8

*Batch NI23 was used to determine the amount of protein that absorbs nonspecifically to nanoparticles. The amount of protein absorbed nonspecifically was found < 3%.