Figure 1

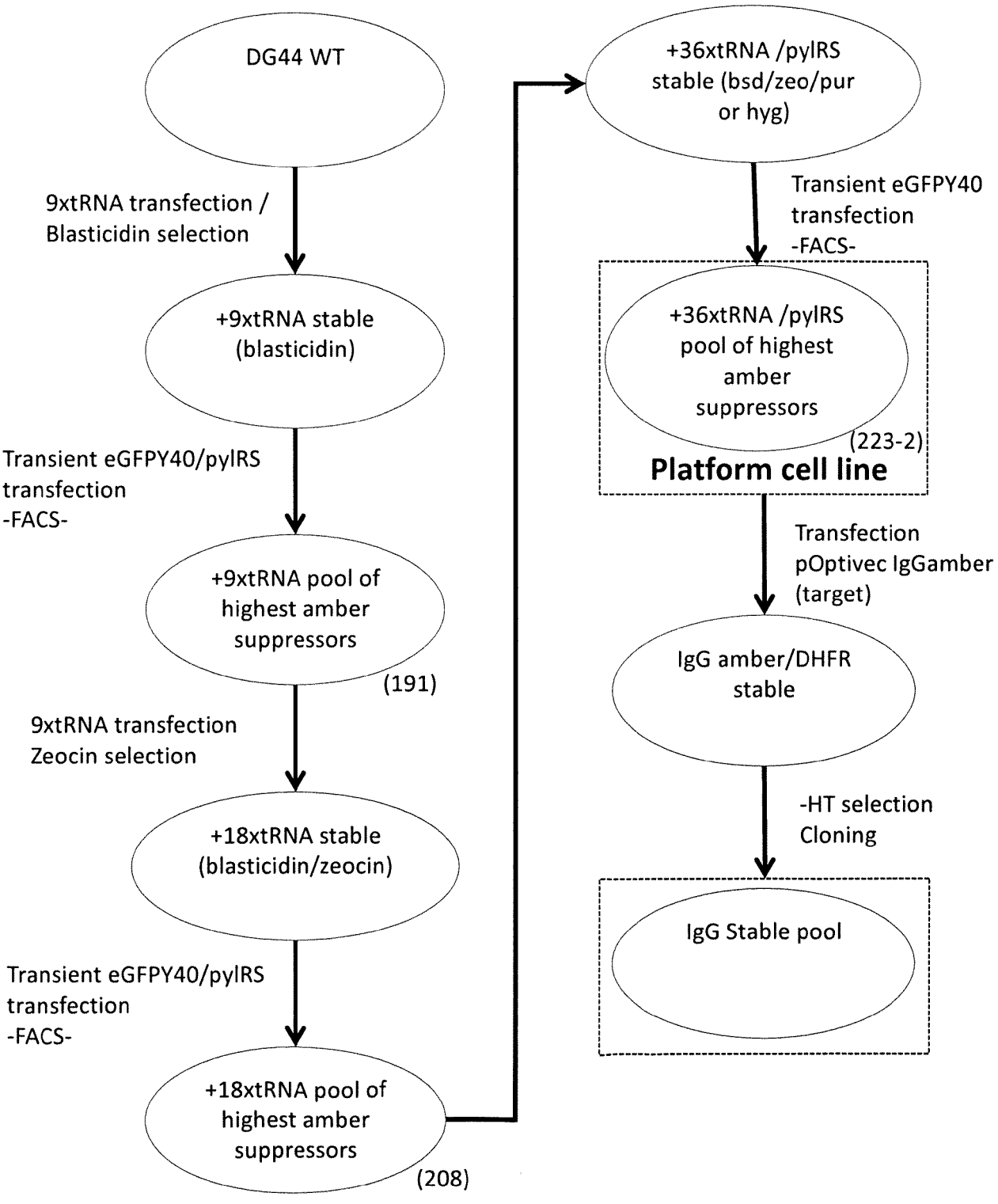

DG44 WT
9xtRNA transfection / Blasticidin selection
+9xtRNA stable (blasticidin)
Transient eGFPY40/pylRS transfection -FACS-
+9xtRNA pool of highest amber suppressors
(191)
9xtRNA transfection Zeocin selection
+18xtRNA stable (blasticidin/zeocin)
Transient eGFPY40/pylRS transfection -FACS-
+18xtRNA pool of highest amber suppressors
(208)
+36xtRNA /pylRS stable (bsd/zeo/pur or hyg)
Transient eGFPY40 transfection -FACS-
+36xtRNA /pylRS pool of highest amber suppressors
(223-2)
Platform cell line
Transfection pOptivec IgGamber (target)
IgG amber/DHFR stable
-HT selection Cloning
IgG Stable pool

Figure 2

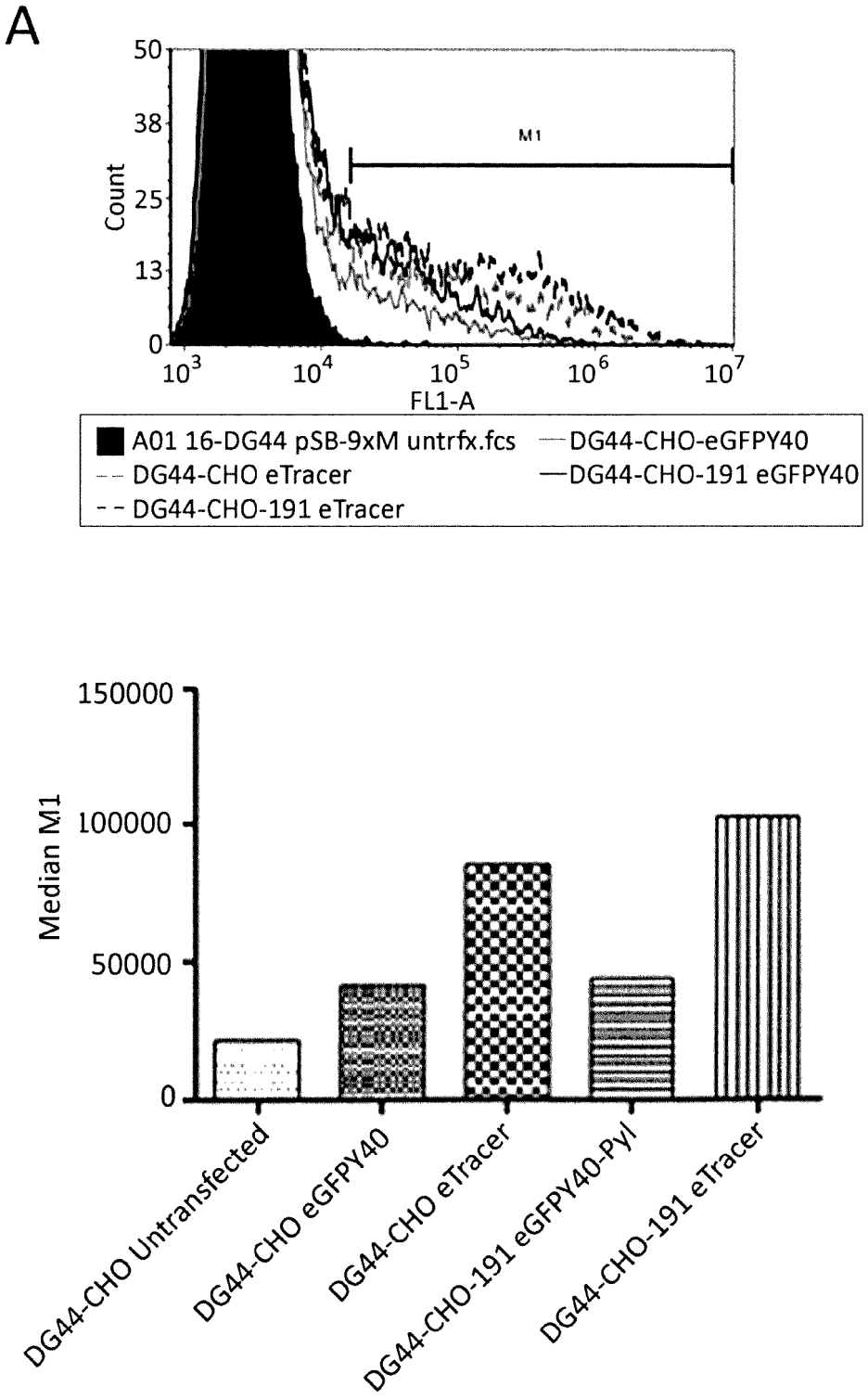
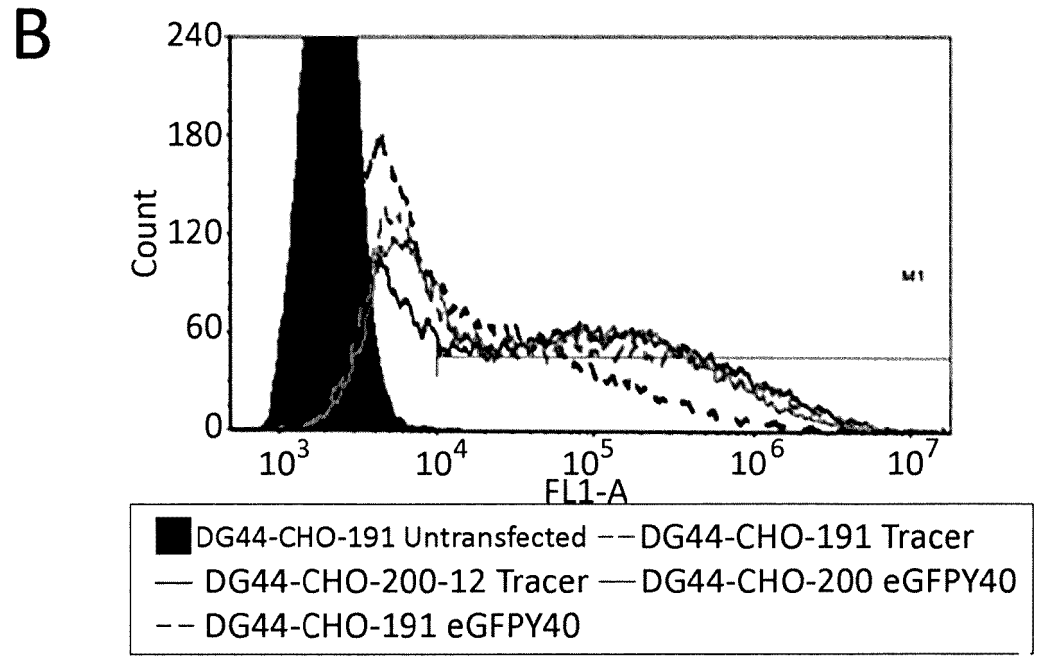

A
50
38
25
13
0
Count
M1
10^3
10^4
10^5
10^6
10^7
FL1-A
A01 16-DG44 pSB-9xM untrfx.fcs
DG44-CHO eTracer
DG44-CHO-191 eTracer
DG44-CHO-eGFPY40
DG44-CHO-191 eGFPY40
150000
100000
50000
0
Median M1
DG44-CHO Untransfected
DG44-CHO eGFPY40
DG44-CHO eTracer
DG44-CHO-191 eGFPY40-Pyl
DG44-CHO-191 eTracer

Figure 2 cont



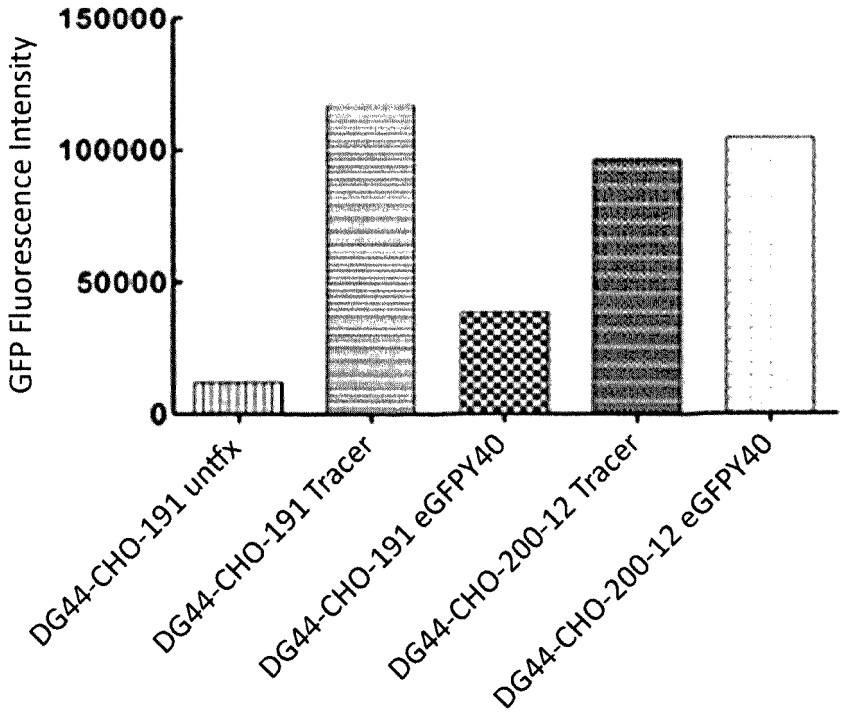
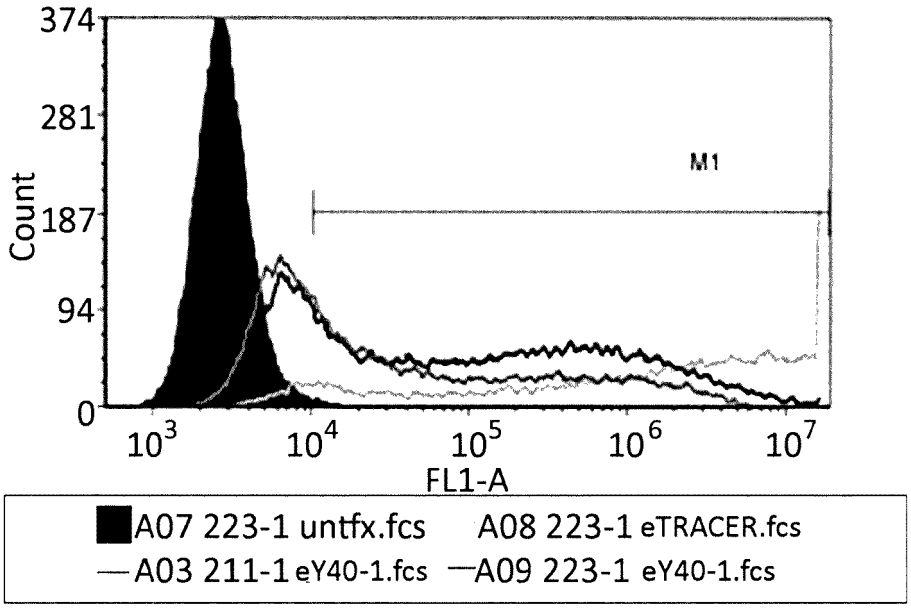


Figure 2 cont

C



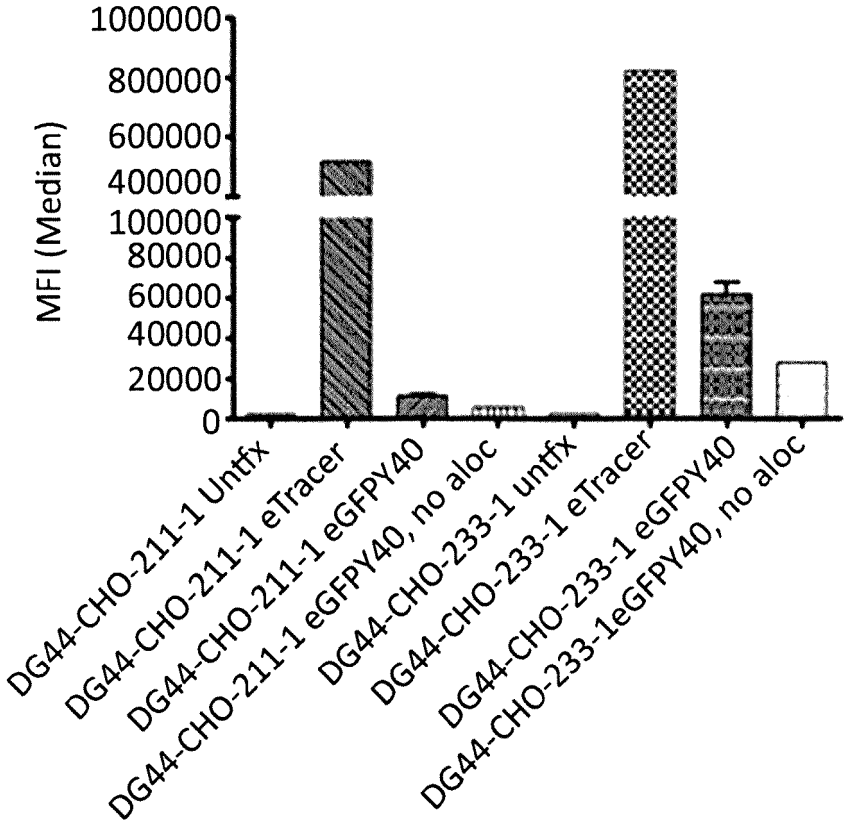


Figure 3

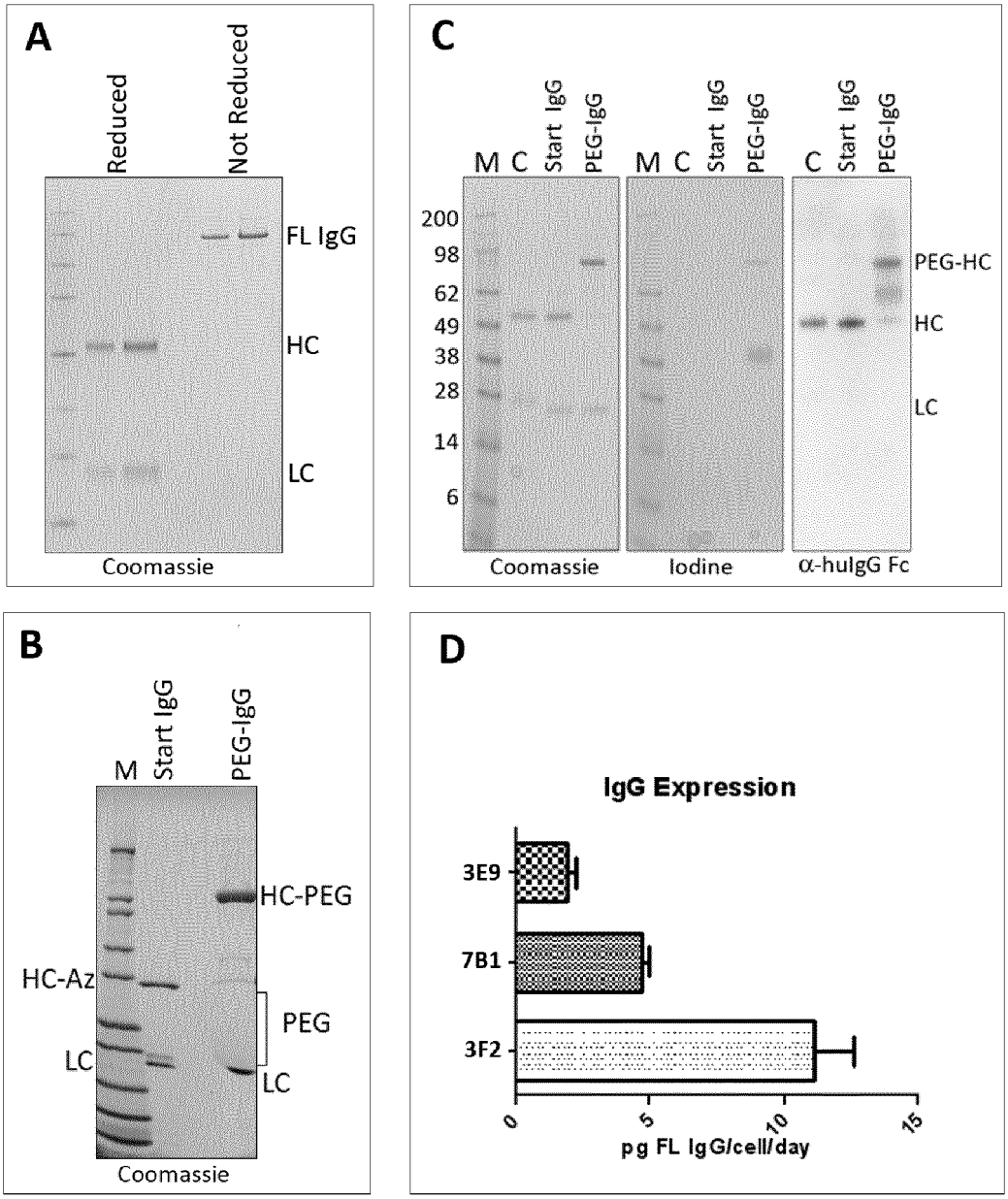

A
Reduced
Not Reduced
FL IgG
HC
LC
Coomassie
C
M C Start IgG PEG-IgG
M C Start IgG PEG-IgG
C Start IgG PEG-IgG
200
98
62
49
38
28
14
6
PEG-HC
HC
LC
Coomassie
Iodine
α-huIgG Fc
B
M
Start IgG
PEG-IgG
HC-PEG
HC-Az
PEG
LC
LC
Coomassie
D
IgG Expression
3E9
7B1
3F2
0
5
10
15
pg FL IgG/cell/day

Figure 4

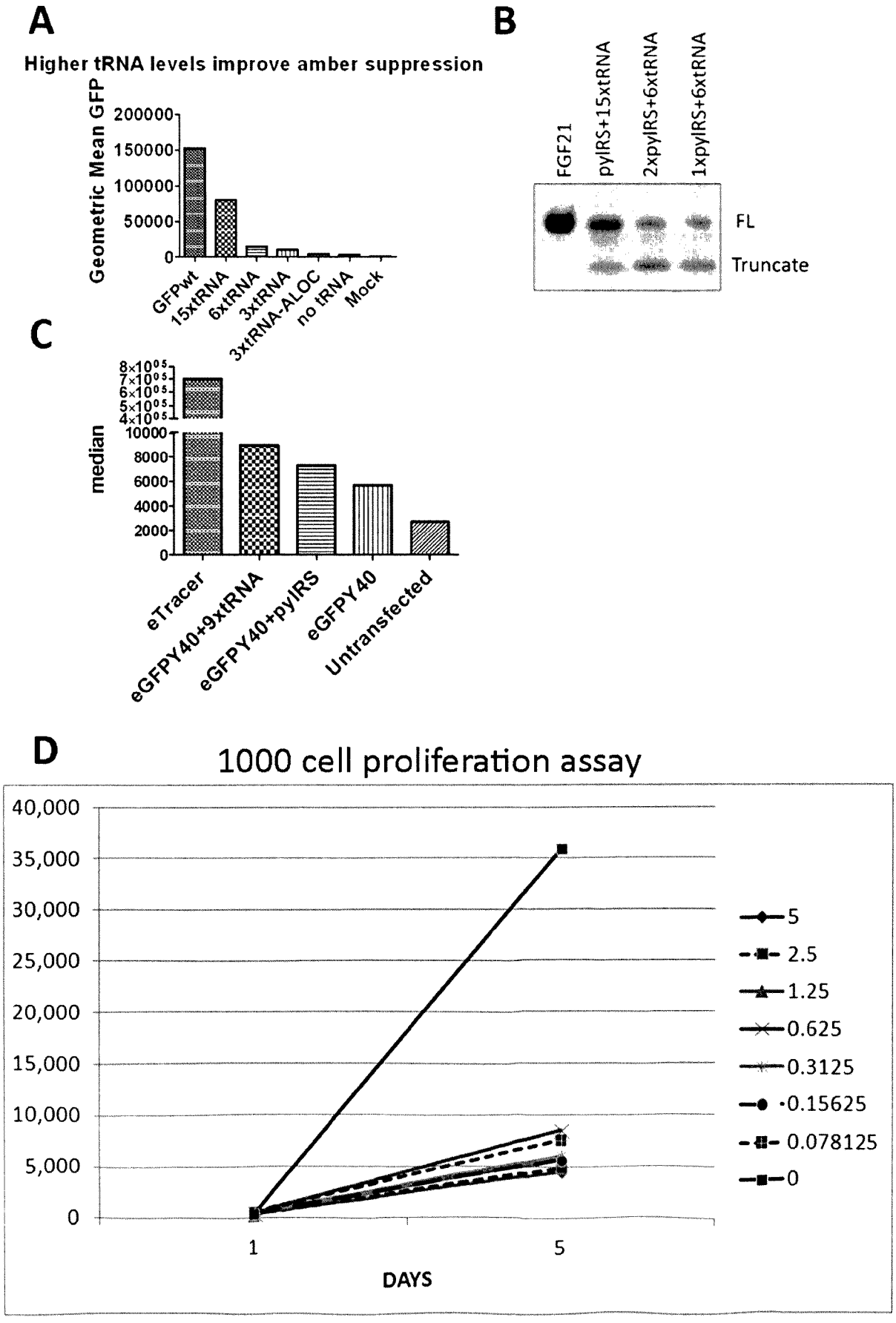

A
Higher tRNA levels improve amber suppression
Geometric Mean GFP
200000
150000
100000
50000
0
GFPwt
15xtRNA
6xtRNA
3xtRNA
3xtRNA-ALOC
no tRNA
Mock
B
FGF21
pylRS+15xtRNA
2xpylRS+6xtRNA
1xpylRS+6xtRNA
FL
Truncate
C
median
8×10^05
7×10^05
6×10^05
5×10^05
4×10^05
10000
8000
6000
4000
2000
0
eTracer
eGFPY40+9xtRNA
eGFPY40+pylRS
eGFPY40
Untransfected
D
1000 cell proliferation assay
40,000
35,000
30,000
25,000
20,000
15,000
10,000
5,000
0
1
5
DAYS
5
2.5
1.25
0.625
0.3125
0.15625
0.078125
0

Figure 4 cont

E

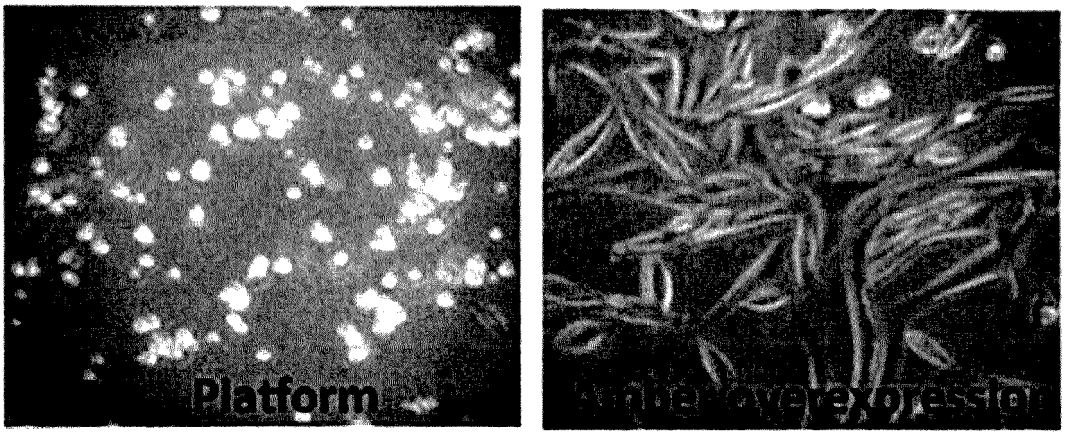


Figure 5

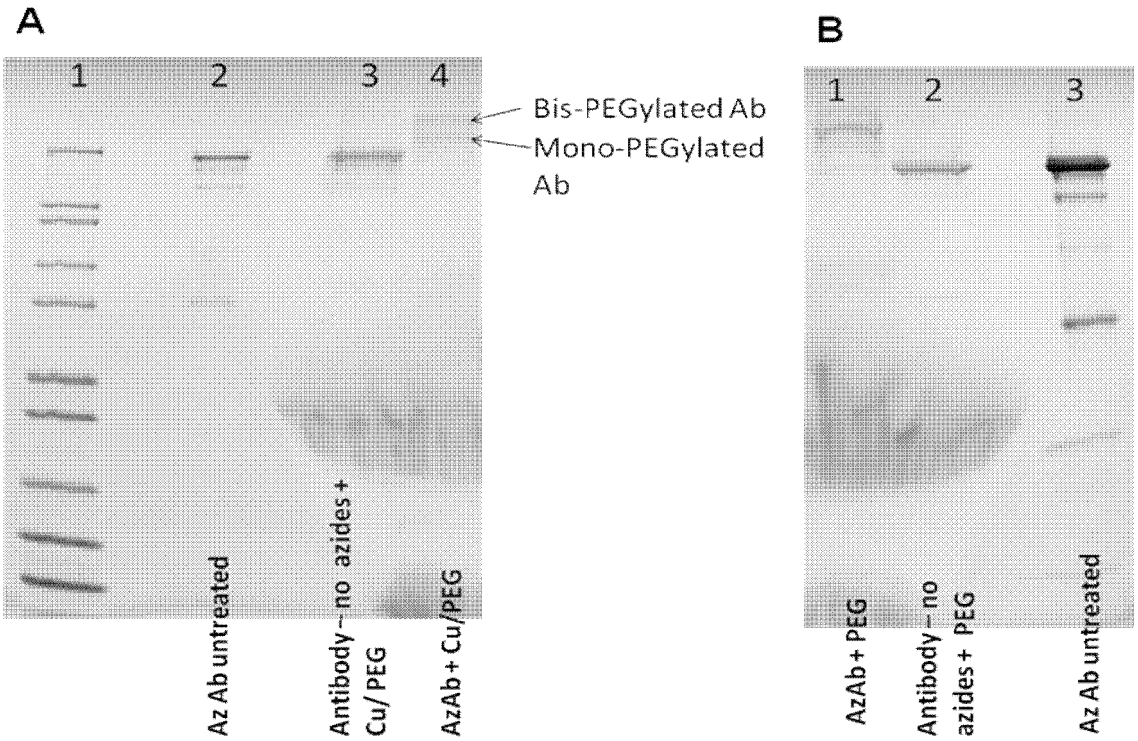


Figure 6

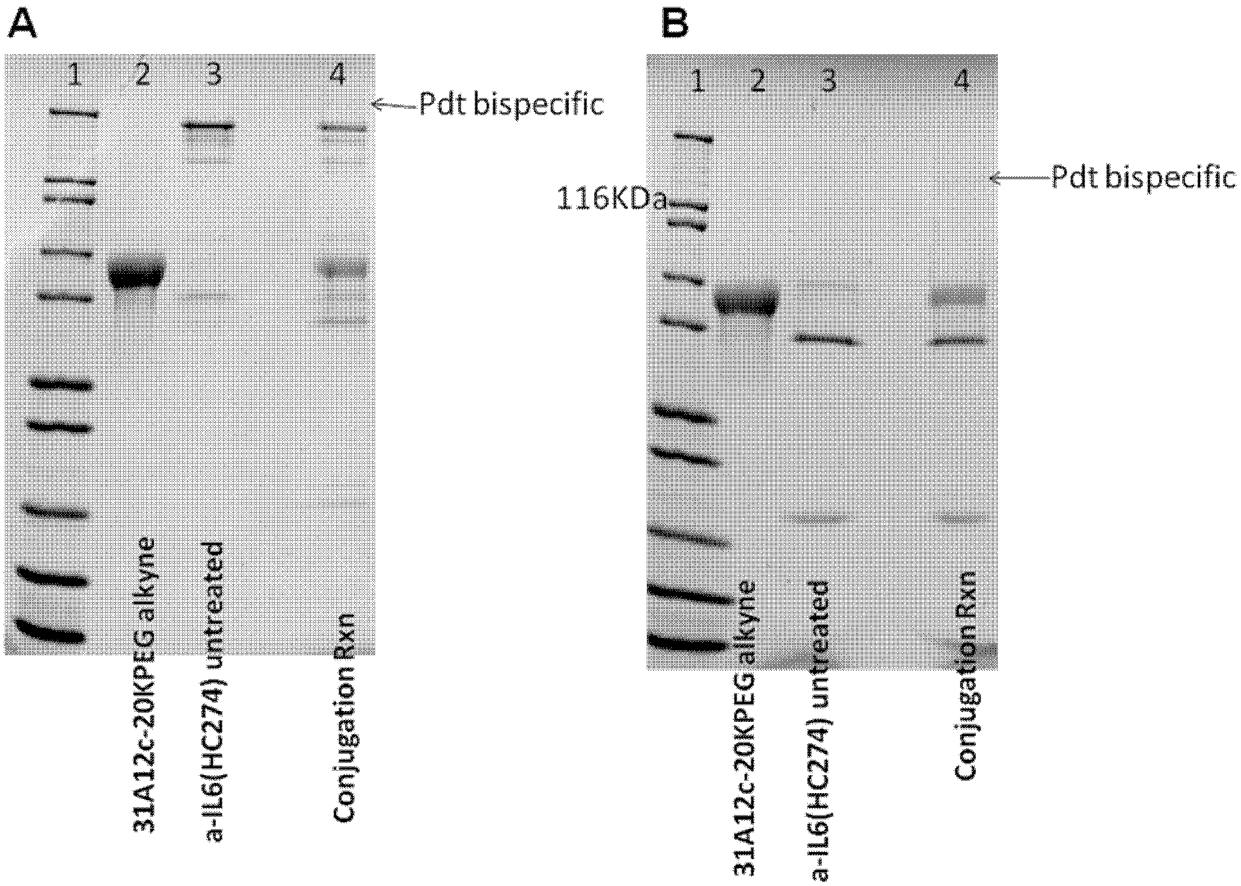


Figure 7

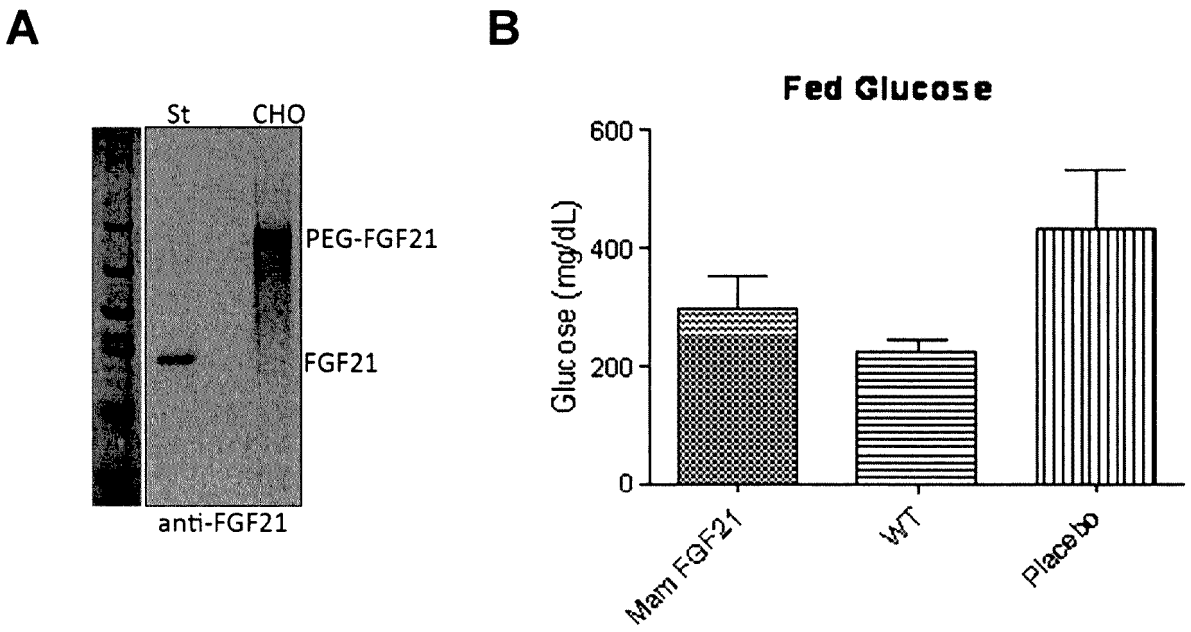


Figure 8

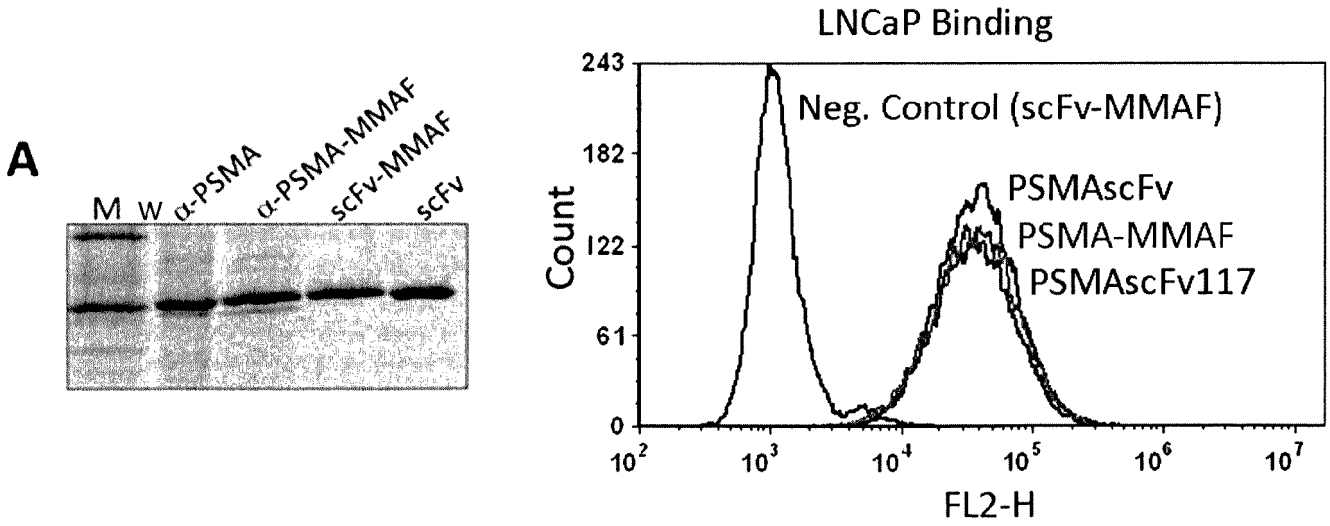
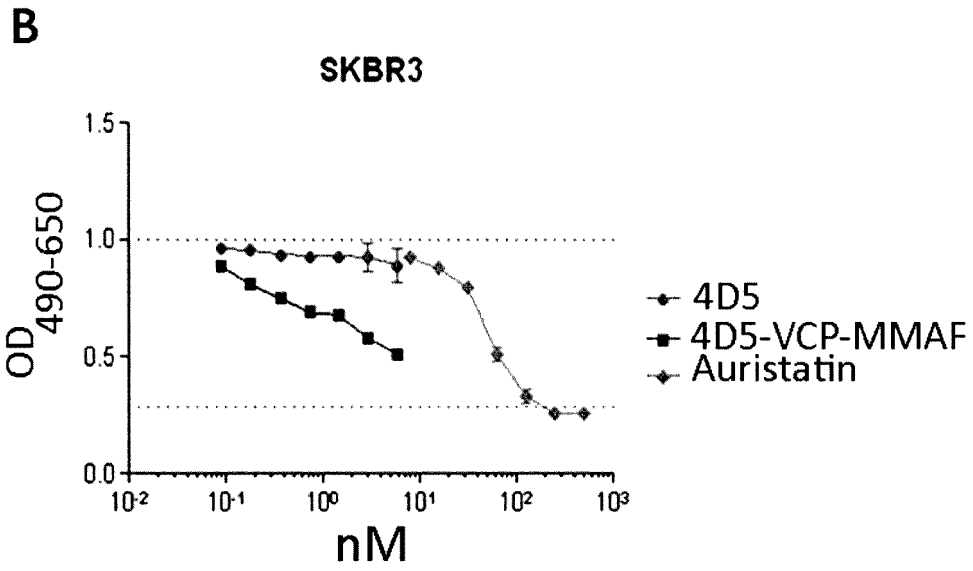


Figure 8 cont



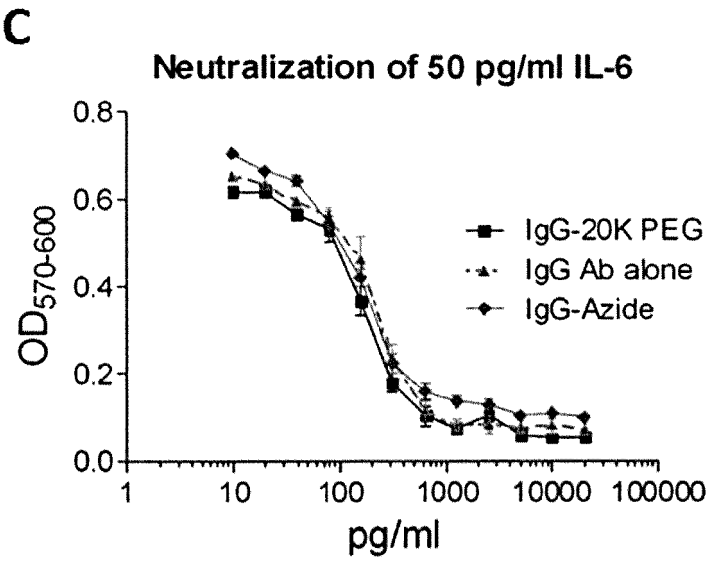


Figure 9

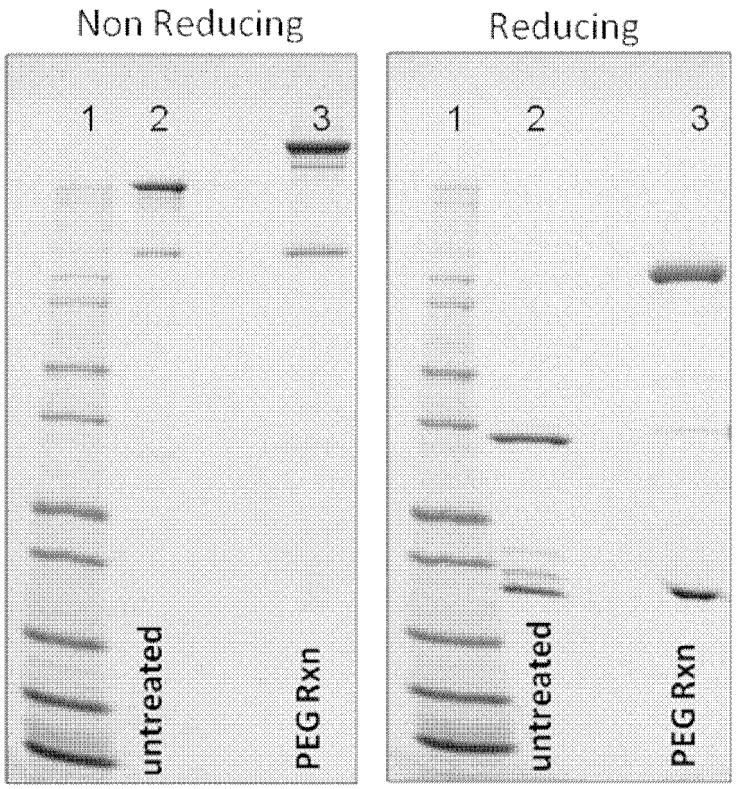


Figure 10

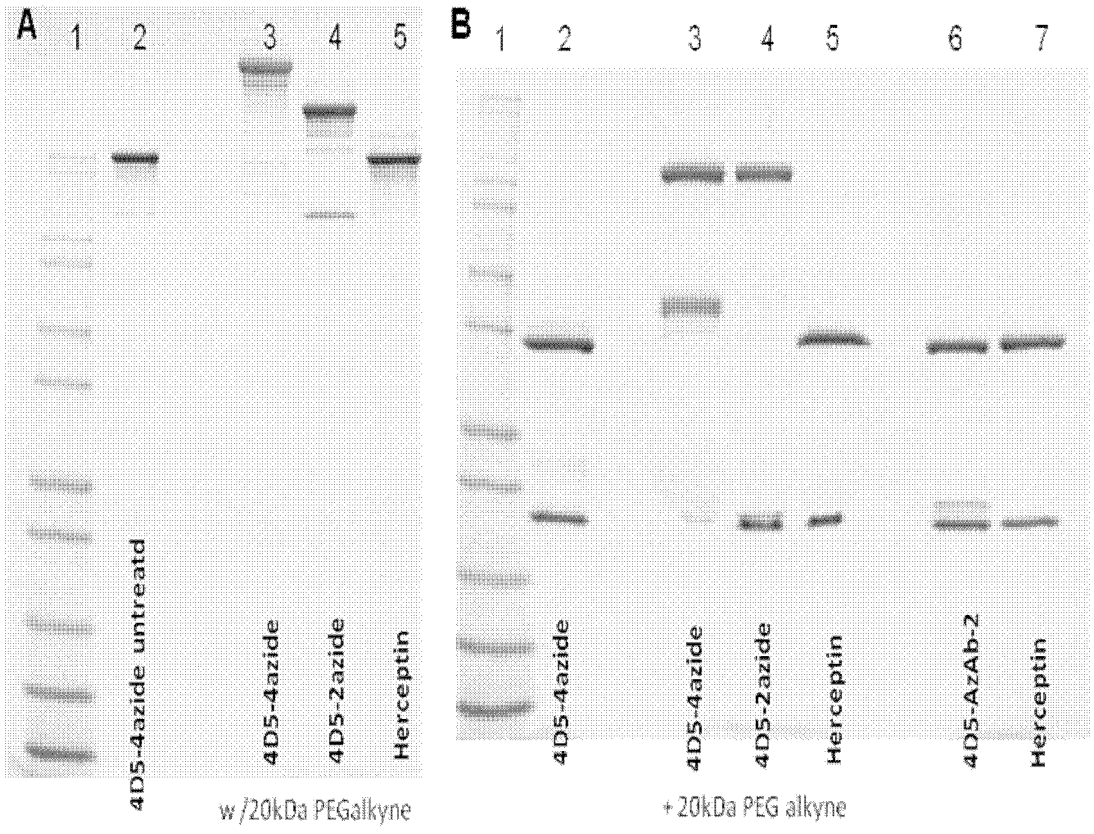


Figure 11

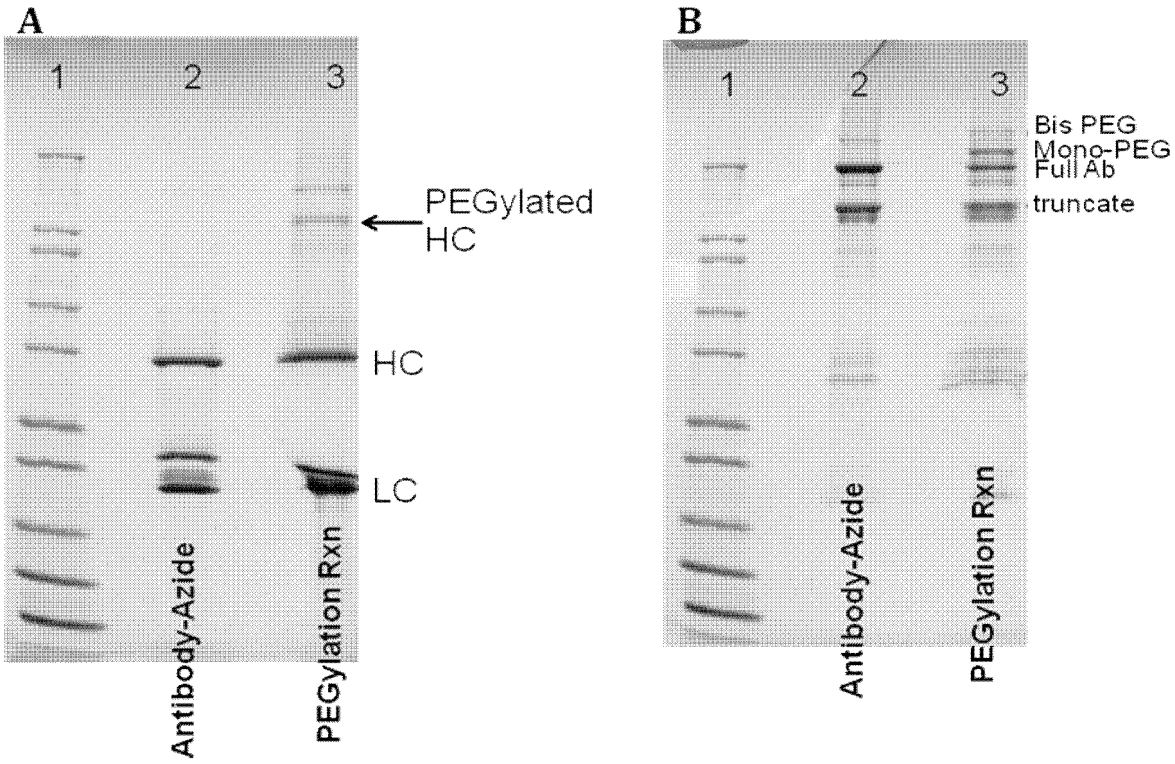


Figure 12

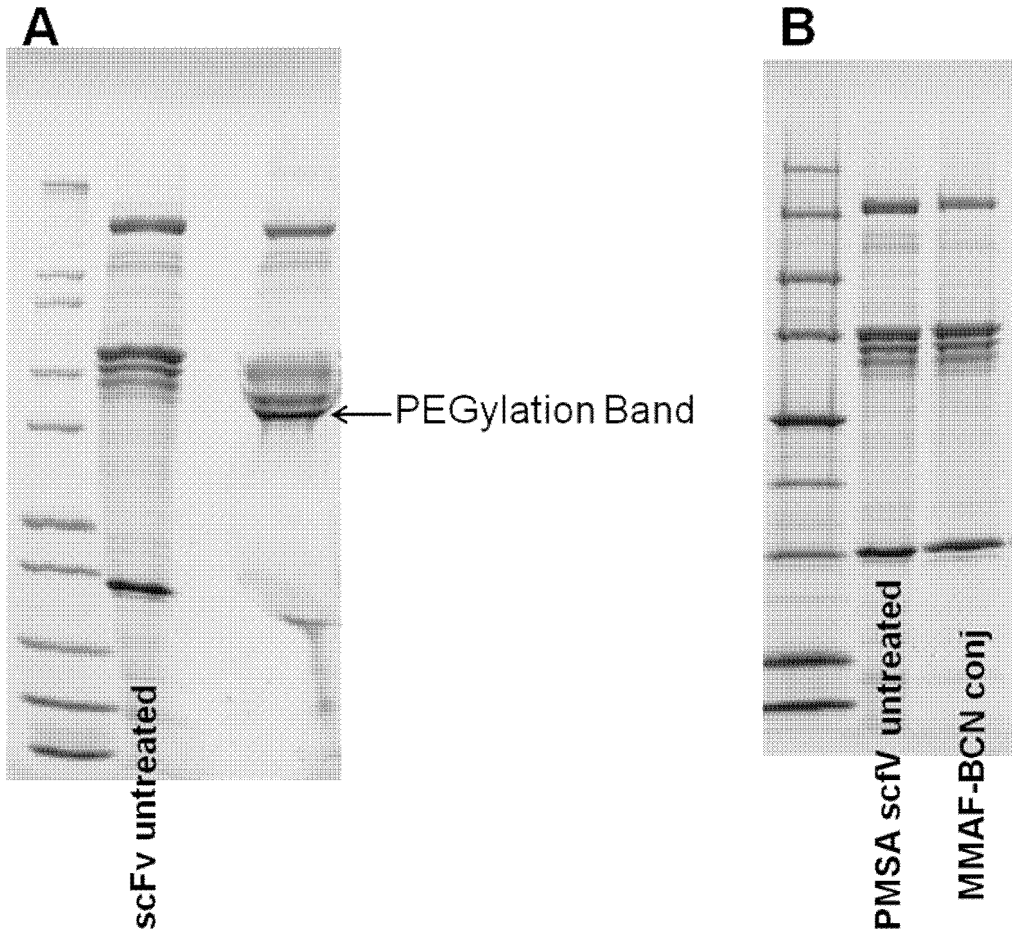
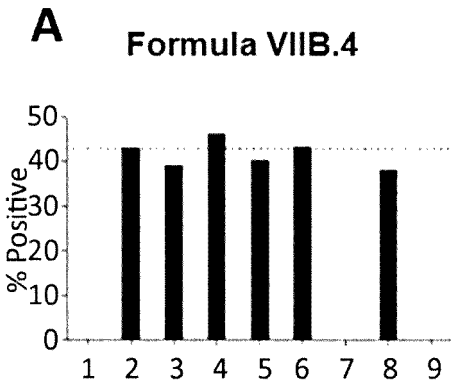


Figure 13



1. untransfected
2. GFP
3. GFP + Lys Azide (0.5 nM)
4. GFP + Decoy (2 nM)
5. GFP + Decoy (1 nM)
6. GFP + Decoy (0.5 nM)
7. GFP + Lys azide + Decoy (2 nM)
8. GFP + Lys azide + decoy (1 nM)
9. GFP + Lys azide + Decoy (0.5 n

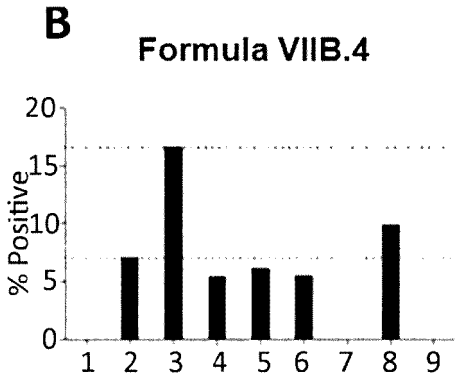
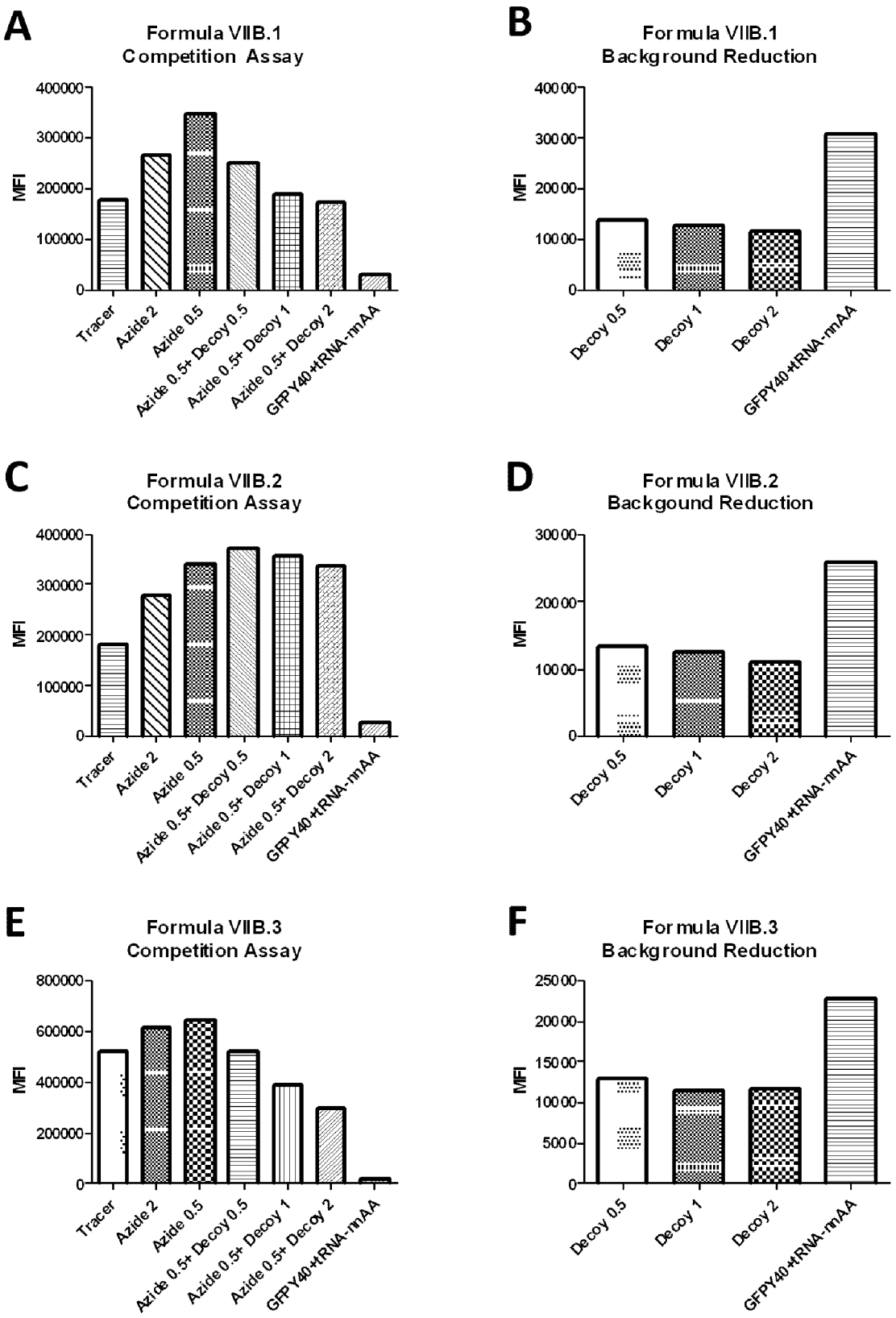
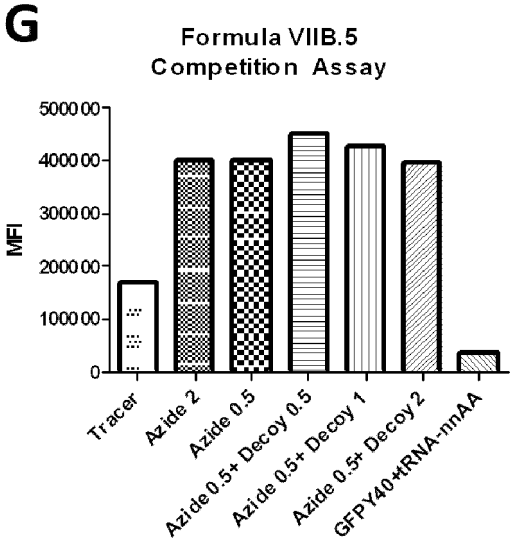


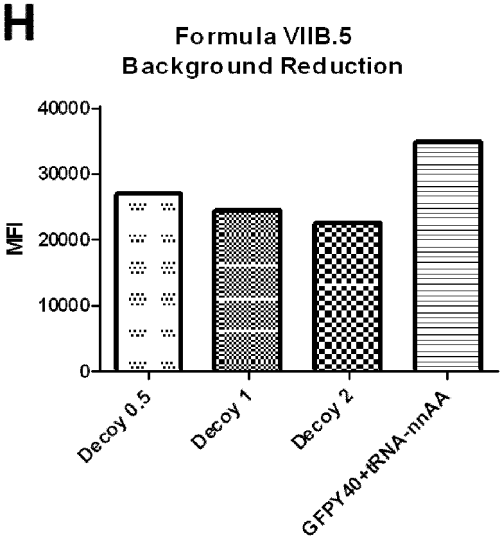
Figure 14


A
Formula VIIB.1
Competition Assay
MFI
400000
300000
200000
100000
0
Tracer
Azide 2
Azide 0.5
Azide 0.5+ Decoy 0.5
Azide 0.5+ Decoy 1
Azide 0.5+ Decoy 2
GFPY40+tRNA-mAA
B
Formula VIIB.1
Background Reduction
MFI
40000
30000
20000
10000
0
Decoy 0.5
Decoy 1
Decoy 2
GFPY40+tRNA-mAA
C
Formula VIIB.2
Competition Assay
MFI
400000
300000
200000
100000
0
Tracer
Azide 2
Azide 0.5
Azide 0.5+ Decoy 0.5
Azide 0.5+ Decoy 1
Azide 0.5+ Decoy 2
GFPY40+tRNA-mAA
D
Formula VIIB.2
Backgound Reduction
MFI
30000
20000
10000
0
Decoy 0.5
Decoy 1
Decoy 2
GFPY40+tRNA-mAA
E
Formula VIIB.3
Competition Assay
MFI
800000
600000
400000
200000
0
Tracer
Azide 2
Azide 0.5
Azide 0.5+ Decoy 0.5
Azide 0.5+ Decoy 1
Azide 0.5+ Decoy 2
GFPY40+tRNA-mAA
F
Formula VIIB.3
Background Reduction
MFI
25000
20000
15000
10000
5000
0
Decoy 0.5
Decoy 1
Decoy 2
GFPY40+tRNA-mAA

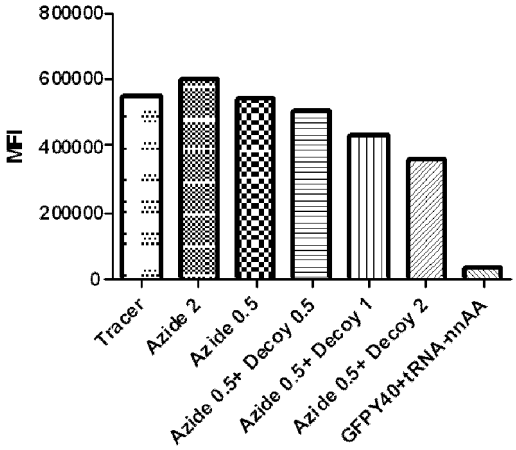
G


Formula VIIB.5
Competition Assay
MFI
5000000
4000000
3000000
2000000
1000000
0
Tracer
Azide 2
Azide 0.5
Azide 0.5+ Decoy 0.5
Azide 0.5+ Decoy 1
Azide 0.5+ Decoy 2
GFPY40+tRNA-nnAA

H


Formula VIIB.5
Background Reduction
MFI
40000
30000
20000
10000
0
Decoy 0.5
Decoy 1
Decoy 2
GFPY40+tRNA-nnAA

I


Formula VIIB.6
Competition Assay
MFI
800000
600000
400000
200000
0
Tracer
Azide 2
Azide 0.5
Azide 0.5+ Decoy 0.5
Azide 0.5+ Decoy 1
Azide 0.5+ Decoy 2
GFPY40+tRNA-nnAA

J

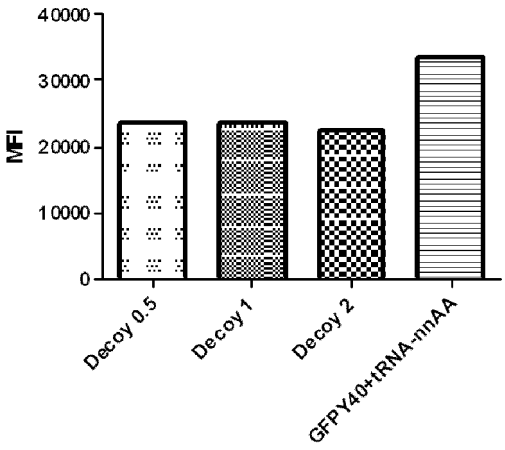
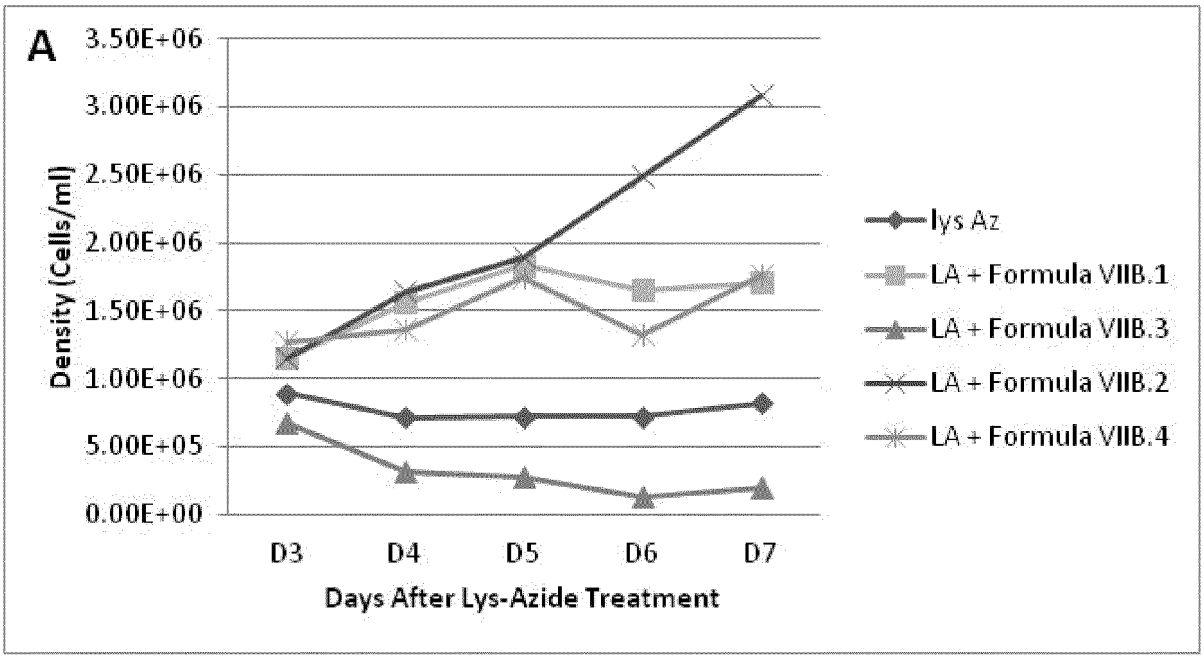

Formula VIIB.6
Background Reduction
MFI
40000
30000
20000
10000
0
Decoy 0.5
Decoy 1
Decoy 2
GFPY40+tRNA-nnAA

Figure 15


A
3.50E+06
3.00E+06
2.50E+06
2.00E+06
1.50E+06
1.00E+06
5.00E+05
0.00E+00
Density (Cells/ml)
D3
D4
D5
D6
D7
Days After Lys-Azide Treatment
lys Az
LA + Formula VIIB.1
LA + Formula VIIB.3
LA + Formula VIIB.2
LA + Formula VIIB.4

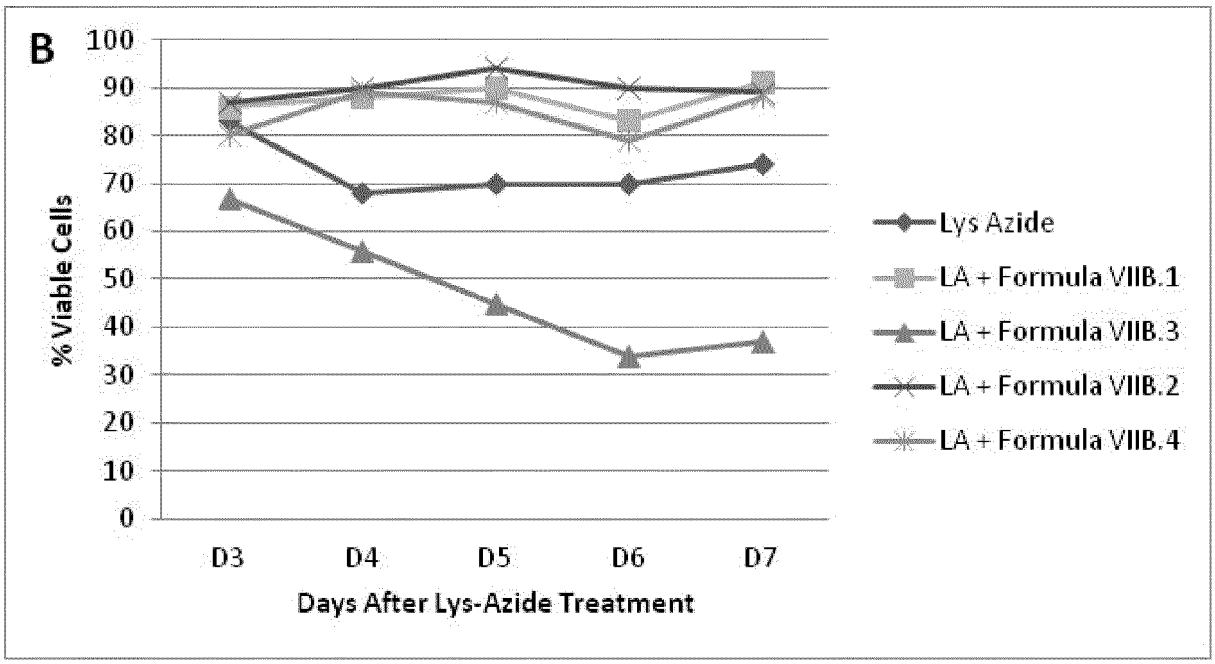
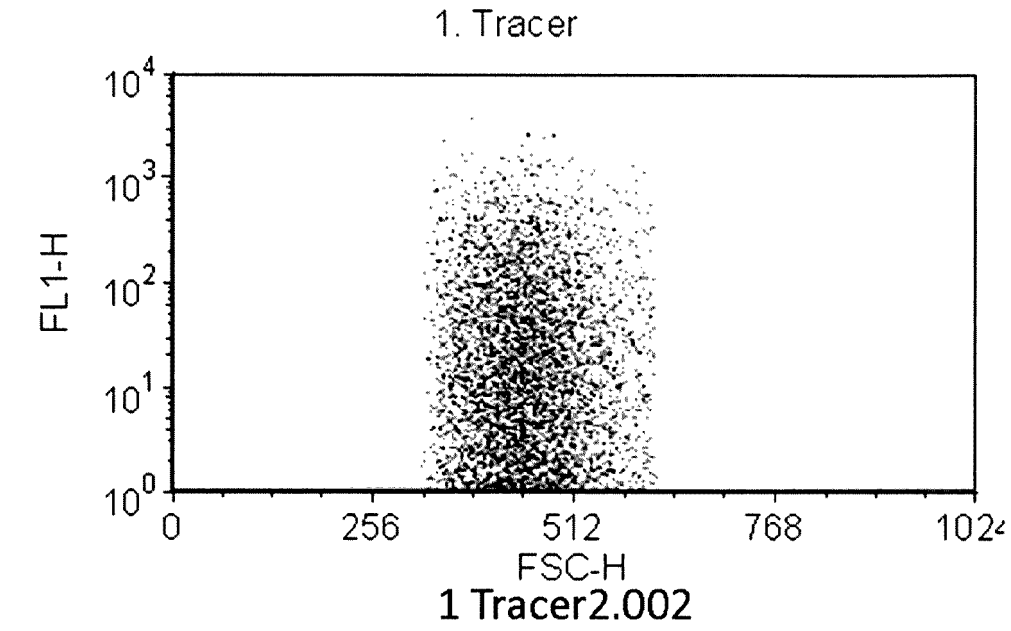

B
100
90
80
70
60
50
40
30
20
10
0
% Viable Cells
D3
D4
D5
D6
D7
Days After Lys-Azide Treatment
Lys Azide
LA + Formula VIIB.1
LA + Formula VIIB.3
LA + Formula VIIB.2
LA + Formula VIIB.4

Figure 16


1. Tracer
FL1-H
FSC-H
1 Tracer2.002

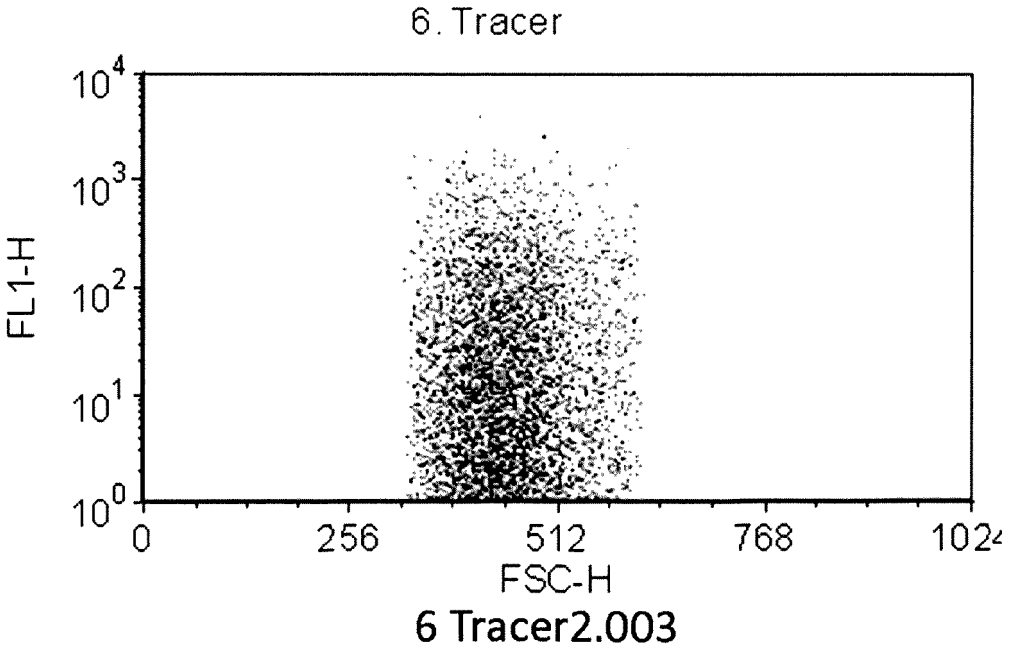
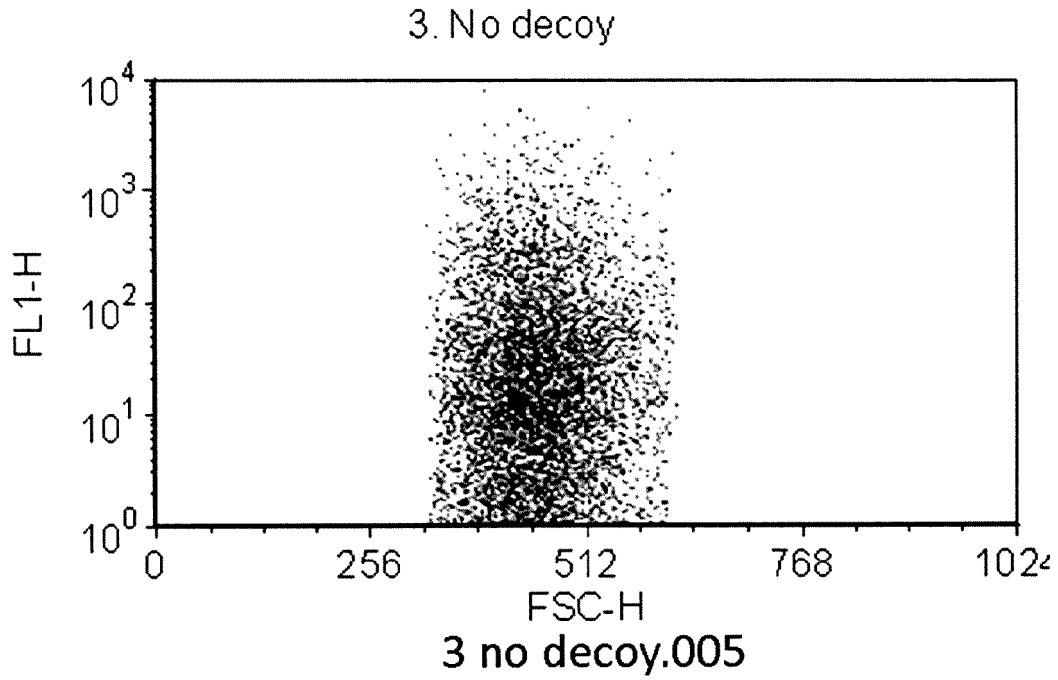

6. Tracer
FL1-H
FSC-H
6 Tracer2.003

Figure 16 cont



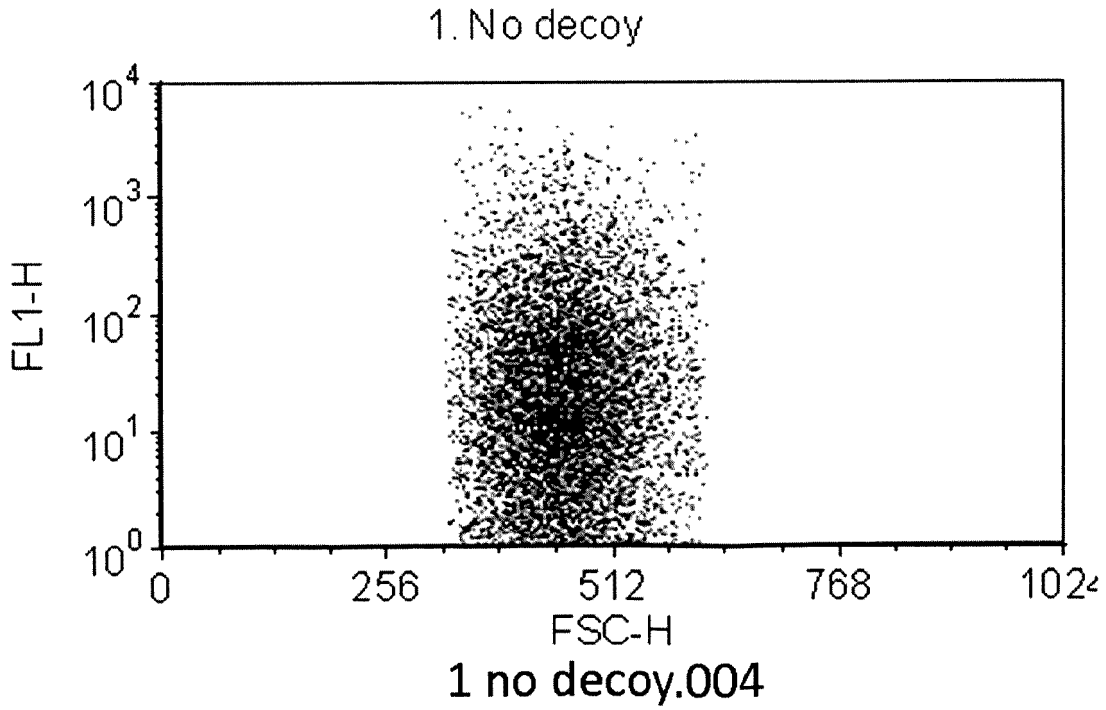
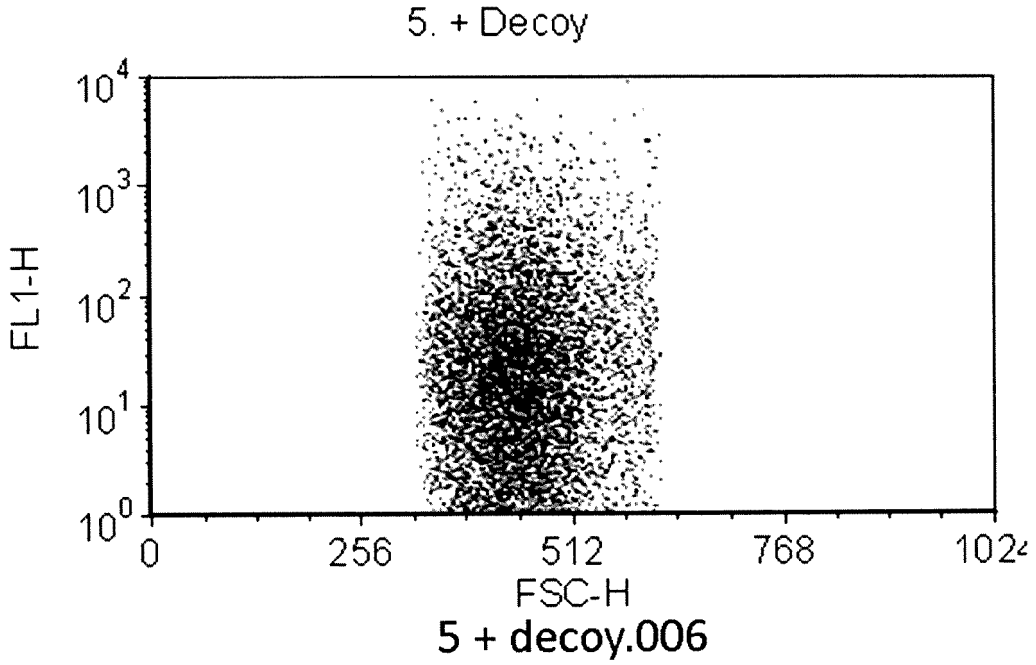


Figure 16 cont



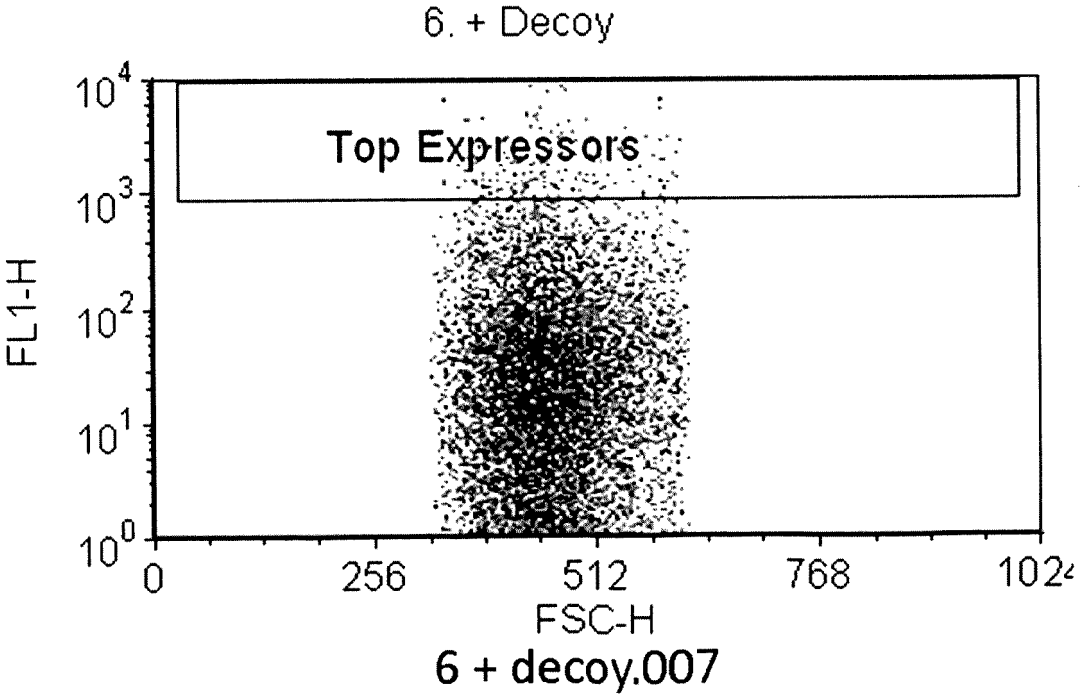


Figure 17

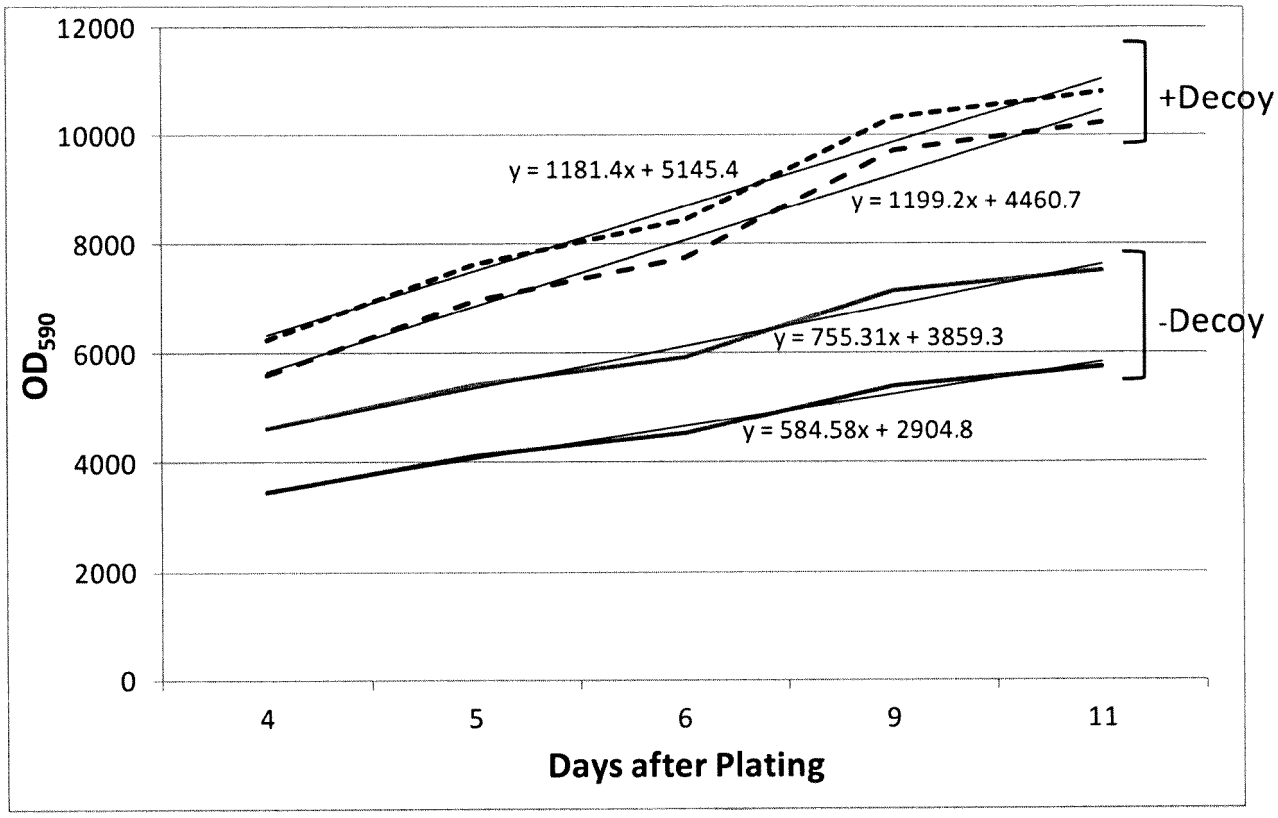

12000
10000
8000
6000
4000
2000
0
OD590
4
5
6
9
11
Days after Plating
y = 1181.4x + 5145.4
y = 1199.2x + 4460.7
y = 755.31x + 3859.3
y = 584.58x + 2904.8
+Decoy
-Decoy

Figure 18

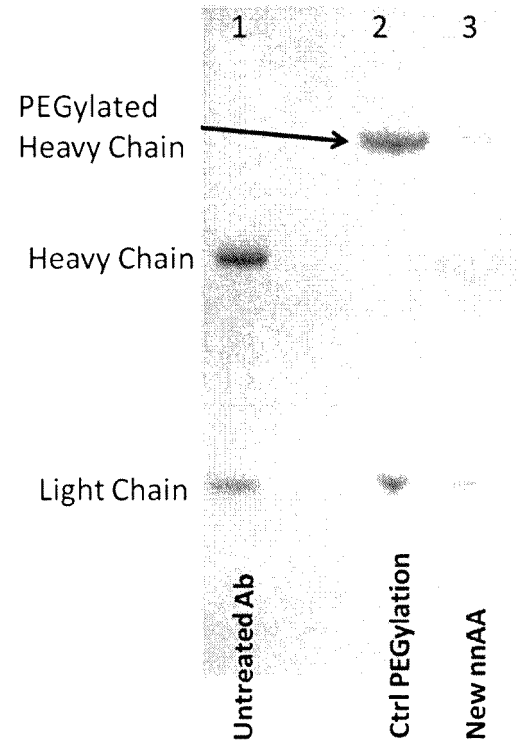

1
2
3
PEGylated
Heavy Chain
Heavy Chain
Light Chain
Untreated Ab
Ctrl PEGylation
New nnAA

Figure 19

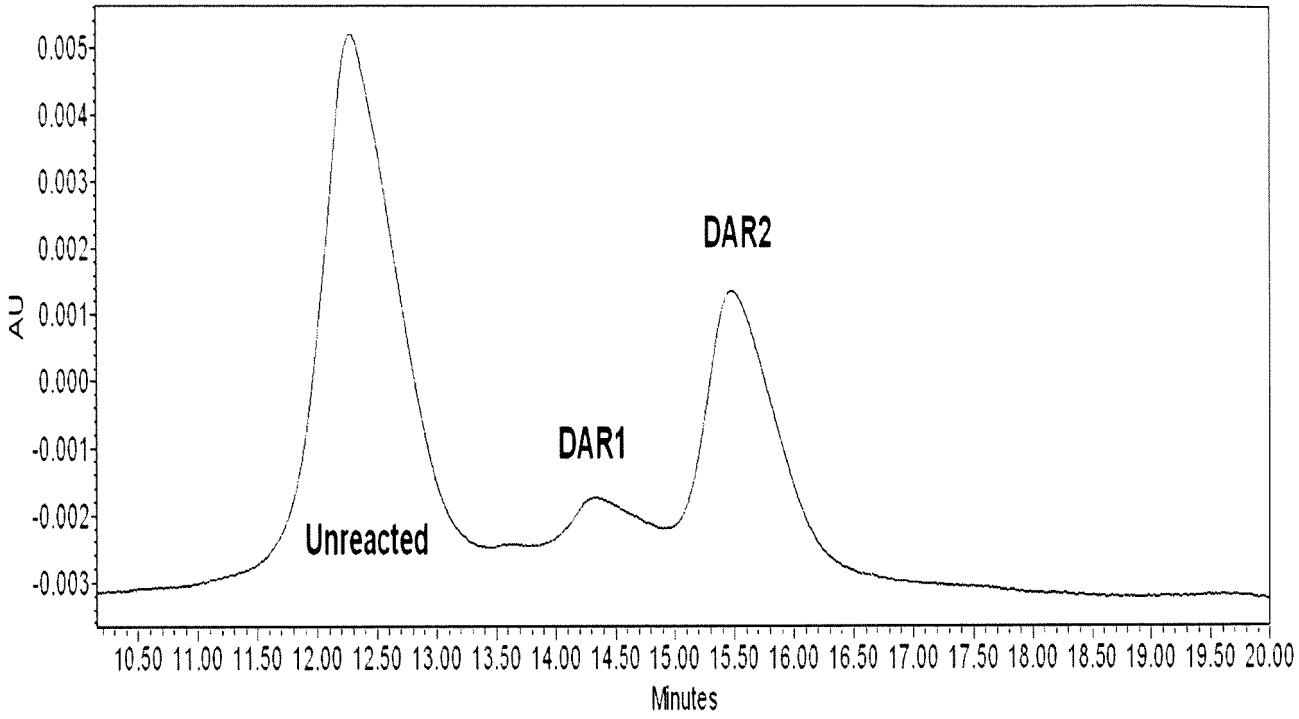

0.005
0.004
0.003
0.002
0.001
0.000
-0.001
-0.002
-0.003
AU
DAR2
DAR1
Unreacted
10.50 11.00 11.50 12.00 12.50 13.00 13.50 14.00 14.50 15.00 15.50 16.00 16.50 17.00 17.50 18.00 18.50 19.00 19.50 20.00
Minutes

Figure 20

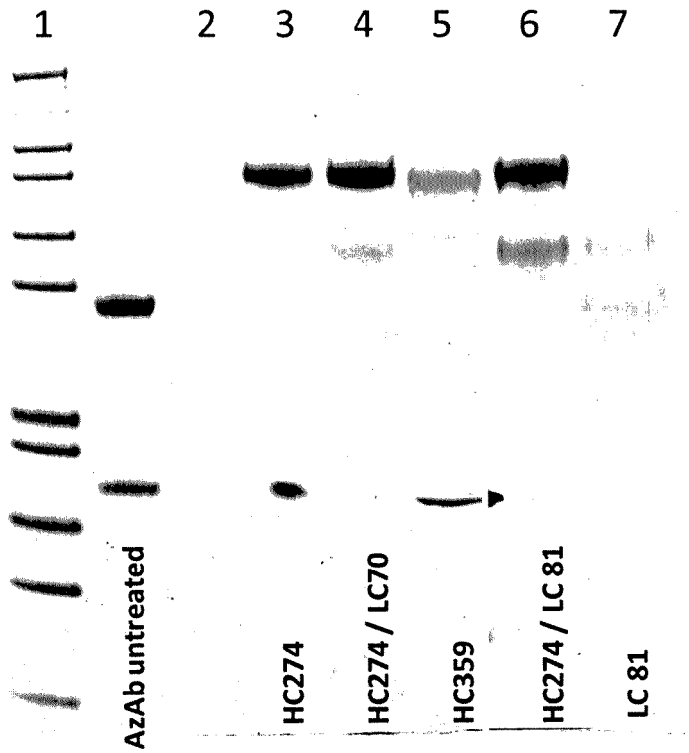


Figure 21

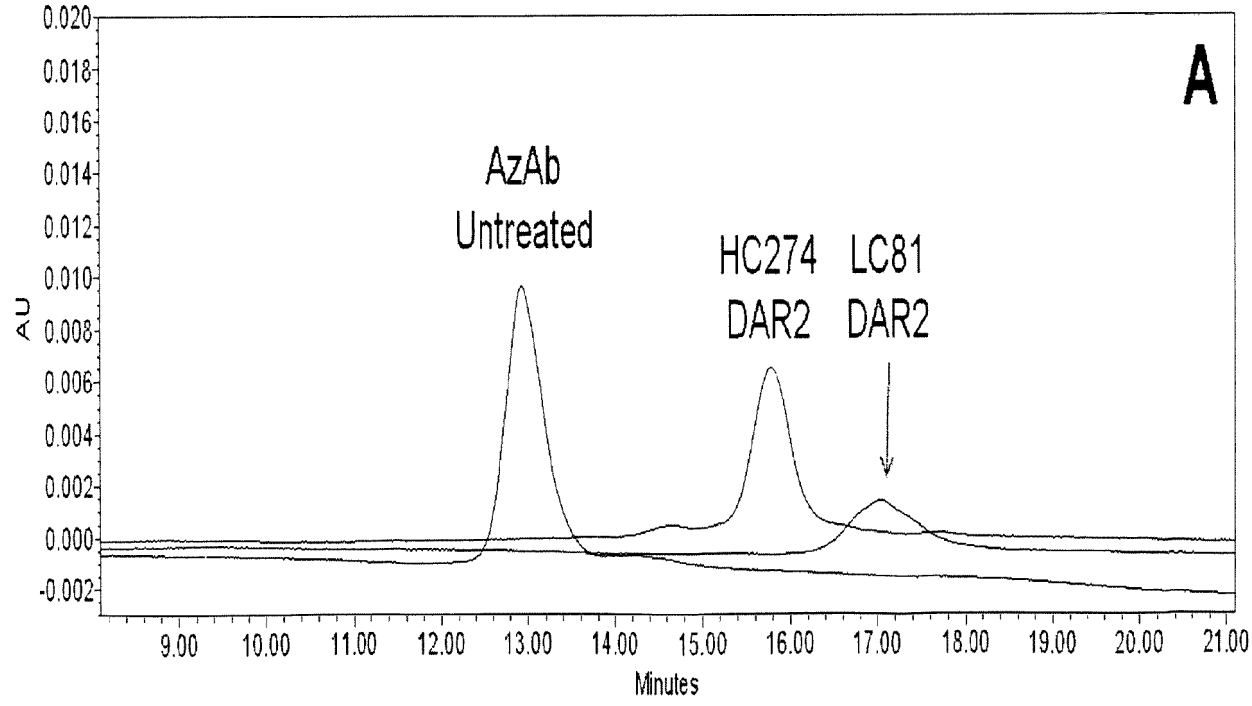
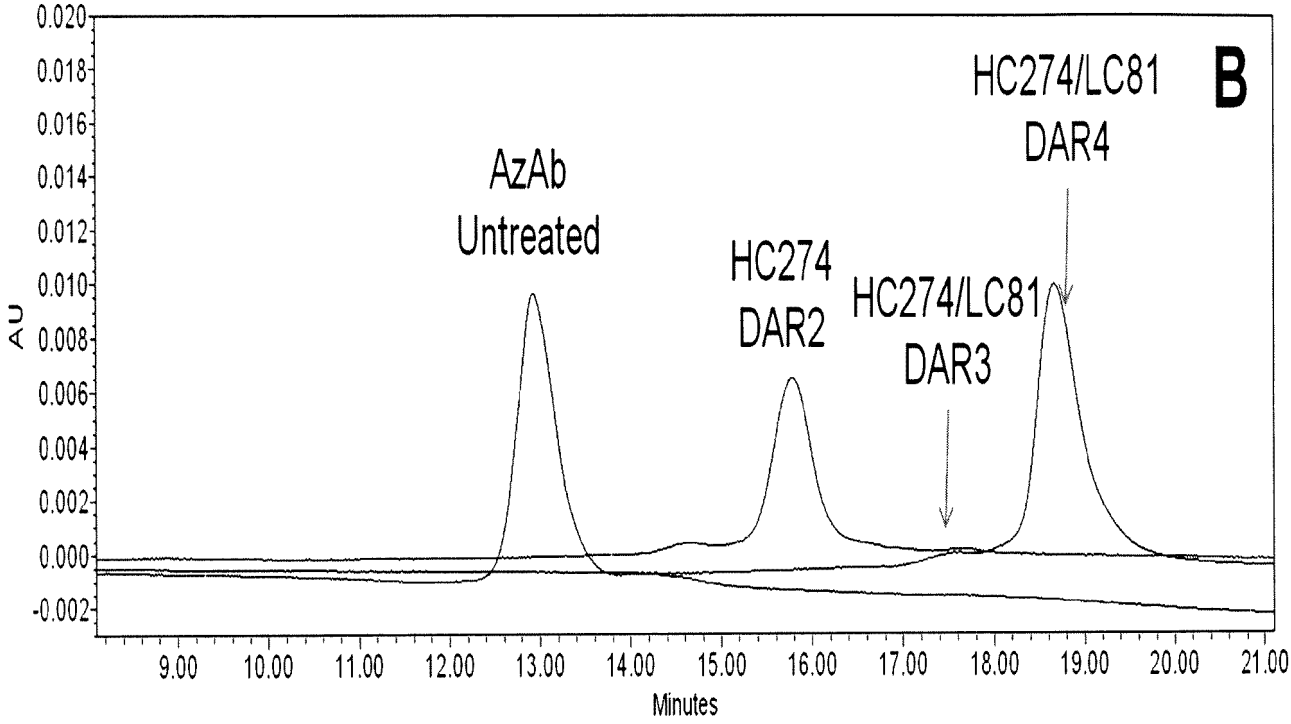


Figure 21 cont



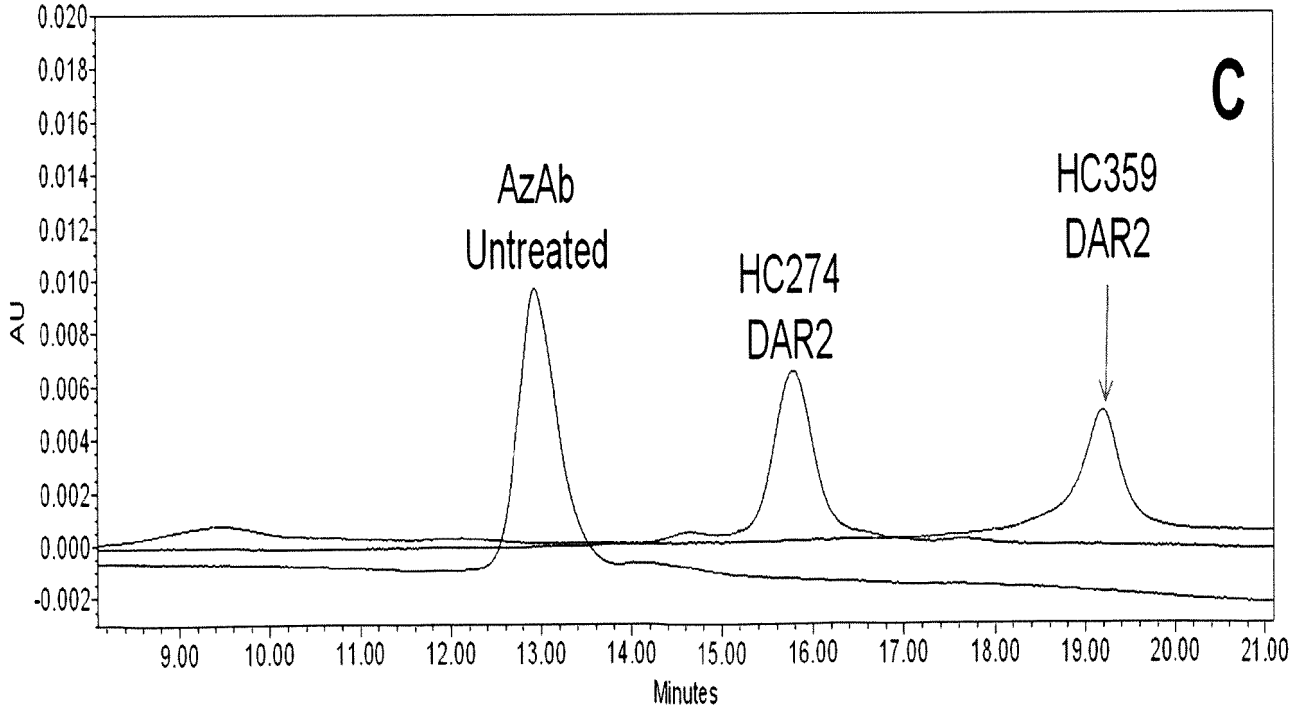


Figure 22.

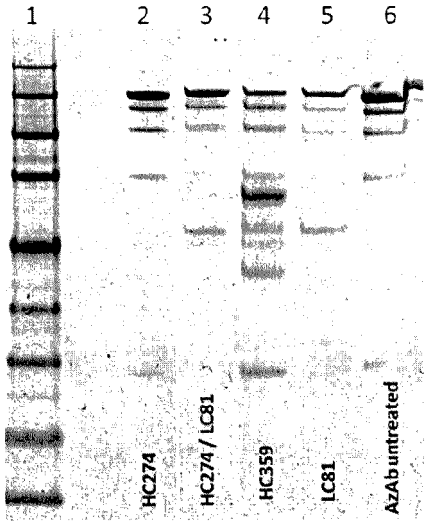


Figure 23

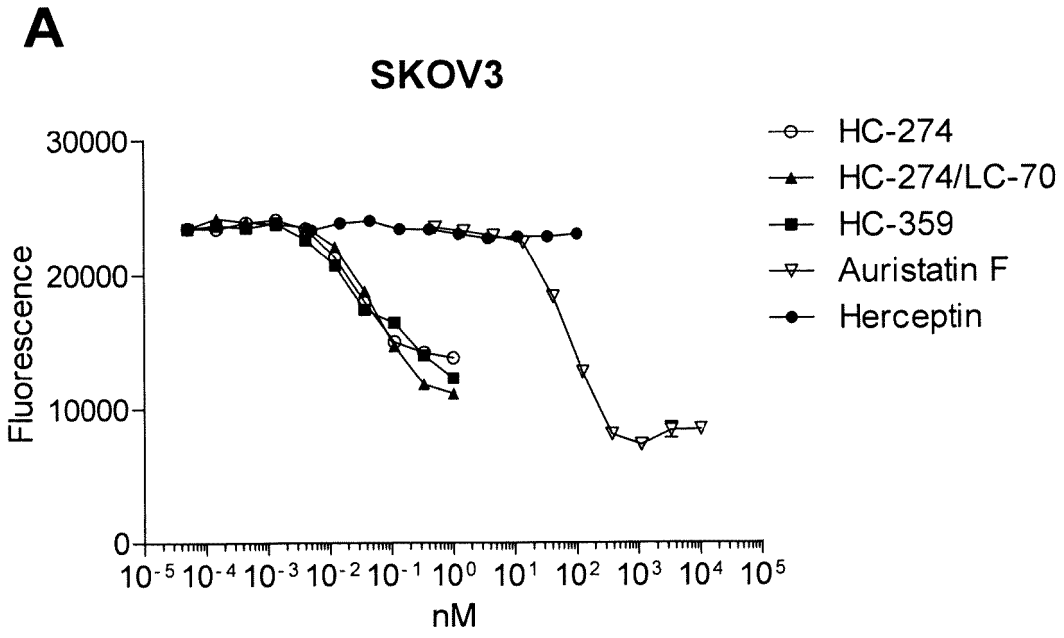
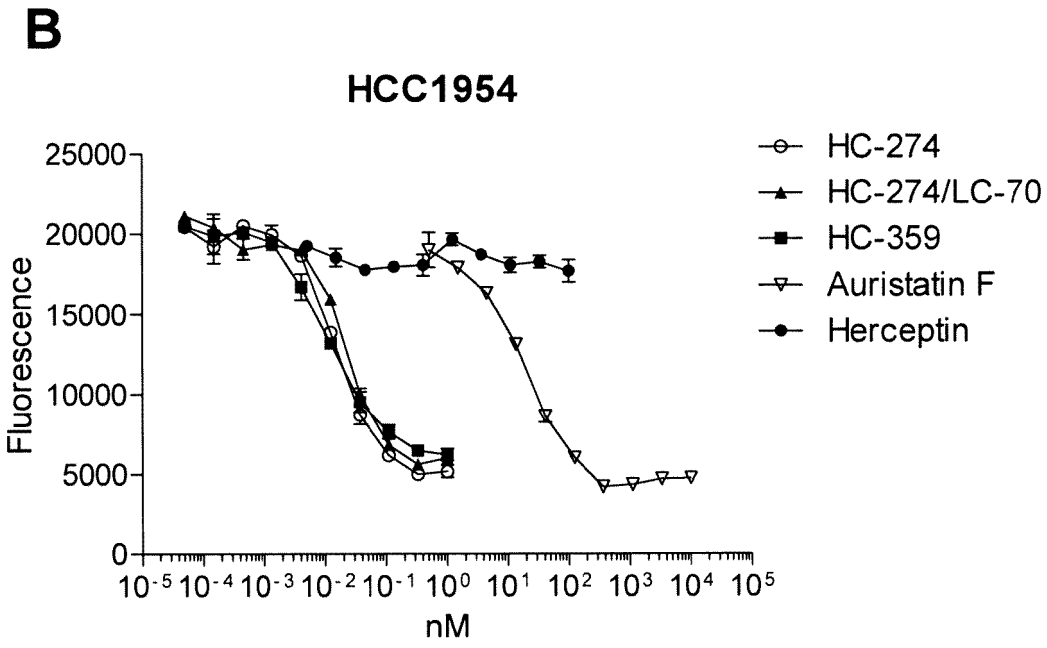


Figure 23 cont



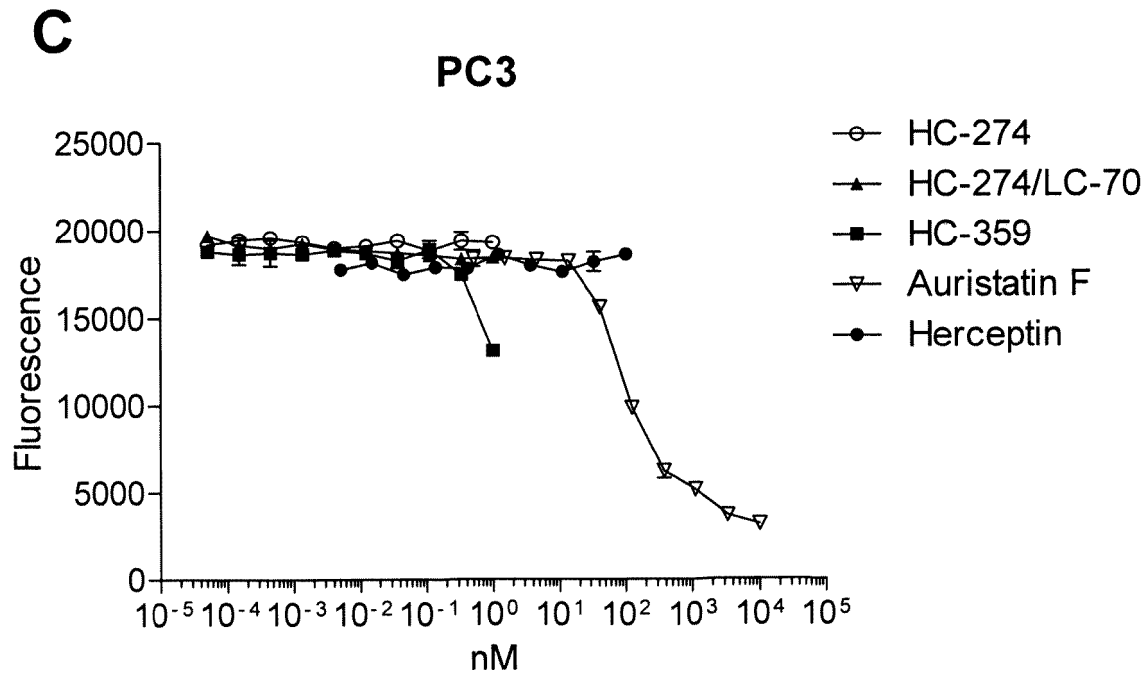
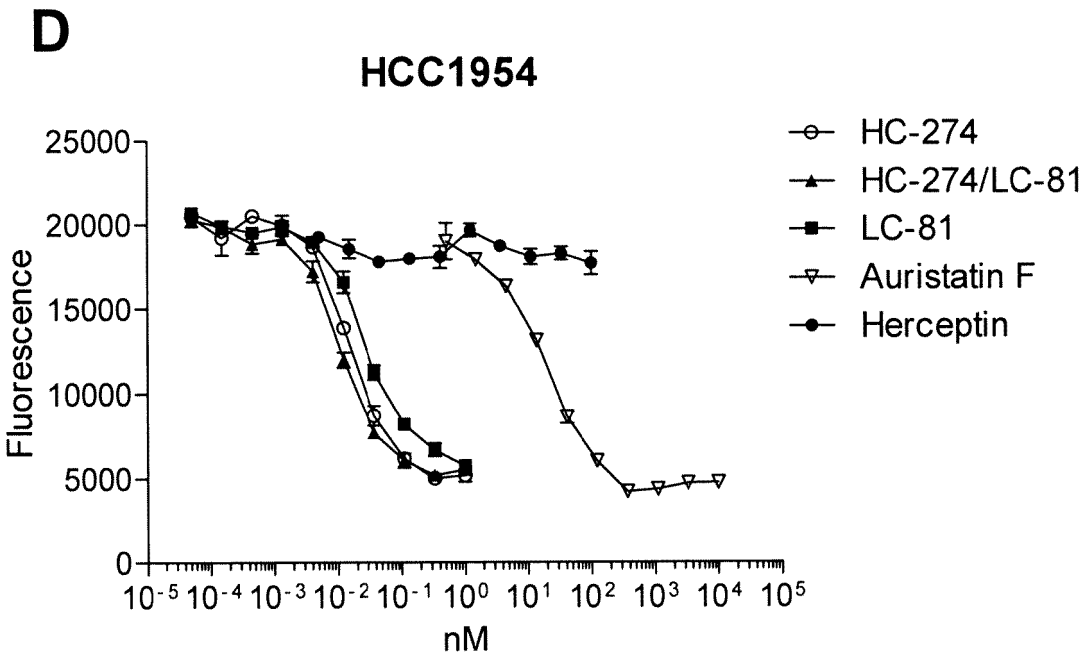


Figure 23 cont



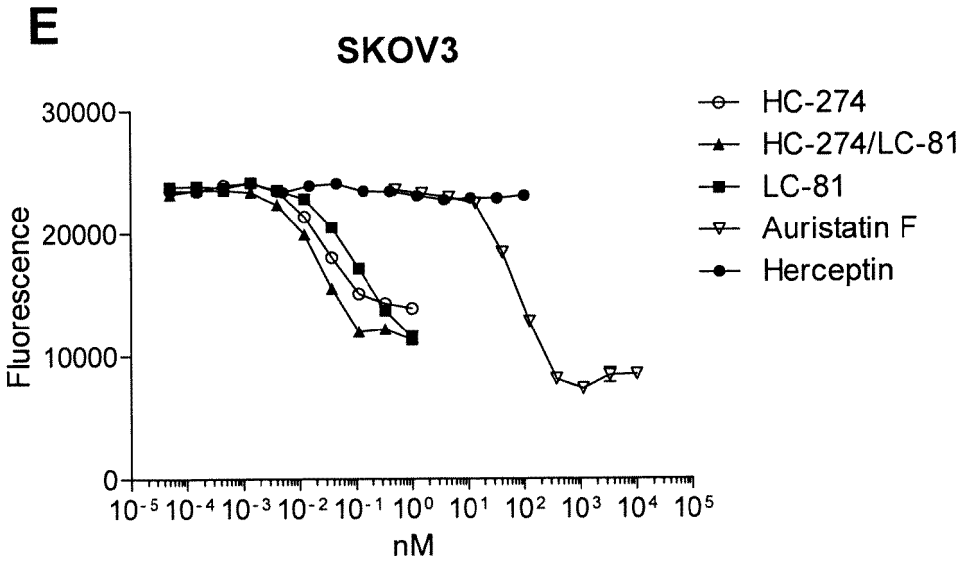


Figure 23 cont

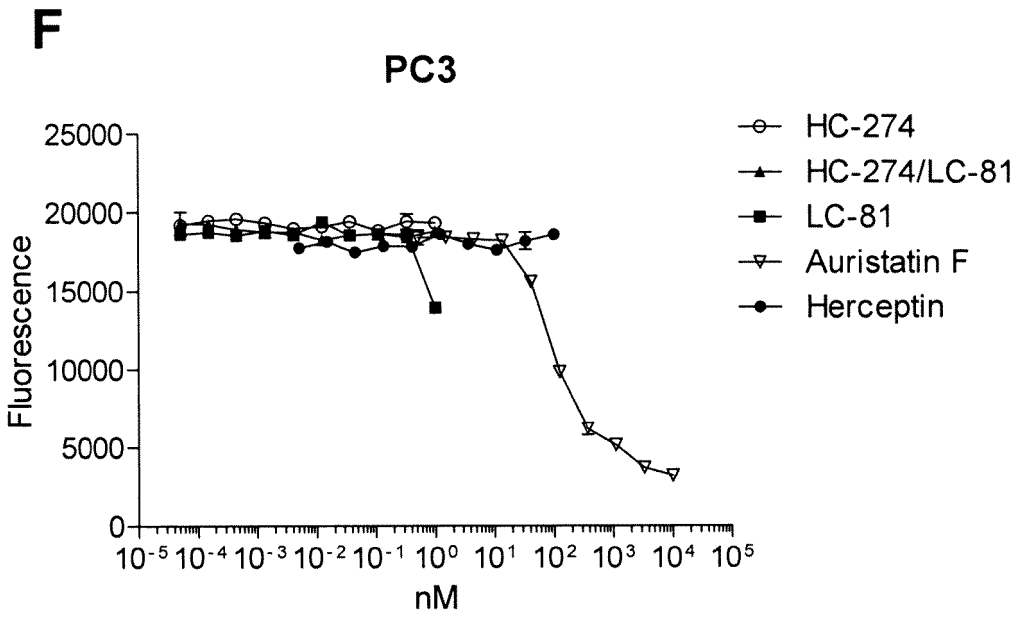


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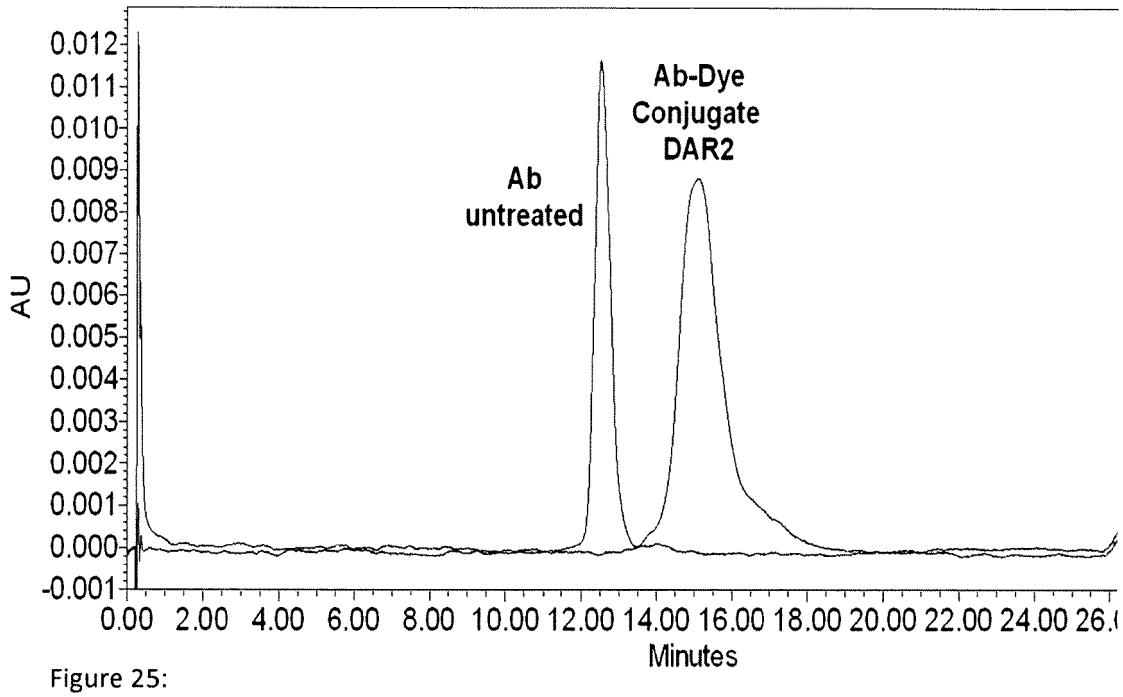


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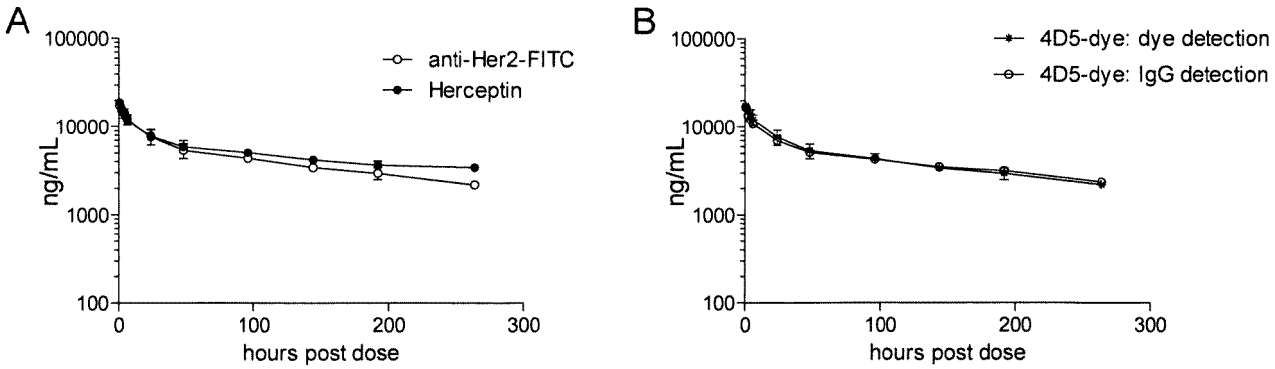
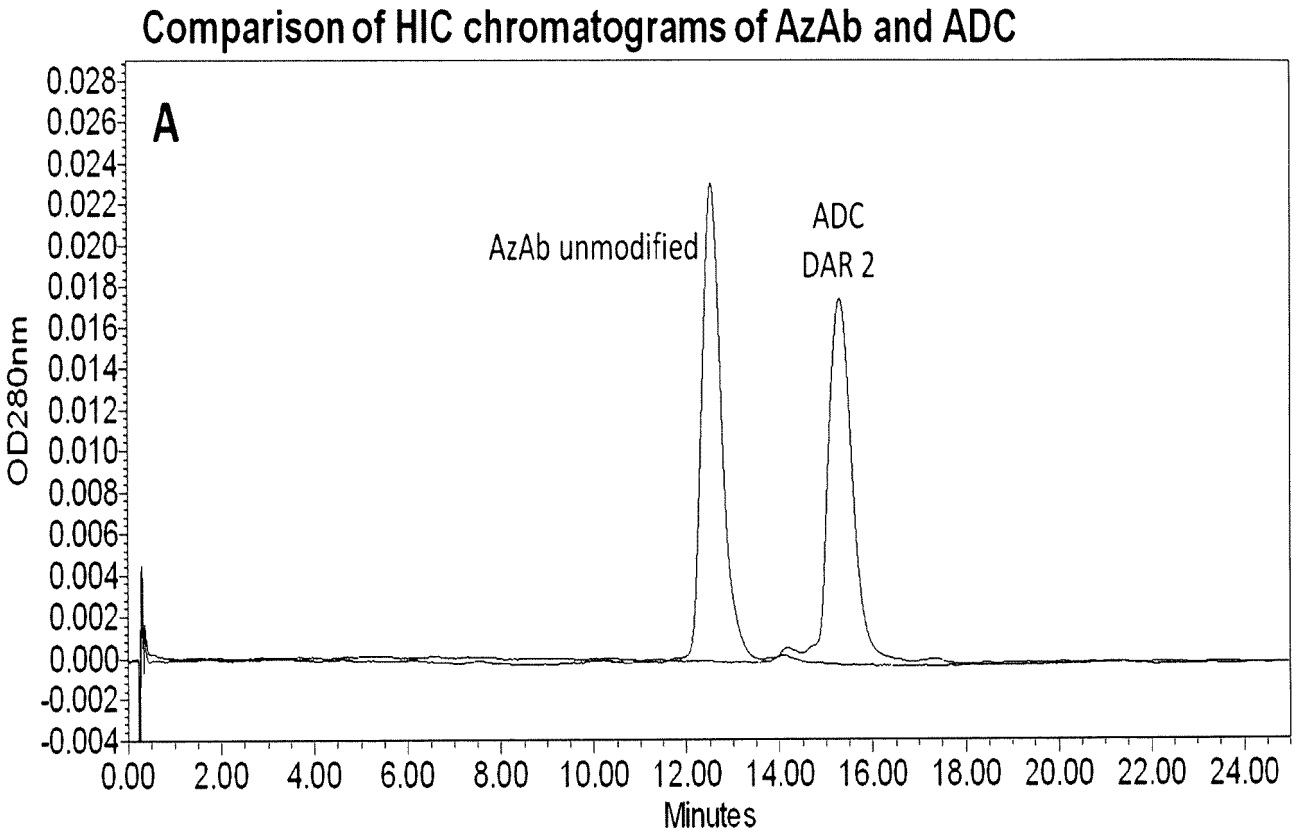


Figure 26


Comparison of HIC chromatograms of AzAb and ADC
A
AzAb unmodified
ADC
DAR 2
OD280nm
0.028
0.026
0.024
0.022
0.020
0.018
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
-0.002
-0.004
0.00
2.00
4.00
6.00
8.00
10.00
12.00
14.00
16.00
18.00
20.00
22.00
24.00
Minutes

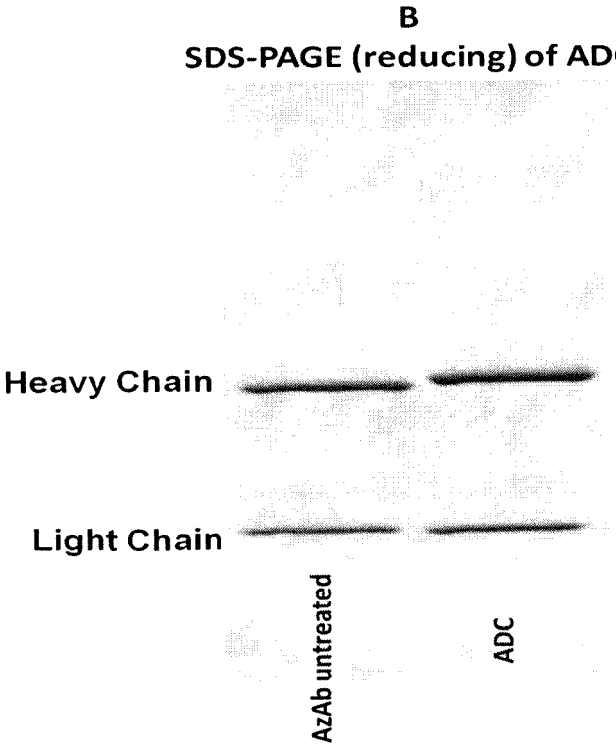

B
SDS-PAGE (reducing) of ADC
Heavy Chain
Light Chain
AzAb untreated
ADC

Figure 27

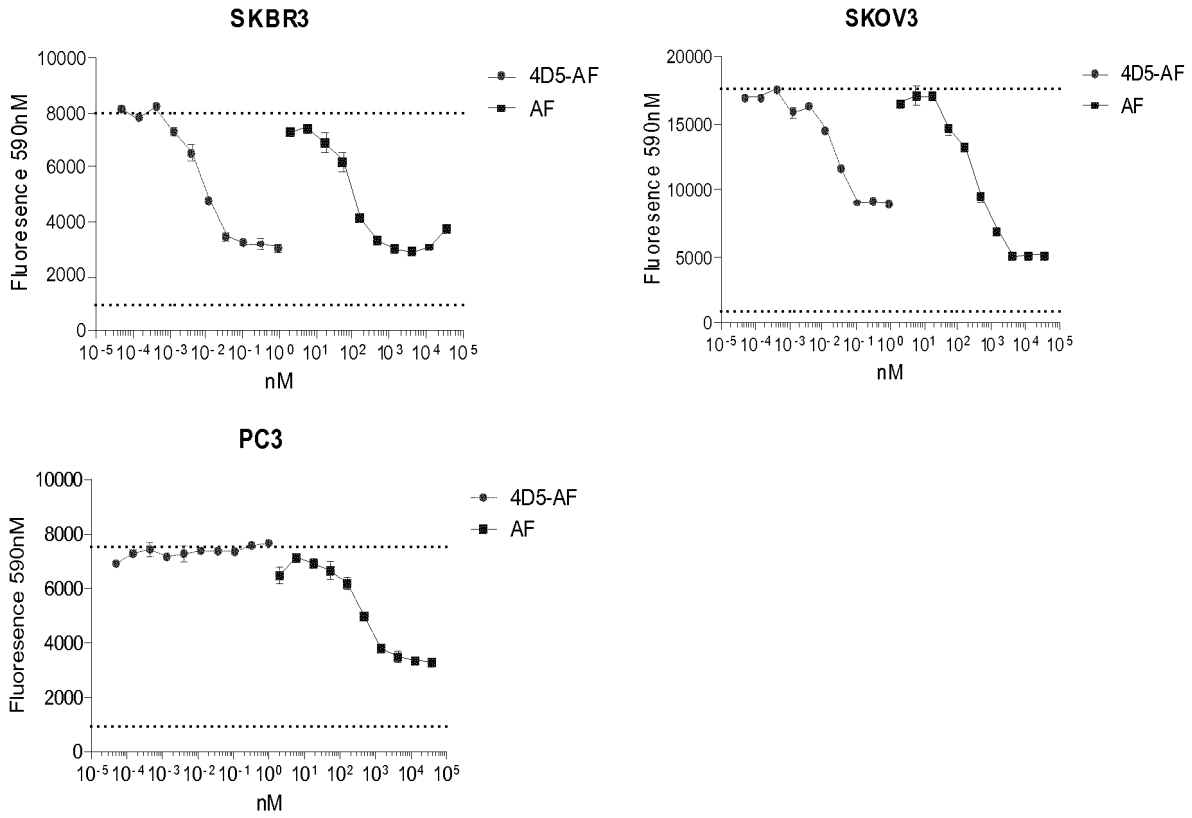


Figure 28

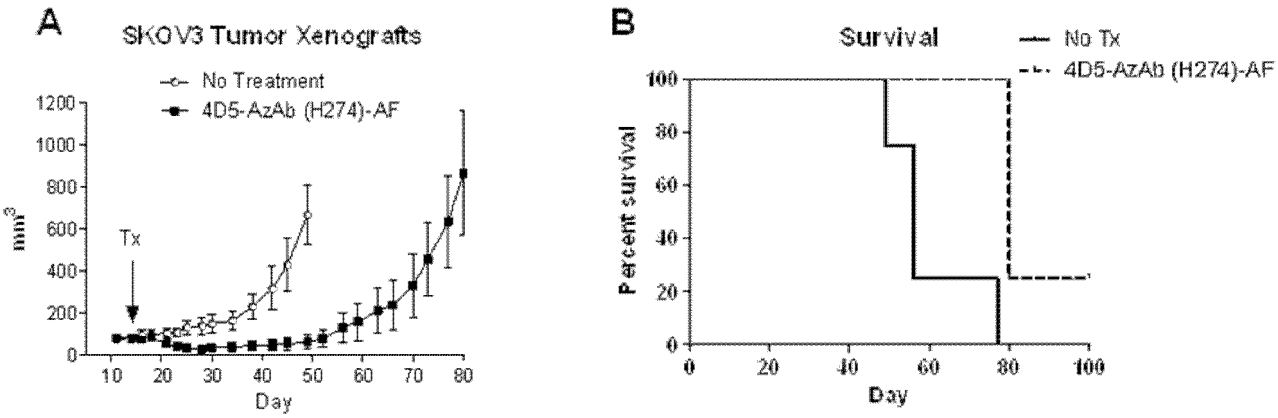


Figure 29

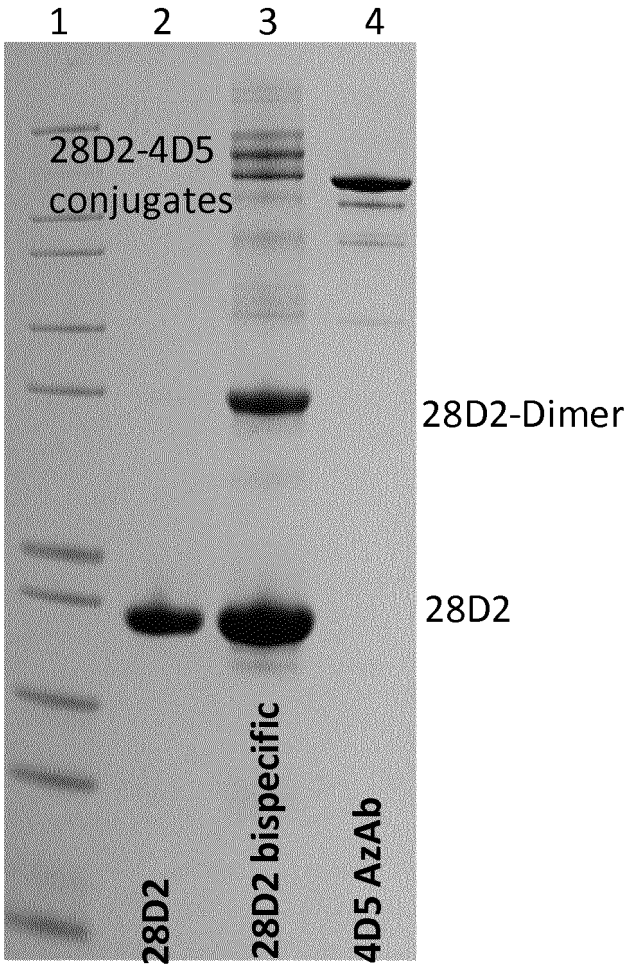
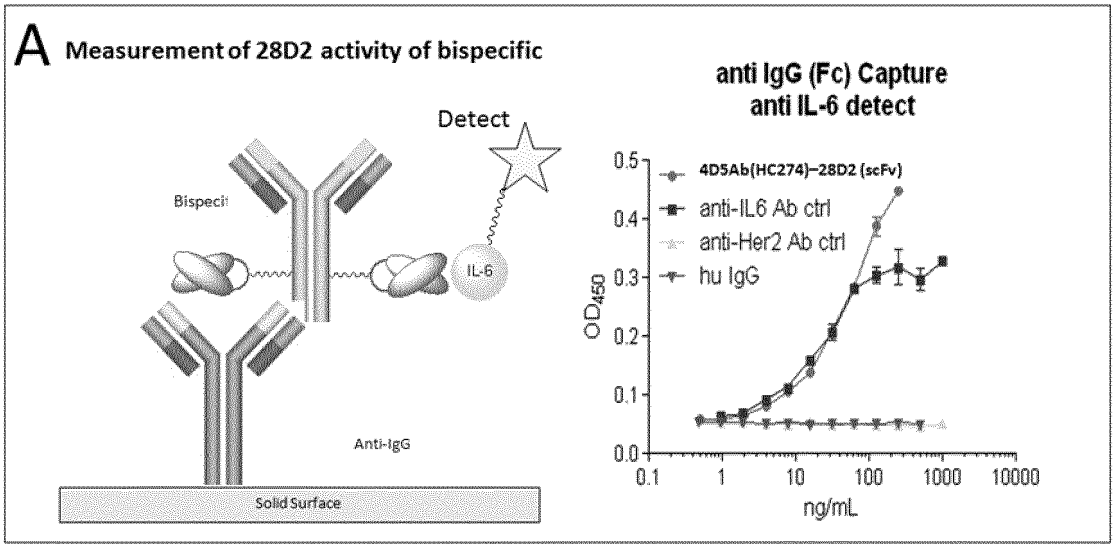
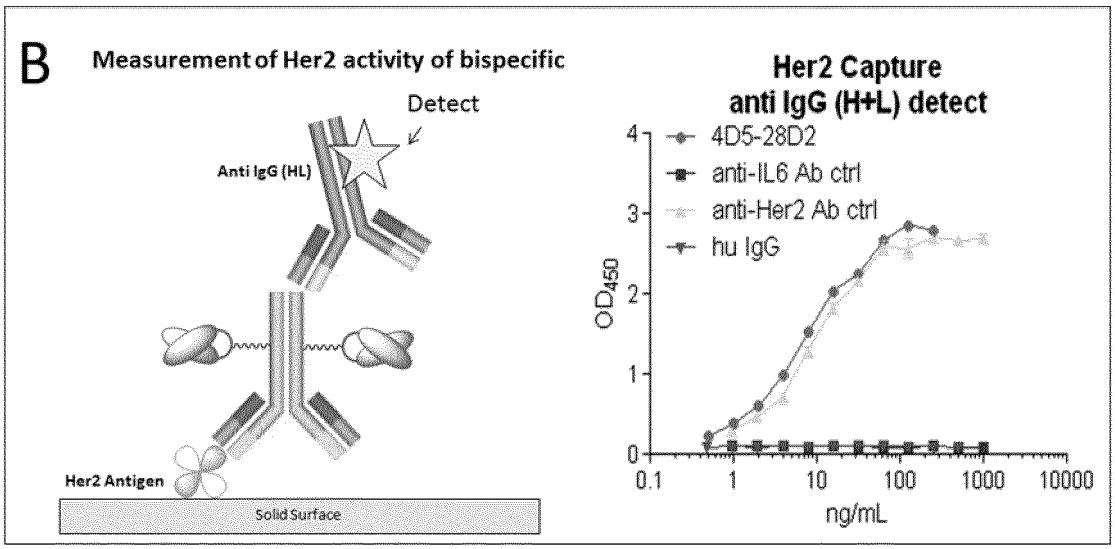

1
2
3
4
28D2-4D5
conjugates
28D2-Dimer
28D2
28D2
28D2 bispecific
4D5 AzAb

Figure 30


A
Measurement of 28D2 activity of bispecific
Detect
Bispecif
IL-6
Anti-IgG
Solid Surface
anti IgG (Fc) Capture
anti IL-6 detect
4D5Ab(HC274)–28D2 (scFv)
anti-IL6 Ab ctrl
anti-Her2 Ab ctrl
hu IgG
OD450
ng/mL


B
Measurement of Her2 activity of bispecific
Detect
Anti IgG (HL)
Her2 Antigen
Solid Surface
Her2 Capture
anti IgG (H+L) detect
4D5-28D2
anti-IL6 Ab ctrl
anti-Her2 Ab ctrl
hu IgG
OD450
ng/mL

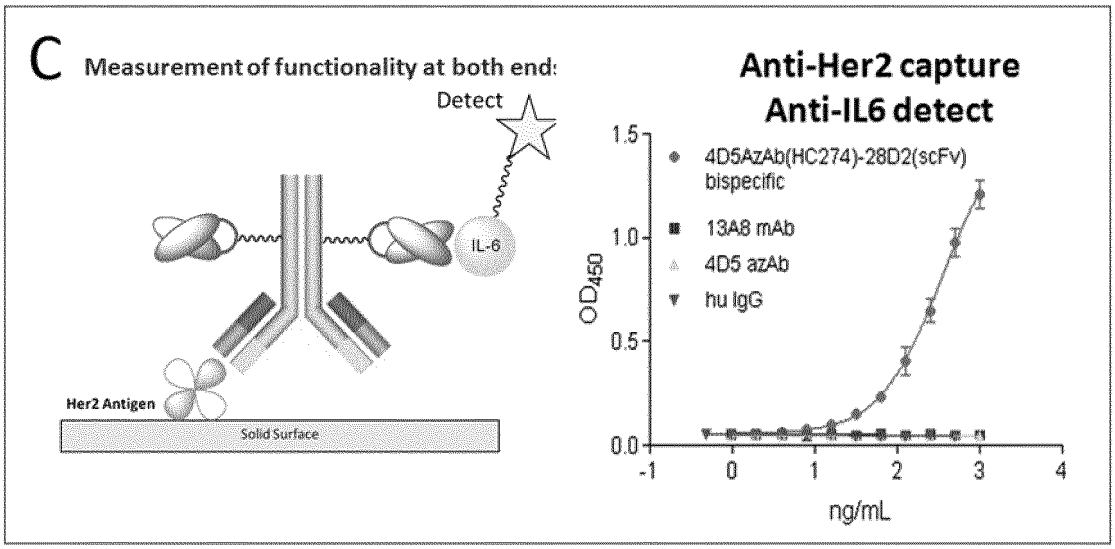

C
Measurement of functionality at both end
Detect
IL-6
Her2 Antigen
Solid Surface
Anti-Her2 capture
Anti-IL6 detect
4D5AzAb(HC274)-28D2(scFv)
bispecific
13A8 mAb
4D5 azAb
hu IgG
OD450
ng/mL

Figure 31

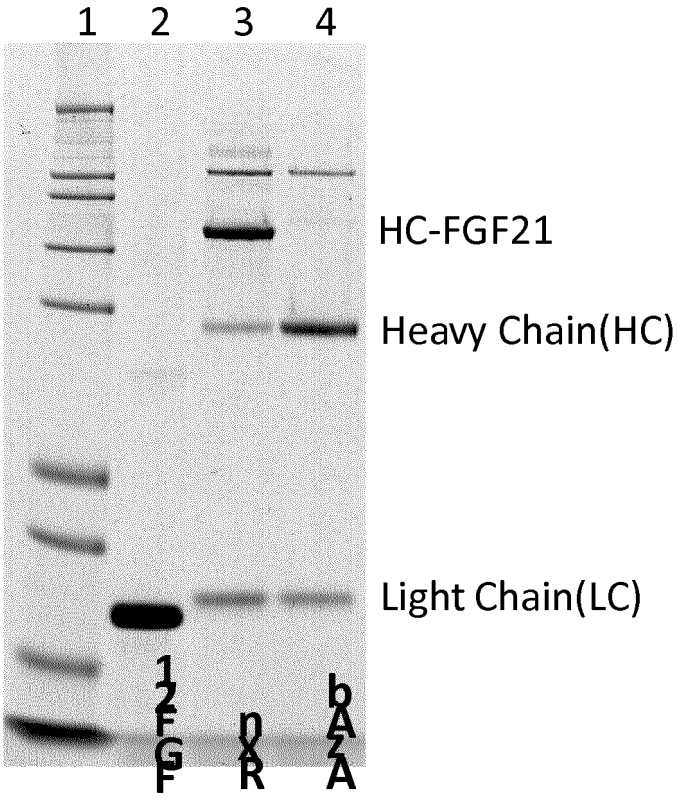


Figure 32

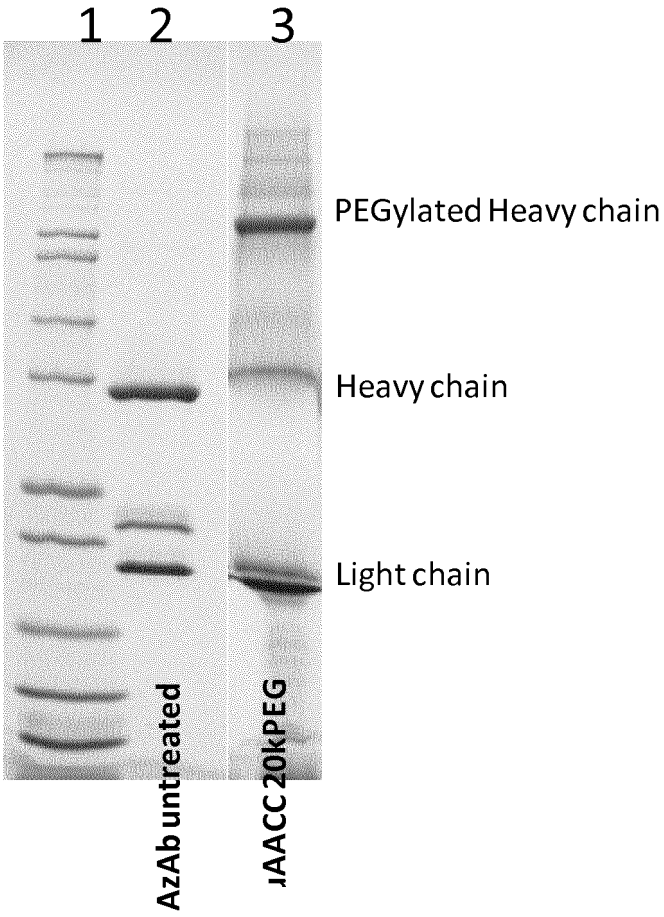


Figure 33

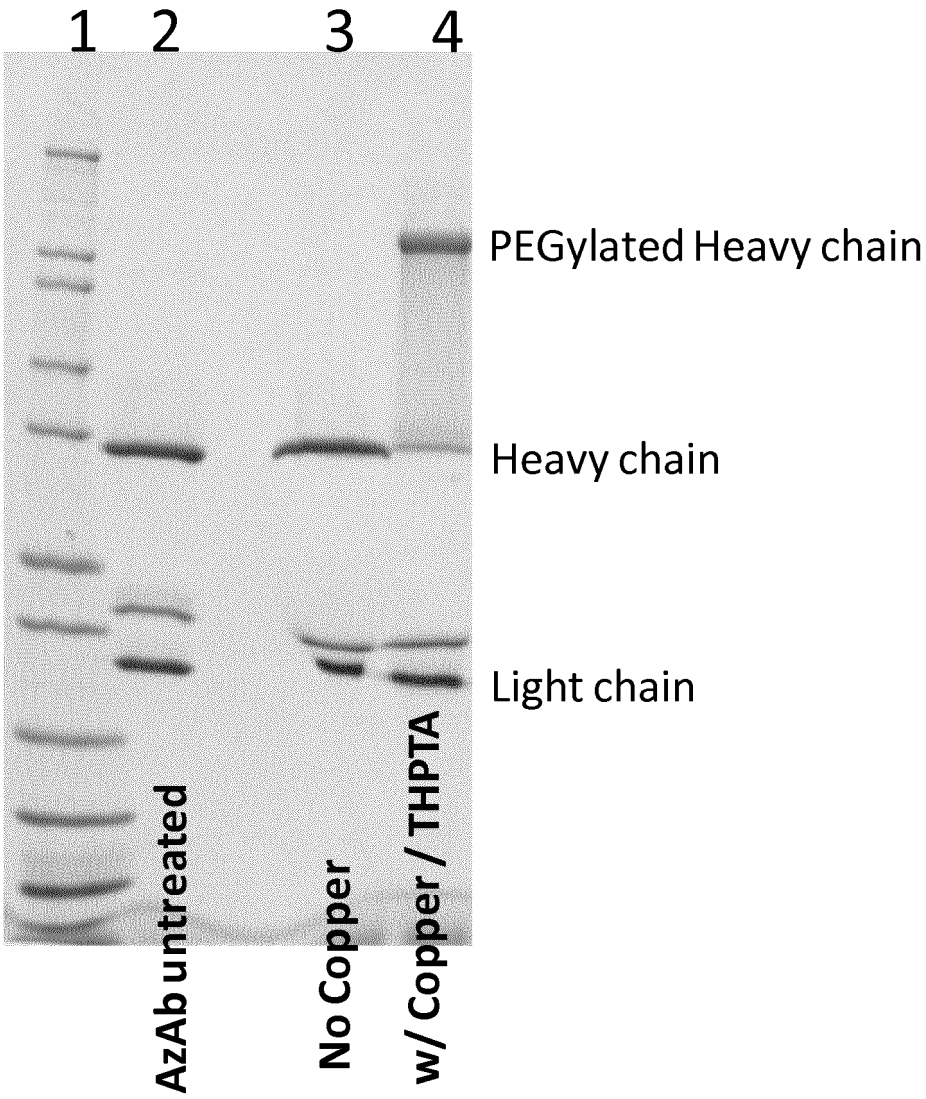

1
2
3
4
PEGylated Heavy chain
Heavy chain
Light chain
AzAb untreated
No Copper
w/ Copper / THPTA

Figure 34

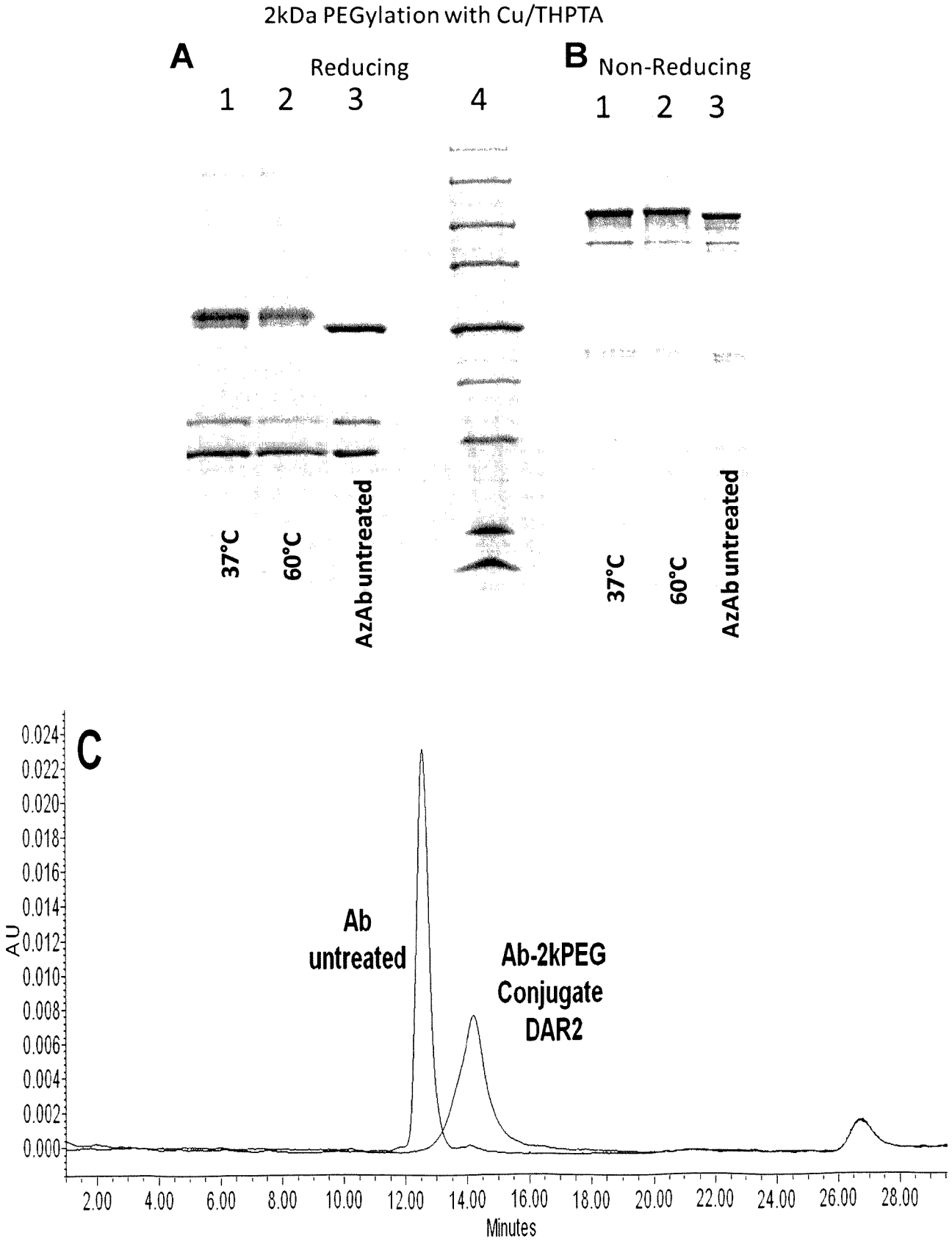

2kDa PEGylation with Cu/THPTA
A
Reducing
1
2
3
4
37°C
60°C
AzAb untreated
B
Non-Reducing
1
2
3
37°C
60°C
AzAb untreated
C
AU
0.024
0.022
0.020
0.018
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
Ab
untreated
Ab-2kPEG
Conjugate
DAR2
2.00
4.00
6.00
8.00
10.00
12.00
14.00
16.00
18.00
20.00
22.00
24.00
26.00
28.00
Minutes

Figure 35

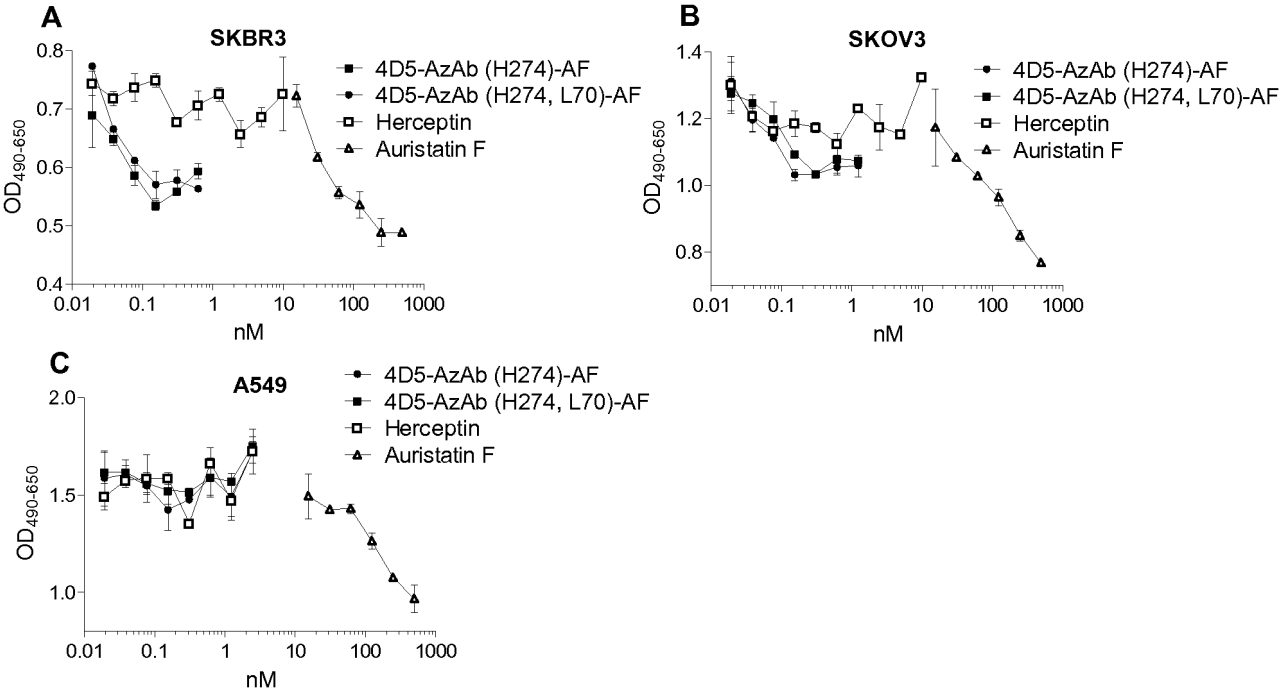


Figure 36 :

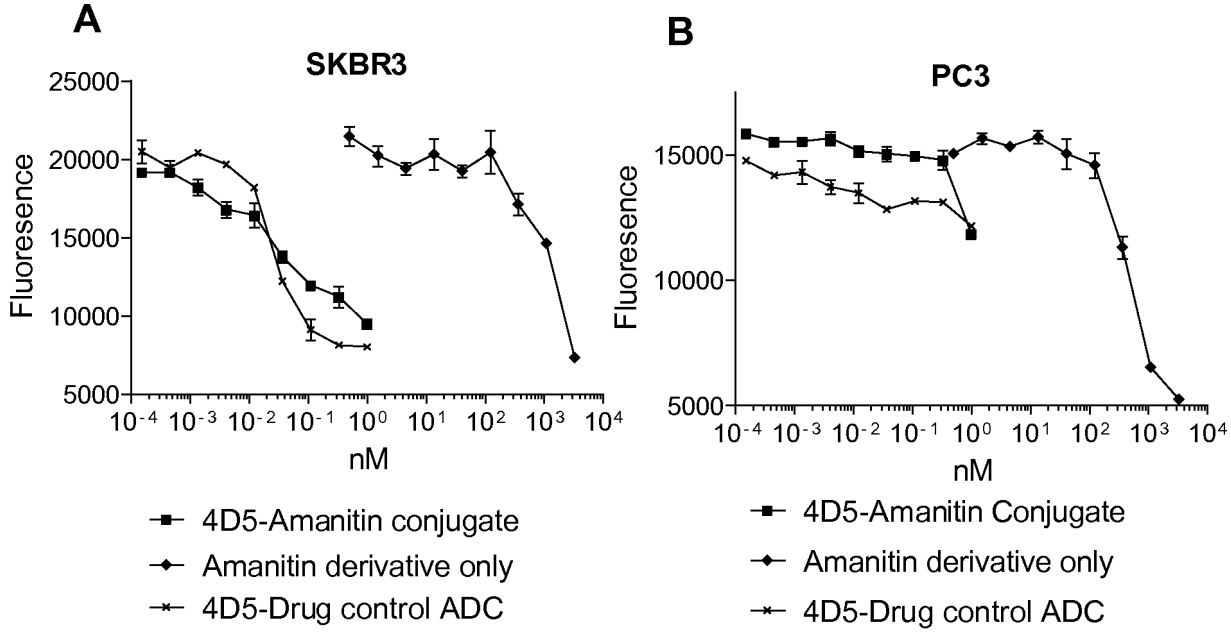
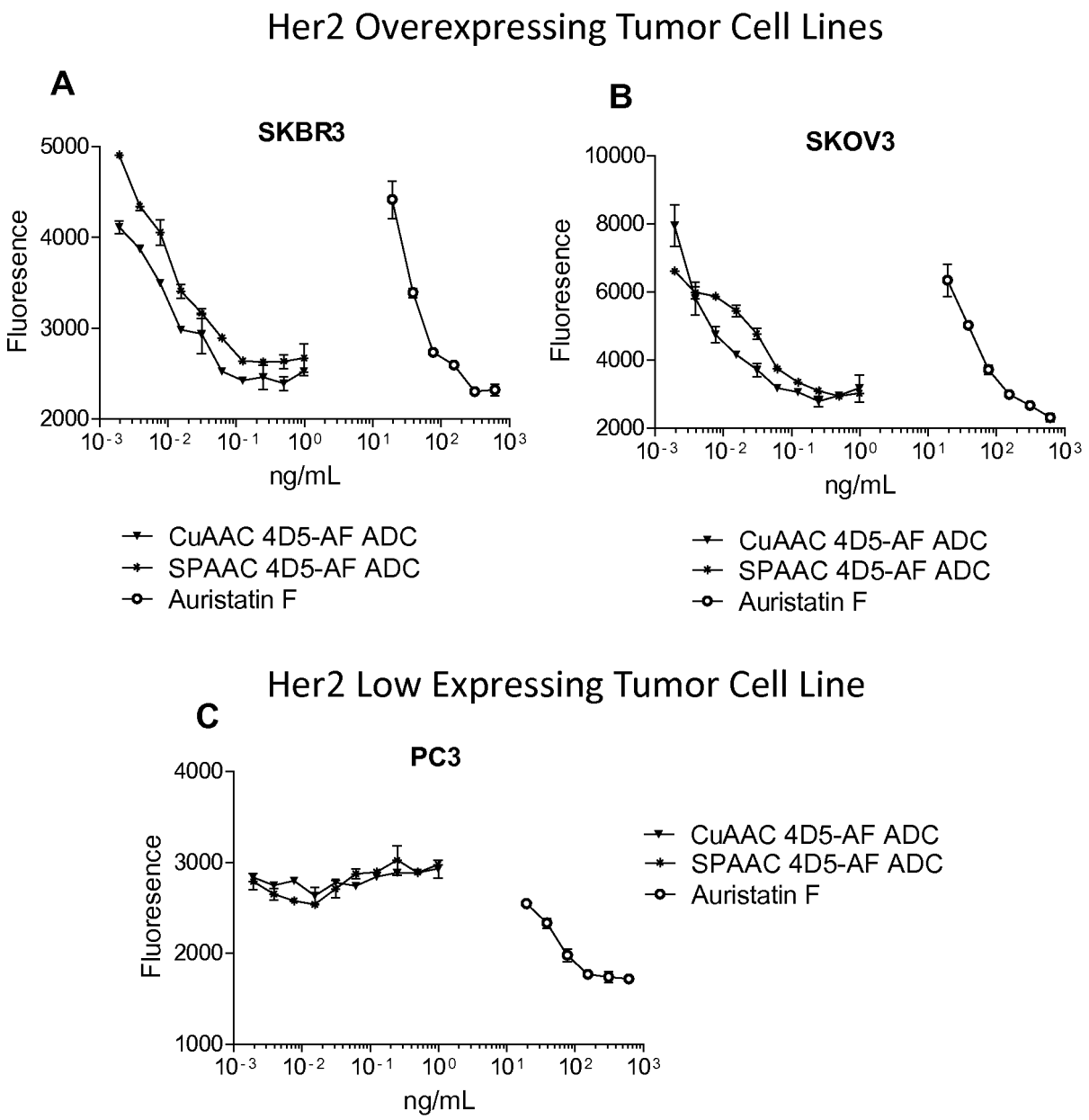


Figure 37


Her2 Overexpressing Tumor Cell Lines
A
SKBR3
Fluoresence
5000
4000
3000
2000
10-3 10-2 10-1 100 101 102 103
ng/mL
B
SKOV3
Fluoresence
10000
8000
6000
4000
2000
10-3 10-2 10-1 100 101 102 103
ng/mL
CuAAC 4D5-AF ADC
SPAAC 4D5-AF ADC
Auristatin F
CuAAC 4D5-AF ADC
SPAAC 4D5-AF ADC
Auristatin F
Her2 Low Expressing Tumor Cell Line
C
PC3
Fluoresence
4000
3000
2000
1000
10-3 10-2 10-1 100 101 102 103
ng/mL
CuAAC 4D5-AF ADC
SPAAC 4D5-AF ADC
Auristatin F

Overlay of HIC chromatograms of a CuAAC derived 4D5-2AzAb(HC274)ADC with the untreated antibody.

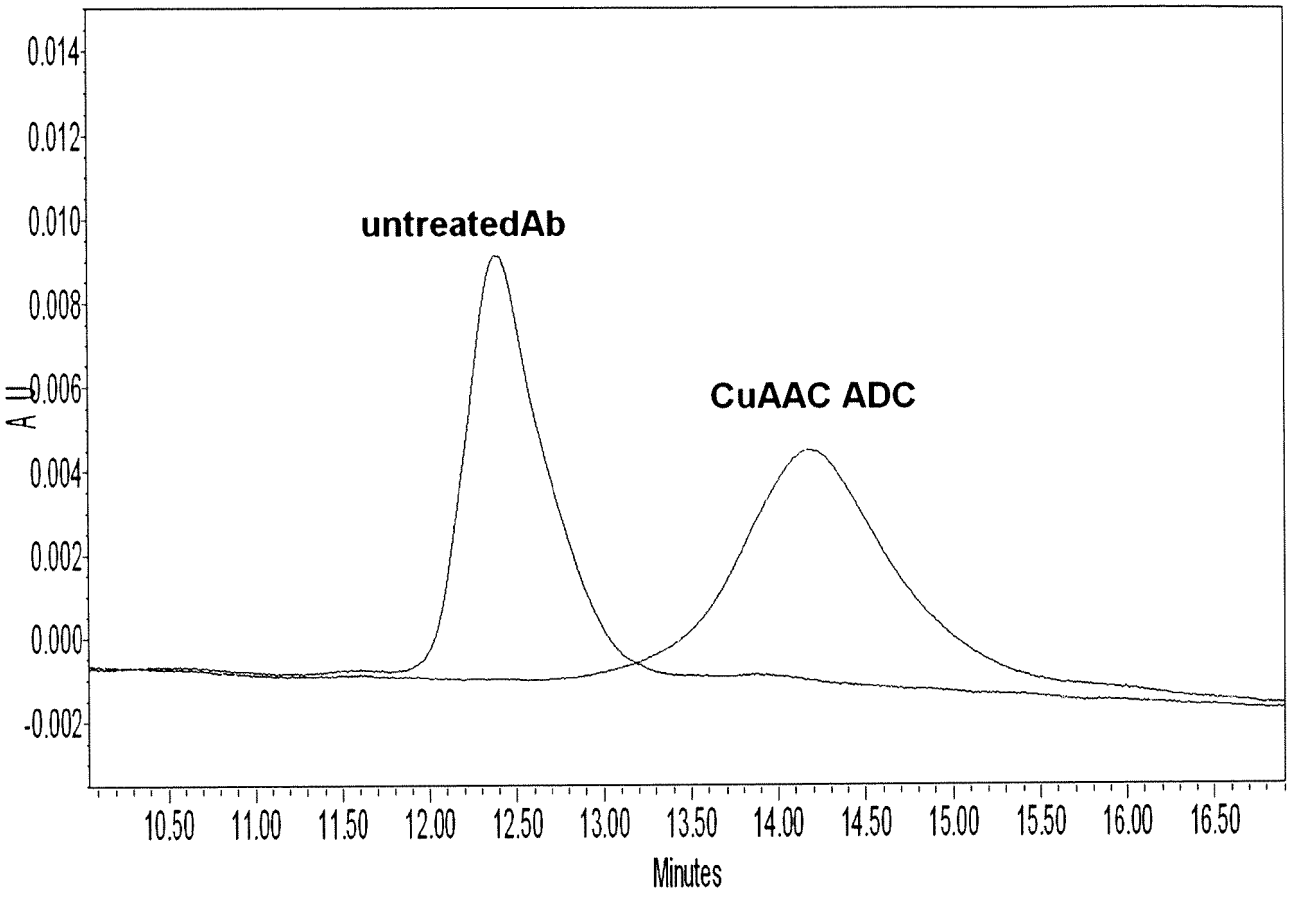


Figure 39

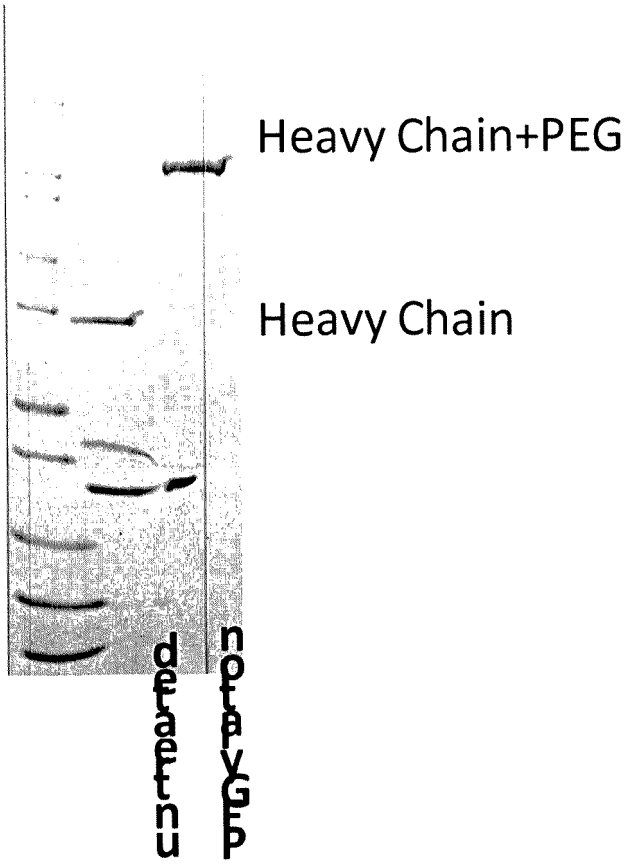


Figure 40

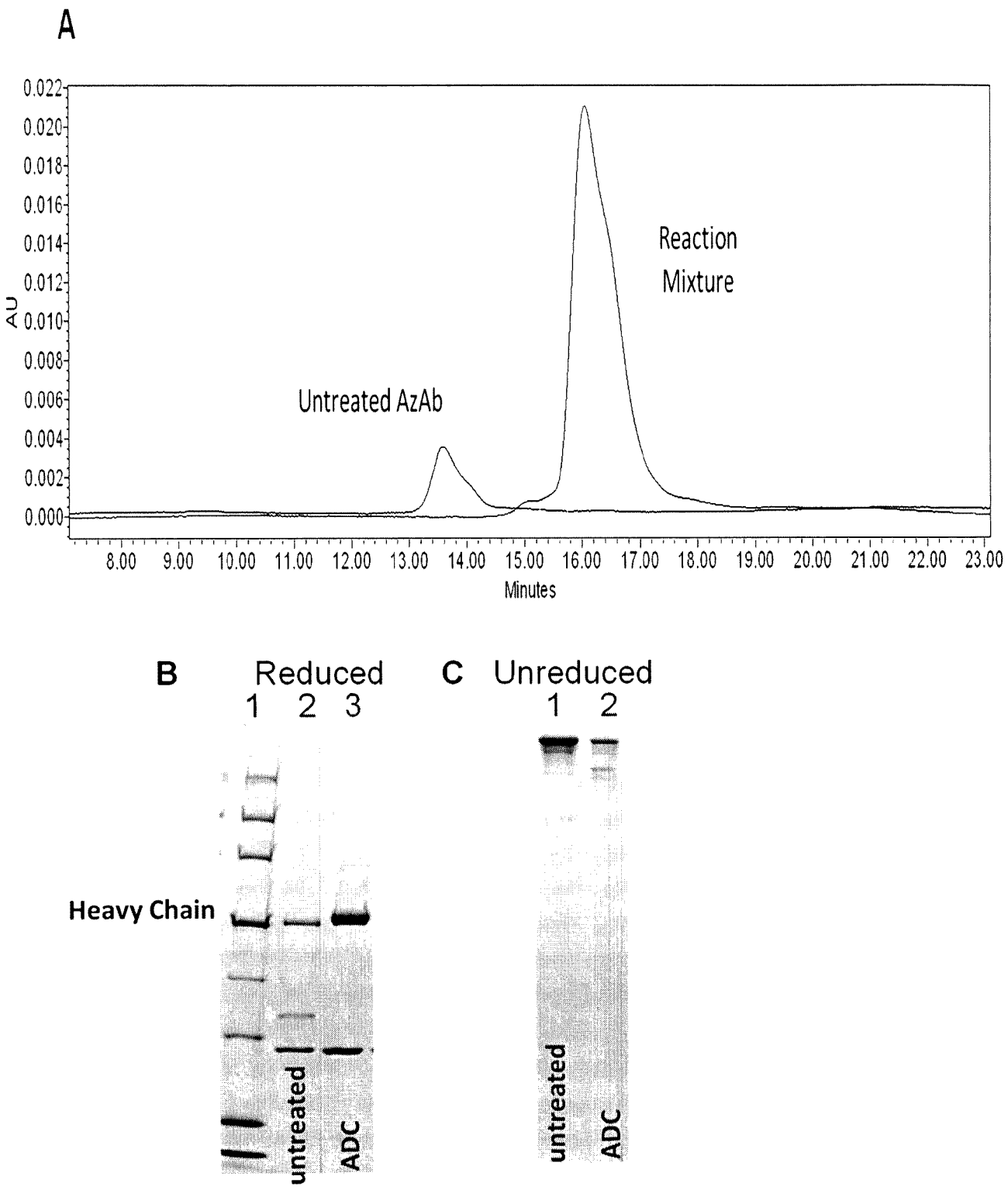
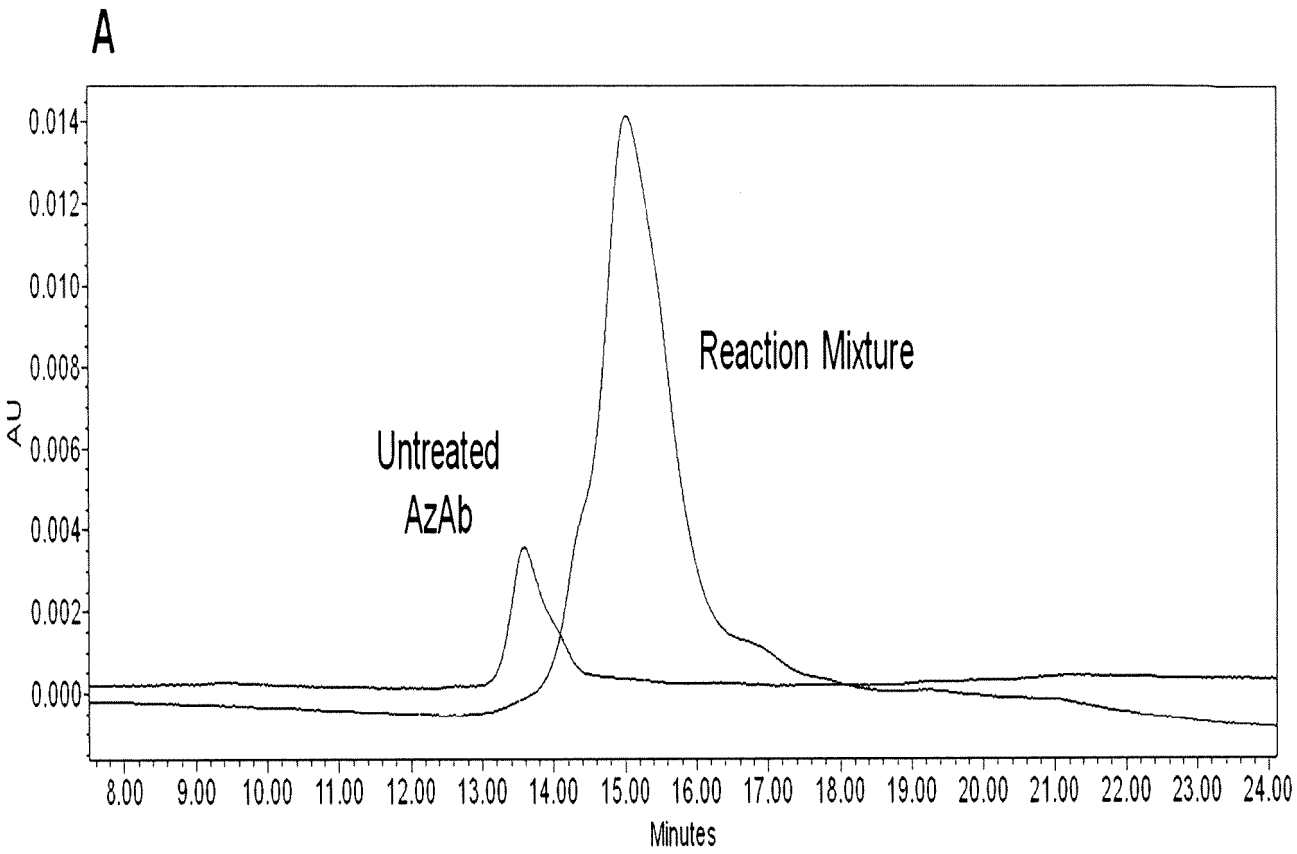

A
AU
0.022
0.020
0.018
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
Untreated AzAb
Reaction
Mixture
8.00
9.00
10.00
11.00
12.00
13.00
14.00
15.00
16.00
17.00
18.00
19.00
20.00
21.00
22.00
23.00
Minutes
B
Reduced
1 2 3
Heavy Chain
untreated
ADC
C
Unreduced
1 2
untreated
ADC

Figure 41


A
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
AU
Reaction Mixture
Untreated
AzAb
8.00
9.00
10.00
11.00
12.00
13.00
14.00
15.00
16.00
17.00
18.00
19.00
20.00
21.00
22.00
23.00
24.00
Minutes

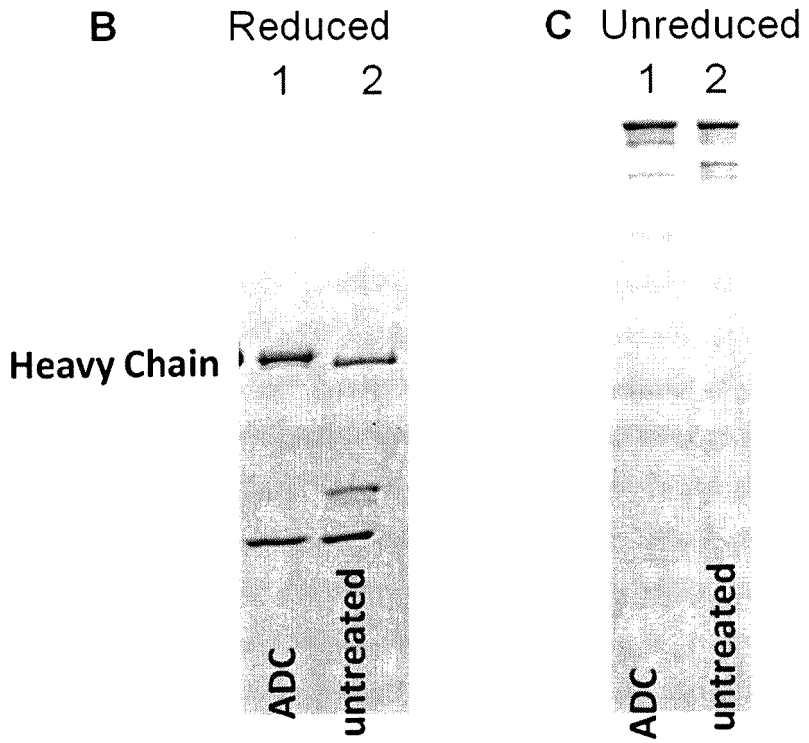
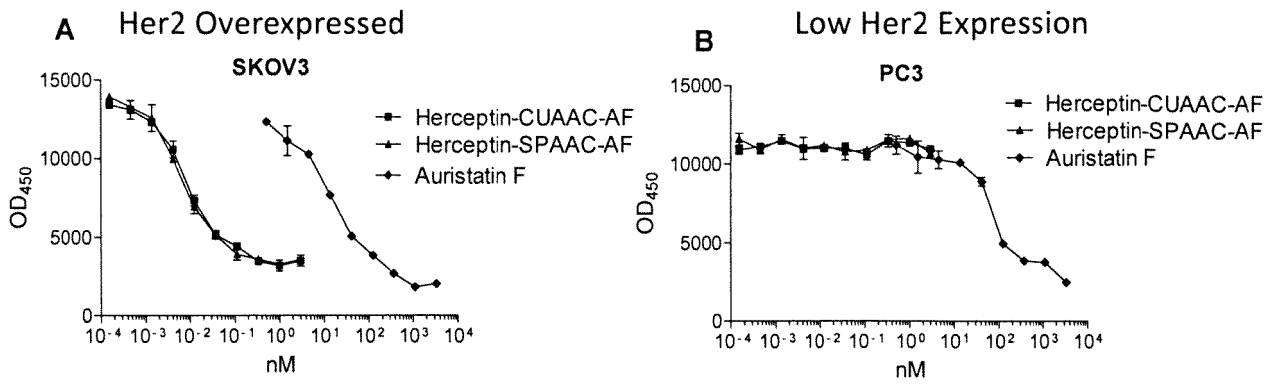

B
Reduced
1
2
Heavy Chain
ADC
untreated
C
Unreduced
1
2
ADC
untreated

Figure 42


A
Her2 Overexpressed
SKOV3
15000
10000
5000
0
OD450
10-4 10-3 10-2 10-1 100 101 102 103 104
nM
Herceptin-CUAAC-AF
Herceptin-SPAAC-AF
Auristatin F
B
Low Her2 Expression
PC3
15000
10000
5000
0
OD450
10-4 10-3 10-2 10-1 100 101 102 103 104
nM
Herceptin-CUAAC-AF
Herceptin-SPAAC-AF
Auristatin F

SEQUENCE LISTING

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<120> Cell lines

<130> ALL-P1457PCT

<150> US 61/705,116
<151> 2012-09-24

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<151> 2013-08-05

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Met Ser Arg Thr Gly Thr Ile His Lys Ile Lys His His Glu Val Ser
            20                  25                  30

Arg Ser Lys Ile Tyr Ile Glu Met Ala Cys Gly Asp His Leu Val Val
        35                  40                  45

Asn Asn Ser Arg Ser Ser Arg Thr Ala Arg Ala Leu Arg His His Lys
    50                  55                  60

Tyr Arg Lys Thr Cys Lys Arg Cys Arg Val Ser Asp Glu Asp Leu Asn
65                  70                  75                  80

Lys Phe Leu Thr Lys Ala Asn Glu Asp Gln Thr Ser Val Lys Val Lys
                85                  90                  95

Val Val Ser Ala Pro Thr Arg Thr Lys Lys Ala Met Pro Lys Ser Val
            100                 105                 110

Ala Arg Ala Pro Lys Pro Leu Glu Asn Thr Glu Ala Ala Gln Ala Gln
        115                 120                 125

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

Ser Val Ser Val Pro Ala Ser Val Ser Thr Ser Ile Ser Ser Ile Ser
145                 150                 155                 160

Thr Gly Ala Thr Ala Ser Ala Leu Val Lys Gly Asn Thr Asn Pro Ile
                165                 170                 175
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Thr Ser Met Ser Ala Pro Val Gln Ala Ser Ala Pro Ala Leu Thr Lys
            180                 185                 190

Ser Gln Thr Asp Arg Leu Glu Val Leu Leu Asn Pro Lys Asp Glu Ile
        195                 200                 205

Ser Leu Asn Ser Gly Lys Pro Phe Arg Glu Leu Glu Ser Glu Leu Leu
    210                 215                 220

Ser Arg Arg Lys Lys Asp Leu Gln Gln Ile Tyr Ala Glu Glu Arg Glu
225                 230                 235                 240

Asn Tyr Leu Gly Lys Leu Glu Arg Glu Ile Thr Arg Phe Phe Val Asp
                245                 250                 255

Arg Gly Phe Leu Glu Ile Lys Ser Pro Ile Leu Ile Pro Leu Glu Tyr
            260                 265                 270

Ile Glu Arg Met Gly Ile Asp Asn Asp Thr Glu Leu Ser Lys Gln Ile
        275                 280                 285

Phe Arg Val Asp Lys Asn Phe Cys Leu Arg Pro Met Leu Ala Pro Asn
    290                 295                 300

Leu Tyr Asn Tyr Leu Arg Lys Leu Asp Arg Ala Leu Pro Asp Pro Ile
305                 310                 315                 320

Lys Ile Phe Glu Ile Gly Pro Cys Tyr Arg Lys Glu Ser Asp Gly Lys
                325                 330                 335

Glu His Leu Glu Glu Phe Thr Met Leu Asn Phe Cys Gln Met Gly Ser
            340                 345                 350

Gly Cys Thr Arg Glu Asn Leu Glu Ser Ile Ile Thr Asp Phe Leu Asn
        355                 360                 365

His Leu Gly Ile Asp Phe Lys Ile Val Gly Asp Ser Cys Met Val Tyr
    370                 375                 380

Gly Asp Thr Leu Asp Val Met His Gly Asp Leu Glu Leu Ser Ser Ala
385                 390                 395                 400

Val Val Gly Pro Ile Pro Leu Asp Arg Glu Trp Gly Ile Asp Lys Pro
                405                 410                 415

Trp Ile Gly Ala Gly Phe Gly Leu Glu Arg Leu Leu Lys Val Lys His
            420                 425                 430

Asp Phe Lys Asn Ile Lys Arg Ala Ala Arg Ser Glu Ser Tyr Tyr Asn
        435                 440                 445
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Gly Ile Ser Thr Asn Leu
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<212> PRT
<213> Artificial sequence

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<223> Synthetic sequence: PylRS Methanosarcina mazei Y384F mutant amino acid sequence

<400> 2

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1 5 10 15

Met Ser Arg Thr Gly Thr Ile His Lys Ile Lys His His Glu Val Ser
20 25 30

Arg Ser Lys Ile Tyr Ile Glu Met Ala Cys Gly Asp His Leu Val Val
35 40 45

Asn Asn Ser Arg Ser Ser Arg Thr Ala Arg Ala Leu Arg His His Lys
50 55 60

Tyr Arg Lys Thr Cys Lys Arg Cys Arg Val Ser Asp Glu Asp Leu Asn
65 70 75 80

Lys Phe Leu Thr Lys Ala Asn Glu Asp Gln Thr Ser Val Lys Val Lys
85 90 95

Val Val Ser Ala Pro Thr Arg Thr Lys Lys Ala Met Pro Lys Ser Val
100 105 110

Ala Arg Ala Pro Lys Pro Leu Glu Asn Thr Glu Ala Ala Gln Ala Gln
115 120 125

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

Ser Val Ser Val Pro Ala Ser Val Ser Thr Ser Ile Ser Ser Ile Ser
145 150 155 160

Thr Gly Ala Thr Ala Ser Ala Leu Val Lys Gly Asn Thr Asn Pro Ile
165 170 175

Thr Ser Met Ser Ala Pro Val Gln Ala Ser Ala Pro Ala Leu Thr Lys
180 185 190

Ser Gln Thr Asp Arg Leu Glu Val Leu Leu Asn Pro Lys Asp Glu Ile
195 200 205

```
Ser Leu Asn Ser Gly Lys Pro Phe Arg Glu Leu Glu Ser Glu Leu Leu
    210                 215                 220

Ser Arg Arg Lys Lys Asp Leu Gln Gln Ile Tyr Ala Glu Glu Arg Glu
225                 230                 235                 240

Asn Tyr Leu Gly Lys Leu Glu Arg Glu Ile Thr Arg Phe Phe Val Asp
                245                 250                 255

Arg Gly Phe Leu Glu Ile Lys Ser Pro Ile Leu Ile Pro Leu Glu Tyr
            260                 265                 270

Ile Glu Arg Met Gly Ile Asp Asn Asp Thr Glu Leu Ser Lys Gln Ile
        275                 280                 285

Phe Arg Val Asp Lys Asn Phe Cys Leu Arg Pro Met Leu Ala Pro Asn
    290                 295                 300

Leu Tyr Asn Tyr Leu Arg Lys Leu Asp Arg Ala Leu Pro Asp Pro Ile
305                 310                 315                 320

Lys Ile Phe Glu Ile Gly Pro Cys Tyr Arg Lys Glu Ser Asp Gly Lys
                325                 330                 335

Glu His Leu Glu Glu Phe Thr Met Leu Asn Phe Cys Gln Met Gly Ser
            340                 345                 350

Gly Cys Thr Arg Glu Asn Leu Glu Ser Ile Ile Thr Asp Phe Leu Asn
        355                 360                 365

His Leu Gly Ile Asp Phe Lys Ile Val Gly Asp Ser Cys Met Val Phe
    370                 375                 380

Gly Asp Thr Leu Asp Val Met His Gly Asp Leu Glu Leu Ser Ser Ala
385                 390                 395                 400

Val Val Gly Pro Ile Pro Leu Asp Arg Glu Trp Gly Ile Asp Lys Pro
                405                 410                 415

Trp Ile Gly Ala Gly Phe Gly Leu Glu Arg Leu Leu Lys Val Lys His
            420                 425                 430

Asp Phe Lys Asn Ile Lys Arg Ala Ala Arg Ser Glu Ser Tyr Tyr Asn
        435                 440                 445

Gly Ile Ser Thr Asn Leu
    450
```

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<211> 419
<212> PRT
<213> Methanosarcina barkeri

<400> 3

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1               5                  10                  15

Met Ser Arg Thr Gly Thr Leu His Lys Ile Lys His Tyr Glu Val Ser
            20                  25                  30

Arg Ser Lys Ile Tyr Ile Glu Met Ala Cys Gly Asp His Leu Val Val
        35                  40                  45

Asn Asn Ser Arg Ser Cys Arg Thr Ala Arg Ala Phe Arg His His Lys
    50                  55                  60

Tyr Arg Lys Thr Cys Lys Arg Cys Arg Val Ser Asp Glu Asp Ile Asn
65                  70                  75                  80

Asn Phe Leu Thr Arg Ser Thr Glu Gly Lys Thr Ser Val Lys Val Lys
                85                  90                  95

Val Val Ser Ala Pro Lys Val Lys Lys Ala Met Pro Lys Ser Val Ser
            100                 105                 110

Arg Ala Pro Lys Pro Leu Glu Asn Pro Val Ser Ala Lys Ala Ser Thr
        115                 120                 125

Asp Thr Ser Arg Ser Val Pro Ser Pro Ala Lys Ser Thr Pro Asn Ser
    130                 135                 140

Pro Val Pro Thr Ser Ala Pro Ala Pro Ser Leu Thr Arg Ser Gln Leu
145                 150                 155                 160

Asp Arg Val Glu Ala Leu Leu Ser Pro Glu Asp Lys Ile Ser Leu Asn
                165                 170                 175

Ile Ala Lys Pro Phe Arg Glu Leu Glu Ser Glu Leu Val Thr Arg Arg
            180                 185                 190

Lys Asn Asp Phe Gln Arg Leu Tyr Thr Asn Asp Arg Glu Asp Tyr Leu
        195                 200                 205

Gly Lys Leu Glu Arg Asp Ile Thr Lys Phe Phe Val Asp Arg Asp Phe
    210                 215                 220

Leu Glu Ile Lys Ser Pro Ile Leu Ile Pro Ala Glu Tyr Val Glu Arg
225                 230                 235                 240

Met Gly Ile Asn Asn Asp Thr Glu Leu Ser Lys Gln Ile Phe Arg Val
                245                 250                 255

Asp Lys Asn Leu Cys Leu Arg Pro Met Leu Ala Pro Thr Leu Tyr Asn
```

260 265 270

Tyr Leu Arg Lys Leu Asp Arg Ile Leu Pro Asp Pro Ile Lys Ile Phe
275 280 285

Glu Val Gly Pro Cys Tyr Arg Lys Glu Ser Asp Gly Lys Glu His Leu
290 295 300

Glu Glu Phe Thr Met Val Asn Phe Cys Gln Met Gly Ser Gly Cys Thr
305 310 315 320

Arg Glu Asn Leu Glu Ser Leu Ile Lys Glu Phe Leu Asp Tyr Leu Glu
325 330 335

Ile Asp Phe Glu Ile Val Gly Asp Ser Cys Met Val Tyr Gly Asp Thr
340 345 350

Leu Asp Ile Met His Gly Asp Leu Glu Leu Ser Ser Ala Val Val Gly
355 360 365

Pro Val Pro Leu Asp Arg Glu Trp Gly Ile Asp Lys Pro Trp Ile Gly
370 375 380

Ala Gly Phe Gly Leu Glu Arg Leu Leu Lys Val Met His Gly Phe Lys
385 390 395 400

Asn Ile Lys Arg Ala Ser Arg Ser Glu Ser Tyr Tyr Asn Gly Ile Ser
405 410 415

Thr Asn Leu

<210> 4
<211> 288
<212> PRT
<213> Desulfitobacterium hafniense

<400> 4

Met Phe Leu Thr Arg Arg Asp Pro Pro Leu Ser Ser Phe Trp Thr Lys
1 5 10 15

Val Gln Tyr Gln Arg Leu Lys Glu Leu Asn Ala Ser Gly Glu Gln Leu
20 25 30

Glu Met Gly Phe Ser Asp Ala Leu Ser Arg Asp Arg Ala Phe Gln Gly
35 40 45

Ile Glu His Gln Leu Met Ser Gln Gly Lys Arg His Leu Glu Gln Leu
50 55 60

Arg Thr Val Lys His Arg Pro Ala Leu Leu Glu Leu Glu Glu Lys Leu
65 70 75 80

```
Ala Lys Ala Leu His Gln Gln Gly Phe Val Gln Val Val Thr Pro Thr
                85                  90                  95

Ile Ile Thr Lys Ser Ala Leu Ala Lys Met Thr Ile Gly Glu Asp His
            100                 105                 110

Pro Leu Phe Ser Gln Val Phe Trp Leu Asp Gly Lys Lys Cys Leu Arg
        115                 120                 125

Pro Met Leu Ala Pro Asn Leu Tyr Thr Leu Trp Arg Glu Leu Glu Arg
    130                 135                 140

Leu Trp Asp Lys Pro Ile Arg Ile Phe Glu Ile Gly Thr Cys Tyr Arg
145                 150                 155                 160

Lys Glu Ser Gln Gly Ala Gln His Leu Asn Glu Phe Thr Met Leu Asn
                165                 170                 175

Leu Thr Glu Leu Gly Thr Pro Leu Glu Glu Arg His Gln Arg Leu Glu
            180                 185                 190

Asp Met Ala Arg Trp Val Leu Glu Ala Ala Gly Ile Arg Glu Phe Glu
        195                 200                 205

Leu Val Thr Glu Ser Ser Val Val Tyr Gly Asp Thr Val Asp Val Met
    210                 215                 220

Lys Gly Asp Leu Glu Leu Ala Ser Gly Ala Met Gly Pro His Phe Leu
225                 230                 235                 240

Asp Glu Lys Trp Glu Ile Phe Asp Pro Trp Val Gly Leu Gly Phe Gly
                245                 250                 255

Leu Glu Arg Leu Leu Met Ile Arg Glu Gly Thr Gln His Val Gln Ser
            260                 265                 270

Met Ala Arg Ser Leu Ser Tyr Leu Asp Gly Val Arg Leu Asn Ile Asn
        275                 280                 285


<210>  5
<211>  443
<212>  PRT
<213>  Methanosarcina acetivorans

<400>  5

Met Asp Lys Lys Pro Leu Asp Thr Leu Ile Ser Ala Thr Gly Leu Trp
1               5                   10                  15

Met Ser Arg Thr Gly Met Ile His Lys Ile Lys His His Glu Val Ser
            20                  25                  30
```

```
Arg Ser Lys Ile Tyr Ile Glu Met Ala Cys Gly Glu Arg Leu Val Val
        35                  40                  45

Asn Asn Ser Arg Ser Ser Arg Thr Ala Arg Ala Leu Arg His His Lys
    50                  55                  60

Tyr Arg Lys Thr Cys Arg His Cys Arg Val Ser Asp Glu Asp Ile Asn
65                  70                  75                  80

Asn Phe Leu Thr Lys Thr Ser Glu Glu Lys Thr Thr Val Lys Val Lys
                85                  90                  95

Val Val Ser Ala Pro Arg Val Arg Lys Ala Met Pro Lys Ser Val Ala
            100                 105                 110

Arg Ala Pro Lys Pro Leu Glu Ala Thr Ala Gln Val Pro Leu Ser Gly
        115                 120                 125

Ser Lys Pro Ala Pro Ala Thr Pro Val Ser Ala Pro Ala Gln Ala Pro
    130                 135                 140

Ala Pro Ser Thr Gly Ser Ala Ser Ala Thr Ser Ala Ser Ala Gln Arg
145                 150                 155                 160

Met Ala Asn Ser Ala Ala Ala Pro Ala Ala Pro Val Pro Thr Ser Ala
                165                 170                 175

Pro Ala Leu Thr Lys Gly Gln Leu Asp Arg Leu Glu Gly Leu Leu Ser
            180                 185                 190

Pro Lys Asp Glu Ile Ser Leu Asp Ser Glu Lys Pro Phe Arg Glu Leu
        195                 200                 205

Glu Ser Glu Leu Leu Ser Arg Arg Lys Lys Asp Leu Lys Arg Ile Tyr
    210                 215                 220

Ala Glu Glu Arg Glu Asn Tyr Leu Gly Lys Leu Glu Arg Glu Ile Thr
225                 230                 235                 240

Lys Phe Phe Val Asp Arg Gly Phe Leu Glu Ile Lys Ser Pro Ile Leu
                245                 250                 255

Ile Pro Ala Glu Tyr Val Glu Arg Met Gly Ile Asn Ser Asp Thr Glu
            260                 265                 270

Leu Ser Lys Gln Val Phe Arg Ile Asp Lys Asn Phe Cys Leu Arg Pro
        275                 280                 285

Met Leu Ala Pro Asn Leu Tyr Asn Tyr Leu Arg Lys Leu Asp Arg Ala
    290                 295                 300
```

```
Leu Pro Asp Pro Ile Lys Ile Phe Glu Ile Gly Pro Cys Tyr Arg Lys
305                 310                 315                 320

Glu Ser Asp Gly Lys Glu His Leu Glu Glu Phe Thr Met Leu Asn Phe
                325                 330                 335

Cys Gln Met Gly Ser Gly Cys Thr Arg Glu Asn Leu Glu Ala Ile Ile
            340                 345                 350

Thr Glu Phe Leu Asn His Leu Gly Ile Asp Phe Glu Ile Ile Gly Asp
        355                 360                 365

Ser Cys Met Val Tyr Gly Asn Thr Leu Asp Val Met His Asp Asp Leu
    370                 375                 380

Glu Leu Ser Ser Ala Val Val Gly Pro Val Pro Leu Asp Arg Glu Trp
385                 390                 395                 400

Gly Ile Asp Lys Pro Trp Ile Gly Ala Gly Phe Gly Leu Glu Arg Leu
                405                 410                 415

Leu Lys Val Met His Gly Phe Lys Asn Ile Lys Arg Ala Ala Arg Ser
            420                 425                 430

Glu Ser Tyr Tyr Asn Gly Ile Ser Thr Asn Leu
        435                 440


<210>  6
<211>  416
<212>  PRT
<213>  Methanococcoides  burtonii

<400>  6

Met Glu Lys Gln Leu Leu Asp Val Leu Val Glu Leu Asn Gly Val Trp
1               5                   10                  15

Leu Ser Arg Ser Gly Leu Leu His Gly Ile Arg Asn Phe Glu Ile Thr
            20                  25                  30

Thr Lys His Ile His Ile Glu Thr Asp Cys Gly Ala Arg Phe Thr Val
        35                  40                  45

Arg Asn Ser Arg Ser Ser Arg Ser Ala Arg Ser Leu Arg His Asn Lys
    50                  55                  60

Tyr Arg Lys Pro Cys Lys Arg Cys Arg Pro Ala Asp Glu Gln Ile Asp
65                  70                  75                  80

Arg Phe Val Lys Lys Thr Phe Lys Glu Lys Arg Gln Thr Val Ser Val
                85                  90                  95
```

```
Phe Ser Ser Pro Lys Lys His Val Pro Lys Lys Pro Lys Val Ala Val
            100                 105                 110

Ile Lys Ser Phe Ser Ile Ser Thr Pro Ser Pro Lys Glu Ala Ser Val
        115                 120                 125

Ser Asn Ser Ile Pro Thr Pro Ser Ile Ser Val Val Lys Asp Glu Val
    130                 135                 140

Lys Val Pro Glu Val Lys Tyr Thr Pro Ser Gln Ile Glu Arg Leu Lys
145                 150                 155                 160

Thr Leu Met Ser Pro Asp Asp Lys Ile Pro Ile Gln Asp Glu Leu Pro
                165                 170                 175

Glu Phe Lys Val Leu Glu Lys Glu Leu Ile Gln Arg Arg Arg Asp Asp
            180                 185                 190

Leu Lys Lys Met Tyr Glu Glu Asp Arg Glu Asp Arg Leu Gly Lys Leu
        195                 200                 205

Glu Arg Asp Ile Thr Glu Phe Phe Val Asp Arg Gly Phe Leu Glu Ile
    210                 215                 220

Lys Ser Pro Ile Met Ile Pro Phe Glu Tyr Ile Glu Arg Met Gly Ile
225                 230                 235                 240

Asp Lys Asp Asp His Leu Asn Lys Gln Ile Phe Arg Val Asp Glu Ser
                245                 250                 255

Met Cys Leu Arg Pro Met Leu Ala Pro Cys Leu Tyr Asn Tyr Leu Arg
            260                 265                 270

Lys Leu Asp Lys Val Leu Pro Asp Pro Ile Arg Ile Phe Glu Ile Gly
        275                 280                 285

Pro Cys Tyr Arg Lys Glu Ser Asp Gly Ser Ser His Leu Glu Glu Phe
    290                 295                 300

Thr Met Val Asn Phe Cys Gln Met Gly Ser Gly Cys Thr Arg Glu Asn
305                 310                 315                 320

Met Glu Ala Leu Ile Asp Glu Phe Leu Glu His Leu Gly Ile Glu Tyr
                325                 330                 335

Glu Ile Glu Ala Asp Asn Cys Met Val Tyr Gly Asp Thr Ile Asp Ile
            340                 345                 350

Met His Gly Asp Leu Glu Leu Ser Ser Ala Val Val Gly Pro Ile Pro
        355                 360                 365
```

```
Leu Asp Arg Glu Trp Gly Val Asn Lys Pro Trp Met Gly Ala Gly Phe
    370                 375                 380

Gly Leu Glu Arg Leu Leu Lys Val Arg His Asn Tyr Thr Asn Ile Arg
385                 390                 395                 400

Arg Ala Ser Arg Ser Glu Leu Tyr Tyr Asn Gly Ile Asn Thr Asn Leu
                405                 410                 415
```

<210> 7
<211> 478
<212> PRT
<213> Methanosarcina thermophila

<400> 7

```
Met Asp Lys Lys Pro Leu Asn Thr Leu Ile Ser Ala Thr Gly Leu Trp
1               5                   10                  15

Met Ser Arg Thr Gly Lys Leu His Lys Ile Arg His His Glu Val Ser
            20                  25                  30

Lys Arg Lys Ile Tyr Ile Glu Met Glu Cys Gly Glu Arg Leu Val Val
        35                  40                  45

Asn Asn Ser Arg Ser Cys Arg Ala Ala Arg Ala Leu Arg His His Lys
    50                  55                  60

Tyr Arg Lys Ile Cys Lys His Cys Arg Val Ser Asp Glu Asp Leu Asn
65                  70                  75                  80

Lys Phe Leu Thr Arg Thr Asn Glu Asp Lys Ser Asn Ala Lys Val Thr
                85                  90                  95

Val Val Ser Ala Pro Lys Ile Arg Lys Val Met Pro Lys Ser Val Ala
            100                 105                 110

Arg Thr Pro Lys Pro Leu Glu Asn Thr Ala Pro Val Gln Thr Leu Pro
        115                 120                 125

Ser Glu Ser Gln Pro Ala Pro Thr Thr Pro Ile Ser Ala Ser Thr Thr
    130                 135                 140

Ala Pro Ala Ser Thr Ser Thr Thr Ala Pro Ala Pro Ala Ser Thr Thr
145                 150                 155                 160

Ala Pro Ala Pro Ala Ser Thr Thr Ala Pro Ala Ser Ala Ser Thr Thr
                165                 170                 175

Ile Ser Thr Ser Ala Met Pro Ala Ser Thr Ser Ala Gln Gly Thr Thr
            180                 185                 190

Lys Phe Asn Tyr Ile Ser Gly Gly Phe Pro Arg Pro Ile Pro Val Gln
```

195 200 205

Ala Ser Ala Pro Ala Leu Thr Lys Ser Gln Ile Asp Arg Leu Gln Gly
210 215 220

Leu Leu Ser Pro Lys Asp Glu Ile Ser Leu Asp Ser Gly Thr Pro Phe
225 230 235 240

Arg Lys Leu Glu Ser Glu Leu Leu Ser Arg Arg Arg Lys Asp Leu Lys
245 250 255

Gln Ile Tyr Ala Glu Glu Arg Glu His Tyr Leu Gly Lys Leu Glu Arg
260 265 270

Glu Ile Thr Lys Phe Phe Val Asp Arg Gly Phe Leu Glu Ile Lys Ser
275 280 285

Pro Ile Leu Ile Pro Met Glu Tyr Ile Glu Arg Met Gly Ile Asp Asn
290 295 300

Asp Lys Glu Leu Ser Lys Gln Ile Phe Arg Val Asp Asn Asn Phe Cys
305 310 315 320

Leu Arg Pro Met Leu Ala Pro Asn Leu Tyr Asn Tyr Leu Arg Lys Leu
325 330 335

Asn Arg Ala Leu Pro Asp Pro Ile Lys Ile Phe Glu Ile Gly Pro Cys
340 345 350

Tyr Arg Lys Glu Ser Asp Gly Lys Glu His Leu Glu Glu Phe Thr Met
355 360 365

Leu Asn Phe Cys Gln Met Gly Ser Gly Cys Thr Arg Glu Asn Leu Glu
370 375 380

Ala Ile Ile Lys Asp Phe Leu Asp Tyr Leu Gly Ile Asp Phe Glu Ile
385 390 395 400

Val Gly Asp Ser Cys Met Val Tyr Gly Asp Thr Leu Asp Val Met His
405 410 415

Gly Asp Leu Glu Leu Ser Ser Ala Val Val Gly Pro Val Pro Met Asp
420 425 430

Arg Asp Trp Gly Ile Asn Lys Pro Trp Ile Gly Ala Gly Phe Gly Leu
435 440 445

Glu Arg Leu Leu Lys Val Met His Asn Phe Lys Asn Ile Lys Arg Ala
450 455 460

Ser Arg Ser Glu Ser Tyr Tyr Asn Gly Ile Ser Thr Asn Leu

465 470 475

<210> 8
<211> 427
<212> PRT
<213> Methanosalsum zhilinae

<400> 8

Met Thr Arg Arg Ser Leu Glu Ser Leu Val Ser Glu Lys Glu Val Trp
1 5 10 15

Leu Ser Arg Lys Gly Leu Leu His Glu Ile Lys Asp Tyr Ser Val Thr
20 25 30

Gln Arg Tyr Ile Asn Ile Tyr Thr Thr Cys Gly Glu Ser Phe Ser Val
35 40 45

Arg Asn Ser Arg Arg Gly Arg Ala Ser Arg Val Leu Arg Asn Asn Lys
50 55 60

Tyr Arg Lys Ile Cys Lys His Cys Lys Val Pro Asp Glu Lys Ile Ser
65 70 75 80

Lys Phe Leu Gln Lys Ala Ser Val Asp Ser Thr Ala Lys Val Lys Val
85 90 95

Val Ser Ser Thr Lys Pro Ser Gln Ser Lys Lys Ala Val Pro Lys Ala
100 105 110

Val Lys Ala Lys Lys Lys Gly Thr Glu Asn Ser Asn Gly Ser Leu Ile
115 120 125

Gln Ser Lys Val Lys Asp Gln Gly Ser Val Asn Ala Ile Ser Ser Gly
130 135 140

Gln Pro Arg Ser Lys Ile Gln Pro Thr Glu Glu Arg Asn Asn Ile Pro
145 150 155 160

Ala Phe Thr Pro Ser Gln Lys Lys Arg Leu Glu Ala Leu Leu Met Pro
165 170 175

Glu Glu Val Ile Pro Asp Pro Ser Glu Asn Leu Asn Phe Gln Glu Leu
180 185 190

Glu Ser Ser Leu Val Asn Arg Arg Lys Lys Asp Ile Val Lys Ile Tyr
195 200 205

Glu Asp Asp Arg Glu Asn Gln Leu Gly Lys Ile Glu Arg Ile Ile Thr
210 215 220

Lys Phe Phe Val Asp Arg Gly Phe Leu Glu Ile Lys Ser Pro Ile Leu
225 230 235 240

```
Ile Pro Ile Glu Tyr Ile Glu Arg Met Gly Ile Thr Glu Asp Lys Glu
                245                 250                 255

Leu Phe Glu Gln Val Phe Lys Val Asp Lys Asn Met Cys Leu Arg Pro
            260                 265                 270

Met Leu Ala Pro Gly Leu Tyr Asn His Leu Arg Lys Phe Asp Lys Val
        275                 280                 285

Leu Pro Asp Pro Ile Arg Ile Phe Glu Ile Gly Pro Cys Tyr Arg Lys
    290                 295                 300

Glu Ser Asp Gly Ser Gln His Leu Glu Glu Phe Thr Met Leu Asn Phe
305                 310                 315                 320

Cys Gln Met Gly Ser Met Cys Thr Arg Lys Thr Leu Glu Asn Leu Ile
                325                 330                 335

Asp Glu Leu Leu Glu Phe Met Asp Ile Glu Tyr Glu Ile Val Ser Asp
            340                 345                 350

Asn Cys His Val Tyr Gly Ala Thr Ile Asp Val Leu His Lys Asp Met
        355                 360                 365

Glu Leu Ala Ser Ala Val Val Gly Pro Ile Pro Lys Asp Ala Asp Trp
    370                 375                 380

Gly Ile Thr Lys Pro Trp Ile Gly Ala Gly Phe Gly Leu Glu Arg Leu
385                 390                 395                 400

Leu Lys Val Met His Asn Tyr Lys Asn Ile Arg Arg Ala Ser Arg Ser
                405                 410                 415

Glu Ser Tyr Tyr Asn Gly Ile Thr Thr Asn Leu
            420                 425


<210>  9
<211>  414
<212>  PRT
<213>  Methanohalobium evestigatum

<400>  9

Met Ser Lys Lys Ser Leu Ala Ser Leu Ile Ser Asp Leu Gln Val Trp
1               5                   10                  15

Val Ser Arg Ser Gly Leu Leu His Glu Ile Lys Asn Tyr Glu Val Ser
            20                  25                  30

Gln Arg Tyr Ile His Met Glu Met Asp Cys Gly Glu Lys Ile Thr Val
        35                  40                  45
```

```
Arg Asn Ser Arg Asn Ser Arg Thr Ala Arg Ile Leu Arg Leu Lys Lys
    50                  55                  60

Tyr Lys Lys Pro Cys Lys Asn Cys Lys Val Ser Asp Glu Val Ile Asn
65                  70                  75                  80

Arg Phe Leu Gln Lys His Thr Asp Arg Thr Asp Thr Lys Val Thr Ala
                85                  90                  95

Phe Ser Tyr Ser Glu Ser Lys Lys Lys Lys Ser Lys Gln Leu Gly His
            100                 105                 110

Lys Lys Lys Lys Gln Ser Lys Val Gln Val Asn Pro Thr Thr Glu Ser
        115                 120                 125

Ile Gln Ser Asn Thr Ser Val Ser Glu Asp Lys Thr Asp Asn Lys Ile
    130                 135                 140

Glu Pro Glu Thr Phe Thr Ser Ala Gln Lys Glu Arg Ile Asn Glu Leu
145                 150                 155                 160

Leu Leu Pro Gly Glu Lys Ile Pro Phe Ser Asn Glu Pro Ser Lys Phe
                165                 170                 175

Lys Glu Ile Glu Ser Glu Leu Val Asn Lys Arg Arg Asn Asp Phe Lys
            180                 185                 190

Gln Met Tyr Glu Asn Asp Arg Glu Glu Gln Ile Ala Lys Leu Glu Arg
        195                 200                 205

Thr Ile Ser Gln Phe Phe Val Asp Lys Gly Phe Ile Glu Ile Lys Ala
    210                 215                 220

Pro Ile Ile Ile Asp Ile Asp Ser Val Lys Lys Met Gly Ile Asp Thr
225                 230                 235                 240

Asp His Lys Leu Ser Lys Gln Ile Phe Tyr Leu Asp Asn Lys His Cys
                245                 250                 255

Leu Arg Pro Met Leu Ala Pro Gly Leu Tyr Gln Trp Leu Lys Asn Phe
            260                 265                 270

Asp Lys Ile Leu Pro Asp Pro Ile Lys Ile Phe Glu Ile Gly Pro Cys
        275                 280                 285

Tyr Arg Lys Glu Ser Glu Gly Ser Gln His Leu Glu Glu Phe Thr Met
    290                 295                 300

Phe Asn Phe Cys Gln Met Gly Ser Gly Ala Asn Arg Glu Asn Leu Leu
305                 310                 315                 320
```

```
Asn His Ile Asp Asp Leu Leu Lys His Leu Asn Ile Asp Tyr Lys Ile
                325                 330                 335

Ile Asp Asp Asn Cys His Val Tyr Gly Glu Thr Ile Asp Ile Val His
            340                 345                 350

Gly Asp Leu Glu Leu Ser Ser Ala Val Val Gly Pro Val Pro Ile Asp
        355                 360                 365

Met Asn Trp Gly Ile Asp Lys Thr Trp Ile Gly Ala Gly Leu Gly Leu
    370                 375                 380

Glu Arg Leu Leu Lys Val Lys His Gly Tyr Lys Asn Ile Lys Arg Ala
385                 390                 395                 400

Ser Lys Ser His Ser Tyr Tyr Asn Gly Ile Ser Thr Asn Leu
                405                 410


<210>  10
<211>  404
<212>  PRT
<213>  Methanohalophilus mahii

<400>  10

Met Glu Arg Lys Pro Leu Asp Leu Leu Ile Asp Thr Asn Gly Val Trp
1               5                   10                  15

Leu Ser Arg Asn Gly Leu Leu His Gly Val Lys Asn Phe Glu Val Ser
            20                  25                  30

Arg Asn His Ile His Ile Thr Thr Asp Cys Gln Ser Arg Phe Thr Val
        35                  40                  45

Arg Asn Ser Arg Arg Ser Arg Ser Ala Arg Ala Leu Arg Asn Asn Lys
    50                  55                  60

Tyr Arg Lys Ala Cys Lys Asn Cys Lys Leu Ser Asp Glu Arg Ile Thr
65                  70                  75                  80

Arg Phe Val Thr Lys Asp Phe Gly Arg Gly Ser Gln Ala Arg Val Ile
                85                  90                  95

Thr Ser Ser Lys Thr Lys Lys Ser Lys Ser Pro Lys Glu Ala Val Val
            100                 105                 110

Lys Ser Val Ser Ser Lys Ala Asn Glu Met Pro Pro Val Val Glu Ala
        115                 120                 125

Lys Lys Glu Lys Pro Val Lys Pro Asp Tyr Thr Pro Ala Gln Lys Lys
    130                 135                 140
```

```
Arg Ile Thr Thr Leu Leu Ser Pro Ala Asp Asp Leu Ser Ser Ile Lys
145                 150                 155                 160

Glu Leu Pro Thr Phe Lys Glu Leu Glu Thr Glu Leu Val Lys Lys Arg
                165                 170                 175

Lys Gln Asp Leu Arg Gln Met Tyr Glu Asp Asp Arg Arg His Gln Leu
            180                 185                 190

Ala Gln Leu Glu Arg Asp Ile Ser Leu Phe Leu Ile Glu Lys Gly Phe
        195                 200                 205

Met Glu Val Arg Thr Ser Val Leu Ile Pro Ala Lys Phe Ile Glu Arg
    210                 215                 220

Met Gly Ile Thr Glu Glu Asp Pro Leu Tyr Lys Gln Ile Phe Arg Val
225                 230                 235                 240

Asp Glu Asn Thr Cys Leu Arg Pro Met Leu Ala Pro Gly Leu Tyr Asn
                245                 250                 255

Tyr Leu His Asn Phe Asp Asn Ile Met Pro Asp Pro Leu Lys Ile Phe
            260                 265                 270

Glu Ile Gly Thr Cys Tyr Arg Lys Glu Ser Asp Gly Lys Glu His Leu
        275                 280                 285

Glu Glu Phe Thr Met Val Asn Phe Cys Gln Met Gly Ser Gly Cys Thr
    290                 295                 300

Lys Glu Asn Leu Leu Asn Ile Ile Asp Asp Leu Leu Lys Tyr Leu Asn
305                 310                 315                 320

Ile Asp Tyr Glu Val Ile Ser Asp Asn Cys Met Val Tyr Gly Asp Thr
                325                 330                 335

Ile Asp Ile Met His Gly Asp Met Glu Ile Ser Ser Ala Val Val Gly
            340                 345                 350

Pro Ile Pro Gln Asp Leu Asp Trp Gly Val Thr Lys Pro Trp Met Gly
        355                 360                 365

Ala Gly Met Gly Ile Glu Arg Leu Leu Lys Val Lys His Lys Tyr Thr
    370                 375                 380

Asn Ile Lys Arg Ser Ser Arg Ser Ile Ser Tyr Tyr Asn Gly Ile Thr
385                 390                 395                 400

Thr Asn Leu Arg
```

<210> 11
<211> 277
<212> PRT
<213> Desulfotomaculum gibsoniae

<400> 11

```
Met Ile Asn Trp Ser Ile Ser Gln Lys Gln Lys Leu Ile Glu Leu Asn
1               5                  10                  15

Gly Lys Ser Glu Leu Leu Asp Leu Arg Phe Gln Asp Lys Gln Lys Arg
            20                  25                  30

Asp Gln Thr Phe Gln Lys Ile Glu Lys Glu Leu Val Lys Lys Asn Lys
        35                  40                  45

Asp His Leu Leu Glu Leu Lys Glu Val Ile His Arg Pro Leu Leu Ser
    50                  55                  60

Ser Leu Glu Ile Gln Leu Ser Asn Leu Leu Cys Lys Thr Gly Phe Val
65                  70                  75                  80

Gln Val Asn Thr Pro Ile Ile Leu Pro Lys Ala Met Leu His Lys Met
                85                  90                  95

Thr Ile Thr Pro Glu His Pro Leu Tyr Lys Gln Val Phe Trp Val Asp
            100                 105                 110

Asn Asn Lys Cys Leu Arg Pro Met Leu Ala Pro Asn Leu Tyr His Tyr
        115                 120                 125

Leu Lys Ile Leu Asp Arg Leu Trp Ser Lys Pro Val Arg Ile Phe Glu
    130                 135                 140

Ile Gly Pro Cys Phe Arg Lys Glu Ser Gln Gly Ala Gln His Leu Asn
145                 150                 155                 160

Glu Phe Thr Met Leu Asn Leu Val Glu Leu Gly Val Asp Lys Gly Lys
                165                 170                 175

Gln Thr Glu Arg Leu Lys Glu Leu Gly Ser Leu Val Met Glu Glu Ile
            180                 185                 190

Gly Val Lys Asn Tyr Glu Phe Val Glu Thr Glu Ser Glu Ile Tyr Gly
        195                 200                 205

Ile Thr Val Asp Val Val Phe Asp Asp Leu Glu Leu Gly Ser Gly Ala
    210                 215                 220

Phe Gly Pro Leu Lys Met Asp Glu Gln Trp Gly Ile Phe Glu Pro Trp
225                 230                 235                 240

Val Gly Ile Gly Phe Gly Leu Glu Arg Leu Ala Met Thr Leu Gln Gly
```

245 250 255

His Arg Asn Ile Arg Arg Val Gly Arg Gly Leu Thr Tyr Leu Asp Gly
260 265 270

Ser Leu Leu Asn Ile
275

<210> 12
<211> 277
<212> PRT
<213> Desulfosporosinus meridiei

<400> 12

Met Ser Ile Thr Trp Thr Pro Ile Gln Lys Gln Arg Leu Gln Glu Leu
1 5 10 15

Asn Ala Ser Glu Val Leu Gln Glu Met Cys Phe Glu Ser His Gln Glu
20 25 30

Arg Asp Arg Ala Tyr Gln Glu Gln Glu His Leu Leu Val Ile Arg Gly
35 40 45

Lys Gln Lys Leu Gln Glu Leu Leu Glu Thr Asn Arg Arg Pro Ser Leu
50 55 60

Ser Val Leu Glu Gln Gln Leu Val Glu Ala Leu Thr Gln Glu Gly Phe
65 70 75 80

Val Gln Val Val Thr Pro Thr Ile Ile Ser Lys Thr Ala Leu Ala Lys
85 90 95

Met Ser Val Ser Asp Asp His Pro Leu Phe Ser Gln Val Phe Trp Leu
100 105 110

Asp Ser Lys Arg Cys Leu Arg Pro Met Leu Ala Pro Asn Leu Tyr Thr
115 120 125

Leu Trp Arg Asp Leu Leu Arg Leu Trp Glu Lys Pro Ile Arg Ile Phe
130 135 140

Glu Ile Gly Thr Cys Tyr Arg Lys Glu Ser Lys Gly Ser Leu His Leu
145 150 155 160

Asn Glu Phe Thr Met Leu Asn Leu Thr Glu Leu Gly Leu Pro Leu Asp
165 170 175

Gln Arg His Gln Arg Leu Lys Glu Leu Ala Asp Leu Val Met Asn Thr
180 185 190

Val Gly Ile Asp Asp Tyr Gln Leu Glu Ser Glu Ser Ser Val Val Tyr
195 200 205

```
Gly Asp Thr Leu Asp Val Val Lys Gly Ile Glu Leu Gly Ser Ser Ala
    210                 215                 220

Met Gly Pro His Val Leu Asp Asp Gln Trp Gly Ile Phe Asp Pro Trp
225                 230                 235                 240

Val Gly Ile Gly Phe Gly Leu Glu Arg Leu Leu Met Ile Lys Glu Gly
                245                 250                 255

Ser Gln Asn Val Gln Ser Met Gly Arg Ser Leu Thr Tyr Leu Asn Gly
            260                 265                 270

Val Arg Leu Asn Ile
        275


<210>  13
<211>  278
<212>  PRT
<213>  Desulfotomaculum acetoxidans

<400>  13

Met Ser Phe Leu Trp Thr Val Ser Gln Gln Lys Arg Leu Ser Glu Leu
1               5                   10                  15

Asn Ala Ser Glu Glu Glu Lys Asn Met Ser Phe Ser Ser Thr Ser Asp
            20                  25                  30

Arg Glu Ala Ala Tyr Lys Arg Val Glu Met Arg Leu Ile Asn Glu Ser
        35                  40                  45

Lys Gln Arg Leu Asn Lys Leu Arg His Glu Thr Lys Arg Pro Ala Ile
    50                  55                  60

Cys Ala Leu Glu Asn Arg Leu Ala Ala Ala Leu Arg Gly Ala Gly Phe
65                  70                  75                  80

Val Gln Val Ala Thr Pro Val Ile Leu Ser Lys Lys Leu Leu Gly Lys
                85                  90                  95

Met Thr Ile Thr Asp Glu His Ala Leu Phe Ser Gln Val Phe Trp Ile
            100                 105                 110

Glu Glu Asn Lys Cys Leu Arg Pro Met Leu Ala Pro Asn Leu Tyr Tyr
        115                 120                 125

Ile Leu Lys Asp Leu Leu Arg Leu Trp Glu Lys Pro Val Arg Ile Phe
    130                 135                 140

Glu Ile Gly Ser Cys Phe Arg Lys Glu Ser Gln Gly Ser Asn His Leu
145                 150                 155                 160
```

```
Asn Glu Phe Thr Met Leu Asn Leu Val Glu Trp Gly Leu Pro Glu Glu
                165                 170                 175

Gln Arg Gln Lys Arg Ile Ser Glu Leu Ala Lys Leu Val Met Asp Glu
            180                 185                 190

Thr Gly Ile Asp Glu Tyr His Leu Glu His Ala Glu Ser Val Val Tyr
        195                 200                 205

Gly Glu Thr Val Asp Val Met His Arg Asp Ile Glu Leu Gly Ser Gly
    210                 215                 220

Ala Leu Gly Pro His Phe Leu Asp Gly Arg Trp Gly Val Val Gly Pro
225                 230                 235                 240

Trp Val Gly Ile Gly Phe Gly Leu Glu Arg Leu Leu Met Val Glu Gln
                245                 250                 255

Gly Gly Gln Asn Val Arg Ser Met Gly Lys Ser Leu Thr Tyr Leu Asp
            260                 265                 270

Gly Val Arg Leu Asn Ile
        275
```

<210> 14
<211> 1365
<212> DNA
<213> Methanosarcina mazei

<400> 14

```
atggataaaa aaccactaaa cactctgata tctgcaaccg ggctctggat gtccaggacc     60

ggaacaattc ataaaataaa acaccacgaa gtctctcgaa gcaaaatcta tattgaaatg    120

gcatgcggag accaccttgt tgtaaacaac tccaggagca gcaggactgc aagagcgctc    180

aggcaccaca aatacaggaa gacctgcaaa cgctgcaggg tttcggatga ggatctcaat    240

aagttcctca caaaggcaaa cgaagaccag acaagcgtaa aagtcaaggt cgtttctgcc    300

cctaccagaa cgaaaaaggc aatgccaaaa tccgttgcga gagccccgaa acctcttgag    360

aatacagaag cggcacaggc tcaaccttct ggatctaaat tttcacctgc gataccggtt    420

tccacccaag agtcagtttc tgtcccggca tctgtttcaa catcaatatc aagcatttct    480

acaggagcaa ctgcatccgc actggtaaaa gggaatacga accccattac atccatgtct    540

gcccctgttc aggcaagtgc ccccgcactt acgaagagcc agactgacag gcttgaagtc    600

ctgttaaacc caaaagatga gatttccctg aattccggca agcctttcag ggagcttgag    660

tccgaattgc tctctcgcag aaaaaaagac ctgcagcaga tctacgcgga agaaagggag    720

aattatctgg ggaaactcga gcgtgaaatt accaggttct ttgtggacag gggttttctg    780

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<220>
<223> Synthetic sequence: PylRS Methanosarcina mazei Y384F mutant nucleotide sequence

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<213> Methanosalum zhilinae

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<213> Desulfotomaculum gibsoniae

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<213> Methanohalophilus mahii

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gactgccaaa gccgctttac agtacgcaat tcaagaagaa gtcgctctgc aagggcgcta 180

cgcaacaata aatatcgcaa agcatgcaaa aactgcaaac tttccgatga gcgtattact 240

cgttttgtca caaaagattt tggcagggga agccaggcac gtgttatcac atcttcaaaa 300

acaaaaaaga gtaaatctcc aaaggaagca gtggtaaaat ctgtatccag caaggcaaat 360

gaaatgccac ctgttgtaga ggcaaaaaaa gaaaagcctg taaaaccgga ttacacgcct 420

gcccagaaga aaaggattac aacactgctt agccctgcag acgaccttag ttcaataaaa 480

gaactcccca ccttcaagga gctggagaca gaacttgtta aaaaaagaaa acaagacctg 540

cgccagatgt atgaggatga ccgcagacat cagctggccc agctcgaaag ggacatctcc 600

ctatttttaa tagaaaaagg attcatggaa gtacgtactt ctgtcctgat acctgccaaa 660

ttcattgaaa gaatgggcat cacagaagaa gacccccctct acaagcagat cttccgggtg 720

gatgagaata catgcctgcg gcccatgctt gccccgggat tatataatta tcttcacaat 780

tttgataaca taatgcccga ccccctcaag atattcgaga tcggtacctg ctacagaaag 840

gaatccgacg gcaaagaaca tcttgaagag tttacaatgg ttaatttctg ccagatgggt 900

tcgggatgca caaaagaaaa cctgttaaat attatcgatg acctgctcaa atatctaaac 960

atcgattacg aagtaatctc ggataattgc atggtgtatg gagataccat tgacataatg 1020

catggggata tggaaatatc ttcagccgtt gtgggaccca ttccacagga cctcgactgg 1080

ggagtgacca aaccctggat gggtgcagga atgggaattg agagattact caaggtaaag 1140

cacaaataca caaacataaa gcgctcaagc aggtctattt catactataa cggaattaca 1200

accaatctca ggtga 1215

<210> 26
<211> 67
<212> RNA
<213> Methanosarcina barkeri

<400> 26
ggaaaccuga ucauguagau cguggacucu aaauccgcag ccggguagau ucccgggguu 60

uccgcca 67

<210> 27
<211> 72
<212> DNA
<213> Methanosarcina acetivorans

<400> 27
ggaaacctga tcatgtagat cgaatggact ctaaatccgt tcagccgggt tagattcccg 60

gggtttccgc ca 72

<210> 28
<211> 72
<212> DNA
<213> Methanosarcina mazei

<400> 28
ggaaacctga tcatgtagat cgaatggact ctaaatccgt tcagccgggt tagattcccg 60

gggtttccgc ca 72

<210> 29
<211> 72
<212> DNA
<213> Methanococcoides burtonii

<400> 29
ggagacttga tcatgtagat cgaacggact ctaaatcctt tcagccgggt tagattcccg 60

gagtttccgc ca 72

<210> 30
<211> 67
<212> RNA
<213> Desulfobacterium hafniense

<400> 30
ggaaaccuga ucauguagau cguggacucu aaauccgcag ccggguagau ucccgggguu 60

uccgcca 67

<210> 31
<211> 101
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: H1/TO promoter

<400> 31
aatatttgca tgtcgctatg tgttctggga aatcaccata aacgtgaaat ccctatcagt 60

gatagagact tataagttcc ctatcagtga tagagacacc a 101

<210> 32
<211> 250
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: U6 snRNA promoter

<400> 32
agagggccta tttcccatga ttccttcata tttgcatata cgatacaagg ctgttagaga 60

gataattaga attaatttga ctgtaaacac aaagatatta gtacaaaata cgtgacgtag 120

aaagtaataa tttcttgggt agtttgcagt tttaaaatta tgttttaaaa tggactatca 180

tatgcttacc gtaacttgaa agtatttcga tttcttggct ttatatatct tgtggaaagg 240

acgaaacacc 250

<210> 33
<211> 269
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: SNR52 promoter

<400> 33
tctttgaaaa gataatgtat gattatgctt tcactcatat ttatacagaa acttgatgtt 60

ttctttcgag tatatacaag gtgattacat gtacgtttga agtacaactc tagattttgt 120

agtgccctct tgggctagcg gtaaaggtgc gcatttttc acaccctaca atgttctgtt 180

caaaagattt tggtcaaacg ctgtagaagt gaaagttggt gcgcatgttt cggcgttcga 240

aacttctccg cagtgaaaga taaatgatc 269

<210> 34
<211> 221
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: H1 promoter

<400> 34
gaacgctgac gtcatcaacc cgctccaagg aatcgcgggc ccagtgtcac taggcgggaa 60

cacccagcgc gcgtgcgccc tggcaggaag atggctgtga gggacagggg agtggcgccc 120

tgcaatattt gcatgtcgct atgtgttctg ggaaatcacc ataaacgtga aatgtctttg 180

gatttgggaa tcttataagt tctgtatgag accacagatc t 221

<210> 35
<211> 372
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: U6-tRNApyl construct

<400> 35
aaggtcgggc aggaagaggg cctatttccc atgattcctt catatttgca tatacgatac 60

aaggctgtta gagagataat tagaattaat ttgactgtaa acacaaagat attagtacaa 120

aatacgtgac gtagaaagta ataatttctt gggtagtttg cagtttttaa aattatgttt 180

taaaatggac tatcatatgc ttaccgtaac ttgaaagtat ttcgatttct tggctttata 240

tatcttgtgg aaaggacgaa acaccgaatt ctctagactc gagggaaacc tgatcatgta 300

gatcgaatgg actctaaatc cgttcagccg ggttagattc ccggggtttc cggacaagtg 360

cggtttttgt tt 372

<210> 36
<211> 1104
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: GFP nucleotide sequence

<400> 36
atggcctcca aaggagaaga acttttcact ggagttgtcc caattcttgt tgaattagat 60

ggtgatgtta atgggcacaa attttctgtc agtggagagg gtgaaggtga tgctacatac 120

ggaaagctta cccttaaatt tatttgcact actggaaaac tacctgttcc atggccaaca 180

cttgtcacta ctttctctta tggtgttcaa tgcttttccc gttatccgga tcatatgaaa 240

cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaacg cactatatct 300

ttcaaagatg acgggaacta caagacgcgt gctgaagtca agtttgaagg tgataccctt 360

gttaatcgta tcgagttaaa aggtattgat tttaaagaag atggaaacat tctcggacac 420

aaactcgagt acaactataa ctcacacaat gtatacatca cggcagacaa acaaaagaat 480

ggaatcaaag ctaacttcaa aattcgtcac aacattgaag atggatccgt tcaactagca 540

gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaaccat 600

tacctgtcga cacaatctgc cctttcgaaa gatcccaacg aaaagcgtga ccacatggtc 660

cttcttgagt ttgtaactgc tgctgggatt acacatggca tggatcaggc caagcctttg 720

tctcaagaag aatccaccct cattgaaaga gcaacggcta caatcaacag catccccatc 780

tctgaagact acagcgtcgc cagcgcagct ctctctagcg acggccgcat cttcactggt 840

gtcaatgtat atcattttac tgggggacct tgtgcagaac tcgtggtgct gggcactgct 900

gctgctgcgg cagctggcaa cctgacttgt atcgtcgcga tcggaaatga gaacaggggc 960

atcttgagcc cctgcggacg gtgccgacag gtgcttctcg atctgcatcc tgggatcaaa 1020

gccatagtga aggacagtga tggacagccg acggcagttg ggattcgtga attgctgccc 1080

tctggttatg tgtgggaggg ctaa 1104

<210> 37
<211> 367
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: GFP amino acid sequence

<400> 37

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Gln Ala Lys Pro Leu
225                 230                 235                 240

Ser Gln Glu Glu Ser Thr Leu Ile Glu Arg Ala Thr Ala Thr Ile Asn
                245                 250                 255

Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala Ser Ala Ala Leu Ser
            260                 265                 270

Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val Tyr His Phe Thr Gly
        275                 280                 285

Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr Ala Ala Ala Ala Ala
    290                 295                 300

Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn Arg Gly
305                 310                 315                 320

Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His
                325                 330                 335

Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp Gly Gln Pro Thr Ala
            340                 345                 350

Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr Val Trp Glu Gly
        355                 360                 365


<210>  38
<211>  367
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic sequence: GFPY40 Amino acid Sequence

<220>
<221>  SITE
<222>  (40)..(40)
<223>  Xaa is nnAA, a non natural amino acid.

<400>  38

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1               5                   10                  15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
            20                  25                  30
```

```
Glu Gly Glu Gly Asp Ala Thr Xaa Gly Lys Leu Thr Leu Lys Phe Ile
        35                  40                  45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
    50                  55                  60

Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65                  70                  75                  80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
                85                  90                  95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
            100                 105                 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
        115                 120                 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
    130                 135                 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145                 150                 155                 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
                165                 170                 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
            180                 185                 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
        195                 200                 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
    210                 215                 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Gln Ala Lys Pro Leu
225                 230                 235                 240

Ser Gln Glu Glu Ser Thr Leu Ile Glu Arg Ala Thr Ala Thr Ile Asn
                245                 250                 255

Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala Ser Ala Ala Leu Ser
            260                 265                 270

Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val Tyr His Phe Thr Gly
        275                 280                 285

Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr Ala Ala Ala Ala Ala
    290                 295                 300
```

```
Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly Asn Glu Asn Arg Gly
305                 310                 315                 320

Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val Leu Leu Asp Leu His
                325                 330                 335

Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp Gly Gln Pro Thr Ala
            340                 345                 350

Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr Val Trp Glu Gly
        355                 360                 365
```

<210> 39
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-IL-6 (28D2) Gamma Nucleotide Sequence

<400> 39

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atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag     60

tcgctggggg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgc    120

acagtctctg gattatccct cagtaagaat gcaattgcct gggtccgcca ggctccaggg    180

aagggactgg aatggatcgg aatcatttat gctggtggtg ccacaaccta cgcgagctgg    240

gcgaaaggcc gattcaccat ctccaagtcc tcgaccacgg tggatctgaa gatcaccagt    300

ccgacaacag tggacacggc cacctatttc tgtgccaggg aatatgctgg tgatagttat    360

tatactggat acactcagtt ggatctctgg ggcccaggca ccctggtcac cgtctcgagt    420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg    480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca    600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc    660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc    720

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga    780

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct    840

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg    900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac    960

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag   1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc   1080

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag   1140

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc   1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg   1260
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ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 40
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-IL-6 (28D2) Gamma Amino acid Sequence

<400> 40

Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Leu Gly Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30

Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Leu Ser Leu Ser
35 40 45

Lys Asn Ala Ile Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Ile Ile Tyr Ala Gly Gly Ala Thr Thr Tyr Ala Ser Trp
65 70 75 80

Ala Lys Gly Arg Phe Thr Ile Ser Lys Ser Ser Thr Thr Val Asp Leu
85 90 95

Lys Ile Thr Ser Pro Thr Thr Val Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110

Arg Glu Tyr Ala Gly Asp Ser Tyr Tyr Thr Gly Tyr Thr Gln Leu Asp
115 120 125

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

```
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 41
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-IL-6 (28D2) Gamma_amber K274 Nucleotide Sequence

<400> 41
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgctggggg agtccggggg tcgcctggtc acgcctggga cacccctgac actcacctgc 120

acagtctctg gattatccct cagtaagaat gcaattgcct gggtccgcca ggctccaggg 180

aagggactgg aatggatcgg aatcatttat gctggtggtg ccacaaccta cgcgagctgg 240

gcgaaaggcc gattcaccat ctccaagtcc tcgaccacgg tggatctgaa gatcaccagt 300

ccgacaacag tggacacggc cacctatttc tgtgccaggg aatatgctgg tgatagttat 360

tatactggat acactcagtt ggatctctgg ggcccaggca ccctggtcac cgtctcgagt 420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 840

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcta gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1260

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 42
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-IL-6 (28D2) Gamma_amber K274 amino acid Sequence

<220>
<221> SITE
<222> (297)..(297)
<223> Xaa is nnAA, a non natural amino acid.

<400> 42

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Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                  10                  15

Val Gln Cys Gln Ser Leu Gly Glu Ser Gly Gly Arg Leu Val Thr Pro
            20                  25                  30

Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Leu Ser Leu Ser
        35                  40                  45

Lys Asn Ala Ile Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
    50                  55                  60

Trp Ile Gly Ile Ile Tyr Ala Gly Gly Ala Thr Thr Tyr Ala Ser Trp
65                  70                  75                  80

Ala Lys Gly Arg Phe Thr Ile Ser Lys Ser Ser Thr Thr Val Asp Leu
                85                  90                  95

Lys Ile Thr Ser Pro Thr Thr Val Asp Thr Ala Thr Tyr Phe Cys Ala
            100                 105                 110

Arg Glu Tyr Ala Gly Asp Ser Tyr Tyr Thr Gly Tyr Thr Gln Leu Asp
        115                 120                 125

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
```

```
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Xaa Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470


<210>  43
<211>  726
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic sequence: anti-IL-6 (28D2)  Kappa Nucleotide Sequence
```

<400> 43
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggcgcc 60

agatgtgccc ttgtgatgac ccagactcca gcctccgtgt ctgccgctgt gggaggcaca 120

gtgaccatca attgccaggc cagtgaggac ctttttagta gtttggcctg gtttcagcag 180

aaaccagggc agcctcccaa actcctgatc tattctgcat ccactctggc atctggggtc 240

ccatcgcggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcgacctg 300

gaatgtgccg atgctgccac ttactactgt ctaggccttt actattatct tactcctgat 360

cctatttatg ggttcggcgg agggaccaag gtggtggtgg tccgtacggt ggctgcacca 420

tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 480

tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 540

ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 600

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 660

tgcgaagtca cccatcaggg cctgagttcg cccgtcacaa agagcttcaa caggggagag 720

tgttaa 726

<210> 44
<211> 241
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-IL-6 (28D2) Kappa amino acid Sequence

<400> 44

Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser
20 25 30

Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala Ser
35 40 45

Glu Asp Leu Phe Ser Ser Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln
50 55 60

Pro Pro Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Ala Ser Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Leu Gly
100 105 110

Leu Tyr Tyr Tyr Leu Thr Pro Asp Pro Ile Tyr Gly Phe Gly Gly Gly
115 120 125

```
Thr Lys Val Val Val Val Arg Thr Val Ala Ala Pro Ser Val Phe Ile
    130                 135                 140

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145                 150                 155                 160

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                165                 170                 175

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
            180                 185                 190

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
    210                 215                 220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225                 230                 235                 240

Cys
```

<210> 45
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma Nucleotide sequence

<400> 45

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atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt     60

gaggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcgggtc cctgcgcctc    120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttcactgggt ccgtcaggca    180

cctggcaagg gtctggagtg ggtgagccgc atttatccta ccaatggtta cactcgctac    240

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccctgtat    300

ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc    360

ggtgatggct tttacgcgat ggactactgg ggccagggca ccctggtcac cgtctcgagt    420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg    480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg    540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca    600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc    660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc    720

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga    780
```

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 840

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1260

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 46
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma amino acid sequence

<400> 46

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
35 40 45

Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Trp Val Ser Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

```
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
```

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 47
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma_K274amber nucleotide sequence

<400> 47
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt 60

gaggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcgggtc cctgcgcctc 120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttcactgggt ccgtcaggca 180

cctggcaagg gtctggagtg ggtgagccgc atttatccta ccaatggtta cactcgctac 240

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccctgtat 300

ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc 360

ggtgatggct tttacgcgat ggactactgg ggccagggca ccctggtcac cgtctcgagt 420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 840

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcta gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1140

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1260

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 48
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma_K274amber amino acid sequence

<220>
<221> SITE
<222> (297)..(297)
<223> Xaa is nnAA, a non natural amino acid.

<400> 48

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
35 40 45

Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Trp Val Ser Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

```
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Xaa Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
```

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 49
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma_T359amber nucleotide sequence

<400> 49
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt 60

gaggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcgggtc cctgcgcctc 120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttcactgggt ccgtcaggca 180

cctggcaagg gtctggagtg ggtgagccgc atttatccta ccaatggtta cactcgctac 240

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccctgtat 300

ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc 360

ggtgatggct tttacgcgat ggactactgg ggccagggca ccctggtcac cgtctcgagt 420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 840

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1020

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140

atgtagaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1260

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 50
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5) gamma_T359amber amino acid sequence

<220>
<221> SITE
<222> (382)..(382)
<223> Xaa is nnAA, a non natural amino acid.

<400> 50

```
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
            20                  25                  30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
        35                  40                  45

Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Val Ser Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65                  70                  75                  80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
                85                  90                  95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
```

```
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Xaa Lys Asn
    370                 375                 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460

Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 51
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5)Kappa nucleotide sequence

<400> 51
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga ccgtgtcaca 120

atcacttgcc gtgctagcca ggatgtgaat acagcggtgg cctggtatca gcagaaacct 180

ggcaaagccc ctaagctcct gatctattct gcatcctttt tgtacagcgg cgtgccgagc 240

cgcttcagcg gcagccgttc tggtaccgat ttcactctca ccatcagctc tctgcaaccg 300

gaagattttg caacttacta ctgtcaacag cactacacca ctcctccgac gttcggccaa 360

gggaccaagg tggaaatcga acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

ctgagttcgc ccgtcacaaa gagcttcaac aggggagagt gttaa 705

<210> 52
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 (4D5)Kappa amino acid sequence

<400> 52

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

```
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110

Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 53
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 Kappa D70amber nucleotide sequence

<400> 53

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atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt     60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga ccgtgtcaca    120

atcacttgcc gtgctagcca ggatgtgaat acagcggtgg cctggtatca gcagaaacct    180

ggcaaagccc ctaagctcct gatctattct gcatcctttt tgtacagcgg cgtgccgagc    240

cgcttcagcg gcagccgttc tggtacctag ttcactctca ccatcagctc tctgcaaccg    300

gaagattttg caacttacta ctgtcaacag cactacacca ctcctccgac gttcggccaa    360

gggaccaagg tggaaatcga acgtacggtg gctgcaccat ctgtcttcat cttcccgcca    420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat    480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag    540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg    600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc    660

ctgagttcgc ccgtcacaaa gagcttcaac aggggagagt gttaa                    705
```

<210> 54
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 Kappa D70amber amino acid sequence

<220>
<221> SITE
<222> (90)..(90)
<223> Xaa is nnAA, a non natural amino acid.

<400> 54

```
Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1               5                  10                  15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
        35                  40                  45

Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Arg Ser Gly Thr Xaa Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110

Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205
```

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 55
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 Kappa E81amber nucleotide sequence

<400> 55
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga ccgtgtcaca 120

atcacttgcc gtgctagcca ggatgtgaat acagcggtgg cctggtatca gcagaaacct 180

ggcaaagccc ctaagctcct gatctattct gcatcctttt tgtacagcgg cgtgccgagc 240

cgcttcagcg gcagccgttc tggtaccgat ttcactctca ccatcagctc tctgcaaccg 300

taggattttg caacttacta ctgtcaacag cactacacca ctcctccgac gttcggccaa 360

gggaccaagg tggaaatcga acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

ctgagttcgc ccgtcacaaa gagcttcaac aggggagagt gttaa 705

<210> 56
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-Her2 Kappa E81amber amino acid sequence

<220>
<221> SITE
<222> (101)..(101)
<223> Xaa is nnAA, a non natural amino acid.

<400> 56

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

```
Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                85                  90                  95

Ser Leu Gln Pro Xaa Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr
            100                 105                 110

Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  57
<211>  825
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic sequence: anti-PSMA scFv nucleotide sequence

<400>  57
atggaggcgc cagcgcagct tctcttcttg ctcctgctct ggctgccgga cacgacggga     60

gacatcgtca tgactcagtc acacaagttc atgtcgactt cggtgggaga tagggtgtcc    120

atcatttgca aagcaagcca agatgtaggg acagcggtcg actggtatca gcagaagccc    180

ggtcagtccc ctaaactcct catctactgg gcatcgacgc gacacacggg cgtcccggac    240

cgcttcacgg gatcgggatc aggtactgac tttacattga caattacaaa cgtccaatcg    300
```

gaggaccttg cggattactt ctgtcaacag tacaattcgt atcccctgac gttcggggct 360

gggacaaagc tcgacttgaa gggcggtgga gggtcaggtg gaggaggctc cggtggggga 420

gggagcggag ggggtggttc ggaggtgcag ttgcagcaat caggcccgga acttaagaaa 480

cccgggacct cagtaagaat cagctgtaag acaagcgggt acacgtttac cgaatatact 540

atccattggg tgaagcagtc gcatggaaaa tcgcttgaat ggatcgggaa cattaatcct 600

aataacgggg gaaccacgta caaccagaag tttgaggata aagccaccct tactgtggac 660

aaatcctcca gcactgccta tatggaattg cggtccctga cctcggagga ttcagccgta 720

tactactgcg cggcaggatg gaattttgat tattgggggc agggaacaac attgacagtc 780

tcgagcggtc cacctcctcc acctcaccat caccatcatc actga 825

<210> 58
<211> 274
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-PSMA scFv amino acid sequence

<400> 58

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
20 25 30

Thr Ser Val Gly Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp
35 40 45

Val Gly Thr Ala Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

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

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr
85 90 95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Asp Leu Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys
145 150 155 160

```
Pro Gly Thr Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
                165                 170                 175

Thr Glu Tyr Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
            180                 185                 190

Glu Trp Ile Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn
        195                 200                 205

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

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
225                 230                 235                 240

Tyr Tyr Cys Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr
                245                 250                 255

Thr Leu Thr Val Ser Ser Gly Pro Pro Pro Pro His His His His
            260                 265                 270

His His
```

<210> 59
<211> 828
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-PSMA scFv_117amber nucleotide sequence

<400> 59

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atggaggcgc cagcgcagct tctcttcttg ctcctgctct ggctgccgga cacgacggga     60

gacatcgtca tgactcagtc acacaagttc atgtcgactt cggtgggaga tagggtgtcc    120

atcatttgca aagcaagcca agatgtaggg acagcggtcg actggtatca gcagaagccc    180

ggtcagtccc ctaaactcct catctactgg gcatcgacgc gacacacggg cgtcccggac    240

cgcttcacgg gatcgggatc aggtactgac tttacattga caattacaaa cgtccaatcg    300

gaggaccttg cggattactt ctgtcaacag tacaattcgt atcccctgac gttcggggct    360

gggacaaagc tcgacttgaa gggcggtgga gggtcaggtg gaggaggctc cggtggggga    420

gggagcggag ggggtggttc ggaggtgcag ttgcagcaat caggcccgga acttaagaaa    480

cccgggacct cagtaagaat cagctgtaag acaagcgggt acacgtttac cgaatatact    540

atccattggg tgaagcagtc gcatggaaaa tcgcttgaat ggatcgggaa cattaatcct    600

aataacgggg gaaccacgta caaccagaag tttgaggata aagccaccct tactgtggac    660

aaatcctcca gcactgccta tatggaattg cggtccctga cctcggagga ttcagccgta    720

tactactgcg cggcaggatg gaattttgat tattgggggc agggaacaac attgacagtc    780
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tcgagctagg gtccacctcc tccacctcac catcaccatc atcactga 828

<210> 60
<211> 275
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: anti-PSMA scFv_amber amino acid sequence

<220>
<221> SITE
<222> (263)..(263)
<223> Xaa is nnAA, a non natural amino acid.

<400> 60

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
20 25 30

Thr Ser Val Gly Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp
35 40 45

Val Gly Thr Ala Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

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

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr
85 90 95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Asp Leu Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys
145 150 155 160

Pro Gly Thr Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
165 170 175

Thr Glu Tyr Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu
180 185 190

Glu Trp Ile Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn

195 200 205

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

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
225 230 235 240

Tyr Tyr Cys Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr
245 250 255

Thr Leu Thr Val Ser Ser Xaa Gly Pro Pro Pro Pro Pro His His His
260 265 270

His His His
275

<210> 61
<211> 612
<212> DNA
<213> Homo sapiens

<400> 61
atgtctgcac ttctgatcct agctcttgtt ggagctgcag ttgctaagct tcaccatcac 60

catcaccatc cgattccaga ctcatctccg ttgctgcagt ttggcgggca ggtgcggcag 120

cgctatctgt acaccgacga cgcacagcaa acagaggctc atcttgaaat ccgggaggat 180

ggcactgttg gcggtgcggc ggatcagagt cccgagtcac tgcttcaact taaggccttg 240

aaaccaggag tgattcaaat cctcggtgtg aaaacgagta gattcctctg ccaaaggccc 300

gatggcgccc tgtacggaag cctccacttc gaccctgagg catgtagctt tcgcgaactc 360

ctgttggaag atgggtataa cgtctatcag tccgaggcac acggccttcc tctccacctc 420

cccgggaata agtcaccgca cagggacccc gctccaaggg gtcccgcacg attcctgccc 480

ttgccagggc tgccacccgc cctgccagaa ccgcctggaa ttctggcccc tcagccacct 540

gacgtcgggt ctagcgaccc cctgagtatg gtaggaccta gccagggcag atccccctcc 600

tacgcctcct aa 612

<210> 62
<211> 219
<212> PRT
<213> Homo sapiens

<400> 62

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu

35 40 45

Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
50 55 60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65 70 75 80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
85 90 95

Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu
100 105 110

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

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
130 135 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145 150 155 160

Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro
165 170 175

Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
180 185 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
195 200 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
210 215

<210> 63
<211> 612
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 R131amber nucleotide sequence

<400> 63
atgtctgcac ttctgatcct agctcttgtt ggagctgcag ttgctaagct tcaccatcac 60

catcaccatc cgattccaga ctcatctccg ttgctgcagt ttggcgggca ggtgcggcag 120

cgctatctgt acaccgacga cgcacagcaa acagaggctc atcttgaaat ccgggaggat 180

ggcactgttg gcggtgcggc ggatcagagt cccgagtcac tgcttcaact taaggccttg 240

aaaccaggag tgattcaaat cctcggtgtg aaaacgagta gattcctctg ccaaaggccc 300

gatggcgccc tgtacggaag cctccacttc gaccctgagg catgtagctt tcgcgaactc 360

ctgttggaag atgggtataa cgtctatcag tccgaggcac acggccttcc tctccacctc 420

cccgggaata agtcaccgca cagggacccc gctccatagg gtcccgcacg attcctgccc 480

ttgccagggc tgccacccgc cctgccagaa ccgcctggaa ttctggcccc tcagccacct 540

gacgtcgggt ctagcgaccc cctgagtatg gtaggaccta gccagggcag atccccctcc 600

tacgcctcct aa 612

<210> 64
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 R131amber amino acid sequence

<220>
<221> SITE
<222> (169)..(169)
<223> Xaa is nnAA, a non natural amino acid.

<400> 64

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu
35 40 45

Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
50 55 60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65 70 75 80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
85 90 95

Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu
100 105 110

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

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
130 135 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145 150 155 160

Ser Pro His Arg Asp Pro Ala Pro Xaa Gly Pro Ala Arg Phe Leu Pro
165 170 175

Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
180 185 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
195 200 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
210 215

<210> 65
<211> 660
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 F12amber nucleotide sequence

<400> 65
atgtctgctc ttctgatact cgccttggta ggggctgctg ttgccgacta taaggatcac 60

gacggcgatt acaaggacca tgatatcgat tacaaagatg acgacgacaa gtctcatccg 120

attccagact catctccgtt gctgcagtag ggcgggcagg tgcggcagcg ctatctgtac 180

accgacgacg cacagcaaac agaggctcat cttgaaatcc gggaggatgg cactgttggc 240

ggtgcggcgg atcagagtcc cgagtcactg cttcaactta aggccttgaa accaggagtg 300

attcaaatcc tcggtgtgaa aacgagtaga ttcctctgcc aaaggcccga tggcgccctg 360

tacggaagcc tccacttcga ccctgaggca tgtagctttc gcgaactcct gttggaagat 420

gggtataacg tctatcagtc cgaggcacac ggccttcctc tccacctccc cgggaataag 480

tcaccgcaca gggaccccgc tccaaggggt cccgcacgat tcctgccctt gccagggctg 540

ccacccgccc tgccagaacc gcctggaatt ctggcccctc agccacctga cgtcgggtct 600

agcgaccccc tgagtatggt aggacctagc cagggcagat ccccctccta cgcctcctaa 660

<210> 66
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 F12amber amino acid sequence

<220>
<221> SITE
<222> (50)..(50)
<223> Xaa is nnAA, a non natural amino acid.

<400> 66

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys
20 25 30

```
Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu
        35                  40                  45

Gln Xaa Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
    50                  55                  60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65                  70                  75                  80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
                85                  90                  95

Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu
            100                 105                 110

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

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
    130                 135                 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145                 150                 155                 160

Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro
                165                 170                 175

Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
            180                 185                 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
        195                 200                 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
    210                 215


<210>  67
<211>  612
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Synthetic sequence: FGF21 L60amber nucleotide sequence

<400>  67
atgtctgcac ttctgatcct agctcttgtt ggagctgcag ttgctaagct tcaccatcac     60

catcaccatc cgattccaga ctcatctccg ttgctgcagt ttggcgggca ggtgcggcag    120

cgctatctgt acaccgacga cgcacagcaa acagaggctc atcttgaaat ccgggaggat    180

ggcactgttg gcggtgcggc ggatcagagt cccgagtcac tgcttcaact taaggccttg    240

aaaccaggag tgattcaaat ctagggtgtg aaaacgagta gattcctctg ccaaaggccc    300
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gatggcgccc tgtacggaag cctccacttc gaccctgagg catgtagctt tcgcgaactc 360

ctgttggaag atgggtataa cgtctatcag tccgaggcac acggccttcc tctccacctc 420

cccgggaata agtcaccgca cagggacccc gctccaaggg gtcccgcacg attcctgccc 480

ttgccagggc tgccacccgc cctgccagaa ccgcctggaa ttctggcccc tcagccacct 540

gacgtcgggt ctagcgaccc cctgagtatg gtaggaccta gccagggcag atccccctcc 600

tacgcctcct aa 612

<210> 68
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 L60amber amino acid sequence

<220>
<221> SITE
<222> (104)..(104)
<223> Xaa is nnAA, a non natural amino acid.

<400> 68

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu
35 40 45

Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
50 55 60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65 70 75 80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
85 90 95

Lys Pro Gly Val Ile Gln Ile Xaa Gly Val Lys Thr Ser Arg Phe Leu
100 105 110

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

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
130 135 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145 150 155 160

Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro
165 170 175

Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
180 185 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
195 200 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
210 215

<210> 69
<211> 612
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21P 90amber nucleotide sequence

<400> 69
atgtctgcac ttctgatcct agctcttgtt ggagctgcag ttgctaagct tcaccatcac 60

catcaccatc cgattccaga ctcatctccg ttgctgcagt ttggcgggca ggtgcggcag 120

cgctatctgt acaccgacga cgcacagcaa acagaggctc atcttgaaat ccgggaggat 180

ggcactgttg gcggtgcggc ggatcagagt cccgagtcac tgcttcaact taaggccttg 240

aaaccaggag tgattcaaat cctcggtgtg aaaacgagta gattcctctg ccaaaggccc 300

gatggcgccc tgtacggaag cctccacttc gactaggagg catgtagctt tcgcgaactc 360

ctgttggaag atgggtataa cgtctatcag tccgaggcac acggccttcc tctccacctc 420

cccgggaata agtcaccgca cagggacccc gctccaaggg gtcccgcacg attcctgccc 480

ttgccagggc tgccacccgc cctgccagaa ccgcctggaa ttctggcccc tcagccacct 540

gacgtcgggt ctagcgaccc cctgagtatg gtaggaccta gccagggcag atccccctcc 600

tacgcctcct aa 612

<210> 70
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 P90amber amino acid sequence

<220>
<221> SITE
<222> (128)..(128)
<223> Xaa is nnAA, a non natural amino acid.

<400> 70

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys

20 25 30

Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu
35 40 45

Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
50 55 60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65 70 75 80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
85 90 95

Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu
100 105 110

Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Xaa
115 120 125

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
130 135 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145 150 155 160

Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro
165 170 175

Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
180 185 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
195 200 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
210 215

<210> 71
<211> 612
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 P140amber nucleotide sequence

<400> 71
atgtctgcac ttctgatcct agctcttgtt ggagctgcag ttgctaagct tcaccatcac 60

catcaccatc cgattccaga ctcatctccg ttgctgcagt ttggcgggca ggtgcggcag 120

cgctatctgt acaccgacga cgcacagcaa acagaggctc atcttgaaat ccgggaggat 180

ggcactgttg gcggtgcggc ggatcagagt cccgagtcac tgcttcaact taaggccttg 240

aaaccaggag tgattcaaat cctcggtgtg aaaacgagta gattcctctg ccaaaggccc 300

gatggcgccc tgtacggaag cctccacttc gaccctgagg catgtagctt tcgcgaactc 360

ctgttggaag atgggtataa cgtctatcag tccgaggcac acggccttcc tctccacctc 420

cccgggaata agtcaccgca cagggacccc gctccaaggg gtcccgcacg attcctgccc 480

ttgtaggggc tgccacccgc cctgccagaa ccgcctggaa ttctggcccc tcagccacct 540

gacgtcgggt ctagcgaccc cctgagtatg gtaggaccta gccagggcag atccccctcc 600

tacgcctcct aa 612

<210> 72
<211> 219
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: FGF21 P140amber amino acid sequence

<220>
<221> SITE
<222> (178)..(178)
<223> Xaa is nnAA, a non natural amino acid.

<400> 72

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

Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr Lys
20 25 30

Asp Asp Asp Asp Lys Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu
35 40 45

Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala
50 55 60

Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly
65 70 75 80

Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu
85 90 95

Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu
100 105 110

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

Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val
130 135 140

Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys
145 150 155 160

```
Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro
                165                 170                 175

Leu Xaa Gly Leu Pro Pro Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala
            180                 185                 190

Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly
        195                 200                 205

Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
    210                 215
```

<210> 73
<211> 1104
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: GFPY40 Nucleotide Sequence

<400> 73

```
atggcctcca aaggagaaga acttttcact ggagttgtcc caattcttgt tgaattagat     60

ggtgatgtta atgggcacaa attttctgtc agtggagagg gtgaaggtga tgctacatag    120

ggaaagctta cccttaaatt tatttgcact actggaaaac tacctgttcc atggccaaca    180

cttgtcacta ctttctctta tggtgttcaa tgcttttccc gttatccgga tcatatgaaa    240

cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaacg cactatatct    300

ttcaaagatg acgggaacta caagacgcgt gctgaagtca agtttgaagg tgataccctt    360

gttaatcgta tcgagttaaa aggtattgat tttaaagaag atggaaacat tctcggacac    420

aaactcgagt acaactataa ctcacacaat gtatacatca cggcagacaa acaaaagaat    480

ggaatcaaag ctaacttcaa aattcgtcac aacattgaag atggatccgt tcaactagca    540

gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaaccat    600

tacctgtcga cacaatctgc cctttcgaaa gatcccaacg aaaagcgtga ccacatggtc    660

cttcttgagt ttgtaactgc tgctgggatt acacatggca tggatcaggc caagcctttg    720

tctcaagaag aatccaccct cattgaaaga gcaacggcta caatcaacag catccccatc    780

tctgaagact acagcgtcgc cagcgcagct ctctctagcg acggccgcat cttcactggt    840

gtcaatgtat atcattttac tgggggacct tgtgcagaac tcgtggtgct gggcactgct    900

gctgctgcgg cagctggcaa cctgacttgt atcgtcgcga tcggaaatga gaacaggggc    960

atcttgagcc cctgcggacg gtgccgacag gtgcttctcg atctgcatcc tgggatcaaa   1020

gccatagtga aggacagtga tggacagccg acggcagttg ggattcgtga attgctgccc   1080

tctggttatg tgtgggaggg ctaa                                         1104
```

<210> 74
<211> 1416

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin Nucleotide sequence Gamma Chain

<400> 74
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt 60

gaggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcgggtc cctgcgcctc 120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttcactgggt ccgtcaggca 180

cctggcaagg gtctggagtg ggtggcccgc atttatccta ccaatggtta cactcgctac 240

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccgcttat 300

ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc 360

ggtgatggct tttacgcgat ggactactgg ggccagggca ccctggtcac cgtctcgagt 420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720

cctaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggac 1140

gagctcacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acgcagaaga gcctctccct gtctccgggt aaataa 1416

<210> 75
<211> 471
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin amino acid sequence Gamma Chain

<400> 75

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

```
Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
            20                  25                  30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
        35                  40                  45

Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65                  70                  75                  80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
                85                  90                  95

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
```

```
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 76
<211> 1416
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin H274 Nucleotide sequence Gamma Chain

<400> 76

```
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt     60

gaggtgcagc tggtggagtc tggcggtggc ttggtacagc cgggcgggtc cctgcgcctc    120

tcctgtgccg cttccggatt caacatcaaa gacacgtata ttcactgggt ccgtcaggca    180

cctggcaagg gtctggagtg ggtggcccgc atttatccta ccaatggtta cactcgctac    240
```

gccgactctg tgaagggccg cttcaccatc agcgccgaca cgtccaagaa caccgcttat 300

ctgcaaatga acagcctgcg tgccgaggac accgcggtgt attactgcag ccgctggggc 360

ggtgatggct tttacgcgat ggactactgg ggccagggca ccctggtcac cgtctcgagt 420

gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720

cctaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 780

ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt ctagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 960

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggac 1140

gagctcacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acgcagaaga gcctctccct gtctccgggt aaataa 1416

<210> 77
<211> 471
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin 274 amino acid sequence Gamma Chain

<220>
<221> SITE
<222> (298)..(298)
<223> Xaa is nnAA, a non natural amino acid.

<400> 77

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn
35 40 45

```
Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
65                  70                  75                  80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
                85                  90                  95

Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
            100                 105                 110

Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Xaa Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
```

```
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 78
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin nucleotide sequence Kappa Chain

<400> 78

```
atggaggctc ccgcccagct gctctttctg ctccttctct ggcttcccga cacaaccggt     60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga ccgtgtcaca    120

atcacttgcc gtgctagcca ggatgtgaat acagcggtgg cctggtatca gcagaaacct    180

ggcaaagccc ctaagctcct gatctattct gcatcctttt tgtacagcgg cgtgccgagc    240

cgcttcagcg gcagccgttc tggtaccgat ttcactctca ccatcagctc tctgcaaccg    300

gaagattttg caacttacta ctgtcaacag cactacacca ctcctccgac gttcggccaa    360

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca    420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat    480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag    540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg    600
```

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

ctgagttcgc ccgtcacaaa gagcttcaac aggggagagt gttaa 705

<210> 79
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Herceptin amino acid sequence Kappa Chain

<400> 79

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr
100 105 110

Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 80
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: 3 x Flag tag sequence

<400> 80

Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1 5 10 15

Lys Asp Asp Asp Asp Lys Ser
20

<210> 81
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: 5xPro-6xHis tag

<400> 81

Pro Pro Pro Pro Pro His His His His His His
1 5 10

<210> 82
<211> 330
<212> PRT
<213> Homo sapiens

<400> 1

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 83
<211> 17
<212> PRT
<213> Homo sapiens

<400> 1

Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
1 5 10 15

Gln

<210> 84
<211> 15
<212> PRT
<213> Homo sapiens

<400> 2

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
1 5 10 15