Figure 1

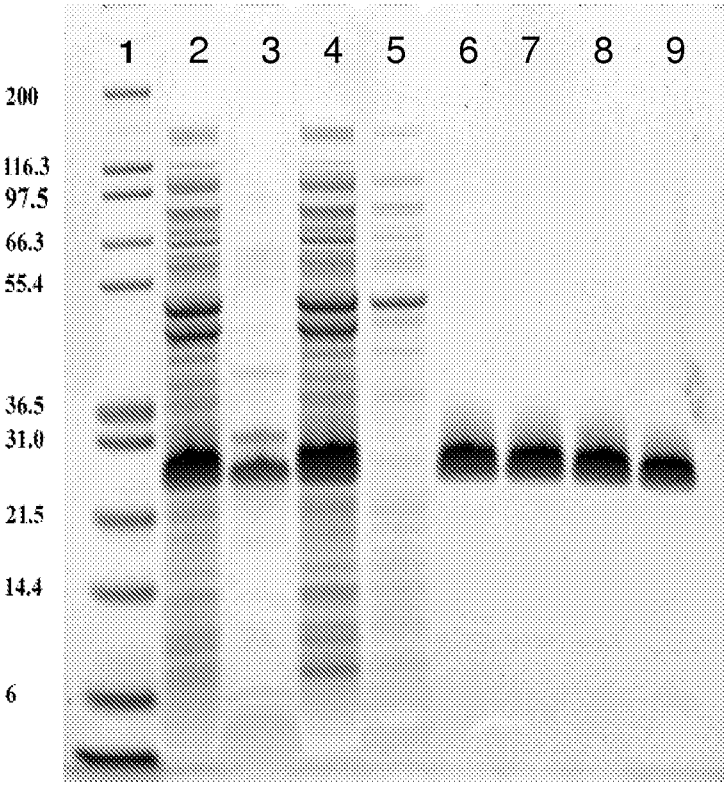
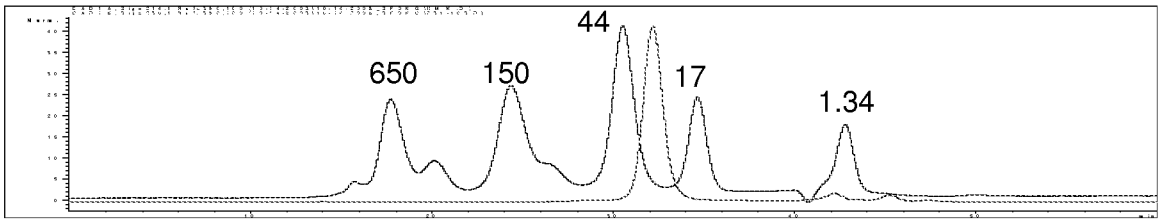



Figure 2

A




B

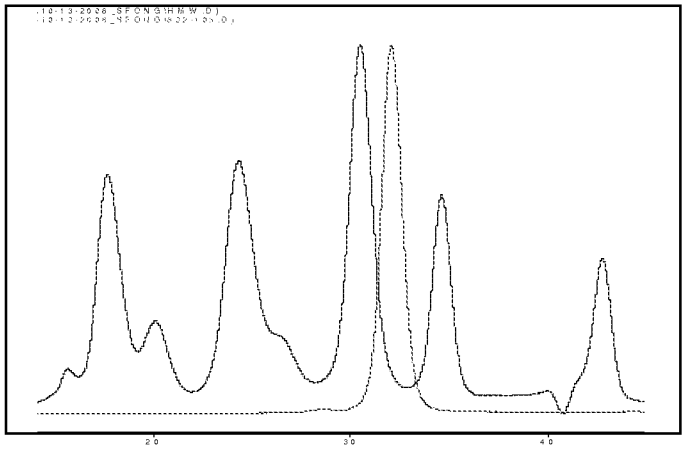
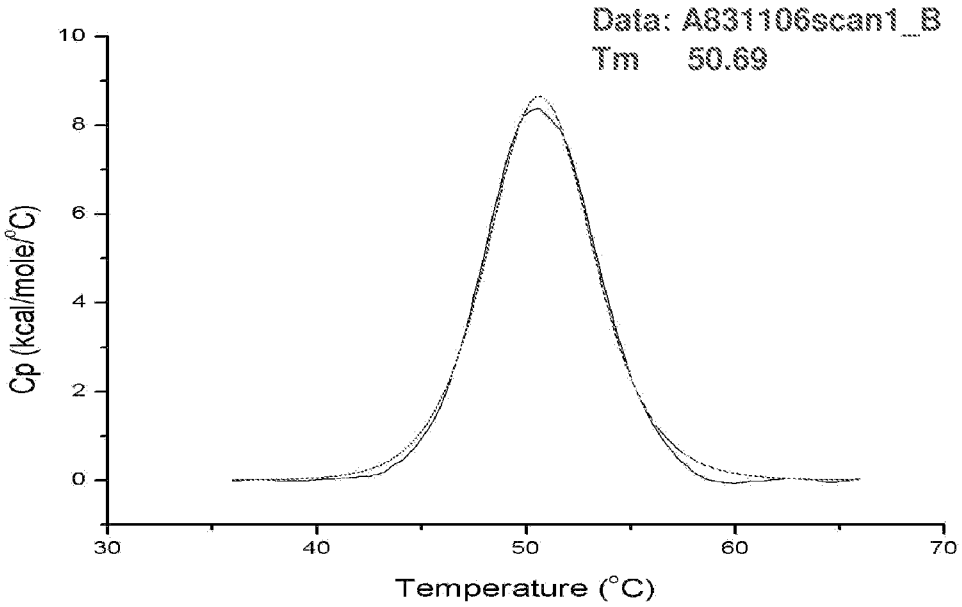


Figure 3

A


Data: A831106scan1_B
Tm 50.69
Cp (kcal/mole/°C)
Temperature (°C)
10
8
6
4
2
0
30
40
50
60
70

B

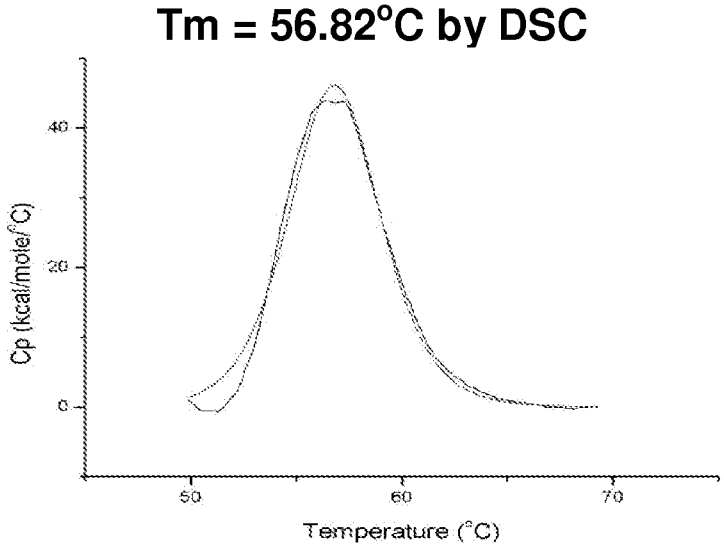

Tm = 56.82°C by DSC
Cp (kcal/mole/°C)
Temperature (°C)
40
20
0
50
60
70

Figure 4

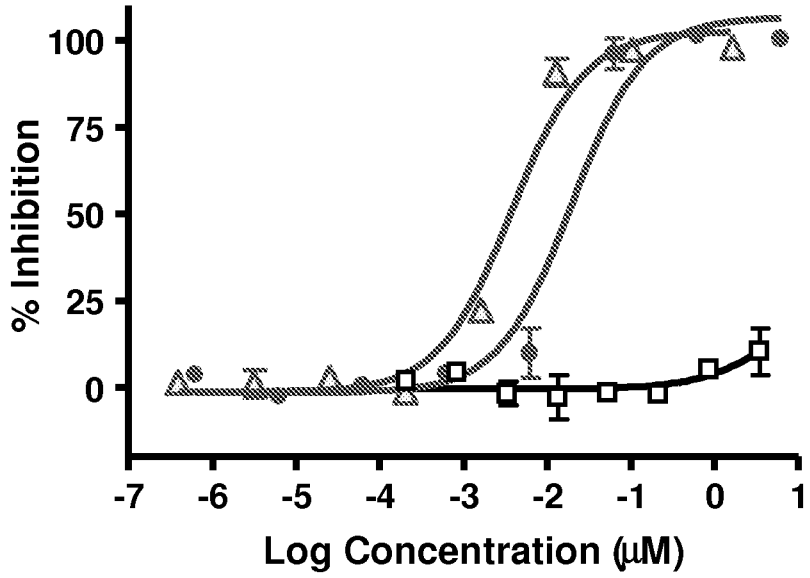



Figure 5

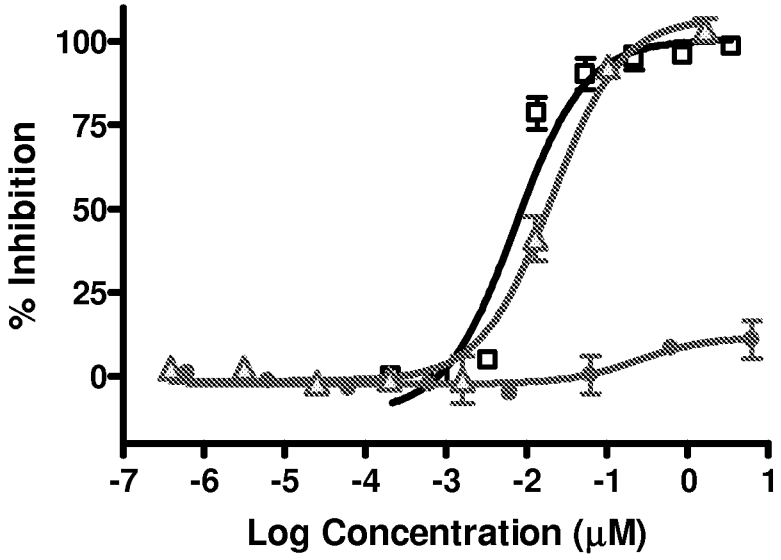


Figure 6

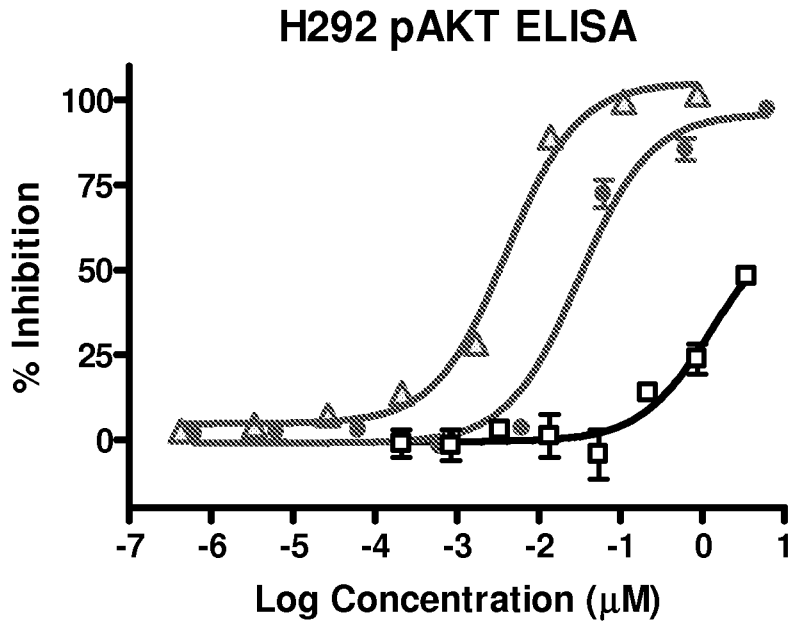



Figure 7

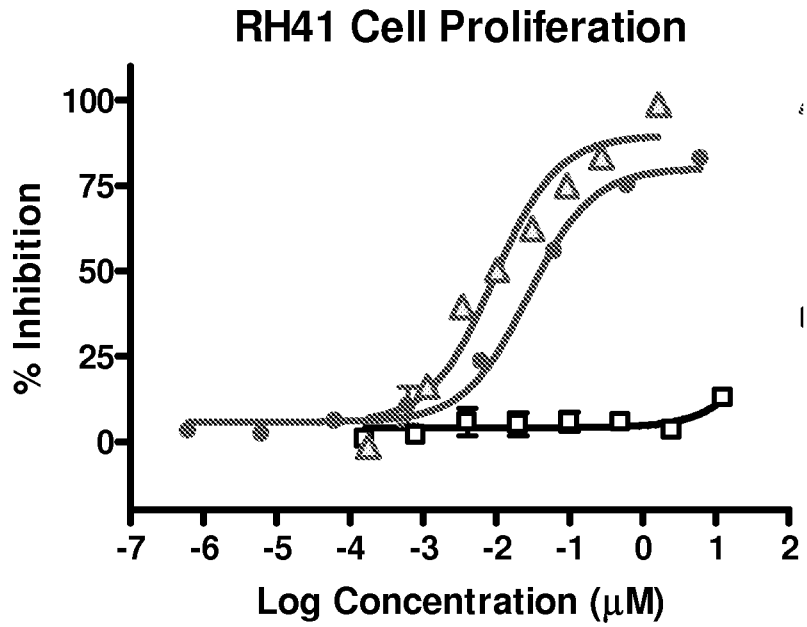


Figure 8

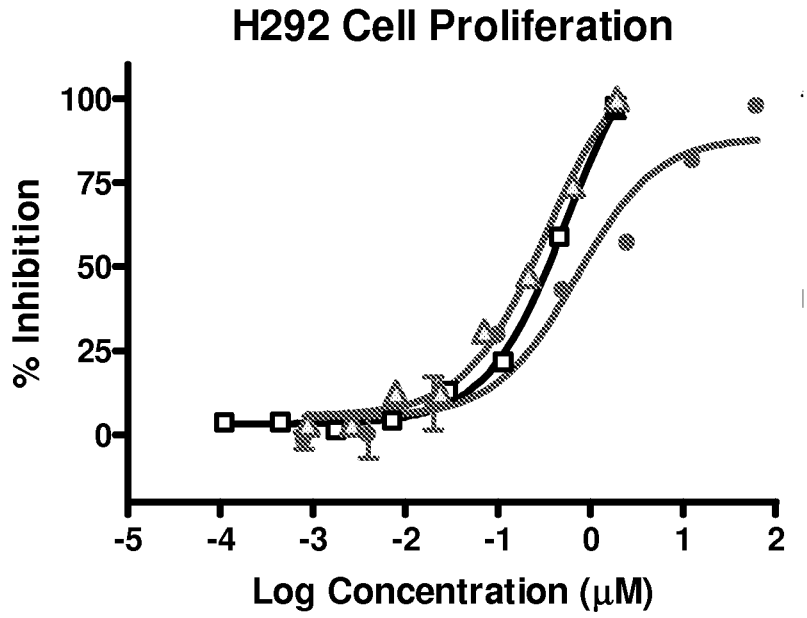



Figure 9

SUMMARY OF ACTIVITY IN CELL BASED ASSAYS

| NAME | H292 pEGFR ELISA (nM) | H292 pIGFR ELISA (nM) | H292 pAKT ELISA (nM) | A431 pEGFR ICW (nM) | A431 pERK ICW (nM) |
|---|---|---|---|---|---|
| E1 | 8 | --- | | 24 | 13 |
| E1-GS10-I1 (Pegylated) | 123 | 4 | 5 | 297 | 295 |
| E1-GS10-I1 | 30 | 1 | 1 | 36 | 51 |
| I1-GS10-E1 (Pegylated) | 127 | 0.9 | 0.8 | 302 | 300 |
| I1-GS10-E1 | 42 | 1 | 1 | 93 | 99 |
| | | | | | |
| E2 | 31 | --- | | 38 | 40 |
| E2-GS10-I1 (Pegylated) | 32 | 0.3 | 0.6 | 77 | 78 |
| E2-GS10-I1 | 8 | 0.1 | 0.1 | 19 | 20 |
| I1-GS10-E2 (Pegylated) | 47 | 0.8 | 0.6 | 97 | 118 |
| I1-GS10-E2 | 8 | 0.1 | 0.1 | 11 | 15 |
| | | | | | |
| E3 | 21 | --- | | 14 | 11 |
| E3-GS10-I1 (Pegylated) | 10 | 6 | 4 | 42 | 40 |
| E3-GS10-I1 | 7 | 6 | 3 | 14 | 12 |
| I1GS10-E3 (Pegylated) | 46 | 2 | 2 | 47 | 50 |
| I1-GS10-E3 | 25 | 19 | 26 | 47 | 42 |

Figure 10

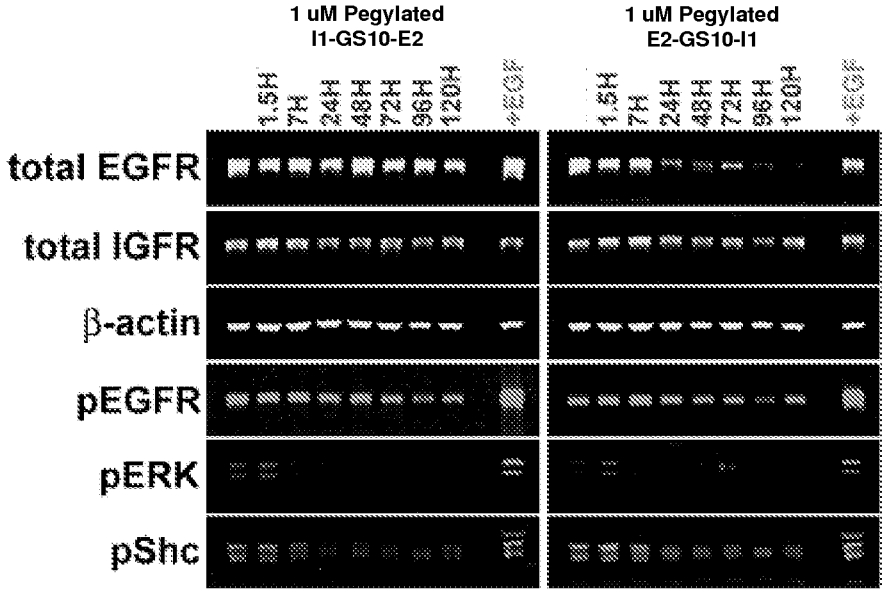



Figure 11

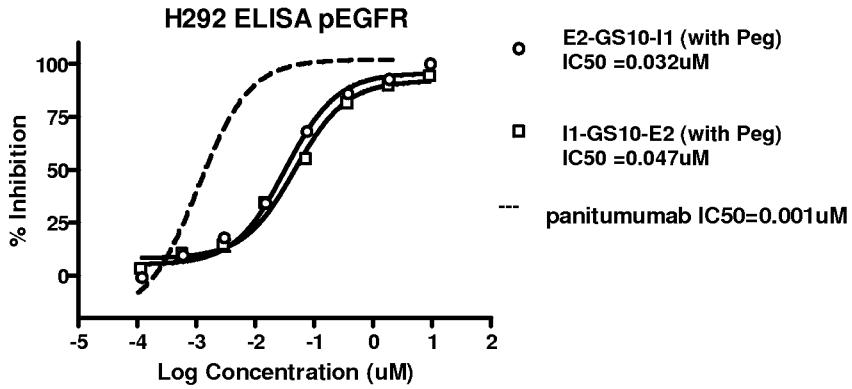


Figure 12A

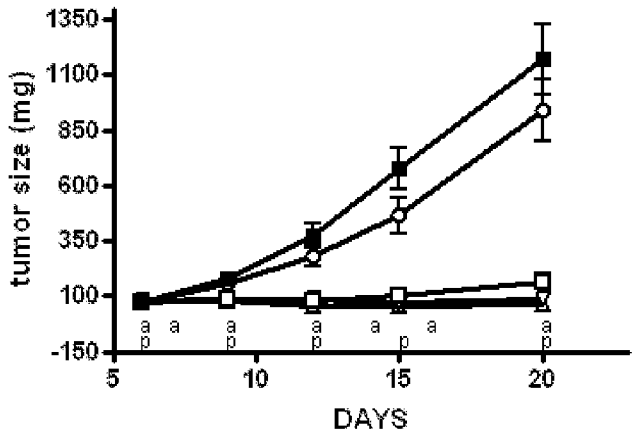



Figure 12B

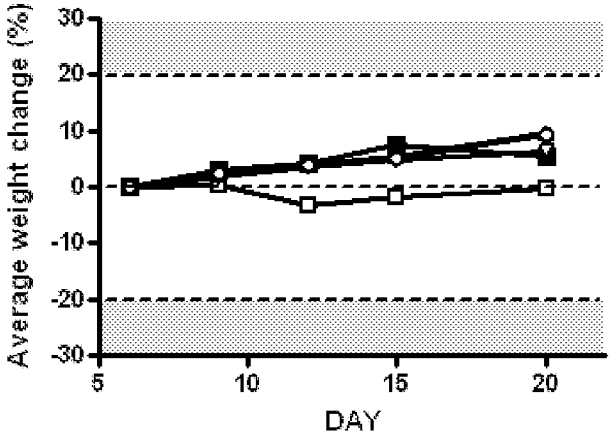


Figure 13

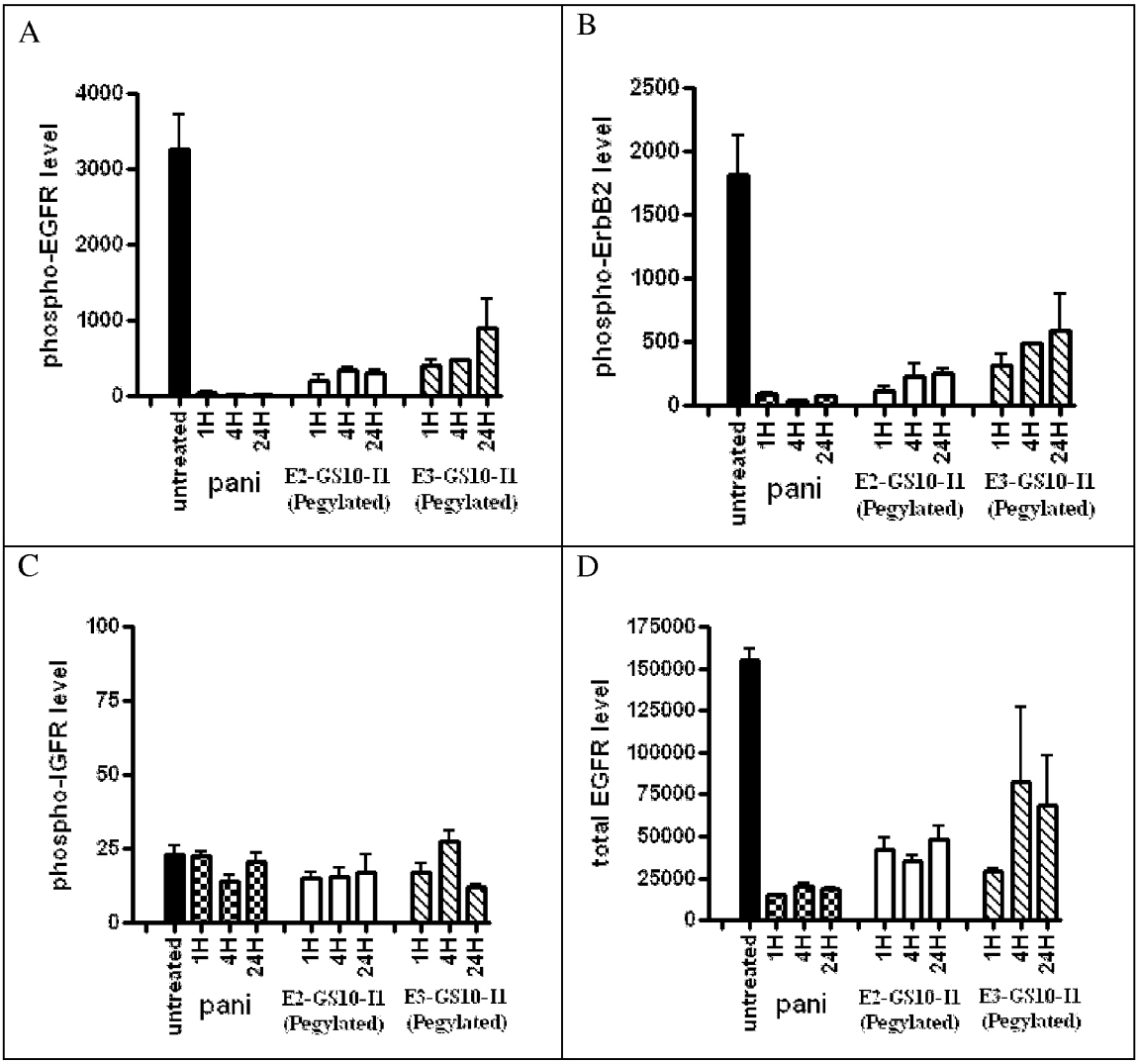

A
phospho-EGFR level
4000
3000
2000
1000
0
untreated
1H
4H
24H
pani
E2-GS10-I1 (Pegylated)
E3-GS10-I1 (Pegylated)
B
phospho-ErbB2 level
2500
2000
1500
1000
500
0
C
phospho-IGFR level
100
75
50
25
0
D
total EGFR level
175000
150000
125000
100000
75000
50000
25000
0

Figure 14

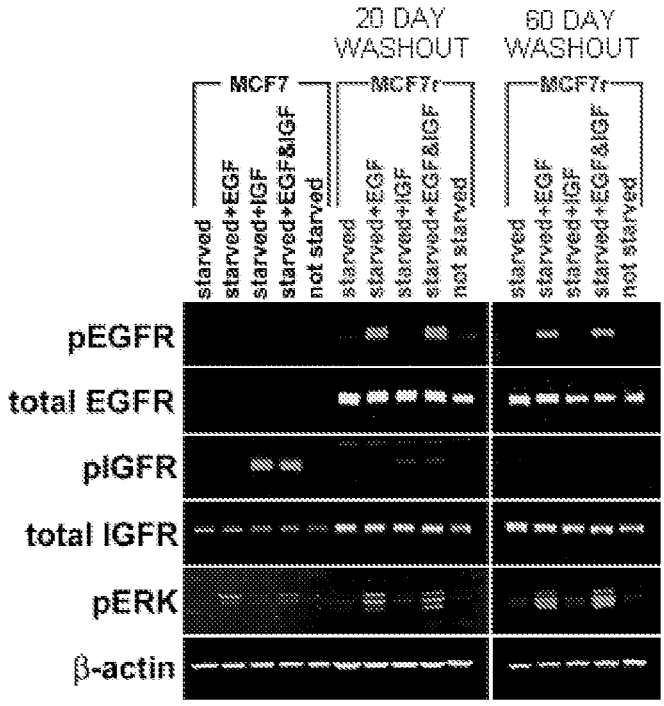



Figure 15

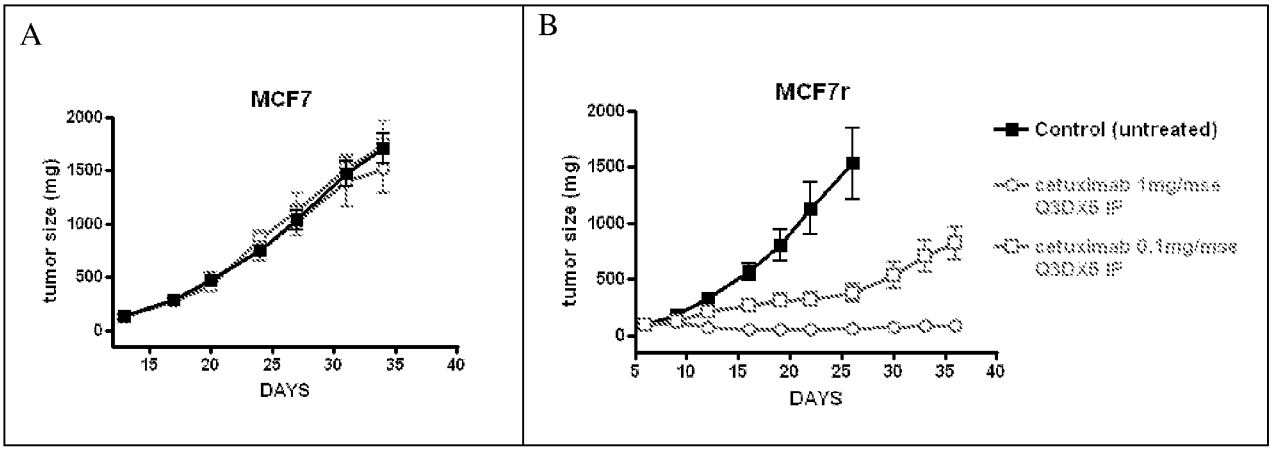
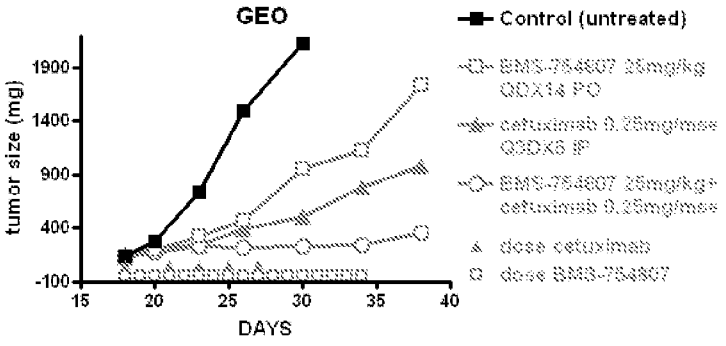
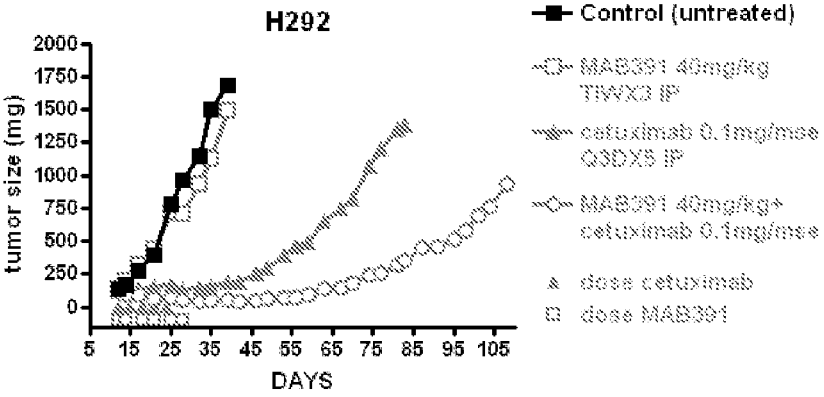


Figure 16




Doses of BMS-754807 and cetuximab are indicated by small boxes and small filled triangles on the x-axis

Figure 17




Doses of BMS-754807 and cetuximab are indicated by small boxes and small filled triangles on the x-axis

Figure 18

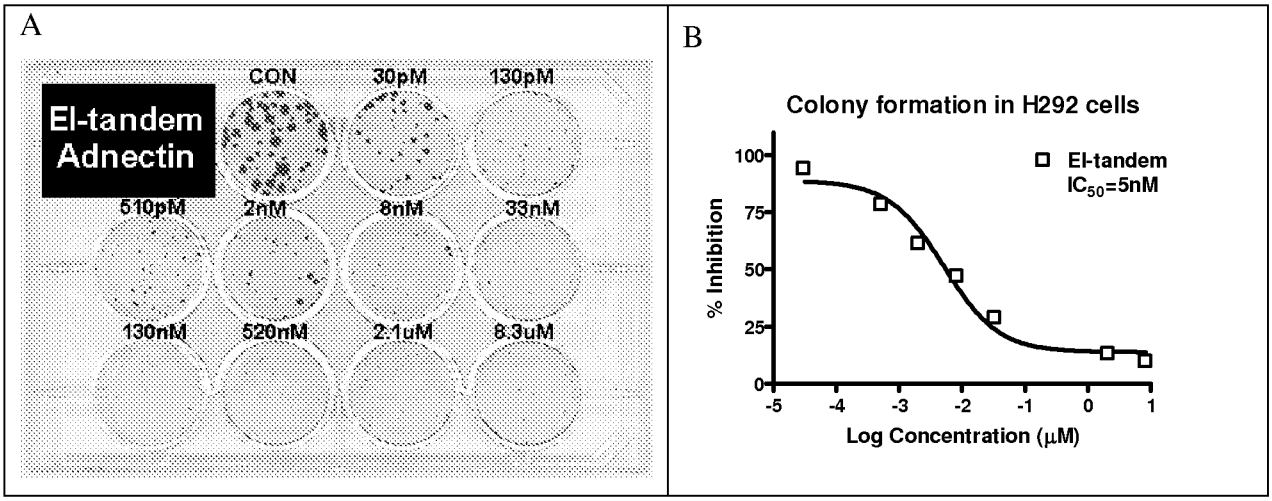



Figure 19

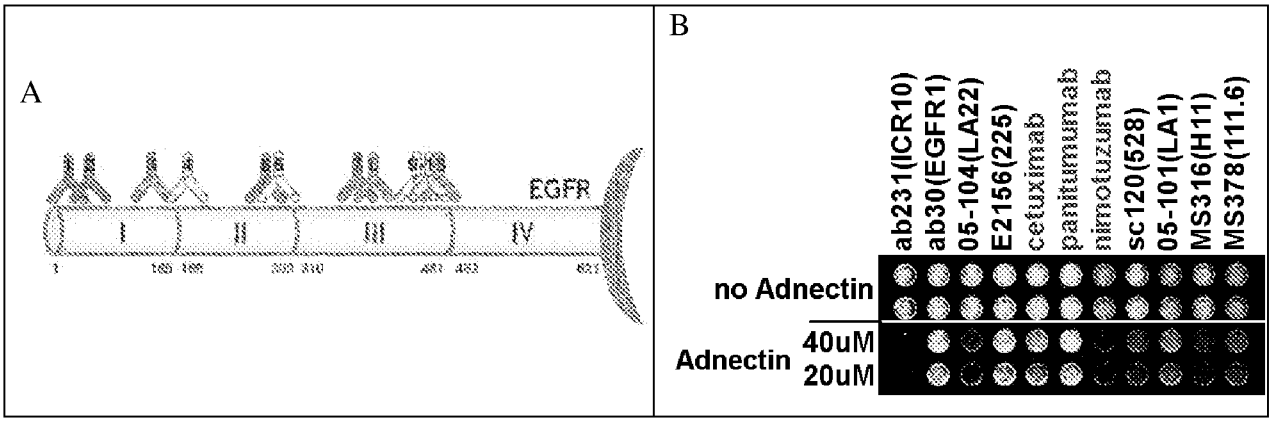


Figure 20

Tm = 55.2°C

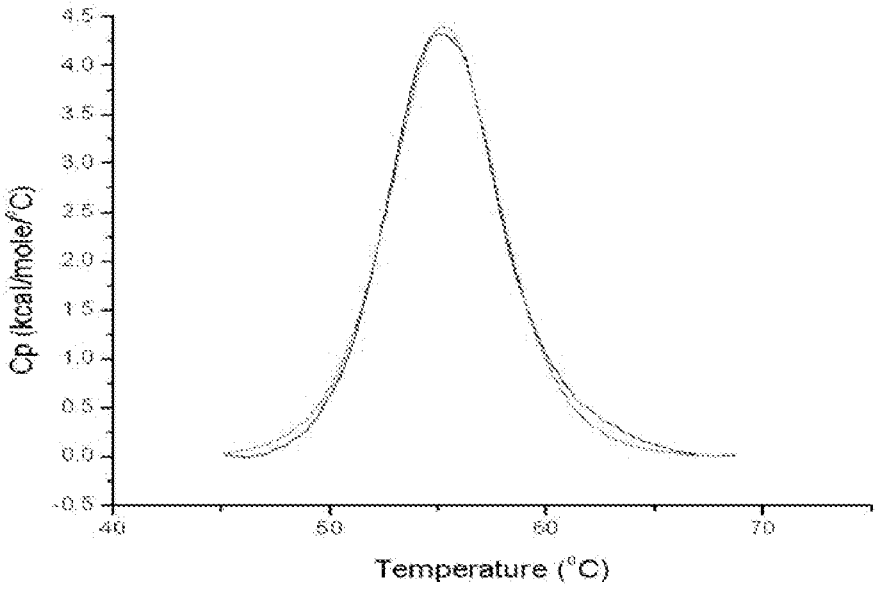



Figure 21

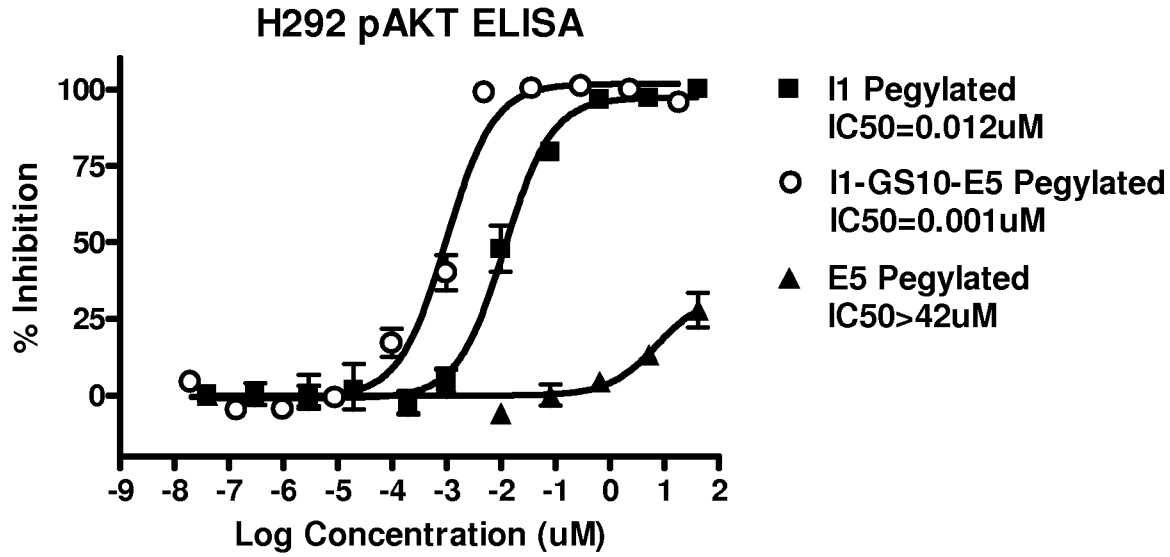


Figure 22

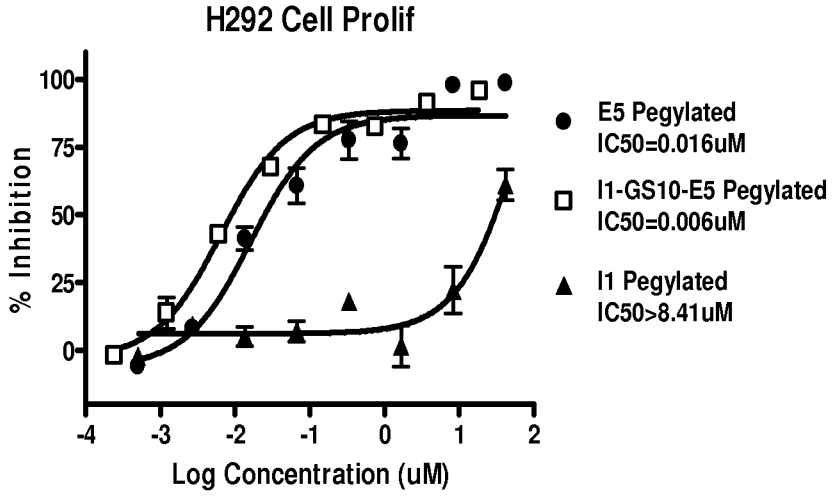



Figure 23

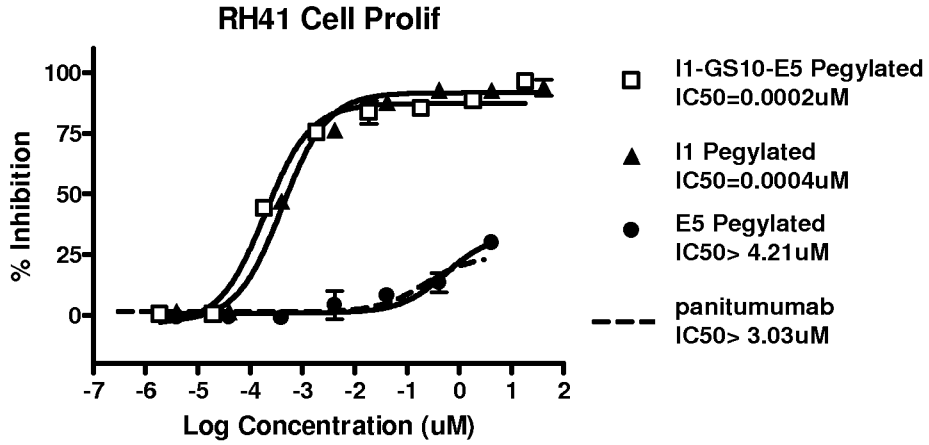
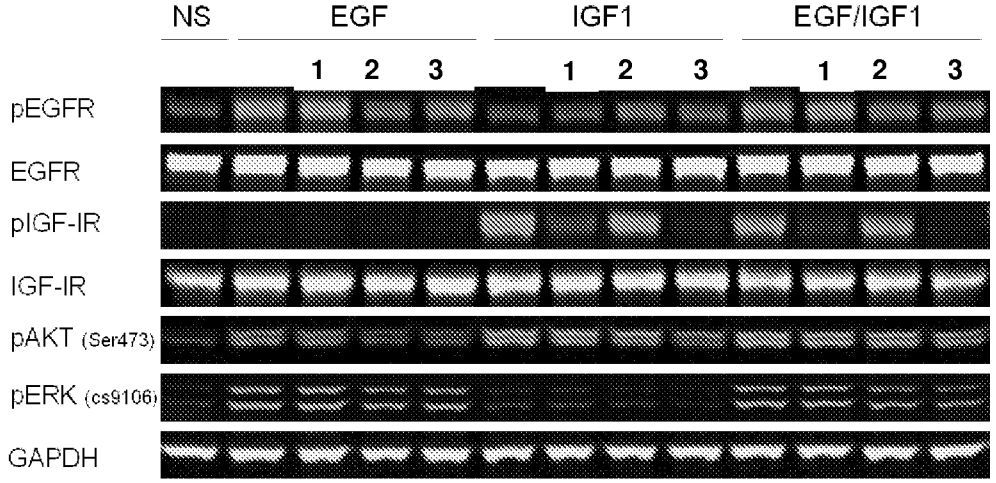


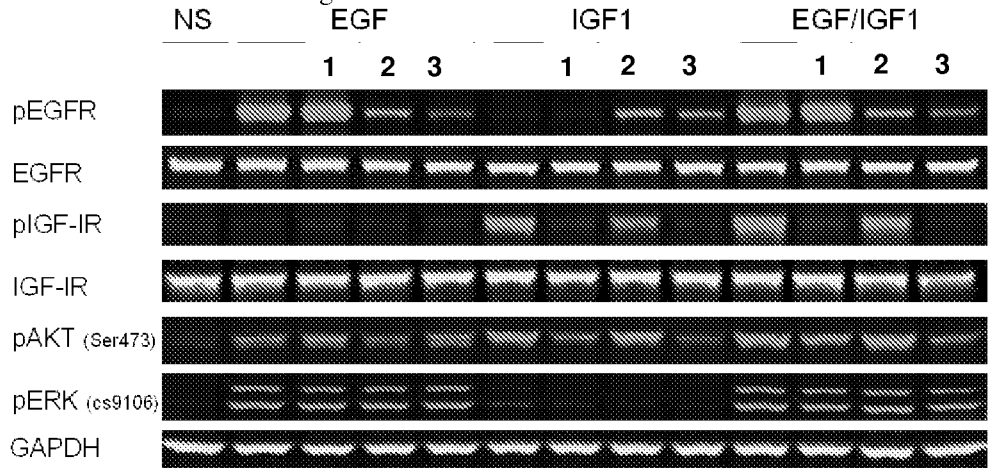
Figure 24

1=I1 pegylated; 2= E5 pegylated; 3=I1-GS10-E5 pegylated

A. DiFi colon carcinoma cells treated with 1uM of $^{10}$Fn3-based binders




B. H292 non-small cell lung carcinoma cells treated with 1uM of $^{10}$Fn3-based binders




C. BxPC3 pancreatic carcinoma cells treated with 0.1 uM of $^{10}$Fn3-based binders

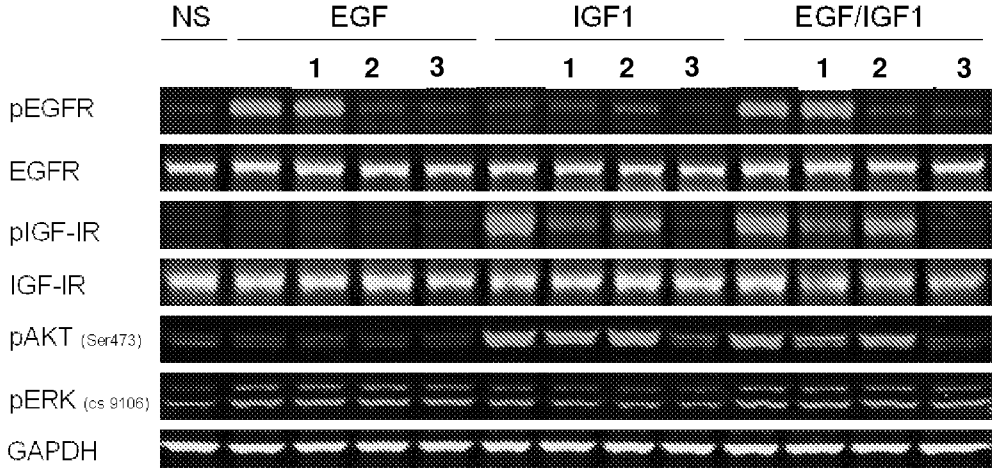
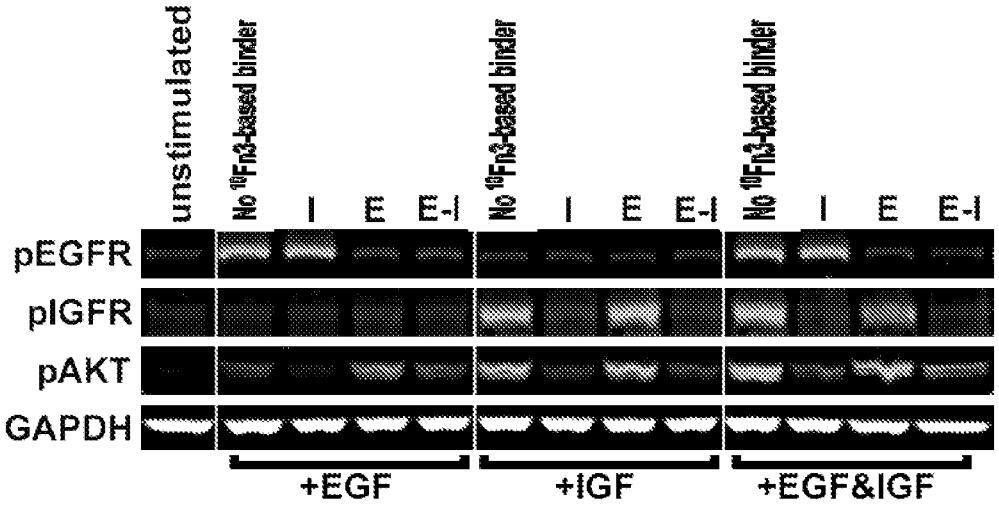


Figure 25




Abbreviations are as follows: I = I1 (unpegylated); E = E2 (unpegylated); EI=E2-GS10-I1 (unpegylated)

Figure 26

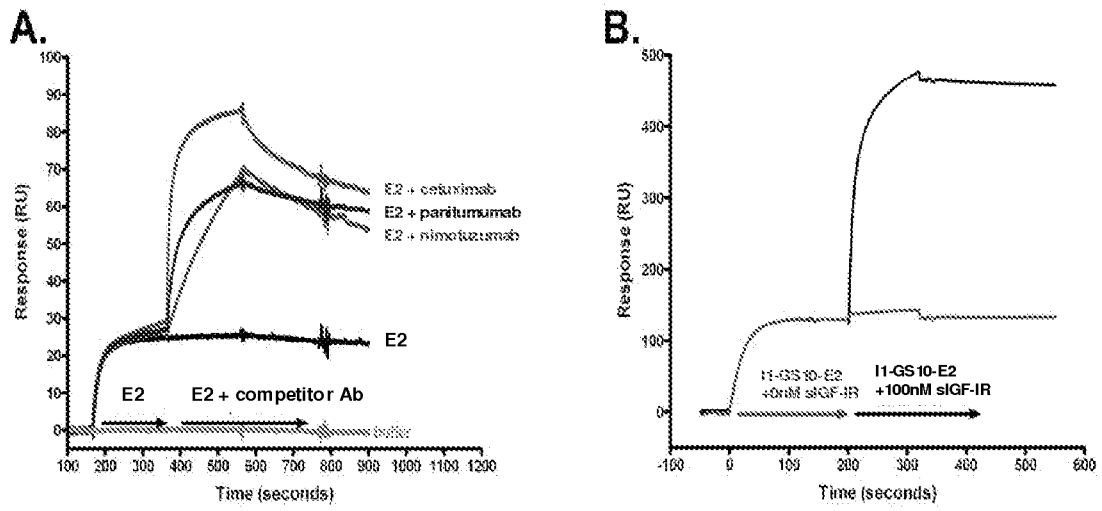


Figure 27

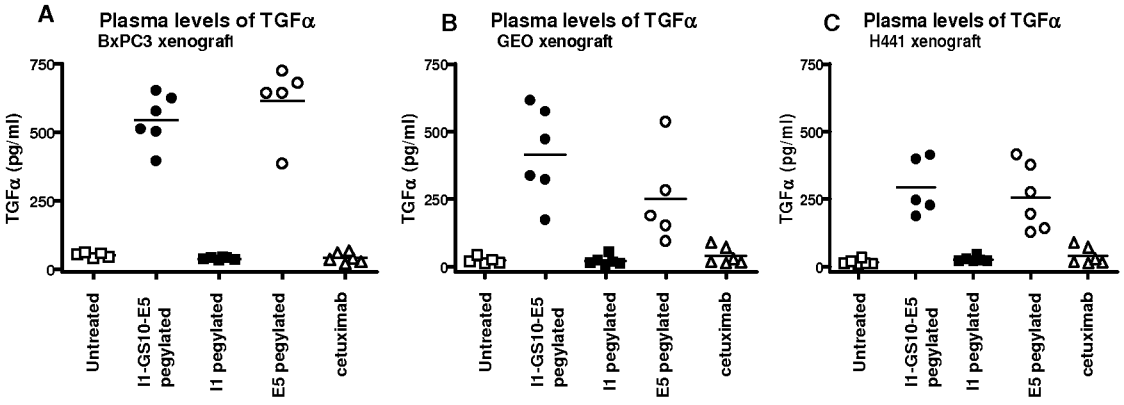



Figure 28

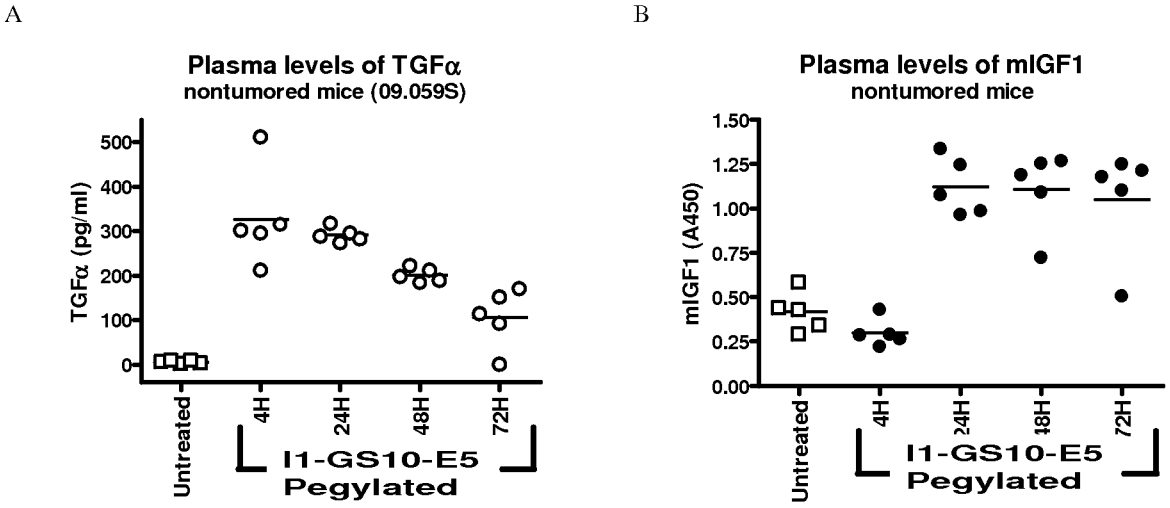
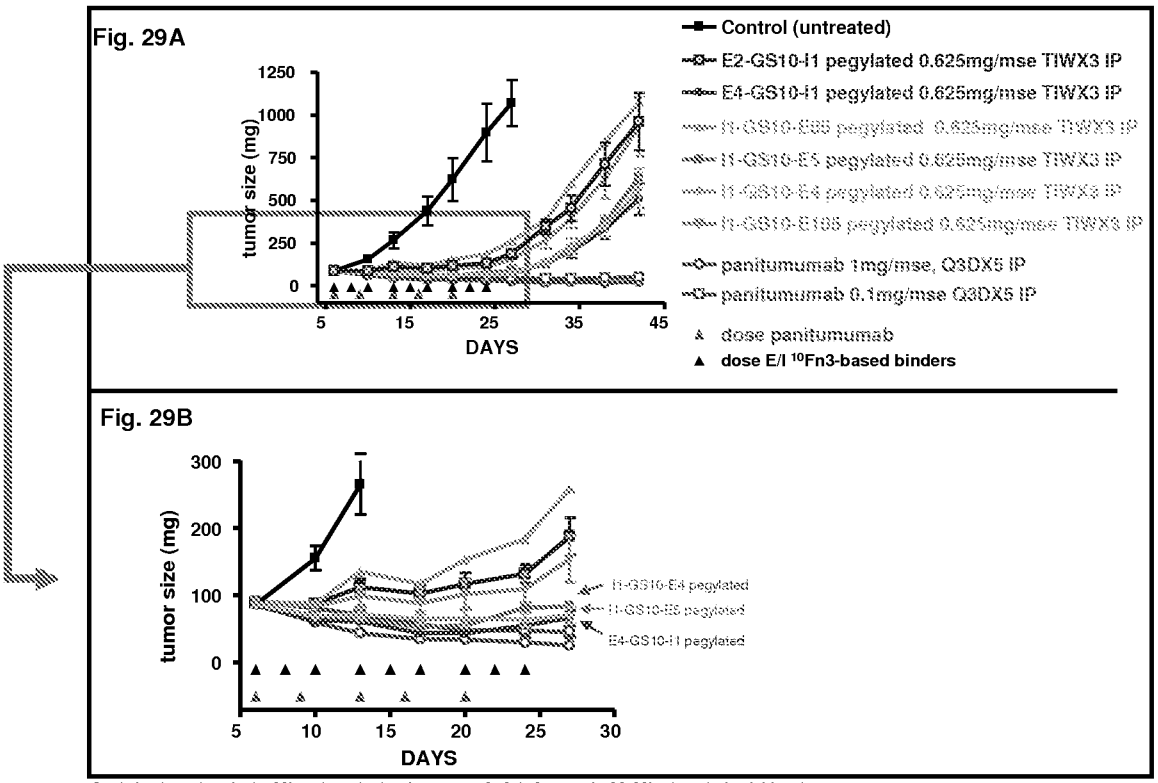
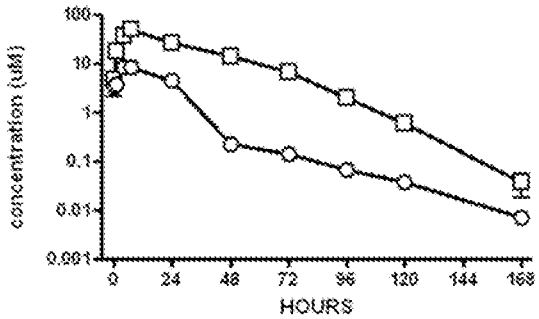


Figure 29




Study implanted on (4-14-09) and reached a size range of 50-150mg on (4-20-09) when dosing initiated.

Figure 30. Pharmacokinetic profile of E2-GS10-I1 pegylated in mice




| Dose (mg/kg) | $t_{1/2}$ (h) | $C_{max}$ (µg/mL) | AUC (h*µg/mL) | Vz_F-obs (mL/kg) | Cl_F-obs (mL/h/kg) |
|---|---|---|---|---|---|
| 10 | 15.8 | 205.7 | 3159 | 45.6 | 2.0 |
| 100 | 16.9 | 1209.6 | 34491.9 | 77.9 | 3.2 |

Plasma levels E2-GS10-I1 pegylated after dosing this construct at 100 mg/kg (□) and 10 mg/kg (○) by the ip route.

Figure 31

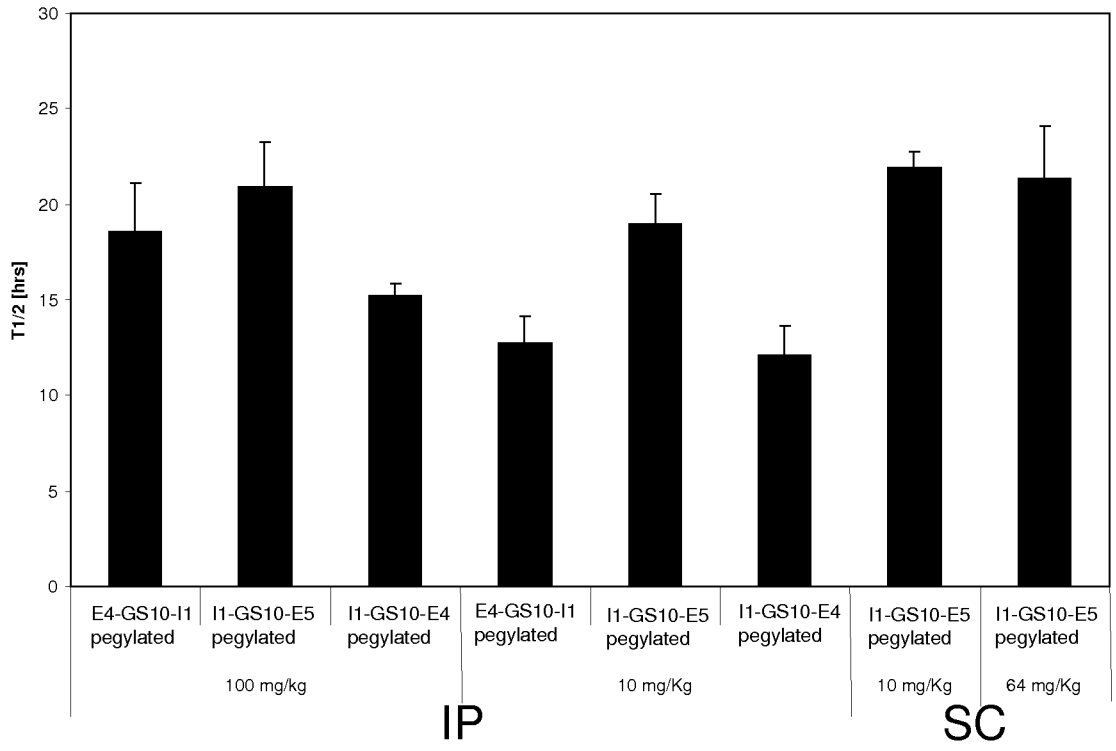



Figure 32

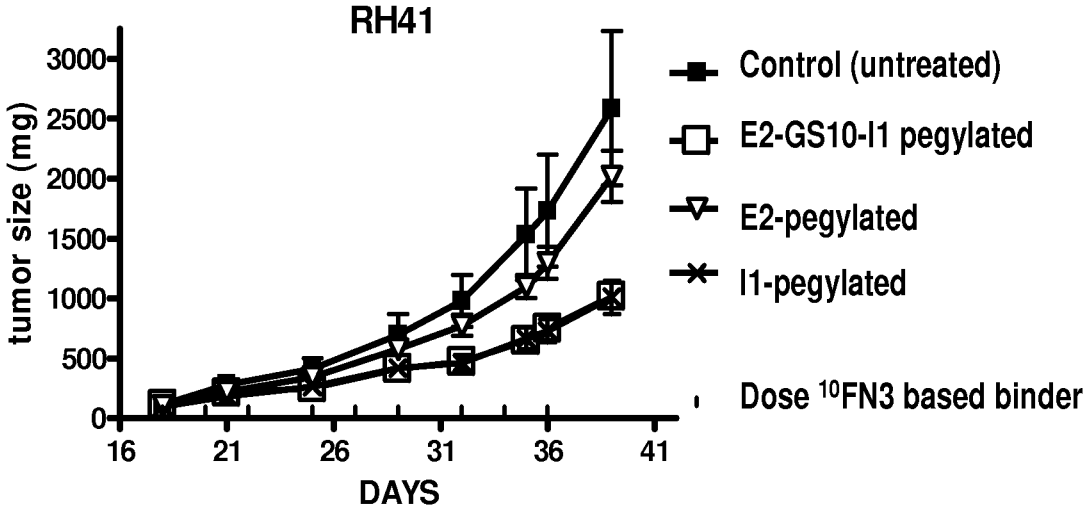


Figure 33

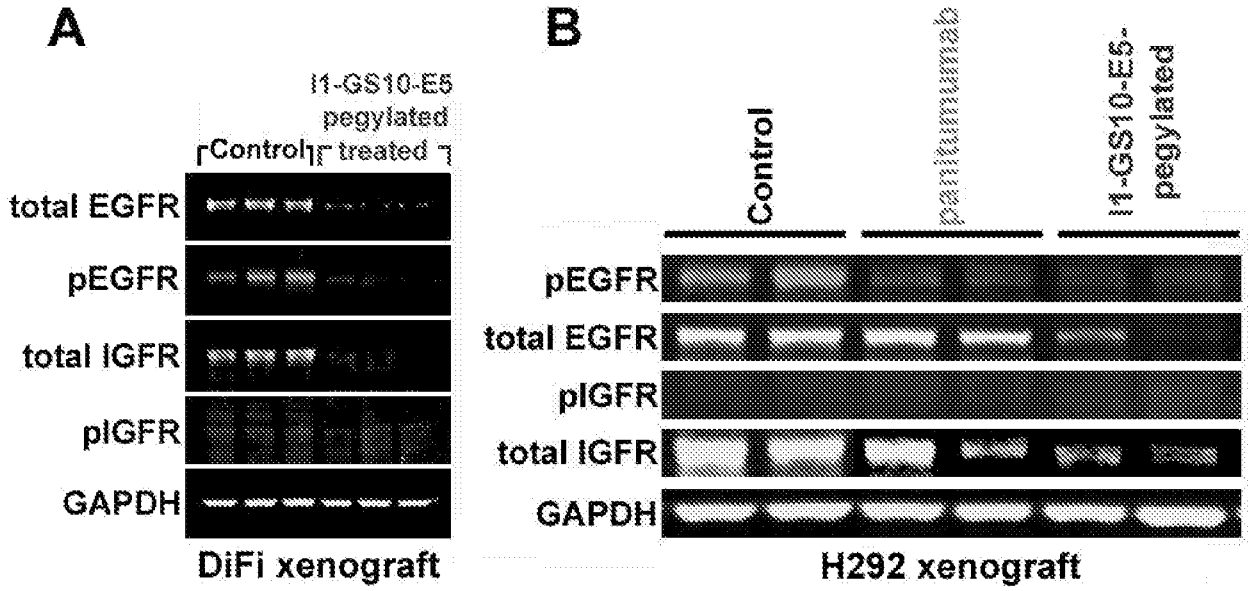



Figure 34

BC loop DE loop

MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPGGVRTATISGL

FG loop

KPGVDYTITVYAVTDYMHSEYRQYPISINYRTEIDKPSQHHHHHH

Figure 35

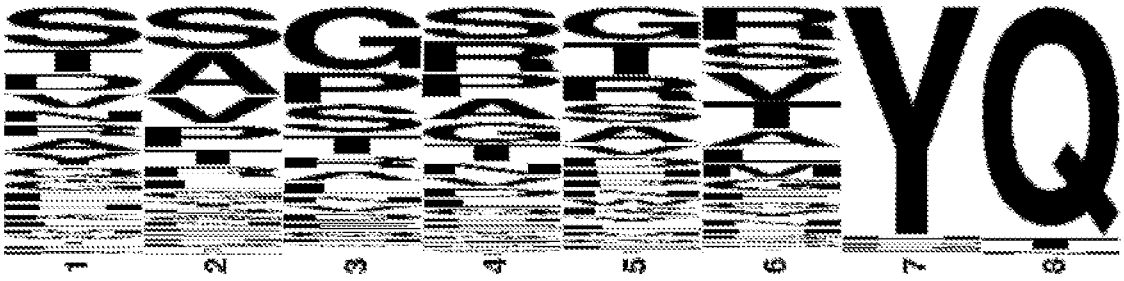


Figure 36



Figure 37

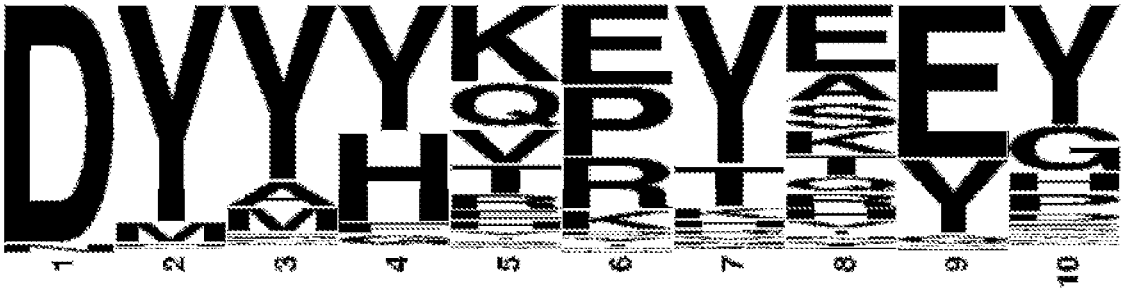


Figure 38



Figure 39

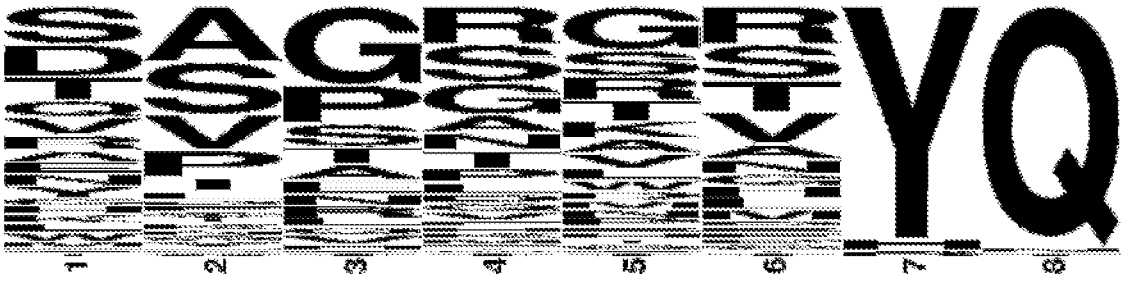


Figure 40



Figure 41



Figure 42

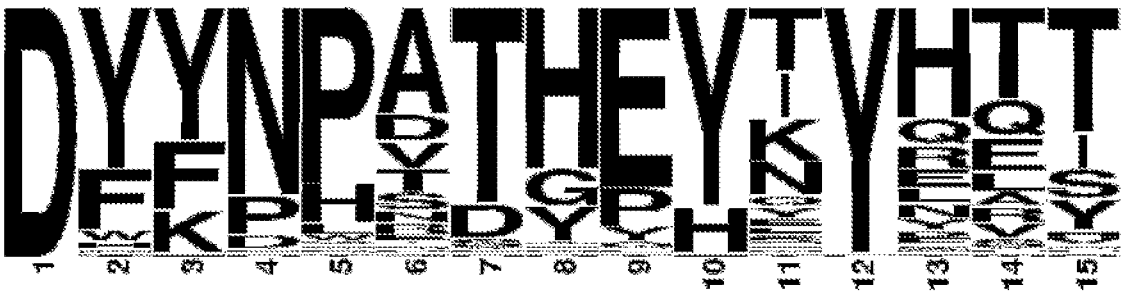


Figure 43

| | a | b | c | d | e | f | g | h | i | j | k | l |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CLONE NAME | A431 pEGFR ICW (nM)* | A431 pERK ICW (nM)* | H292 pEGFR ELISA (nM)* | H292 pIGFR ELISA (nM)* | De-grades EGFR | De-grades IGFR | EGFR KD (nM) | IGFR KD (nM) | EGF Blocking ELISA (nM) | Inhibition of Colony Forma-tion (nM) | Tm | % Mono-mer |
| E1-GS10-I1 pegylated | 297 | 295 | 123 | 4 | + | + | 57.9 | 2.43 | 238 | --- | 49 | >95% |
| E3-GS10-I1 pegylated | 42 | 40 | 10 | 6 | ++ | ++ | 10.4 | 0.74 | 89 | --- | 52.5 | >95% |
| E2-GS10-I1 pegylated | 77 | 78 | 32 | 0.3 | ++ | (-) | 10.1 | 1.17 | 25 | 560 | 57.5 | >95% |
| E4-GS10-I1 pegylated | 12±0 | 12±2 | 1.3±0.5 | 0.4±0.2 | (-) | (-) | 4.77 | 0.77 | 19.5 | 5 | 55.5 | >95% |
| E96-GS10-I1 pegylated | 61±1 | 54±21 | 10±1 | 0.4 | (-) | (-) | 24.2 | 0.96 | 43.8 | --- | 55 | >95% |
| E5-GS10-I1 pegylated | 44±1 | 47±7 | 12±4 | 0.4 | + | + | 12.4 | 1.16 | 119.3 | --- | 54.5 | >95% |
| E85-GS10-I1 pegylated | 15±0 | 15±2 | 4±1 | 0.3 | (-) | + | 4.76 | 0.75 | 65.9 | --- | 55.5 | >95% |
| E90-GS10-I1 pegylated | 65±0 | 63±9 | 10±1 | 0.4 | --- | --- | 13.5 | 1.5 | 69.1 | --- | 49.5 | >95% |
| E105-GS10-I1 pegylated | 56±0 | 61±6 | 15±4 | 0.5 | ++ | ++ | 9.28 | 1.35 | 75 | --- | 58.5 | >95% |
| E105-GS10-I1 pegylated | 61±11 | 49±17 | 16±6 | 0.5 | --- | --- | 7.65 | 1.19 | 93.8 | --- | 56.5 | >95% |
| I1-GS10-E5 pegylated | 54±33 | 58±13 | 12±4 | 0.4±0.1 | + | ++ | 7.66 | 0.4 | 150.8 | 1 | 56 | >95% |
| I1-GS10-E85 pegylated | 22±15 | 23±4 | 8±3 | 0.7±0.5 | (-) | (-) | 5.97 | 0.43 | 37.8 | --- | 58 | >95% |
| I1-GS10-E4 pegylated | 12±4 | 13±1 | 4±1 | 0.2 | (-) | + | 3.63 | 0.46 | 38.1 | 6 | 60 | >95% |
| I1-GS10-E105 pegylated | 53±9 | 48±3 | 13±3 | 0.5±0.2 | ++ | ++ | 4.28 | 0.37 | 61.2 | --- | 59.5 | >95% |
| I1-GS10-E112 pegylated | 116 | 94 | 16 | 0.3 | --- | --- | 3.35 | 0.38 | 104.3 | --- | 62.5 | >95% |
| cetuximab | 5±4 | 9±1 | 5±3 | --- | ++ | --- | 0.39 | --- | 1 | 770 | --- | --- |
| panitumumab | 6±4 | 5±2 | 5±2 | --- | ++ | --- | 0.05 | --- | 24.4 | 140 | --- | --- |
| nimotuzumab | >3 | >3 | >3 | --- | + | --- | 1 | --- | 13.6 | --- | --- | --- |
| I1 | --- | --- | --- | 0.4±0.2 | --- | (-) | --- | 0.11 | --- | 15,510 | 65.3 | >95% |

Figure 44

| Dose | Molecule | | HL_Lambda_z (hr) | Cmax (ug/mL) | AUCINF_obs (hr*ug/mL) | Cl_F_obs (mL/hr/kg) | Vz_F_obs (mL/kg) | MRTINF_obs (hr) |
|---|---|---|---|---|---|---|---|---|
| 100 mg/kg | E4-GS10-I1 pegylated | N | 3 | 3 | 3 | 3 | 3 | 3 |
| | | Mean | **18.5** | 521.1 | 20811.4 | 4.8 | 128.3 | 34.1 |
| | | SD | 2.6 | 75.7 | 2058.7 | 0.5 | 6.4 | 2.0 |
| | | Min | 16.6 | 434.2 | 18824.8 | 4.4 | 122.4 | 31.8 |
| | | Max | 21.5 | 573.0 | 22935.3 | 5.3 | 135.2 | 35.6 |
| | | CV% | 14.0 | 14.5 | 9.9 | 9.8 | 5.0 | 6.0 |
| | I1-GS10-E5 pegylated | N | 3 | 3 | 3 | 3 | 3 | 3 |
| | | Mean | **20.9** | 719.5 | 25730.1 | 3.9 | 117.4 | 33.0 |
| | | SD | 2.3 | 90.4 | 2983.3 | 0.4 | 4.1 | 2.2 |
| | | Min | 18.6 | 623.7 | 23362.5 | 3.4 | 114.9 | 30.6 |
| | | Max | 23.2 | 803.4 | 29080.9 | 4.3 | 122.1 | 34.8 |
| | | CV% | 11.0 | 12.6 | 11.6 | 11.1 | 3.5 | 6.7 |
| | I1-GS10-E4 pegylated | N | 3 | 3 | 3 | 3 | 3 | 3 |
| | | Mean | **15.2** | 757.1 | 28344.0 | 3.6 | 77.7 | 34.5 |
| | | SD | 0.6 | 202.9 | 2777.8 | 0.4 | 6.7 | 2.0 |
| | | Min | 14.6 | 533.9 | 25411.7 | 3.2 | 70.3 | 32.4 |
| | | Max | 15.9 | 930.4 | 30936.0 | 3.9 | 83.1 | 36.5 |
| | | CV% | 4.1 | 26.8 | 9.8 | 10.0 | 8.6 | 5.9 |
| 10mg/kg | E4-GS10-I1 pegylated | N | 3 | 3 | 3 | 3 | 3 | 3 |
| | | Mean | **12.7** | 67.2 | 1721.2 | 6.0 | 108.4 | 19.6 |
| | | SD | 1.4 | 12.9 | 336.7 | 1.3 | 15.1 | 0.9 |
| | | Min | 11.6 | 52.5 | 1338.0 | 5.1 | 95.5 | 18.7 |
| | | Max | 14.3 | 76.8 | 1969.5 | 7.5 | 125.0 | 20.6 |
| | | CV% | 11.0 | 19.2 | 19.6 | 21.8 | 13.9 | 4.8 |
| | I1-GS10-E5 pegylated | N | 2 | 2 | 2 | 2 | 2 | 2 |
| | | Mean | **19.0** | 80.9 | 2345.6 | 4.4 | 118.7 | 23.7 |
| | | SD | 1.5 | 3.2 | 526.4 | 1.0 | 17.1 | 0.6 |
| | | Min | 17.9 | 78.7 | 1973.4 | 3.7 | 106.6 | 23.3 |
| | | Max | 20.1 | 83.2 | 2717.8 | 5.1 | 130.8 | 24.1 |
| | | CV% | 8.2 | 3.9 | 22.4 | 22.4 | 14.4 | 2.5 |
| | I1-GS10-E4 pegylated | N | 3 | 3 | 3 | 3 | 3 | 3 |
| | | Mean | **12.1** | 85.9 | 1857.1 | 5.6 | 95.5 | 19.6 |
| | | SD | 1.6 | 15.4 | 420.2 | 1.1 | 9.7 | 0.9 |
| | | Min | 10.7 | 69.6 | 1581.1 | 4.3 | 85.0 | 18.6 |
| | | Max | 13.8 | 100.2 | 2340.7 | 6.3 | 104.1 | 20.4 |
| | | CV% | 12.9 | 17.9 | 22.6 | 20.1 | 10.2 | 4.7 |

Figure 45

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 219 | E6 | 80.0 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 220 | E7 | 89.4 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDVHTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 221 | E8 | 92.4 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDLTTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 222 | E9 | 77.3 | MGVSDVPRDLEVVAATPTSLLISWEANPSRYQYYRITYGETGGNSPVQEFTVPHDLNTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 223 | E10 | 84.7 | MGVSDVPRDLEVVAATPTSLLISWYPGSRTYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYY HPATYEHEYHAHPISINYRTEIDKPSQ |
| 224 | E11 | 83.7 | MGVSDVPRDLEVVAATPTSLLISWTPANKSYQYYRITYGETGGNSPVQEFTVPYDGTTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 225 | E12 | 76.5 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPHDVYTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 226 | E13 | 86.7 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPGQVYTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 227 | E14 | 80.4 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDVTTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 228 | E15 | 88.8 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPHDLRTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 229 | E16 | 97.7 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDLVTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHESPISINYRTEIDKPSQ |
| 230 | E3 | 87.5 | MGVSDVPRDLEVVAATPTSLLISWLPGKLRYQYYRITYGETGGNSPVQEFTVPHDLRTATISGLKPGVDYTITVYAVTNMM HVEYSEYPISINYRTEIDKPSQH |
| 231 | E1 | 85.9 | MGVSDVPRDLEVVAATPTSLLISWVAGAEDYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDMM HVEYTEHPISINYRTEIDKPSQ |
| 232 | E17 | 75.5 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPGMVHTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHESPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 233 | E18 | 91.1 | MGVSDVPRDLEVVAATPTSLLISWFVTHVAYQYYRITYGETGGNSPVQEFTVPGGLSTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 234 | E19 | 84.6 | MGVSDVPRDLEVVAATPTSLLISWETESNAYQYYRITYGETGGNSPVQEFTVPGQIYTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 235 | E20 | 80.2 | MGVSDVPRDLEVVAATPTSLLISWMTSPSVYQYYRITYGETGGNSPVQEFTVPGPVQTATISGLKPGVDYTITVYAVTDYK EHQHAPHQYTAHPISINYRTEIDKPSQ |
| 236 | E2 | 80.5 | MGVSDVPRDLEVVAATPTSLLISWDSGRGSYQYYRITYGETGGNSPVQEFTVPGPVHTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHESPISINYRTEIDKPSQ |
| 237 | E22 | 83.7 | MGVSDVPRDLEVVAATPTSLLISWSTGRTTYQYYRITYGETGGNSPVQEFTVPHDLDTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 238 | E23 | 81.1 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPYDVITATISGLKPGVDYTITVYAVTDMM HVEYAEYPISINYRTEIDKPSQ |
| 239 | E24 | 90.3 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPGQVPTATISGLKPGVDYTITVYAVTDSY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 240 | E25 | 77.1 | MGVSDVPRDLEVVAATPTSLLISWGYQSGGYTYYRITYGETGGNSPVQEFTVPHDLRTATISGLKPGVDYTITVYAVTDYA YKEYQEHPISINYRTEIDKPSQ |
| 241 | E26 | 75.4 | MGVSDVPRDLEVVAATPTSLLISWWIGIPVYQYYRITYGETGGNSPVQEFTVPYDGKTATISGLKPGVDYTITVYAVTDMM HVEYAEYPISINYRTEIDKPSQ |
| 242 | E27 | 94.6 | MGVSDVPRDLEVVAATPTSLLISWSKGSKSYQYYRITYGETGGNSPVQEFTVPYHVYTATISGLKPGVDYTITVYAVTDYY NPATYEYIYLTTPISINYRTEIDKPSQ |
| 243 | E28 | 85.3 | MGVSDVPRDLEVVAATPTSLLISWNPGSKSYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDFY NPDTHEYLYNQYPISINYRTEIDKPSQ |
| 244 | E29 | 87.9 | MGVSDVPRDLEVVAATPTSLLISWQPGTTHYQYYRITYGETGGNSPVQEFTVPYDLMTATISGLKPGVDYTITVYAVTDYY NPNTYEYIYLTTPISINYRTEIDKPSQ |
| 245 | E30 | 87.3 | MGVSDVPRDLEVVAATPTSLLISWAIGTIVYQYYRITYGETGGNSPVQEFTVPAGVYTATISGLKPGVDYTITVYAVTDYY DWATHEYNYHTAPISINYRTEIDKPSQ |
| 246 | E31 | 75.8 | MGVSDVPRDLEVVAATPTSLLISWTYNDGSYQYYRITYGETGGNSPVQEFTVPYAVYTATISGLKPGVDYTITVYAVTDFY NPATYEYIYHTTPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 247 | E32 | 86.0 | MGVSDVPRDLEVVAATPTSLLISWVSLVGFYQYYRITYGETGGNSPVQEFTVPGGVHTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 248 | E33 | 75.8 | MGVSDVPRDLEVVAATPTSLLISWASRKEVYQYYRITYGETGGNSPVQEFTVPGWLNTATISGLKPGVDYTITVYAVTDYM HVEYAEYPISINYRTEIDKPSQ |
| 249 | E34 | 80.4 | MGVSDVPRDLEVVAATPTSLLISWLAPFWRYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 250 | E35 | 90.2 | MGVSDVPRDLEVVAATPTSLLISWTPPGHQHQYYRITYGETGGNSPVQEFTVPGQVTTATISGLKPGVDYTITVYAVTDYY NPATHYYTYYTTPISINYRTEIDKPSQ |
| 251 | E36 | 81.3 | MGVSDVPRDLEVVAATPTSLLISWESGSRTYQYYRITYGETGGNSPVQEFTVPGGVHTATISGLKTGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 252 | E37 | 80.8 | MGVSDVPRDLEVVAATPTSLLISWERTSTHYQYYRITYGETGGNSPVQEFTVPGRVYTATISGLKPGVDYTITVYAVTDYY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 253 | E38 | 89.8 | MGVSDVPRDLEVVAATPTSLLISWNARTDAYQYYRITYGETGGNSPVQEFTVPRDLETATISGLKPGVDYTITVYAVTDYK PHADGPHTYQESPISINYRTEIDKPSQ |
| 254 | E39 | 76.7 | MGVSDVPRDLEVVAATPTSLLISWQVSAFRYQYYRITYGETGGNSPVQEFTVPGMVSTATISGLKPGVDYTITVYAVTDYK PHADGPHTYSEYPISINYRTEIDKPSQ |
| 255 | E40 | 89.6 | MGVSDVPRDLEVVAATPTSLLISWVLGRRVYQYYRITYGETGGNSPVQEFTVPGAVYTATISGLKPGVDYTITVYAVTDYF NPATHEYQYELTPISINYRTEIDKPSQ |
| 256 | E41 | 75.2 | MGVSDVPRDLEVVAATPTSLLISWTPPNSGHNYYRITYGETGGNSPVQEFTVPHDLTTATISGLKPGVDYTITVYAVTDYY NPNTYEYTYQFTPISINYRTEIDKPSQ |
| 257 | E42 | 77.3 | MGVSDVPRDLEVVAATPTSLLISWVVPNWMYQYYRITYGETGGNSPVQEFTVPGMLETATISGLKPGVDYTITVYAVTDYY NPTTYEYTYFTYPISINYRTEIDKPSQ |
| 258 | E43 | 75.0 | MGVSDVPRDLEVVAATPTSLLISWSGGFMRYQYYRITYGETGGNSPVQEFTVPGQVYTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 259 | E44 | 83.3 | MGVSDVPRDLEVVAATPTSLLISWDSEGPSYQYYRITYGETGGNSPVQEFTVPYAVYTATISGLKPGVDYTITVYAVTDYY NPRTHELFFQQYPISINYRTEIDKPSQ |
| 260 | E45 | 80.4 | MGVSDVPRDLEVVAATPTSLLISWQVPRPMYQYYRITYGEKGGNSPVQEFTVPHDLRTATISGLKPGVDYTITVYAVTDYY DPTSNLYNYNQTPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 261 | E46 | 77.0 | MGVSDVPRDLEVVAATPTSLLISWQVGSVVYQYYRITYGETGGNSPVQEFTVPRDVLTATISGLKPGVDYTITVYAVTDYK PKPDGPHIYQAVPISINYRTEIDKPSQ |
| 262 | E47 | 76.9 | MGVSDVPRDLEVVAATPTSLLISWNPASKDYQYYRITYGETGGNSPVQEFTVPGQVPTATISGLKPGVDYTITVYAVTDFY NPATHEYKYDSTPISINYRTEIDKPSQ |
| 263 | E48 | 88.6 | MGVSDVPRDLEVVAATPTSLLISWRSSATAYQYYRITYGETGGNSPVQEFTVPGRVYTATISGLKPGVDYTITVYAVTDFF NWATHEYIYHSTPISINYRTEIDKPSQ |
| 264 | E49 | 83.5 | MGVSDVPRDLEVVAATPTSLLISWHSGPREYQYYRITYGETGGNSPVQEFTVPGQVYTATISGLKPGVDYTITVYAVTDFF NPITHYYYYELTPISINYRTEIDKPSQ |
| 265 | E50 | 77.4 | MGVSDVPRDLEVVAATPTSLLISWTVGLSVYQYYRITYGETGGNSPVQEFTVPGMVSTATISGLKPSVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 266 | E51 | 82.8 | MGVSDVPRDLEVVAATPTSLLISWGGHRAVYQYYRITYGETGGNSPVQEFTVPGAVYTATISGLKPGVDYTITVYAVTDYY NPDTHEYKYHQYPISINYRTEIDKPSQ |
| 267 | E52 | 75.3 | MGVSDVPRDLEVVSATPTSLLISWQVPRPMYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYW FKEYREDPISINYRTEIDKPSQ |
| 268 | E53 | 79.8 | MGVSDVPRDLEVVAATPTSLLISWSVGGMIYQYYRITYGETGGNSPVQEFTVPGMVTTATISGLKPGVDYTITVYAVTDYY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 113, wherein X = Ser | E5 | 99.1 | MGVSDVPRDLEVVAATPTSLLISWWAPVDRYQYYRITYGETGGNSPVQEFTVPRDVYTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 269 | E54 | 76.1 | MGVSDVPRDLEVVAATPTSLLISWKASYTGYNYYRITYGETGGNSPVQEFTVPRDVMTATISGLKPGVDYTITVYAVTDFY NPDTHQYTYRRIPISINYRTEIDKPSQ |
| 270 | E55 | 99.1 | MGVSDVPRDLEVVAATPTSLLISWSVGQVFYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDYY NPATHEYKYHQTPISINYRTEIDKPSQ |
| 271 | E56 | 84.2 | MGVSDVPRDLEVVAATPTSLLISWYSGDYHYQYYRITYGETGGNSPVQEFTVPHDLETATISGLKPGVDYTITVYAVTDYY NPATHYYKYEQTPISINYRTEIDKPSQ |
| 272 | E57 | 75.5 | MGVSDVPRDLEVVAATPTSLLISWIVQGGRYQYYRITYGETGGNSPVQEFTVPGMVTTATISGLKPGVDYTITVYAVTDYY NPSTHEYKYHQTPISINYRTEIDKPSQ |
| 273 | E58 | 79.7 | MGVSDVPRDLEVVAATPTSLLISWSAVRWRYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDFY NPRTHVYIYDQFPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 274 | E59 | 76.3 | MGVSDVPRDLEVVAATPTSLLISWRARRLQYQYYRITYGETGGNSPVQEFTVPGMVTTATISGLKPGVDYTITVYAVTDFY NPATMEYTYQRTPISINYRTEIDKPSQ |
| 275 | E60 | 100.0 | MGVSDVPRDLEVVAATPTSLLISWLQPLWRYQYYRITYGETGGNSPVQEFTVPGGLDTATISGLKPGVDYTITVYAVTDYK PHVDGPHAYHEYPISINYRTEIDKPSQ |
| 276 | E61 | 79.8 | MGVSDVPRDLEVVAATPTSLLISWDASQGNYQYYRITYGETGGNSPVQEFTVPGAVKTATISGLKPGVDYTITVYAVTDFF NPATHEYIYHTTPISINYRTEIDKPSQ |
| 277 | E62 | 78.9 | MGVSDVPRDLEVVAATPTSLLISWCLDGQLYQYYRITYGETGGNSPVQEFTVPGSIVTATISGLKPGVDYTITVYAVTDWY NLATHEYNYRVTPISINYRTEIDKPSQ |
| 278 | E63 | 76.2 | MGVSDVPRDLEVVAATPTSLLISWDTSGASYQYYRITYGETGGNSPVQEFTVPYSVYTATISGLKPGVDYTITVYAVTDYY DPDSHYYNYNMVPISINYRTEIDKPSQ |
| 279 | E64 | 78.2 | MGVSDVPRDLEVVAATPTSLLISWDSGNGTYQYYRITYGETGGNSPVQEFTVPYRVYTATISGLKPGVDYTITVYAVTDYY NPATHEYTYELRPISINYRTEIDKPSQ |
| 280 | E65 | 80.7 | MGVSDVPRDLEVVATTPTSLLISWRPTSQVYQYYRITYGETGGNSPVQEFTVPYNVYTATISGLKPGVDYTITVYAVTDFF NYATHEYIYHTIPISINYRTEIDKPSQ |
| 281 | E66 | 75.0 | MGVSDVPRDLEVVAATPTSLLISWKSYGSAYQYYRITYGETGGNSPVQEFTVPGDLQTATISGLKPGVDYTITVYAITDYY NPDTHEYKYHVSPISINYRTEIDKPSQ |
| 282 | E67 | 75.3 | MGVSDVPRDLEVVAATPTSLLISWSSVMGLYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDYY NPSTYEYKYNTTPISINYRTEIDKPSQ |
| 283 | E68 | 78.5 | MGVSDVPRDLEVVAATPTSLLISWKTEPGRHQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDWY NLVSHEYVYHTTPISINYRTEIDKPSQ |
| 284 | E69 | 85.1 | MGVSDVPRDLEVVAATPTSLLISWHAGMAVYQYYRITYGETGGNSPVQEFTVPGDVLTATISGLKPGVDYTITVYAVTDFF NPVTHEYMYHTIPISINYRTEIDKPSQ |
| 285 | E70 | 76.8 | MGVSDVPRDLEVVAATPTSLLISWVSARGRYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYY NLETYEYHYYRTPISINYRTEIDKPSQ |
| 286 | E71 | 80.4 | MGVSDVPRDLEVVAATPTSLLISWWFGTSSYQYYRITYGETGGNSPVQEFTVPGDLKTATISGLKPGVDYTITVYAVTDYF NPVTHEYEYHTTPISINYRTEIDKPSQ |
| 287 | E72 | 82.8 | MGVSDVPRDLEVVAATPTSLLISWSATRTLYQYYRITYGETGGNSPVQEFTVPYDVHTATISGLKPGVDYTITVYAVTDYY NMVTYEYNYHLTPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 288 | E73 | 78.8 | MGVSDVPRDLEVVVATPTSLLISWTKLLGGYQYYRITYGETGGNSPVQEFTVPGPVYTATISGLKPGVDYTITVYAVTDFF NPRTHEYQYHTTPISINYRTEIDKPSQ |
| 289 | E74 | 80.9 | MGVSDVPRDLEVVAATPTSLLISWRASGGLYQYYRITYGETGGNSPVQEFTVPGSVNTATISGLKPGVDYTITVYAVTDFY NPATYEYIYHTTPISINYRTEIDKPSQ |
| 290 | E75 | 76.5 | MGVSDVPRDLEVVAATPTSLLISWAAGRATYQYYRITYGETGGNSPVQEFTVPYDVTTATISGLKPGVDYTITVYAVTDFY NPATHEYYYETTPISINYRTEIDKPSQ |
| 291 | E76 | 79.0 | MGVSDVPRDLEVVAATPTSLLISWYSQPLTYQYYRITYGETGGNSPVQEFTVPHDVNTATISGLKPGVDYTITVYAVTDFY NPETHEYTYHLTPISINYRTEIDKPSQ |
| 292 | E77 | 81.1 | MGVSDVPRDLEVVAATPTSLLISWSSATRPYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDFF NPTTHEYYYHTTPISINYRTEIDKPSQ |
| 293 | E78 | 76.9 | MGVSDVPRDLEVVAATPTSLLISWSVERSVYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYY NPSTHEYNYLTTPISINYRTEIDKPSQ |
| 294 | E79 | 99.2 | MGVSDVPRDLEVVAATPTSLLISWQDTSSYHQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYF NPSTHEYIYRTIPISINYRTEIDKPSQ |
| 295 | E80 | 89.6 | MGVSDVPRDLEVVAATPTSLLISWSSSHRRYQYYRITYGETGGNSPVQEFTVPGSVATATISGLKPGVDYTITVYAVTDYF NPDTHEYLYHATPISINYRTEIDKPSQ |
| 296 | E81 | 75.1 | MGVSDVPRDLEVVAATPTSLLISWDNNSNSYQYYRITYGETGGNSPVQEFTVPYDLRTATISGLKPGVDYTITVYAVTDYK PHTEGEHTYHESPISINYRTEIDKPSQ |
| 297 | E82 | 77.2 | MGVSDVPRDLEVVAATPTSLLISWRVLVDMYQYYRITYGETGGNSPVQEFTVPGGVLTATISGLKPGVDYTITVYAVTDYK PHVDGPHTYYESPISINYRTEIDKPSQ |
| 298 | E83 | 90.7 | MGVSDVPRDLEVVAATPTSLLISWMFVGMSYQYYRITYGETGGNSPVQEFTVPYGVHTATISGLKPGVDYTITVYAVTDYF NPATHEYIYHVTPISINYRTEIDKPSQ |
| 299 | E84 | 86.5 | MGVSDVPRDLEVVAATPTSLLISWTLHRKNYQYYRITYGETGGNSPVQEFTVPGGVVTATISGLKPGVDYTITVYAVTDYY NPATHEYDYRTTPISINYRTEIDKPSQ |
| 300 | E85 | 89.3 | MGVSDVPRDLEVVAATPTSLLISWTQGSTHYQYYRITYGETGGNSPVQEFTVPGMVYTATISGLKPGVDYTITVYAVTDYF DRSTHEYKYRTTPISINYRTEIDKPSQ |
| Residues 1-108 of SEQ ID NO: 107, | E4 | 94.3 | MGVSDVPRDLEVVAATPTSLLISWHERDGSRQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYF NPTTHEYIYQTTPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| wherein X = Ser | | | |
| 301 | E86 | 84.7 | MGVSDVPRDLEVVAATPTSLLISWDSGENNYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYY NPKTHEYNYLTIPISINYRTEIDKPSQ |
| 302 | E87 | 87.0 | MGVSDVPRDLEVVAATPTSLLISWGSPLIEYQYYRITYGETGGNSPVQEFTVPGGLSTATISGLKPGVDYTITVYAVTDYF NPATHEYTYHVSPISINYRTEIDKPSQ |
| 303 | E88 | 89.3 | MGVSDVPRDLEVVAATPTSLLISWSATNKTYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYF NPTTHEYIYQTTPISINYRTEIDKPSQ |
| 304 | E89 | 82.6 | MGVSDVPRDLEVVAATPTSLLISWDDPAANRQYYRITYGETGGNSPVQEFTVPYDLRTATISGLKPGVDYTITVYAVTDYY NPATHQYKYSQSPISINYRTEIDKPSQ |
| 305 | E90 | 81.3 | MGVSDVPRDLEVVAATPTSLLISWYWEGLPYQYYRITYGETGGNSPVQEFTVPRDVNTATISGLKPGVDYTITVYAVTDWY NPDTHEYIYHTIPISINYRTEIDKPSQ |
| 306 | E91 | 84.7 | MGVSDVPRDLEVVAATPTSLLISWSAPWRTYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDYL NPNTLEYTYQRIPISINYRTEIDKPSQ |
| 307 | E92 | 88.5 | MGVSDVPRDLEVVAATPTSLLISWQAANHSYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDFF NPVTHEYKYRTIPISINYRTEIDKPSQ |
| 308 | E93 | 76.9 | MGVSDVPRDLEVVAATPTSLLISWDSGRGSYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 309 | E94 | 78.7 | MGVSDVPRDLEVVAATPTSLLISWNNGGRNYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 310 | E95 | 98.0 | MGVSDVPRDLEVVAATPTSLLISWVVPQGMYQYYRITYGETGGNSPVQEFTVPGGVSTATISGLKPGVDYTITVYAVTDYF NPATHEYNYHSIPISINYRTEIDKPSQ |
| 311 | E96 | 91.7 | MGVSDVPRDLEVVAATPTSLLISWASNRGTYQYYRITYGETGGNSPVQEFTVPGGVSTATISGLKPGVDYTITVYAVTDAF NPTTHEYNYFTTPISINYRTEIDKPSQ |
| 312 | E97 | 89.3 | MGVSDVPRDLEVVAATPTSLLISWLPGKLRYQYYRITYGETGGNSPVQEFTVPHDLRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 313 | E98 | 75.8 | MGVSDVPRDLEVVAATPTSLLISWDAPTSRYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHEYPISINYRTEIDKPSQ |

**Figure 45 Con't**

| SEQ ID NO | Binder | % inhibition at 100nM | Amino Acid Sequence |
|---|---|---|---|
| 314 | E99 | 84.7 | MGVSDVPRDLEVVAATPTSLLISWDAPTSRYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 315 | E100 | 83.3 | MGVSDVPRDLEVVAATPTSLLISWTPANKSYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 316 | E101 | 90.9 | MGVSDVPRDLEVVAATPTSLLISWDAPAVTYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 317 | E102 | 80.0 | MGVSDVPRDLEVVAATPTSLLISWTPANKSYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHESPISINYRTEIDKPSQ |
| 318 | E103 | 76.3 | MGVSDVPRDLEVVAATPTSLLISWTPANKSYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTNMM HVEYSEYPISINYRTEIDKPSQ |
| 319 | E104 | 89.3 | MGVSDVPRDLEVVAATPTSLLISWDAGAVTYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDHK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 320 | E105 | 87.0 | MGVSDVPRDLEVVAATPTSLLISWDAPTSRYQYYRITYGETGGNSPVQEFTVPGGLSTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 321 | E106 | 84.0 | MGVSDVPRDLEVVAATPTSLLISWDAPAVTYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |
| 322 | E107 | 75.8 | MGVSDVPRDLEVVAATPTSLLISWDSGRGSYQYYRITYGETGGNSPVQEFTVPYDVYTATISGLKPGVDYTITVYAVTDMM HVEYTEHPISINYRTEIDKPSQH |
| 323 | E108 | 80.0 | MGVSDVPRDLEVVAATPTSLLISWDAPAVTYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 324 | E109 | 90.9 | MGVSDVPRDLEVVAATPTSLLISWDAPTSRYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 325 | E110 | 81.3 | MGVSDVPRDLEVVAATPTSLLISWDAGAVTYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHESPISINYRTEIDKPSQ |
| 326 | E111 | 85.5 | MGVSDVPRDLEVVAATPTSLLISWDAPTSRYQYYRITYGETGGNSPVQEFTVPHDLVTATISGLKPGVDYTITVYAVTNMM HVEYSEYPISINYRTEIDKPSQ |
| 327 | E112 | 86.2 | MGVSDVPRDLEVVAATPTSLLISWDAGAVTYQYYRITYGETGGNSPVQEFTVPGGVRTATISGLKPGVDYTITVYAVTDYK PHADGPHTYHEYPISINYRTEIDKPSQ |

Figure 46

```
                  21        30                  51  56                  76        87
WT    EVVAATPTSLLI SWDAPAVTVR YYRITYGETGGNSPVQEFTV PGSKST ATISGLKPGVDYTITVYAV TGRGDSPASSK     P ISINYRT
I1    EVVAATPTSLLI SWSARLKVAR YYRITYGETGGNSPVQEFTV PKNVYT ATISGLKPGVDYTITVYAV TRFRDYQ        P ISINYRT
E1    EVVAATPTSLLI SWVAGAEDYQ YYRITYGETGGNSPVQEFTV PHDLVT ATISGLKPGVDYTITVYAV TDMMHVEYTEH    P ISINYRT
E2    EVVAATPTSLLI SWDSGRGSYQ YYRITYGETGGNSPVQEFTV PGPVHT ATISGLKPGVDYTITVYAV TDHKPHADGPHTYHESP ISINYRT
E3    EVVAATPTSLLI SWLPGKLRYQ YYRITYGETGGNSPVQEFTV PHDLRT ATISGLKPGVDYTITVYAV TNMMHVEYSEY    P ISINYRT
E4    EVVAATPTSLLI SWHERDGSRQ YYRITYGETGGNSPVQEFTV PGGVRT ATISGLKPGVDYTITVYAV TDYFNPTTHEYIYQTTP ISINYRT
E5    EVVAATPTSLLI SWWAPVDRYQ YYRITYGETGGNSPVQEFTV PRDVYT ATISGLKPGVDYTITVYAV TDYKPHADGPHTYHESP ISINYRT
E85   EVVAATPTSLLI SWTQGSTHYQ YYRITYGETGGNSPVQEFTV PGMVYT ATISGLKPGVDYTITVYAV TDYFDRSTHEYKYRTTP ISINYRT
E90   EVVAATPTSLLI SWYWEGLPYQ YYRITYGETGGNSPVQEFTV PRDVNT ATISGLKPGVDYTITVYAV TDWYNPDTHEYIYHTIP ISINYRT
E96   EVVAATPTSLLI SWASNRGTYQ YYRITYGETGGNSPVQEFTV PGGVST ATISGLKPGVDYTITVYAV TDAFNPTTHEYNYFTTP ISINYRT
E105  EVVAATPTSLLI SWDAPTSRYQ YYRITYGETGGNSPVQEFTV PGGLST ATISGLKPGVDYTITVYAV TDYKPHADGPHTYHESP ISINYRT
E112  EVVAATPTSLLI SWDAGAVTYQ YYRITYGETGGNSPVQEFTV PGGVRT ATISGLKPGVDYTITVYAV TDYKPHADGPHTYHEYP ISINYRT
```

Figure 47

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 328 | I1 (with Cys tail) | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCGCGTCTG<br>AAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAAAAACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAGGTTCCGCGACTACCAG<br>CCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCACCCACCACCCAC |
| 329 | E6 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 330 | E7 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>CATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 331 | E8 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACCTG<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 332 | E9 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGAAGCTAACCCT<br>TCTCGTTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 333 | E10 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTACCCAGGATCT<br>CGCACCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTACCATCCGGCT<br>ACTTACGAACATGAATACCATGCTCATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 334 | E11 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACCCCTGCTAAT<br>AAATCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGGT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 335 | E12 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 336 | E13 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 337 | E14 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 338 | E15 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 339 | E16 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 340 | E3 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTGCCGGGCAAG<br>CTGAGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAACATGATGCATGTTGAA<br>TACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 341 | E1 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTGGCCGGGGCG<br>GAGGACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACATGATGCATGTTGAA<br>TACACTGAACATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 342 | E17 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>CACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 343 | E18 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTCGTGACGCAC<br>GTCGCCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTCTG<br>TCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 344 | E19 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGAGACGGAGAGC<br>AACGCGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGATC<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 345 | E20 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATGACGTCGCCC<br>TCGGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCCGGTT<br>CAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACAAAGAACATCAG<br>CATGCTCCGCATCAGTACACTGCTCATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 346 | E2 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATTCAGGACGA<br>GGTTCCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCCGGTT<br>CATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 347 | E22 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCAACAGGTCGC<br>ACAACTTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 348 | E23 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>ATCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACATGATGCATGTTGAA<br>TACGCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 349 | E24 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT<br>CCAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTCTTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 350 | E25 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGCTACCAAAGT<br>GGCGGCTATACCTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACGCTTACAAAGAA<br>TACCAGGAACATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 351 | E26 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTGGATCGGCATC<br>CCGGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGGT<br>AAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACATGATGCATGTTGAA<br>TACGCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 352 | E27 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTAAAGGTTCA<br>AAATCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACCATGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTATAACCCGGCT<br>ACTTACGAATACATATACCTTACGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 353 | E28 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAATCCCGGCTCC<br>AAAAGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAATCCGGAT<br>ACTCATGAATACCTATACAATCAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 354 | E29 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAACCCGGCACC<br>ACACATTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACCTG<br>ATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGAAT<br>ACTTATGAGTATATATACTTGACGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 355 | E30 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGCCATCGGCACC<br>ATCGTCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGCTGGTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACGACTGGGCT<br>ACTCATGAATACAATTACCACACCGCTCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

**Figure 47 Con't**

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 356 | E31 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACTTATAATGAT GGCAGCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGCTGTT TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAATCCGGCT ACATATGAATACATATATCACACGACACCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |
| 357 | E32 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTCTCCCTCGTG GGCTTCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT CATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |
| 358 | E33 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGCCTCGAGGAAG GAGGTCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTTGGTTG AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACATGCATGTTGAA TACGCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 359 | E34 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTGGCGCCCTTC TGGCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |
| 360 | E35 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACACCACCAGGA CATCAACATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCAGCT ACTCACTATTACACTTATTATACGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |
| 361 | E36 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGAGTCGGGGTCC AGGACGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT CATACAGCTACCATCAGCGGCCTTAAAACTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT GACGGTCCGCATACTTACCATGAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |
| 362 | E37 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGAGAGGACCTCC ACCCACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCGTGTT TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTACAACCCGGCT ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 363 | E38 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAATGCTCGCACC<br>GACGCTTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACCTG<br>GAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCTCATGCG<br>GACGGACCGCATACTTACCAAGAGTCGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 364 | E39 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTGAGCGCG<br>TTCCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>TCTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 365 | E40 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTGCTGGGCAGG<br>AGGGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGCTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCAGCT<br>ACCCATGAATACCAATACGAGCTTACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 366 | E41 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACTCCACCCAAT<br>TCTGGTCATAATTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGAAT<br>ACCTATGAATACACATATCAATTCACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 367 | E42 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTCGTCCCGAAC<br>TGGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGCTG<br>GAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTATAACCCGACT<br>ACGTATGAATACACATACTTTACCTATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 368 | E43 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCCGGCGGGTTC<br>ATGCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 369 | E44 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATTCCGAAGGT<br>CCTTCTTATCAATATTACCGCATCACTTACGGCGAAAAAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGCTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGAGA<br>ACGCATGAATTATTTTTCCAGCAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 370 | E45 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACGACCCGACA<br>TCTAATCTGTACAATTACAACCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 371 | E46 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTGGGCTCG<br>GTGGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACGTT<br>CTGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGAAGCCT<br>GACGGTCCACATATATACCAGGCAGTGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 372 | E47 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAACCCTGCTTCT<br>AAAGACTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT<br>CCGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAACCCGGCT<br>ACTCATGAGTATAAAATATGACTCGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 373 | E48 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGATCATCAGCA<br>ACCGCCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCGTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAACTGGGCC<br>ACTCATGAGTACATATACCACTCAACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 374 | E49 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCATTCCGGTCCA<br>CGAGAATATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCAGGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAACCCGATT<br>ACACATTTACTATTACTACGAGCTGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 375 | E50 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACGGTGGGCCTG<br>AGCGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>TCTACAGCTACCATCAGCGGCCTTAAACCTAGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATATCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 376 | E51 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGGGGGGCACCGG<br>GCGGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGCTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTACAACCCGGAT<br>ACTCATGAATACAAATACCATCAATATCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

**Figure 47 Con't**

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 377 | E52 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTTCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGTTCCGCGT<br>CCGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTGGTTCAAGGAA<br>TACCGTGAAGACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 378 | E53 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGCGTCGGGGGC<br>ATGATCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTACAACCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 379 | E5 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTGGGCCCCCGTC<br>GACCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 380 | E5 (with Cys tail) | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTGGGCCCCCGTC<br>GACCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCACCACCAC<br>CACCAC |
| 381 | E54 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAAAGCCAGCTAT<br>ACCGGCTACAACTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACGTT<br>ATGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTTCTACAATCCGGAT<br>ACTCATCAATACACATACCGTCGCATTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 382 | E55 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCGGTGGGCCAG<br>GTCTTCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACTACAACCCGGCT<br>ACTCATGAATACAAATACCATCAGACTCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 383 | E56 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTACTCTGGTGAT<br>TACCATTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGGCT<br>ACTCATTACTACAAGTACGAGCAGACACCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 384 | E57 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTTGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATCGTCCAGGGG<br>GGGCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCTTCA<br>ACTCATGAATACAAATACCATCAGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 385 | E58 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCGGCCGTCCGC<br>TGGCGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAACCGCGT<br>ACTCATGTATACATATACGATCAGTTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 386 | E59 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCCAGGCGC<br>TTGCAGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAACCGGCT<br>ACTATGGAGTACACATATCAGCGGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 387 | E60 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTGCAGCCCCTC<br>TGGAGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTCTG<br>GACACAGCTACCATCAGCGGACTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGTT<br>GACGGTCCCCATGCTTACCATGAATATCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 388 | E61 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCCTCCCAG<br>GGGAACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGCTGTT<br>AAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAACCCGGCT<br>ACTCATGAATACATATACCATACGACTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 389 | E62 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTGCCTCGACGGG<br>CAGTTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTTCTATC<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTGGTACAACCTCGCG<br>ACTCATGAATACAACTACCGTGTGACTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 390 | E63 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACACTTCAGGT<br>GCTTCATATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACTCTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACGACCCTGAT<br>TCGCATTATTACAACTACAATATGGTTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 391 | E64 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATTCTGGTAAT<br>GGTACTTATCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACCGTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGGCT<br>ACTCACGAATATACATACGAGCTGCGTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 392 | E65 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTACCACCCCCACCAGCCTGCTGATCAGCTGGCGGCCCACCAGC<br>CAGGTCTACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACAACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTTAACTATGCT<br>ACTCACGAATACACATATACCATACCATTTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 393 | E66 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAAGTCGTACGGG<br>TCGGCCTACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGACCTG<br>CAGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTATCACTGACTATTACAACCCGGAT<br>ACACATGAGTATAAATACCATGTGTCGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 394 | E67 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCGTCGGTGATG<br>GGGTTGTACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCTTCT<br>ACTTATGAATACAAATACAAATACGACTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 495 | E68 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAAAACAGAACCA<br>GGCCGCCACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTGGTACAACCTGGTT<br>TCTCATGAATACGTATACCATACTACCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 395 | E69 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCACGCCGGCATG<br>GCGGTGTACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGACGTT<br>CTGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAATCCGGTT<br>ACTCATGAATACATGTATCATACGATTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 396 | E70 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTGTCCGCGAGG<br>GGGCGGTACCAATATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCTAGAA<br>ACTTATGAATATCATTACTATCGCACTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

**Figure 47 Con't**

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 397 | E71 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTGGTTCGGCACC<br>TCGTCCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGACCTG<br>AAAACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTTAACCCGTT<br>ACTCATGAATACGAATATCATACGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 398 | E72 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCCGCGACCCGG<br>ACCCTGTACCAATATTACCGAATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>CATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACATGGTT<br>ACTTATGAATACAACTACCATCTTACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 399 | E73 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGTTGCCACCCCCACCAGCCTGCTGATCAGCTGGACCAAGTTGTTG<br>GGCGGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCCTGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAACCCTCGT<br>ACTCATGAATATCAATATCACACGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 400 | E74 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGGGCGTCGGGC<br>GGGCTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTTCTGTT<br>AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAACCCGGCT<br>ACTTATGAGTACATATACCATACCACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 401 | E75 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGCGGCCGGCGC<br>GCCACGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>ACTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTACAACCCGGCT<br>ACTCATGAATACTACTATGAGACCACGCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 402 | E76 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTACTCGCAGCCC<br>TTGACGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACGTT<br>AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTCTACAACCCGGAG<br>ACACATGAATACACTTACCACCTGACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 403 | E77 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGTTCTGCAACA<br>AGACCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAACCCGACT<br>ACGCACGAATACTATTATCATACGACTCCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 404 | E78 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCCGTCGAGAGG<br>TCCGTGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCGTCT<br>ACTCATGAATACAATTACCTCACGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 405 | E79 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAAGATACCTCC<br>AGTTATCATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCGTCT<br>ACCCATGAATACATCTACCGTACCATTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 406 | E80 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTAGCTCTCAT<br>CGCCGCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTTCGGTT<br>GCTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCAGAC<br>ACTCATGAATACCTATACCATGCCACCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 407 | E81 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATAAATAATTCT<br>AACTCATATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCTCATACT<br>GAGGGTGAGCATACTTATTATCATGAATCGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 408 | E82 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCGCGTGTTGGTC<br>GACATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CTGACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGTT<br>GACGGGCCGCACACCTACTATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 409 | E83 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGATGTTTCGTGGGG<br>ATGTCCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGGTGTT<br>CATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCGGCT<br>ACGCATGAATACATCTACCATGTGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 410 | E84 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACGCTGCACCGG<br>AAGAACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGGCA<br>ACTCATGAATACGACTACCGAACAACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 411 | E85 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTTCTGATCAGCTGGACACAAGGCAGT<br>ACTCATTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTATGGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCGACCGCTCT<br>ACTCATGAGTATAAATACCGTACGACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 412 | E4 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCACGAACGTGAC<br>GGAAGTAGACAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTAACCCGACT<br>ACACATGAATACATATATCAGACAACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 413 | E86 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACTCCGGTGAA<br>AACAATTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGAAG<br>ACTCATGAATATAATTATCTTACTATTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 414 | E87 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGGAGCCCCTTG<br>ATCGAGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTCTG<br>TCTACAGCTACCATCAGCGGCCTCAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCGGCT<br>ACTCATGAATACACATACCATGTGAGTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 415 | E88 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCAACAAAC<br>AAAACTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTTAACCCGACT<br>ACACATGAATACATATATCAGACAACTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 416 | E89 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATGACCCAGCT<br>GCAAACCGACAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTACAACCCGGCT<br>ACCCATCAATACAAATACTCTCAGAGTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 417 | E90 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTACTGGGAGGGG<br>CTGCCCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCGTGACGTT<br>AACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTGGTACAACCCCGAC<br>ACCCATGAGTATATACCATACGATTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 418 | E91 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAGCGCGCCGTGG<br>CGGACCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTAAACCCTAAC<br>ACGCTTGAATACACCTACCAGCGCATTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 419 | E92 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAGGCGGCCAAC<br>CACTCGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTTTTTCAATCCTGTC<br>ACTCATGAATACAAATACCGTACAATTTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 420 | E93 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATTCAGGACGA<br>GGTTCCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCACGCT<br>GACGGTCCGCACACTTACCATGAATATCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 421 | E94 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGAATAACGGAGGA<br>CGCAATTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCACGCT<br>GACGGTCCGCACACTTACCATGAATATCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 422 | E95 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTCGTGCCGCAG<br>GGGATGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>TCTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATTTCAACCCGGCA<br>ACCCATGAATACAATTATCATTCAATTTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 423 | E96 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGCGAGCAACCGG<br>GGGACGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>TCTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACGCTTTCAACCCAACT<br>ACTCATGAATACAATTATTTTACAACTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 424 | E97 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTGCCGGGCAAG<br>CTGAGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 425 | E98 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCAACC<br>TCCCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 426 | E99 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCAACC<br>TCCCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCACGCT<br>GACGGTCCGCACACTTACCATGAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 427 | E100 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACCCCTGCTAAT<br>AAATCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 428 | E101 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCGGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATTCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 429 | E102 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACCCCTGCTAAT<br>AAATCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 430 | E103 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGACCCCTGCTAAT<br>AAATCTTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAACATGATGCATGTTGAA<br>TACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 431 | E104 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTGGTGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 432 | E105 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCAACC<br>TCCCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTCTG<br>TCCACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 433 | E106 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCGGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCACGCT<br>GACGGTCCGCACACTTACCATGAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 434 | E107 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATTCAGGACGA<br>GGTTCCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTTACGACGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACATGATGCATGTTGAA<br>TACACTGAACATCCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCAC |
| 435 | E108 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCGGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 436 | E109 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCAACC<br>TCCCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 437 | E110 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTGGTGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 438 | E111 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTCCAACC<br>TCCCGCTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGACCTG<br>GTTACAGCTACCATCAGCGGCCTTAAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCAC<br>TACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCAC |

Figure 47 Con't

| SEQ ID NO | BINDER | NUCLEOTIDE SEQUENCE |
|---|---|---|
| 439 | E112 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGACGCTGGTGCT<br>GTTACTTACCAGTATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTATAAACCGCACGCT<br>GACGGTCCGCACACTTACCATGAATATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |
| 440 | E113 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTATCCTGGCCAA<br>CCAACATATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCATTGTGCCTTACCTGGTT<br>TACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACTACGCTTACAAAGAA<br>TACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCACCACCAC |
| 441 | E114 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGCAAAGTTCAACC<br>AGCCAATATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTGGTGTT<br>CGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCGCATGCT<br>GACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATCCCAGCACCATCACCAC<br>CACCAC |

Figure 48

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 442 | E3-GS10-I1 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTTGCCGGGCA<br>AGCTGAGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGA<br>CCTGCGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAACATGATGCAT<br>GTTGAATACTCTGAATACCCAATTTCCATTAATTACCGCACACAGAAATTGACAAAGGTAGCGGCTCTGGTTCCGGCAGCGGCT<br>CCGGCAGCGGCTCTGGCAGCGGTTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAG<br>CCTGCTGATCAGCTGGTCTGCGCGTCTGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT<br>GTCCAGGAGTTCACTGTGCCTAAAAACGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTG<br>TGTATGCTGTCACTAGGTTCCGCGACTACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCA<br>CCACCACCACCAC |
| 443 | I1-GS10-E3 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCGCGTC<br>TGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAAAAA<br>CGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAGGTTCCGCGAC<br>TACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAGGTAGCGGCTCTGGTTCCGGCAGCGGCTCCGGCAGCGGCT<br>CTGGCAGCGGTTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG<br>CTGGTTGCCGGGCAAGCTGAGGTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTC<br>ACTGTGCCTCATGACCTGCGTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCA<br>CTAACATGATGCATGTTGAATACTCTGAATACCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCA<br>CCACCACCACCAC |
| 444 | E1-GS10-I1 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGTGGCCGGGG<br>CGGAGGACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTCATGA<br>CCTGGTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACATGATGCAT<br>GTTGAATACACTGAACATCCAATTTCCATTAATTACCGCACAGAAATTGACAAAGGTAGCGGCTCTGGTTCCGGCAGCGGCT<br>CCGGCAGCGGCTCTGGCAGCGGTTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAG<br>CCTGCTGATCAGCTGGTCTGCGCGTCTGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCT<br>GTCCAGGAGTTCACTGTGCCTAAAAACGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTG<br>TGTATGCTGTCACTAGGTTCCGCGACTACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCA<br>CCACCACCACCAC |

**Figure 48 Con't**

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 445 | I1-GS10-E1 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCGCGTC<br>TGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAAAAA<br>CGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAGGTTCCGCGAC<br>TACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAGGTAGCGGCTCTGGTTCCGGCAGCGGCTCCGGCAGCGGCT<br>CTGGCAGCGGTTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG<br>CTGGGTGGCCGGGGCGGAGGACTACCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTC<br>ACTGTGCCTCATGACCTGGTTACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCA<br>CTGACATGATGCATGTTGAATACACTGAACATCCAATTTCCATTAATTACCGCACAGAAATTGACAAACCATGCCAGCACCA<br>CCACCACCACCAC |
| 446 | E2-GS10-I1 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGGATTCAGGAC<br>GAGGTTCCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGTCC<br>GGTTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTGACCATAAACCG<br>CATGCTGACGGTTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAAAGGTAGCGGCTCTG<br>GTTCCGGCAGCGGCTCCGGCAGCGGCTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGC<br>TGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCGCGTCTGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACA<br>GGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAAAAACGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTG<br>ATTATACCATCACTGTGTATGCTGTCACTAGGTTCCGCGACTACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAA<br>ACCATGCCAGCACCACCACCACCACCAC |
| 447 | I1-GS10-E2 | ATGGGAGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAGCTGGTCTGCGCGTC<br>TGAAAGTTGCGCGATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTCACTGTGCCTAAAAA<br>CGTTTACACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCACTAGGTTCCGCGAC<br>TACCAGCCAATTTCCATTAATTACCGCACAGAAATTGACAAAGGTAGCGGCTCTGGTTCCGGCAGCGGCTCCGGCAGCGGCT<br>CTGGCAGCGGTTCTGGTTCCGTTTCTGATGTGCCGCGCGACCTGGAAGTGGTTGCTGCCACCCCCACCAGCCTGCTGATCAG<br>CTGGGATTCAGGACGAGGTTCCTATCAATATTACCGCATCACTTACGGCGAAACAGGAGGCAATAGCCCTGTCCAGGAGTTC<br>ACTGTGCCTGGTCCGGTTCATACAGCTACCATCAGCGGCCTTAAACCTGGCGTTGATTATACCATCACTGTGTATGCTGTCA<br>CTGACCATAAACCGCATGCTGACGGTCCGCATACTTACCATGAATCTCCAATTTCCATTAATTACCGCACAGAAATTGACAA<br>ACCATGCCAGCACCACCACCACCACCAC |
| 448 | E5-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGTGGGCACCGG<br>TTGATCGTTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTCGCGA<br>CGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTACGCCGTTACCGATTATATAAACCG<br>CATGCAGATGGTCCGCATACCTATCATGAAAGCCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |

Figure 48 Con't

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 449 | E85-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGACCCAGGGTA<br>GCACACATTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTGGTAT<br>GGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTACGCCGTTACCGATTATTTCGAT<br>CGGTCCACCCATGAATATAAATATCGGACCACCCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |
| 450 | E4-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGCATGAACGTG<br>ATGGTAGCCGTCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTGGCGG<br>TGTTCGTACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTACGCCGTTACCGATTATTTCAAT<br>CCGACCACCCATGAATATATTTATCAGACCACCCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |
| 451 | E90-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGTATTGGGAAG<br>GTCTGCCGTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTCACCGTTCCTCGCGA<br>CGTTAATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTACGCCGTTACCGATTGGTACAAC<br>CCTGATACCCATGAATATATTTATCATACCATTCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTTCTGGTAGTGGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |
| 452 | E96-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGGCAAGCAATC<br>GTGGCACCTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTGGCGG<br>TGTTTCTACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTACGCCGTTACCGATGCATTTAAT<br>CCGACCACCCATGAATATAATTATTTTACCACCCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |

**Figure 48 Con't**

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 453 | E105-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGGATGCACCGA<br>CCTCTCGTTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTGGCGG<br>TCTGAGCACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTACGCCGTTACCGATTATAAACCG<br>CATGCAGATGGTCCGCATACCTATCATGAAAGCCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCCGAAAAATTGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |
| 454 | E112-GS10-I1 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAGGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTTCTTGGGATGCAGGTG<br>CAGTTACCTATCAGTATTATCGCATCACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCTGGCGG<br>TGTTCGTACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTACGCCGTTACCGATTATAAACCG<br>CATGCAGATGGTCCGCATACCTATCATGAATATCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCG<br>GTTCAGGTAGCGGATCAGGTTCTGGTAGTGGTAGCGGCAGCGTTTCAGATGTGCCTCGCGACCTGGAAGTGGTGGC<br>AGCCACACCGACTTCTCTGCTGATTAGCTGGTCTGCACGTCTGAAAGTTGCCCGTTATTACCGTATTACTTATGGCGAAACA<br>GGCGGAAATAGCCCTGTGCAAGAATTTACCGTGCCGAAAAATGTGTACACAGCCACCATCTCTGGCCTGAAACCTGGCGTGG<br>ACTACACAATCACAGTTTATGCAGTGACCCGTTTTCGTGATTATCAGCCGATCAGCATCAATTATCGTACAGAGATCGATAA<br>ACCGTGCCAGCATCACCACCATCATCAC |
| 455 | I1-GS10-E5 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAAGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCACGTC<br>TGAAAGTTGCCCGTTATTATCGCATTACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCGAAAAA<br>TGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTATGCAGTTACCCGTTTTCGTGAT<br>TATCAGCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTTCTGGTAGCGGTTCAGGTTCTGGTT<br>CTGGTAGTGGTAGCGGCAGCGTTTCAGACGTGCCTCGTGATTTAGAAGTGGTGGCAGCCACACCGACCTCACTGCTGATTTC<br>TTGGTGGGCACCGGTTGATCGTTATATCAGTATTATCGCATCACATACGGCGAAACAGGCGGAAATAGCCCTGTGCAAGAATTC<br>ACCGTACCGCGTGATGTGTATACCGCCACAATTTCTGGTTTAAAACCTGGCGTGGACTACACAATCACAGTTTATGCCGTGA<br>CCGATTATAAACCGCATGCAGATGGTCCGCATACCTATCATGAAAGCCCGATCTCTATCAATTATCGCACAGAGATCGATAA<br>ACCGTGTCAGCATCACCACCATCATCAC |
| 456 | I1-GS10-E85 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAAGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCACGTC<br>TGAAAGTTGCCCGTTATTATCGCATTACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCGAAAAA<br>TGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTATGCAGTTACCCGTTTTCGTGAT<br>TATCAGCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTTCTGGTAGCGGTTCAGGTTCTGGTT<br>CTGGTAGTGGTAGCGGCAGCGTTTCAGACGTGCCTCGTGATTTAGAAGTGGTGGCAGCCACACCGACCTCACTGCTGATTTC<br>TTGGACCCAGGGTAGCACACATTATCAGTATTATCGCATCACATACGGCGAAACAGGCGGAAATAGCCCTGTGCAAGAATTC<br>ACCGTACCGGGTATGGTGTATACCGCCACAATTTCTGGTTTAAAACCTGGCGTGGACTACACAATCACAGTTTATGCCGTGA<br>CCGATTATTTCGATCGCAGCACCCATGAATATAAATATCGTACCACCCCGATCTCTATCAATTATCGCACAGAGATCGATAA<br>ACCGTGTCAGCATCACCACCATCATCAC |

**Figure 48 Con't**

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 457 | I1-GS10-E4 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAAGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCACGTC<br>TGAAAGTTGCCCGTTATTATCGCATTACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCGAAAAA<br>TGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTATGCAGTTACCGTTTTCGTGAT<br>TATCAGCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCGGTTCTGGTAGCGGTTCAGGTTCTGGTT<br>CTGGTAGTGGTAGCGGCAGCGTTCCTCGTGATTTAGAAGTGGTGGCAGCCACACCGACCTCACTGCTGATTTC<br>TTGGCATGAACGTGATGGTAGCCGTCAGTATTATCGCATCACATACGGCGAAACAGGCGGAAATAGCCCTGTGCAAGAATTC<br>ACCGTACCGGGTGGTGTTCGTACCGCCACAATTTCTGGTTTAAAACCTGGCGTGGACTACACAATCACAGTTTATGCCGTGA<br>CCGATTATTTCAATCCGACCACACCCACGAATATATTTATCAGACCACCCCGATCTCTATCAATTATCGCACAGAGATCGATAA<br>ACCGTGTCAGCATCACCACCATCATCAC |
| 458 | I1-GS10-E105 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAAGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCACGTC<br>TGAAAGTTGCCCGTTATTATCGCATTACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCGAAAAA<br>TGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTATGCAGTTACCGTTTTCGTGAT<br>TATCAGCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCGGTTCTGGTAGCGGTTCAGGTTCTGGTT<br>CTGGTAGTGGTAGCGGCAGCGTTCCTCGTGATTTAGAAGTGGTGGCAGCCACACCGACCTCACTGCTGATTTC<br>TTGGGATGCACCGACCAGCCGTTATCAGTATTATCGCATCACATACGGCGAAACAGGCGGAAATAGCCCTGTGCAAGAATTC<br>ACCGTACCGGGTGGTCTGAGCACCGCCACAATTTCTGGTTTAAAACCTGGCGTGGACTACACAATCACAGTTTATGCCGTGA<br>CCGATTATAAACCGCATGCAGATGGTCCGCATACCTATCATGAAAGCCCGATCTCTATCAATTATCGCACAGAGATCGATAA<br>ACCGTGTCAGCATCACCACCATCATCAC |
| 459 | I1-GS10-E112 | ATGGGTGTTTCTGATGTTCCGCGTGATCTGGAAGTTGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCACGTC<br>TGAAAGTTGCCCGTTATTATCGCATTACCTATGGTGAAACCGGTGGTAATTCTCCGGTTCAGGAATTTACCGTTCCGAAAAA<br>TGTTTATACCGCAACCATTAGCGGTCTGAAACCGGGTGTTGATTACACCATTACCGTTTATGCAGTTACCGTTTTCGTGAT<br>TATCAGCCGATTAGCATTAACTATCGCACCGAAATTGATAAAGGTAGCGGTAGCGGTTCTGGTAGCGGTTCAGGTTCTGGTT<br>CTGGTAGTGGTAGCGGCAGCGTTCCTCGTGATTTAGAAGTGGTGGCAGCCACACCGACCTCACTGCTGATTTC<br>TTGGGATGCCGGTGTTCGTACCGCCACAATTTCTGGTTTAAAACCTGGCGTGGACTACACAATCACAGTTTATGCCGTGA<br>CCGATTATAAACCGCATGCAGATGGTCCGCATACCTATCATGAATATCCGATCTCTATCAATTATCGCACAGAGATCGATAA<br>ACCGTGTCAGCATCACCACCATCATCAC |
| 460 | I1-GSGCGS8-E5 | ATGGGCGTGAGTGATGTTCCGCGTGATCTGGAAGTGGTTGCAGCAACCCCGACGAGCCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACTCTCCGGTTCAGGAATTTACCGTGCCGAAAAA<br>TGTTTATACCGCAACGATTAGCGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCCGTTTCCGCGAT<br>TACCAGCCGATTAGCATCAACTATCGTACGGAAATTGAAAAAGGCTCTGGTTGCGGCAGTGGTAGCGGCTCTGGTAGTGGCA<br>GCGGTTCTGGCAGTGGTAGCGTGTCTGACGTCCCGCGCGACCTGGAAGTTGTTGCAGCGACCCCGACCAGCCTGCTGATTAG<br>TTGGTGGGCCCCGGTGGATCGTTACCAGTATTACCGCATCACCTATGGCGAAACCGGTGGTAACAGCCCCGGTGCAAGAATTT<br>ACCGTGCCGCGTGATGTTTATACCGCGACCATCTCTGGTCTGAAACCGGGCGTTGACTACACGATTACCGTTTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAAAGTCCGATTAGCATCAATTATCGGACCGAACATCACCA<br>TCACCATCAC |

Figure 48 Con't

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 461 | I1-GS10-E5-GSGC | ATGGGCGTGTCTGATGTTCCGCGTGATCTGGAAGTGGTTGCGGCCACCCCGACGAGTCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACAGCCCGGTTCAGGAATTTACCGTGCCGAAAAA<br>TGTTTATACCGCAACGATTTCTGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCGTTTCCGCGAT<br>TACCAGCCGATTAGCATCAACTATCGTACGGAAATTGAAAAAGGCAGTGGTAGCGGCTCTGGTAGTGGCAGCGGTTCTGGCA<br>GTGGTAGCGGCTCTGGTAGTGTAAGCGACGTCCCGCGCGATCTGGAAGTGGTTGCAGCGACCCCGACGAGCCTGCTGATTTC<br>TTGGTGGGCCCCGGTGGATCGTTACCAGTATTACCGCATCACCTATGGCGAAACCGGTGGCAATTCTCCGGTGCAAGAATTC<br>ACCGTGCCGCGTGATGTTTATACCGCGACGATTAGCGGTCTGAAACCGGGCGTTGACTACACGATTACCGTGTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAATCTCCGATTAGTATCAATTATCGGACCGAAGGCAGTGG<br>TTGCCATCACCATCACCATCAC |
| 462 | I1(S62C)-GS10-E5 | ATGGGCGTGAGTGATGTTCCGCGTGATCTGGAAGTGGTTGCAGCAACCCCGACGAGCCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACAGCCCGGTTCAGGAATTTACCGTGCCGAAAAA<br>TGTTTATACCGCAACGATTTGCGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCGTTTCCGCGAT<br>TACCAGCCGATTAGCATCAACTATCGTACGGAAATTGAAAAAGGCAGTGGTAGCGGCTCTGGTAGTGGCAGCGGTTCTGGCA<br>GTGGTAGCGGCTCTGGTAGTGTAAGCGACGTCCCGCGCGACCTGGAAGTGGTTGCAGCGACCCCGACGAGCCTGCTGATCTC<br>TTGGTGGGCCCCGGTGGATCGTTACCAGTATTACCGCATCACCTATGGCGAAACCGGTGGTAACTACTCCGGTGCAAGAATTT<br>ACCGTGCCGCGTGATGTTTATACCGCGACGATTTCTGGTCTGAAACCGGGCGTTGACTACACGATTACCGTTTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAATCTCCGATTAGTATCAATTATCGGACCGAACACATCACCA<br>TCACCATCAC |
| 463 | I1-GS10-E5(S62C) | ATGGGCGTGAGTGATGTTCCGCGTGATCTGGAAGTGGTTGCAGCAACCCCGACGAGCCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACTCTCCGGTTCAGGAATTTACCGTGCCGAAAAA<br>TGTTTATACCGCAACGATTAGCGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCGTTTCCGCGAT<br>TACCAGCCGATTAGCATCAACTATCGTACGGAAATTGAAAAAGGCAGTGGTAGCGGCTCTGGTAGTGGCAGCGGTTCTGGCA<br>GTGGTAGCGGCTCTGGTAGTGTAAGCGACGTCCCGCGCGACCTGGAAGTGTTGCAGCGACGCCGACGAGCCTGCTGATCTC<br>TTGGTGGGCCCCGGTGGATCGTTACCAGTATTACCGCATCACCTATGGCGAAACCGGTGGTAACACAGCCCGGTGCAAGAATTT<br>ACCGTGCCGCGTGATGTTTATACCGCGACGATTTGTGGTCTGAAACCGGGCGTTGACTACACGATTACCGTTTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAATCTCCGATTAGTATCAATTATCGGACCGAACACATCACCA<br>TCACCATCAC |
| 464 | I1(S91C)-GS10-E5 | ATGGGCGTGAGTGATGTTCCGCGTGATCTGGAAGTGGTTGCAGCAACCCCGACGAGCCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACTCTCCGGTTCAGGAATTTACCGTGCCGAAAAA<br>TGTTTATACCGCAACGATTAGCGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCGTTTCCGCGAT<br>TACCAGCCGATTTGCATCAACTATCGTACGGAAATTGAAAAAGGCAGTGGTAGCGGCTCTGGTAGTGGCAGCGGTTCTGGCA<br>GTGGTAGCGGCTCTGGTAGTGTAAGCGACGTCCCGCGCGACCTGGAAGTTGTTGCAGCGACGCCGACGAGCCTGCTGATCTC<br>ACCGTGCCGCGTGATGTTTATACCGCGACCATCTCTGGTCTGAAACCGGGCGTTGACTACACGATTACCGTTTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAATCTCCGATTAGTATCAATTATCGGACCGAACACATCACCA<br>TCACCATCAC |

Figure 48 Con't

| SEQ ID NO | Binder | DNA SEQ |
|---|---|---|
| 465 | I1-GS10-E5(S91C) | ATGGGCGTGAGCGATGTTCCGCGTGATCTGGAAGTGGTTGCAGCAACCCCGACCAGCCTGCTGATTAGCTGGTCTGCCCGCC<br>TGAAAGTGGCACGTTATTACCGCATCACCTACGGCGAAACGGGCGGTAACAGTCCGGTTCAGGAATTTACCGTGCCCGAAAAA<br>TGTTTATACCGCAACGATTAGCGGCCTGAAACCGGGTGTGGATTATACCATCACGGTGTACGCGGTTACCCGTTTCCGCGAT<br>TACCAGCCGATTAGCATCAACTATCGTACGGAAATTGAAAAAGGCAGTGGTAGCGGCTCTGGTAGTGGCAGCGGTTCTGGCA<br>GTGGTAGCGGCTCTGGTAGTGTAAGCGACGTCCCGCGCGACCTGGAAGTTGTTGCAGCGACCGACCAGCCTGCTGATCAG<br>TTGGTGGGCCCCGGTGGATCGTTACCAGTATTACCGCATCACCTATGGCGAAACCGGTGGTAACAGCCCGGTGCAAGAATTC<br>ACCGTGCCGCGTGATGTTTATACCGCGACCATCTCTGGTCTGAAACCGGGCGTTGACTACACGATTACCGTTTACGCGGTTA<br>CCGATTATAAACCGCATGCCGATGGTCCGCATACGTACCACGAAAGCCCGATTTGCATCAATTATCGGACCGAACATCACCA<br>TCACCATCAC |