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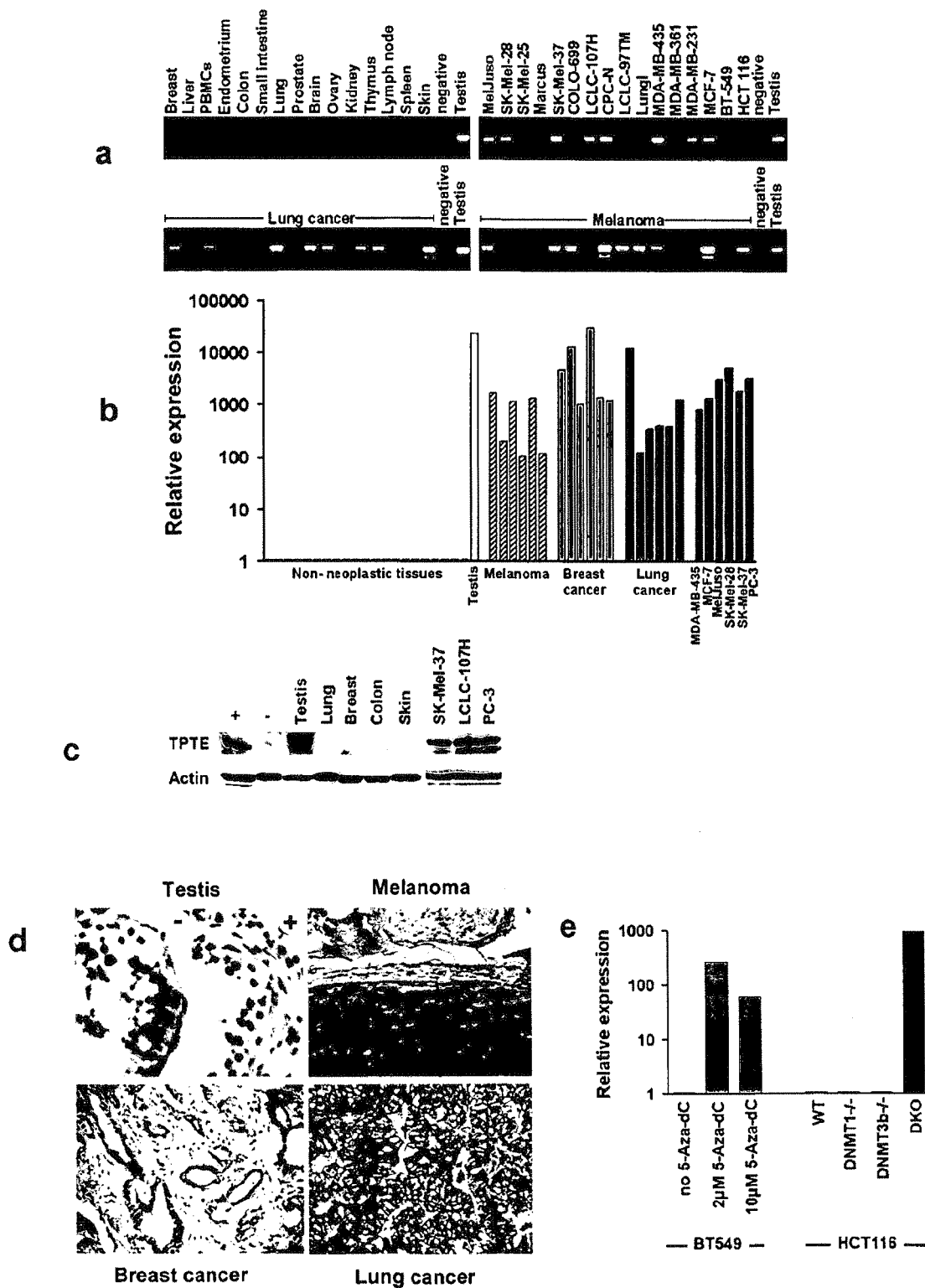


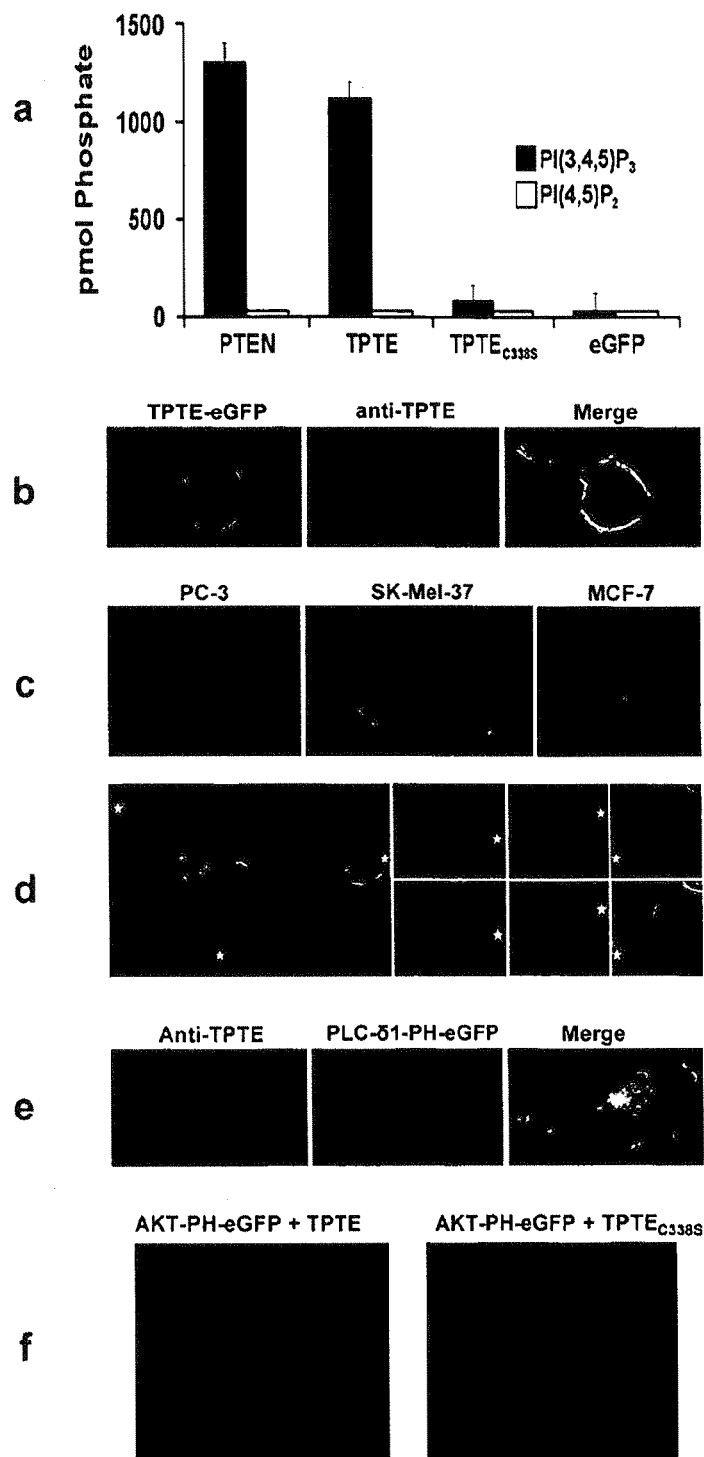
Figure 2

Figure 3

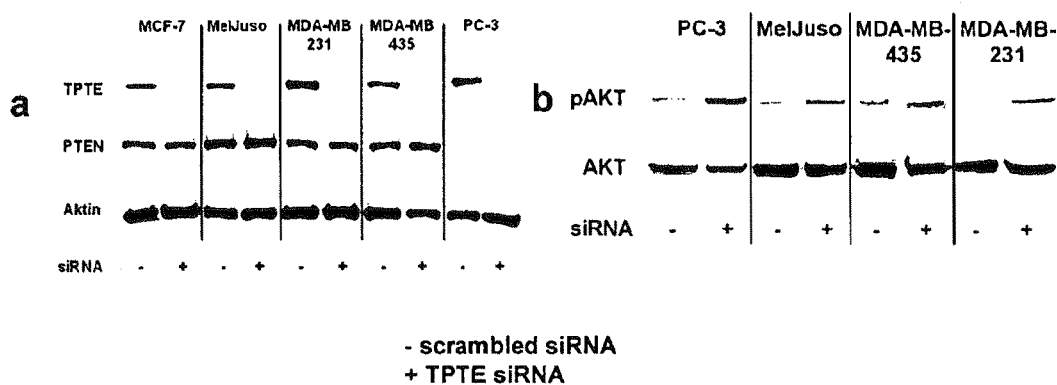
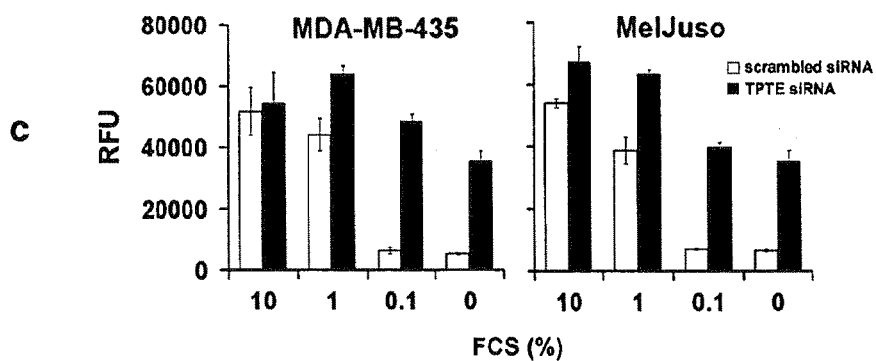
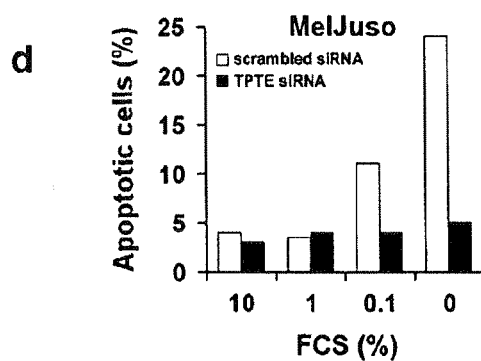


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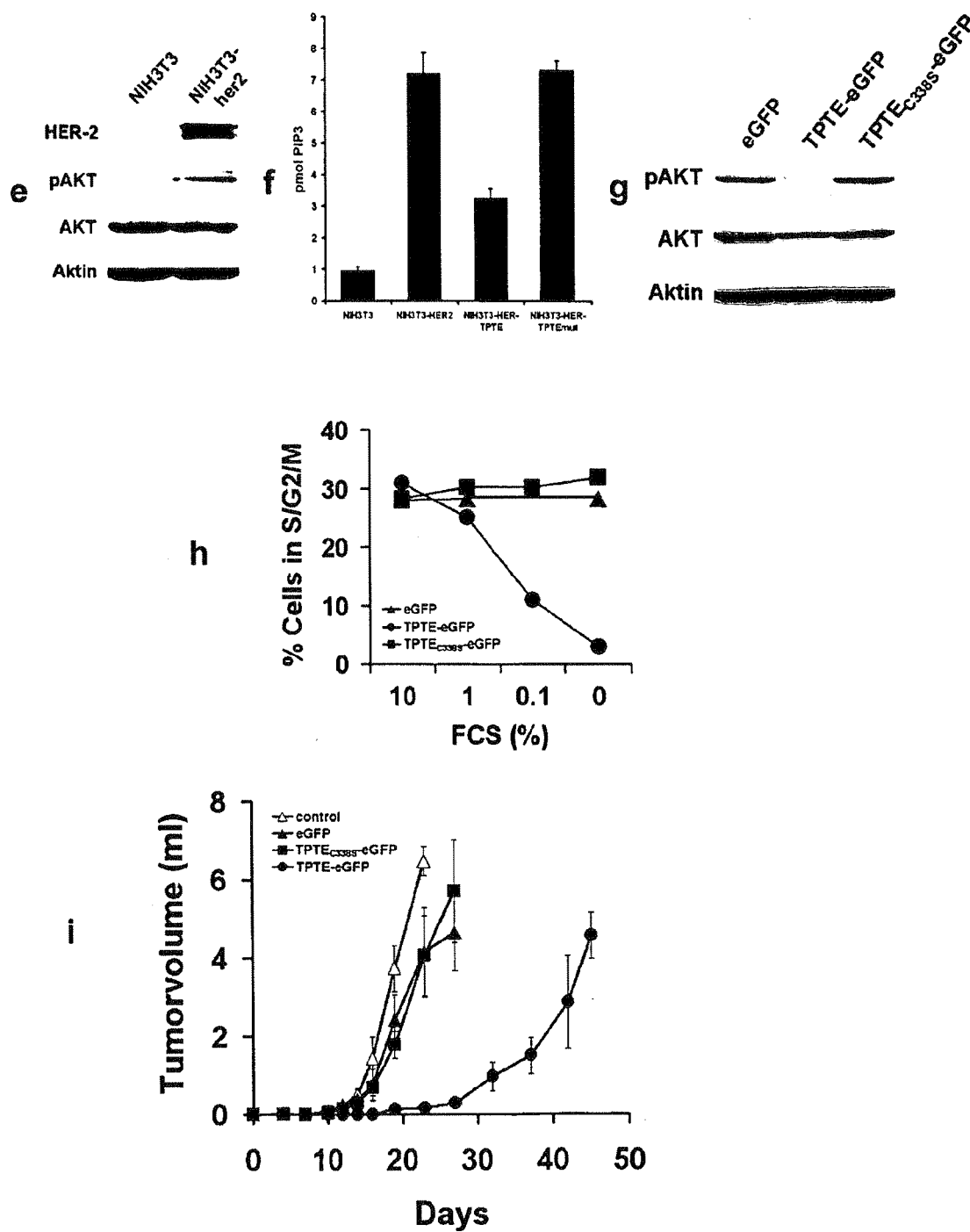


Figure 4

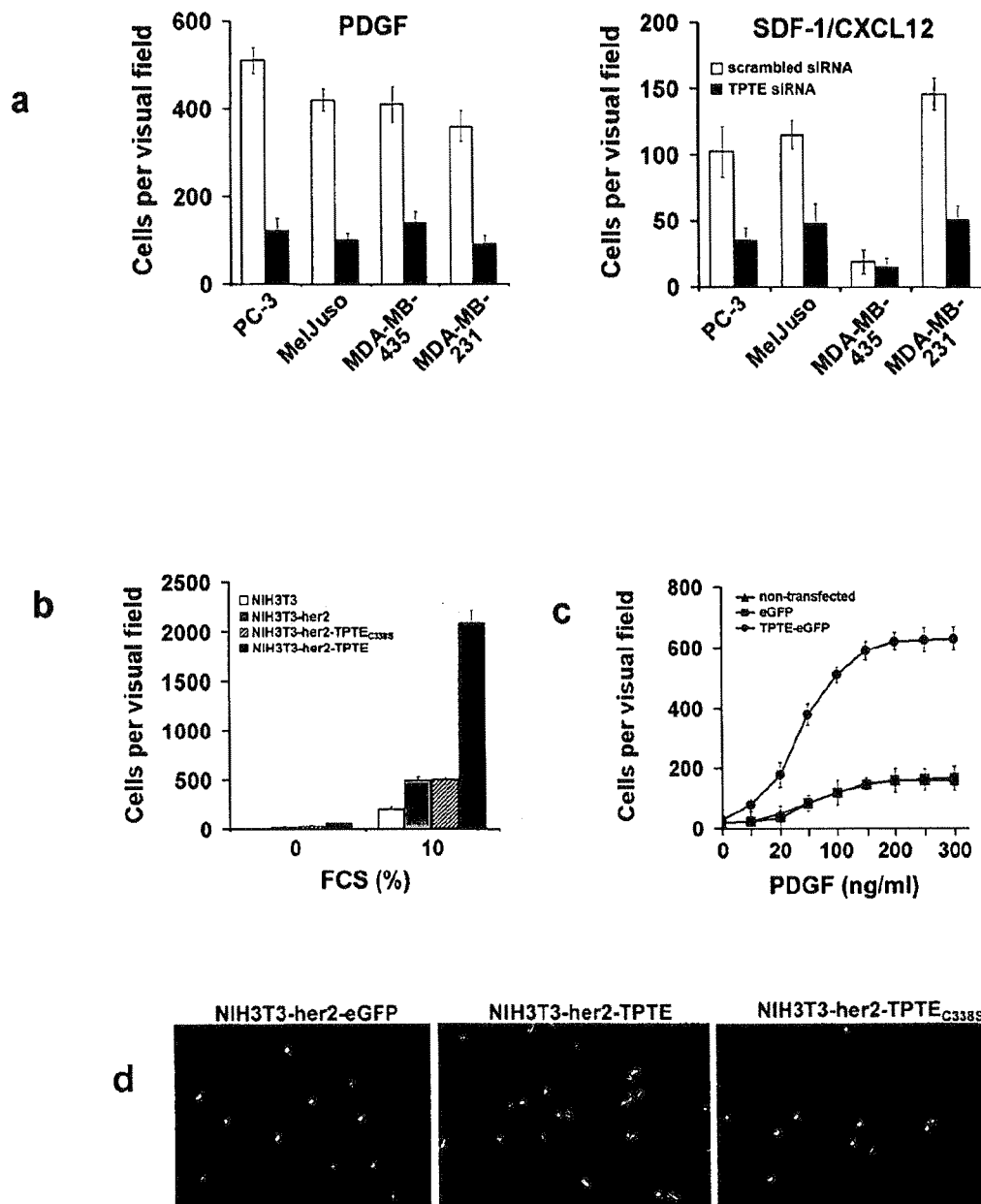
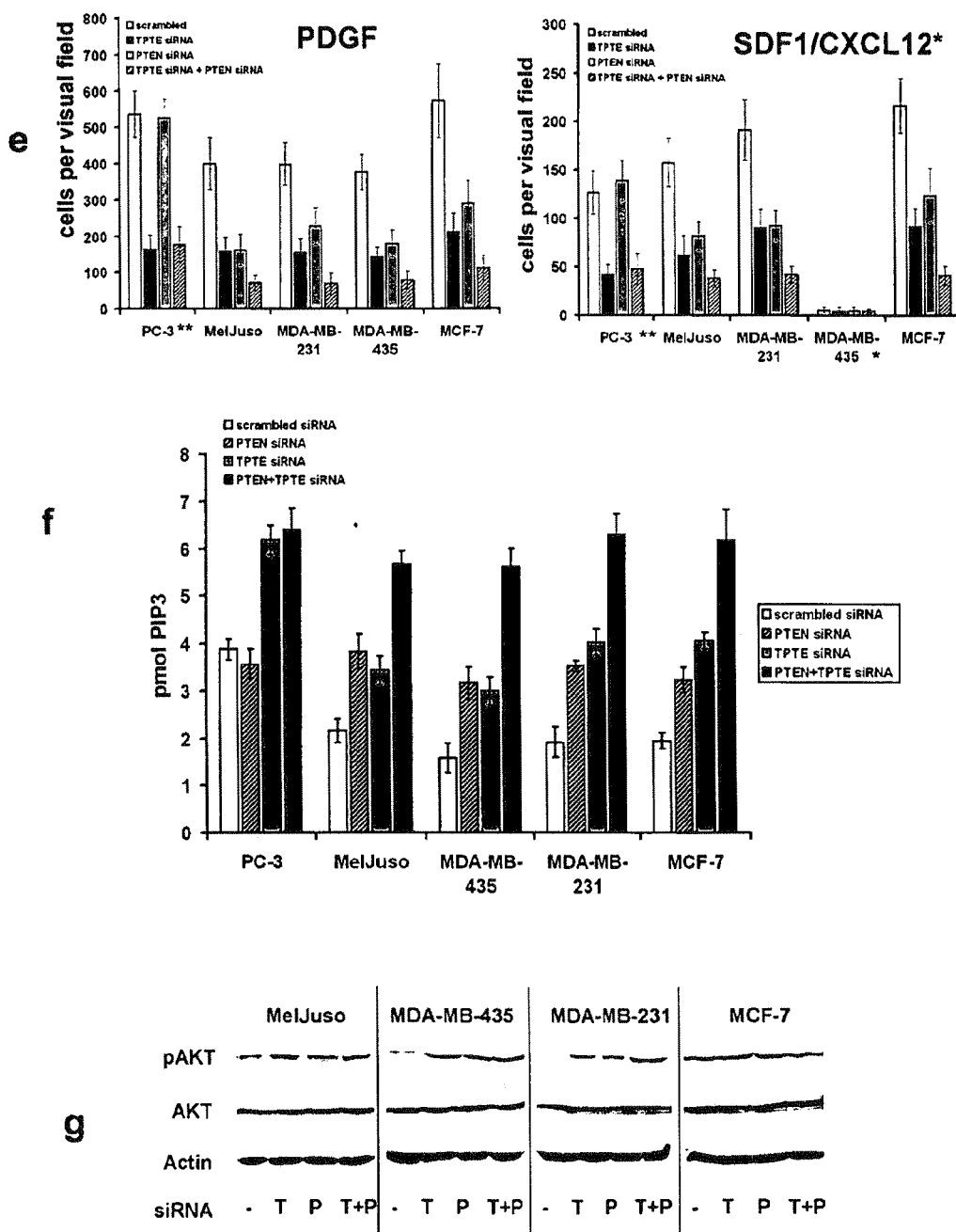


Figure 4 (cont`)



siRNA: -, scrambled control; T, TPTE; P, PTEN

Figure 5

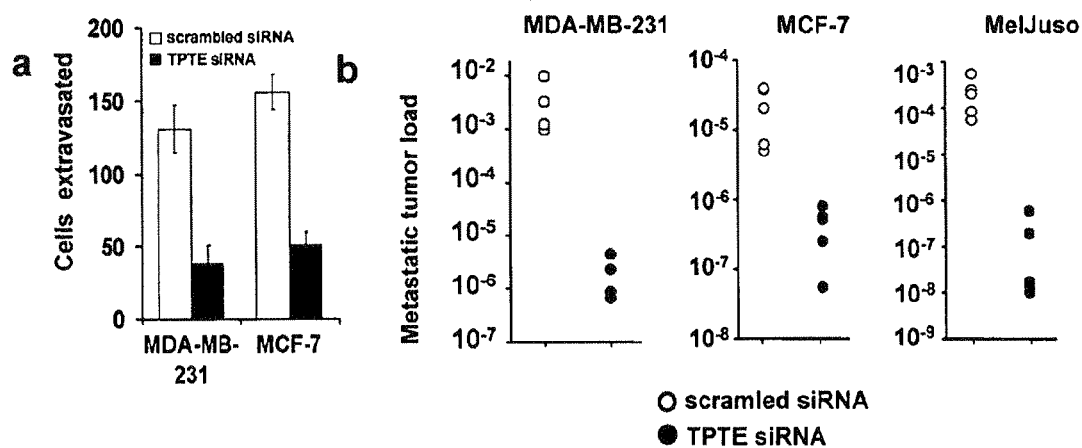
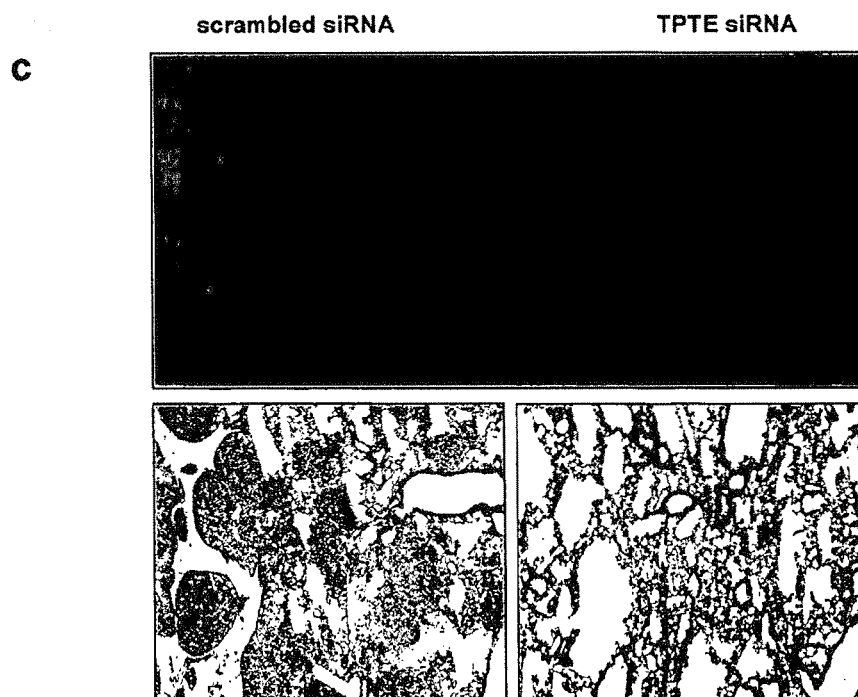
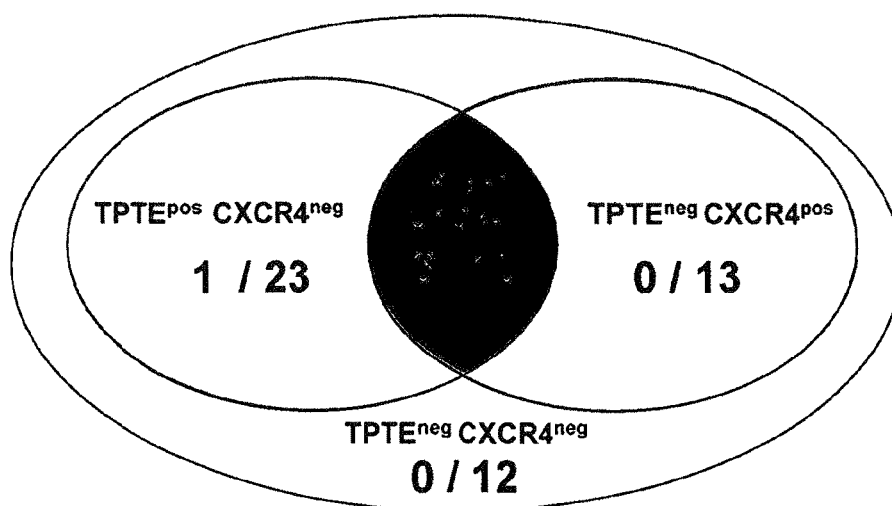


Figure 5 (cont')

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ataagaaggc gggtttcaga aaacaaaagg cgatacacia gggatggatt tgacctagac 660
ctcacttacg ttacagaacg tattattgct atgtcatttc catcttctgg aaggcagtct 720
ttctatagaa atccaatcaa ggaagttgtg cggtttctag ataagaaaca ccgaaaccac 780
tatcgagtct acaatctatg cagtgaaga gcttacgac ctaagcactt ccataatagg 840
gtcgtagaaa tcatgattga tgatcataat gtcccccactc tacatcagat ggtgggtttc 900
accaaggaag taaatgagtg gatggctcaa gatcttgaaa acatcgtagc gattcactgt 960
aaaggaggca caggttatgt acgtgatcta aaaatccaaa tagaaatgga gaaaaagggt 1020
gtcttttcca ctatttcatt aggaaaatgt tcggtacttg ataacattac aacagacaaa 1080
atattaattg atgtattcga cgggccacct ctgtatgatg atgtgaaagt gcagtttttc 1140
tattcgaatc ttctacata ctatgacaat tgctcatttt acttctgggt gcacacatct 1200
tttattgaaa ataacaggct ttatctacca aaaaatgaat tggataatct acataaacia 1260
aaagcacgga gaatttatcc atcagatttt gccgtggaga tacttttttg cgagaaaatg 1320
acttccagtg atgtttagc tggatccgat taa 1353

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<210> 8
 <211> 551
 <212> PRT
 <213> Homo sapiens

<400> 8

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
 20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Pro His Thr Ser Glu Phe Lys Gly
 35 40 45

Ala Ala Arg Val Ser Pro Ile Ser Glu Ser Val Leu Ala Arg Leu Ser
 50 55 60

Lys Phe Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys
 65 70 75 80

Ile Lys Lys Ile Val His Ser Ile Val Ser Ser Phe Ala Phe Gly Leu
 85 90 95

342-33PCT.ST25.txt

Phe Gly Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp
100 105 110

Leu Ile Phe Thr Asp Ser Lys Leu Tyr Ile Pro Leu Glu Tyr Arg Ser
115 120 125

Ile Ser Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg
130 135 140

Val Phe Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile
145 150 155 160

Leu Asp Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr
165 170 175

Ile Phe Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His
180 185 190

Leu Leu Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu
195 200 205

Phe His Gln Lys Arg Gln Leu Glu Lys Leu Ile Arg Arg Arg Val Ser
210 215 220

Glu Asn Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr
225 230 235 240

Tyr Val Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg
245 250 255

Gln Ser Phe Tyr Arg Asn Pro Ile Lys Glu Val Val Arg Phe Leu Asp
260 265 270

Lys Lys His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg
275 280 285

Ala Tyr Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile
290 295 300

Asp Asp His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys
305 310 315 320

Glu Val Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile
325 330 335

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

342-33PCT.ST25.txt

Leu Ile Ala Ser Glu Ile Cys Ser Thr Ala Lys Glu Ser Leu Tyr Tyr
355 360 365

Phe Gly Glu Arg Arg Thr Asp Lys Thr His Ser Glu Lys Phe Gln Gly
370 375 380

Val Glu Thr Pro Ser Gln Lys Arg Tyr Val Ala Tyr Phe Ala Gln Val
385 390 395 400

Lys His Leu Tyr Asn Trp Asn Leu Pro Pro Arg Arg Ile Leu Phe Ile
405 410 415

Lys His Phe Ile Ile Tyr Ser Ile Pro Arg Tyr Val Arg Asp Leu Lys
420 425 430

Ile Gln Ile Glu Met Glu Lys Lys Val Val Phe Ser Thr Ile Ser Leu
435 440 445

Gly Lys Cys Ser Val Leu Asp Asn Ile Thr Thr Asp Lys Ile Leu Ile
450 455 460

Asp Val Phe Asp Gly Pro Pro Leu Tyr Asp Asp Val Lys Val Gln Phe
465 470 475 480

Phe Tyr Ser Asn Leu Pro Thr Tyr Tyr Asp Asn Cys Ser Phe Tyr Phe
485 490 495

Trp Leu His Thr Ser Phe Ile Glu Asn Asn Arg Leu Tyr Leu Pro Lys
500 505 510

Asn Glu Leu Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro
515 520 525

Ser Asp Phe Ala Val Glu Ile Leu Phe Gly Glu Lys Met Thr Ser Ser
530 535 540

Asp Val Val Ala Gly Ser Asp
545 550

<210> 9
<211> 533
<212> PRT
<213> Homo sapiens

<400> 9

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr

Glu Glu Ala Pro Ala Lys Glu Ser Val Leu Ala Arg Leu Ser Lys Phe
 35 40 45

Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys Ile Lys
 50 55 60

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

Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp Leu Ile
 85 90 95

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

Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg Val Phe
 115 120 125

Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile Leu Asp
 130 135 140

Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr Ile Phe
 145 150 155 160

Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His Leu Leu
 165 170 175

Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu Phe His
 180 185 190

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

Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr Tyr Val
 210 215 220

Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg Gln Ser
 225 230 235 240

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

His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg Ala Tyr
 260 265 270

Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile Asp Asp

275

280

285

His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys Glu Val
 290 295 300

Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile His Cys
 305 310 315 320

Lys Gly Gly Thr Asp Arg Thr Gly Thr Met Val Cys Ala Phe Leu Ile
 325 330 335

Ala Ser Glu Ile Cys Ser Thr Ala Lys Glu Ser Leu Tyr Tyr Phe Gly
 340 345 350

Glu Arg Arg Thr Asp Lys Thr His Ser Glu Lys Phe Gln Gly Val Glu
 355 360 365

Thr Pro Ser Gln Lys Arg Tyr Val Ala Tyr Phe Ala Gln Val Lys His
 370 375 380

Leu Tyr Asn Trp Asn Leu Pro Pro Arg Arg Ile Leu Phe Ile Lys His
 385 390 395 400

Phe Ile Ile Tyr Ser Ile Pro Arg Tyr Val Arg Asp Leu Lys Ile Gln
 405 410 415

Ile Glu Met Glu Lys Lys Val Val Phe Ser Thr Ile Ser Leu Gly Lys
 420 425 430

Cys Ser Val Leu Asp Asn Ile Thr Thr Asp Lys Ile Leu Ile Asp Val
 435 440 445

Phe Asp Gly Pro Pro Leu Tyr Asp Asp Val Lys Val Gln Phe Phe Tyr
 450 455 460

Ser Asn Leu Pro Thr Tyr Tyr Asp Asn Cys Ser Phe Tyr Phe Trp Leu
 465 470 475 480

His Thr Ser Phe Ile Glu Asn Asn Arg Leu Tyr Leu Pro Lys Asn Glu
 485 490 495

Leu Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro Ser Asp
 500 505 510

Phe Ala Val Glu Ile Leu Phe Gly Glu Lys Met Thr Ser Ser Asp Val
 515 520 525

Val Ala Gly Ser Asp

530

<210> 10
 <211> 569
 <212> PRT
 <213> Homo sapiens

<400> 10

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
 20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Pro His Thr Ser Glu Phe Lys Gly
 35 40 45

Ala Ala Arg Val Ser Pro Ile Ser Glu Ser Val Leu Ala Arg Leu Ser
 50 55 60

Lys Phe Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys
 65 70 75 80

Ile Lys Lys Ile Val His Ser Ile Val Ser Ser Phe Ala Phe Gly Leu
 85 90 95

Phe Gly Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp
 100 105 110

Leu Ile Phe Thr Asp Ser Lys Leu Tyr Ile Pro Leu Glu Tyr Arg Ser
 115 120 125

Ile Ser Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg
 130 135 140

Val Phe Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile
 145 150 155 160

Leu Asp Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr
 165 170 175

Ile Phe Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His
 180 185 190

Leu Leu Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu
 195 200 205

Phe His Gln Lys Arg Gln Leu Glu Lys Leu Ile Arg Arg Arg Val Ser
 210 215 220

Glu Asn Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr
 225 230 235 240

Tyr Val Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg
 245 250 255

Gln Ser Phe Tyr Arg Asn Pro Ile Lys Glu Val Val Arg Phe Leu Asp
 260 265 270

Lys Lys His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Met Tyr
 275 280 285

Ile Thr Leu Tyr Cys Ala Thr Val Asp Arg Lys Gln Ile Thr Ala Arg
 290 295 300

Glu Arg Ala Tyr Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile
 305 310 315 320

Met Ile Asp Asp His Asn Val Pro Thr Leu His Gln Met Val Val Phe
 325 330 335

Thr Lys Glu Val Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val
 340 345 350

Ala Ile His Cys Lys Gly Gly Thr Asp Arg Thr Gly Thr Met Val Cys
 355 360 365

Ala Phe Leu Ile Ala Ser Glu Ile Cys Ser Thr Ala Lys Glu Ser Leu
 370 375 380

Tyr Tyr Phe Gly Glu Arg Arg Thr Asp Lys Thr His Ser Glu Lys Phe
 385 390 395 400

Gln Gly Val Glu Thr Pro Ser Gln Lys Arg Tyr Val Ala Tyr Phe Ala
 405 410 415

Gln Val Lys His Leu Tyr Asn Trp Asn Leu Pro Pro Arg Arg Ile Leu
 420 425 430

Phe Ile Lys His Phe Ile Ile Tyr Ser Ile Pro Arg Tyr Val Arg Asp
 435 440 445

Leu Lys Ile Gln Ile Glu Met Glu Lys Lys Val Val Phe Ser Thr Ile
 450 455 460

Ser Leu Gly Lys Cys Ser Val Leu Asp Asn Ile Thr Thr Asp Lys Ile
 465 470 475 480

Leu Ile Asp Val Phe Asp Gly Pro Pro Leu Tyr Asp Asp Val Lys Val
485 490 495

Gln Phe Phe Tyr Ser Asn Leu Pro Thr Tyr Tyr Asp Asn Cys Ser Phe
500 505 510

Tyr Phe Trp Leu His Thr Ser Phe Ile Glu Asn Asn Arg Leu Tyr Leu
515 520 525

Pro Lys Asn Glu Leu Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile
530 535 540

Tyr Pro Ser Asp Phe Ala Val Glu Ile Leu Phe Gly Glu Lys Met Thr
545 550 555 560

Ser Ser Asp Val Val Ala Gly Ser Asp
565

<210> 11
<211> 395
<212> PRT
<213> Homo sapiens

<400> 11

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Pro His Thr Ser Glu Phe Lys Gly
35 40 45

Ala Ala Arg Val Ser Pro Ile Ser Glu Ser Val Leu Ala Arg Leu Ser
50 55 60

Lys Phe Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys
65 70 75 80

Ile Lys Lys Ile Val His Ser Ile Val Ser Ser Phe Ala Phe Gly Leu
85 90 95

Phe Gly Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp
100 105 110

Leu Ile Phe Thr Asp Ser Lys Leu Tyr Ile Pro Leu Glu Tyr Arg Ser
115 120 125

342-33PCT.ST25.txt

Ile Ser Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg
130 135 140

Val Phe Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile
145 150 155 160

Leu Asp Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr
165 170 175

Ile Phe Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His
180 185 190

Leu Leu Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu
195 200 205

Phe His Gln Lys Arg Gln Leu Glu Lys Leu Ile Arg Arg Arg Val Ser
210 215 220

Glu Asn Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr
225 230 235 240

Tyr Val Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg
245 250 255

Gln Ser Phe Tyr Arg Asn Pro Ile Lys Glu Val Val Arg Phe Leu Asp
260 265 270

Lys Lys His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg
275 280 285

Ala Tyr Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile
290 295 300

Asp Asp His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys
305 310 315 320

Glu Val Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile
325 330 335

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

Leu Ile Ala Ser Glu Ile Cys Ser Thr Ala Lys Glu Ser Leu Tyr Tyr
355 360 365

Phe Gly Glu Arg Arg Thr Asp Lys Thr His Ser Glu Lys Phe Gln Gly
370 375 380

342-33PCT.ST25.txt

Val Glu Thr Pro Ser Gln Val Met Tyr Val Ile
385 390 395

<210> 12
<211> 468
<212> PRT
<213> Homo sapiens

<400> 12

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Pro His Thr Ser Glu Phe Lys Gly
35 40 45

Ala Ala Arg Val Ser Pro Ile Ser Glu Ser Val Leu Ala Arg Leu Ser
50 55 60

Lys Phe Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys
65 70 75 80

Ile Lys Lys Ile Val His Ser Ile Val Ser Ser Phe Ala Phe Gly Leu
85 90 95

Phe Gly Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp
100 105 110

Leu Ile Phe Thr Asp Ser Lys Leu Tyr Ile Pro Leu Glu Tyr Arg Ser
115 120 125

Ile Ser Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg
130 135 140

Val Phe Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile
145 150 155 160

Leu Asp Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr
165 170 175

Ile Phe Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His
180 185 190

Leu Leu Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu
195 200 205

342-33PCT.ST25.txt

Phe His Gln Lys Arg Gln Leu Glu Lys Leu Ile Arg Arg Arg Val Ser
 210 215 220

Glu Asn Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr
 225 230 235 240

Tyr Val Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg
 245 250 255

Gln Ser Phe Tyr Arg Asn Pro Ile Lys Glu Val Val Arg Phe Leu Asp
 260 265 270

Lys Lys His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg
 275 280 285

Ala Tyr Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile
 290 295 300

Asp Asp His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys
 305 310 315 320

Glu Val Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile
 325 330 335

His Cys Lys Gly Gly Thr Gly Tyr Val Arg Asp Leu Lys Ile Gln Ile
 340 345 350

Glu Met Glu Lys Lys Val Val Phe Ser Thr Ile Ser Leu Gly Lys Cys
 355 360 365

Ser Val Leu Asp Asn Ile Thr Thr Asp Lys Ile Leu Ile Asp Val Phe
 370 375 380

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

Asn Leu Pro Thr Tyr Tyr Asp Asn Cys Ser Phe Tyr Phe Trp Leu His
 405 410 415

Thr Ser Phe Ile Glu Asn Asn Arg Leu Tyr Leu Pro Lys Asn Glu Leu
 420 425 430

Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro Ser Asp Phe
 435 440 445

Ala Val Glu Ile Leu Phe Gly Glu Lys Met Thr Ser Ser Asp Val Val
 450 455 460

Ala Gly Ser Asp
465

<210> 13
<211> 470
<212> PRT
<213> Homo sapiens

<400> 13

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Val Leu Ala Arg Leu Ser Lys Phe
35 40 45

Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys Ile Lys
50 55 60

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

Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp Leu Ile
85 90 95

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

Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg Val Phe
115 120 125

Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile Leu Asp
130 135 140

Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr Ile Phe
145 150 155 160

Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His Leu Leu
165 170 175

Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu Phe His
180 185 190

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

Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr Tyr Val

210 215 220
 Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg Gln Ser
 225 230 235 240
 Phe Tyr Arg Asn Pro Ile Lys Glu Val Val Arg Phe Leu Asp Lys Lys
 245 250 255
 His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg Ala Tyr
 260 265 270
 Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile Asp Asp
 275 280 285
 His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys Glu Val
 290 295 300
 Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile His Cys
 305 310 315 320
 Lys Gly Gly Thr Asp Arg Thr Gly Thr Met Val Cys Ala Phe Leu Ile
 325 330 335
 Ala Ser Glu Ile Cys Ser Thr Ala Lys Glu Ser Leu Tyr Tyr Phe Gly
 340 345 350
 Glu Arg Arg Thr Asp Lys Thr His Ser Glu Lys Phe Gln Gly Val Glu
 355 360 365
 Thr Pro Ser Val Leu Asp Asn Ile Thr Thr Asp Lys Ile Leu Ile Asp
 370 375 380
 Val Phe Asp Gly Pro Pro Leu Tyr Asp Asp Val Lys Val Gln Phe Phe
 385 390 395 400
 Tyr Ser Asn Leu Pro Thr Tyr Tyr Asp Asn Cys Ser Phe Tyr Phe Trp
 405 410 415
 Leu His Thr Ser Phe Ile Glu Asn Asn Arg Leu Tyr Leu Pro Lys Asn
 420 425 430
 Glu Leu Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro Ser
 435 440 445
 Asp Phe Ala Val Glu Ile Leu Phe Gly Glu Lys Met Thr Ser Ser Asp
 450 455 460
 Val Val Ala Gly Ser Asp

465

470

<210> 14
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 14

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

Leu Gly Pro Asn Asp Ser Pro Gln Thr Ser Glu Phe Lys Gly Ala Thr
 20 25 30

Glu Glu Ala Pro Ala Lys Glu Ser Val Leu Ala Arg Leu Ser Lys Phe
 35 40 45

Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys Ile Lys
 50 55 60

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

Val Phe Leu Val Leu Leu Asp Val Thr Leu Ile Leu Ala Asp Leu Ile
 85 90 95

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

Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg Val Phe
 115 120 125

Val Glu Arg Arg Gln Gln Tyr Phe Ser Asp Leu Phe Asn Ile Leu Asp
 130 135 140

Thr Ala Ile Ile Val Ile Leu Leu Leu Val Asp Val Val Tyr Ile Phe
 145 150 155 160

Phe Asp Ile Lys Leu Leu Arg Asn Ile Pro Arg Trp Thr His Leu Leu
 165 170 175

Arg Leu Leu Arg Leu Ile Ile Leu Leu Arg Ile Phe His Leu Phe His
 180 185 190

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

Lys Arg Arg Tyr Thr Arg Asp Gly Phe Asp Leu Asp Leu Thr Tyr Val
 210 215 220

Thr Glu Arg Ile Ile Ala Met Ser Phe Pro Ser Ser Gly Arg Gln Ser
225 230 235 240

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

His Arg Asn His Tyr Arg Val Tyr Asn Leu Cys Ser Glu Arg Ala Tyr
260 265 270

Asp Pro Lys His Phe His Asn Arg Val Val Arg Ile Met Ile Asp Asp
275 280 285

His Asn Val Pro Thr Leu His Gln Met Val Val Phe Thr Lys Glu Val
290 295 300

Asn Glu Trp Met Ala Gln Asp Leu Glu Asn Ile Val Ala Ile His Cys
305 310 315 320

Lys Gly Gly Thr Gly Tyr Val Arg Asp Leu Lys Ile Gln Ile Glu Met
325 330 335

Glu Lys Lys Val Val Phe Ser Thr Ile Ser Leu Gly Lys Cys Ser Val
340 345 350

Leu Asp Asn Ile Thr Thr Asp Lys Ile Leu Ile Asp Val Phe Asp Gly
355 360 365

Pro Pro Leu Tyr Asp Asp Val Lys Val Gln Phe Phe Tyr Ser Asn Leu
370 375 380

Pro Thr Tyr Tyr Asp Asn Cys Ser Phe Tyr Phe Trp Leu His Thr Ser
385 390 395 400

Phe Ile Glu Asn Asn Arg Leu Tyr Leu Pro Lys Asn Glu Leu Asp Asn
405 410 415

Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro Ser Asp Phe Ala Val
420 425 430

Glu Ile Leu Phe Gly Glu Lys Met Thr Ser Ser Asp Val Val Ala Gly
435 440 445

Ser Asp
450

<210> 15
<211> 21

<212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence

<400> 15
 tcggtacttg ataacattac a

21

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA sense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 16
 gguacuugau aacauuacat t

21

<210> 17
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA antisense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 17
 uguaaugua ucaaguaccg a

21

<210> 18
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence

<400> 18
 cagacttgtag ttattctagc a

21

<210> 19
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>

<223> siRNA sense strand

<220>

<221> misc_feature

<222> (1)..(19)

<223> ribonucleotide bases

<400> 19

gacuuguguu auucuagcat t

21

<210> 20

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA antisense strand

<220>

<221> misc_feature

<222> (1)..(19)

<223> ribonucleotide bases

<400> 20

ugcuagaaua acacaaguct g

21

<210> 21

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Target sequence

<400> 21

ctgaaatatg ttcaactgca a

21

<210> 22

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA sense strand

<220>

<221> misc_feature

<222> (1)..(19)

<223> ribonucleotide bases

<400> 22

gaaauauguu caacugcaat t

21

<210> 23

<211> 21

<212> DNA

<213> Artificial sequence

<220>
 <223> siRNA antisense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 23
 uugcaguuga acauauuuga g

21

<210> 24
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence

<400> 24
 cagattggca accaagacta a

21

<210> 25
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA sense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 25
 gauuggcaac caagacuaat t

21

<210> 26
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA antisense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 26
 uuagucuugg uugccaauct g

21

<210> 27
 <211> 21

<212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence

<400> 27
 aaccctgccca catgttcata t

21

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA sense strand

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 28
 cccugccaca uguucauaut t

21

<210> 29
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA antisense strand

<220>
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 <222> (1)..(19)
 <223> ribonucleotide bases

<400> 29
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21

<210> 30
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<220>
 <223> Target sequence

<400> 30
 aatgacagtc cacagacaag t

21

<210> 31
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<220>

<223> siRNA sense strand

<220>

<221> misc_feature

<222> (1)..(19)

<223>

<400> 31

ugacagucca cagacaagut t

21

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<222> (1)..(19)

<223> ribonucleotide bases

<400> 32

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21

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<400> 33

aagctgataa gaaggcgggt t

21

<210> 34

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<212> DNA

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<222> (1)..(19)

<223> ribonucleotide bases

<400> 34

gcugauaaga aggcggguut t

21

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<400> 36
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<210> 37
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<400> 37
ccatagttcc tgttctatct g

21

<210> 38
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<220>
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<400> 38
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21

<210> 39
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<400> 39
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<210> 40
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<223> Oligonucleotide

<400> 40

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21

<210> 41

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<223> Oligonucleotide

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46

<210> 42

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<212> DNA

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<220>

<223> Oligonucleotide

<400> 42

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<223> siRNA sense strand

<220>

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<222> (1)..(19)

<223> ribonucleotide bases

<400> 43

uaacuguaua aucgacuagt t

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<210> 44

<211> 21

<212> DNA

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<223> siRNA antisense strand

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<221> misc_feature

<222> (1)..(19)

<223> ribonucleotide bases

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<210> 45
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 45
cagctgacta aacagaagca g 21

<210> 46
<211> 22
<212> DNA
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<220>
<223> Oligonucleotide

<400> 46
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<210> 47
<211> 1912
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<213> Homo sapiens

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gaaggatata atgaagtcac tatgggaaaa gatggggagg agagttgtag gattctacat 180
taattctctt gtgcccttag cccactactt cagaatttcc tgaagaaagc aagcctgaat 240
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gggtggttggtg ttccagtttc agcacatcat gggtggcctt atcctgcttg gtattgtcat 960
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atgctggttt ttcagttttc aggagtgggt tgatttcagc acctacagtg tacagtcttg 1860
tattaagttg ttaataaaaag tacatgttaa acttaaaaaa aaaaaaaaaa aa 1912

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<210> 48
<211> 1691
<212> DNA
<213> Homo sapiens

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<400> 48
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cagataacta caccgaggaa atgggctcag gggactatga ctccatgaag gaacctgtt 180
tccgtgaaga aaatgctaatt ttcaataaaa ttttctgcc caccatctac tccatcatct 240
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tgagaagcat gacggacaag tacaggctgc acctgtcagt ggcgacctc ctctttgtca 360
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agctgttggc tgaaaagggtg gtctatgttg gcgtctggat cctgcccctc ctgctgacta 600
ttcccgaact catctttgcc aacgtcagtg aggcagatga cagatatatc tgtgaccgct 660

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342-33PCT.ST25.txt

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totaccccaa tgacttgtgg gtgggtgtgt tccagtttca gcacatcatg gttggcctta 720
tctgcctggg tattgtcatc ctgtcctgct attgcattat catctccaag ctgtcacact 780
ccaagggcca ccagaagcgc aaggccctca agaccacagt catcctcatc ctggctttct 840
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<210> 49
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 <213> Homo sapiens

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Thr Glu Glu Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys
          20           25           30

```

```

Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile
          35           40           45

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Tyr Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
          50           55           60

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Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr
          65           70           75           80

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342-33PCT.ST25.txt

Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro
85 90 95

Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu
100 105 110

Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val
115 120 125

Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His
130 135 140

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

Tyr Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe
165 170 175

Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg
180 185 190

Phe Tyr Pro Asn Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile
195 200 205

Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys
210 215 220

Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys
225 230 235 240

Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp
245 250 255

Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu
260 265 270

Ile Ile Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile
275 280 285

Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
290 295 300

Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala
305 310 315 320

Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly
325 330 335

Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser
 340 345 350

Phe His Ser Ser
 355

<210> 50
 <211> 352
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 <213> Homo sapiens

<400> 50

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Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
 20 25 30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile Ile
 35 40 45

Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
 50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
 65 70 75 80

Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
 85 90 95

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
 100 105 110

His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
 115 120 125

Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
 130 135 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
 145 150 155 160

Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
 165 170 175

Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
 180 185 190

Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu

195

200

205

Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
210 215 220

Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225 230 235 240

Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
245 250 255

Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
260 265 270

Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
275 280 285

Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
290 295 300

Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser Val
305 310 315 320

Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
325 330 335

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
340 345 350

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<220>
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<220>
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<222> (1)..(19)
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ggcgauuaca ggaacaaat t

21

<210> 52
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> siRNA antisense strand

342-33PCT.ST25.txt

<220>
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<222> (1)..(19)
<223> ribonucleotide bases

<400> 52
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21