

SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> CHIMERIC MOLECULE FOR TARGETING C-MYC IN CELLS

<130> 9869SG5225

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> H1-control (H1-neg; original unmutated H1 sequence)

<400> 1

Asn Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile
1 5 10

<210> 2

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Cadherin (CAD)

<400> 2

Leu Leu Ile Ile Leu Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala
1 5 10 15

His Ser Lys

<210> 3

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Antenapedia (Int)

<400> 3

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 4

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> TAT

<400> 4

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
1 5 10

<210> 5

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Mutated H1 (S6A, F8A; also referred to as tPE-H1)

<400> 5

Asn Glu Leu Lys Arg Ala Phe Ala Ala Leu Arg Asp Gln Ile
1 5 10

<210> 6

<211> 90

<212> PRT

<213> Artificial sequence

<220>

<223> Omomyc

<400> 6

Thr Glu Glu Asn Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln
1 5 10 15

Arg Arg Asn Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile
20 25 30

Pro Glu Leu Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys
35 40 45

Lys Ala Thr Ala Tyr Ile Leu Ser Val Gln Ala Glu Thr Gln Lys Leu
50 55 60

Ile Ser Glu Ile Asp Leu Leu Arg Lys Gln Asn Glu Gln Leu Lys His
65 70 75 80

Lys Leu Glu Gln Leu Arg Asn Ser Cys Ala
85 90

<210> 7
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Int-H1

<400> 7

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

Asn Glu Leu Lys Arg Ala Phe Ala Ala Leu Arg Asp Gln Ile
20 25 30

<210> 8
<211> 33
<212> PRT
<213> Artificial sequence

<220>
<223> CAD-H1

<400> 8

Leu Leu Ile Ile Leu Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala
1 5 10 15

His Ser Lys Asn Glu Leu Lys Arg Ala Phe Ala Ala Leu Arg Asp Gln
20 25 30

Ile

<210> 9
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> Tat-H1

<400> 9

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Asn Glu Leu
1 5 10 15

Lys Arg Ala Phe Ala Ala Leu Arg Asp Gln Ile
20 25

<210> 10
<211> 364
<212> PRT
<213> Artificial sequence

<220>
<223> tPE (comprising both PE domains Ia and II)

<400> 10

Met Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
165 170 175

Ala Gln Ala Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
195 200 205

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

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys

Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro Ala
20 25 30

Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val Leu
35 40 45

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

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

Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser Trp
85 90 95

Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn Ile
100 105 110

Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His Met
115 120 125

Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys Leu
130 135 140

Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu Met
145 150 155 160

Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met Ala
165 170 175

Gln Ala Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser Gly
180 185 190

Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr Leu
195 200 205

Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile Tyr

210

215

220

Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys Pro
 225 230 235 240

Thr Val Ile Ser His Arg Leu His Phe Pro Glu
 245 250

<210> 12
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>
 <223> tPE comprising only the PE Domain II

<400> 12

Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro
 1 5 10 15

Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu
 20 25 30

Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
 35 40 45

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
 50 55 60

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
 65 70 75 80

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
 85 90 95

Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Ser
 100 105 110

<210> 13
<211> 378
<212> PRT
<213> Artificial sequence

<220>
<223> tPE-H1-control (tPE-H1-neg; H1 portion is highlighted)

<220>
<221> MISC_FEATURE
<222> (365)..(378)
<223> H1 portion

<400> 13

Met Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys

130

135

140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
 145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
 165 170 175

Ala Gln Ala Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
 180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
 195 200 205

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

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
 225 230 235 240

Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
 245 250 255

Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
 260 265 270

Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
 275 280 285

Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
 290 295 300

Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
 305 310 315 320

Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
 325 330 335

Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
340 345 350

Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Ser Asn Glu Leu Lys
355 360 365

Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile
370 375

<210> 14
<211> 378
<212> PRT
<213> Artificial sequence

<220>
<223> tPE-H1 (mutated H1 sequence highlighted)

<220>
<221> MISC_FEATURE
<222> (365)..(378)
<223> mutated H1 sequence

<400> 14

Met Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
165 170 175

Ala Gln Ala Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
195 200 205

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

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
225 230 235 240

Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
245 250 255

Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
260 265 270

Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
275 280 285

Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
290 295 300

Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
305 310 315 320

Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
325 330 335

Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
340 345 350

Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Ser Asn Glu Leu Lys
355 360 365

Arg Ala Phe Ala Ala Leu Arg Asp Gln Ile
370 375

<210> 15
<211> 454
<212> PRT
<213> Artificial sequence

<220>
<223> tPE- Omomyc (Omomyc sequence highlighted)

<220>
<221> MISC_FEATURE
<222> (365)..(454)
<223> Omomyc sequence

<400> 15

Met Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro

20	25	30
Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val		
35	40	45
Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu		
50	55	60
Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu		
65	70	75
Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser		
85	90	95
Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn		
100	105	110
Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His		
115	120	125
Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys		
130	135	140
Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu		
145	150	155
Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met		
165	170	175
Ala Gln Ala Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser		
180	185	190
Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr		
195	200	205
Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile		
210	215	220

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
 225 230 235 240

Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
 245 250 255

Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
 260 265 270

Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
 275 280 285

Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
 290 295 300

Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
 305 310 315 320

Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
 325 330 335

Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
 340 345 350

Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Ser Thr Glu Glu Asn
 355 360 365

Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn Glu
 370 375 380

Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu Glu
 385 390 395 400

Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr Ala
 405 410 415

Tyr Ile Leu Ser Val Gln Ala Glu Thr Gln Lys Leu Ile Ser Glu Ile
420 425 430

Asp Leu Leu Arg Lys Gln Asn Glu Gln Leu Lys His Lys Leu Glu Gln
435 440 445

Leu Arg Asn Ser Cys Ala
450

<210> 16
<211> 19
<212> RNA
<213> Artificial sequence

<220>
<223> Sec61B siRNA sequence

<400> 16
gcaaguacac ucguucgua 19

<210> 17
<211> 19
<212> RNA
<213> Artificial sequence

<220>
<223> SUN2 siRNA sequence

<400> 17
ccuaugggcu gcagacauu 19