

SEQUENCE LISTING

<110> Novo Nordisk A/S

<120> SAFE IMMUNO-STEALTHED CELLS

<130> 190045WO01

<160> 9

<170> PatentIn version 3.5

<210> 1

<211> 337

<212> PRT

<213> homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(337)

<400> 1

Gly Ser His Ser Leu Lys Tyr Phe His Thr Ser Val Ser Arg Pro Gly

1

5

10

15

Arg Gly Glu Pro Arg Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Gln

20

25

30

Phe Val Arg Phe Asp Asn Asp Ala Ala Ser Pro Arg Met Val Pro Arg

35

40

45

Ala Pro Trp Met Glu Gln Glu Gly Ser Glu Tyr Trp Asp Arg Glu Thr

50

55

60

Arg Ser Ala Arg Asp Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr

65

70

75

80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln

85

90

95

Trp Met His Gly Cys Glu Leu Gly Pro Asp Arg Arg Phe Leu Arg Gly

100

105

110

Tyr Glu Gln Phe Ala Tyr Asp Gly Lys Asp Tyr Leu Thr Leu Asn Glu

115 120 125

Asp Leu Arg Ser Trp Thr Ala Val Asp Thr Ala Ala Gln Ile Ser Glu

130 135 140

Gln Lys Ser Asn Asp Ala Ser Glu Ala Glu His Gln Arg Ala Tyr Leu

145 150 155 160

Glu Asp Thr Cys Val Glu Trp Leu His Lys Tyr Leu Glu Lys Gly Lys

165 170 175

Glu Thr Leu Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His

180 185 190

Pro Ile Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe

195 200 205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His

210 215 220

Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr

225 230 235 240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg

245 250 255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu

260 265 270

Arg Trp Lys Pro Ala Ser Gln Pro Thr Ile Pro Ile Val Gly Ile Ile

275 280 285

Ala Gly Leu Val Leu Leu Gly Ser Val Val Ser Gly Ala Val Val Ala

290 295 300

Ala Val Ile Trp Arg Lys Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr

305 310 315 320

Ser Lys Ala Glu Trp Ser Asp Ser Ala Gln Gly Ser Glu Ser His Ser

325

330

335

Leu

<210> 2

<211> 99

<212> PRT

<213> homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(99)

<400> 2

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu

1

5

10

15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro

20

25

30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys

35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu

50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys

65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp

85 90 95

Arg Asp Met

<210> 3

<211> 337

<212> PRT

<213> homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(337)

<400> 3

Gly Ser His Ser Leu Lys Tyr Phe His Thr Ser Val Ser Arg Pro Gly

1 5 10 15

Arg Gly Glu Pro Arg Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Gln

20 25 30

Phe Val Arg Phe Asp Asn Asp Ala Ala Ser Pro Arg Met Val Pro Arg

35 40 45

Ala Pro Trp Met Glu Gln Glu Gly Ser Glu Tyr Trp Asp Arg Glu Thr

50 55 60

Arg Ser Ala Arg Asp Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr

65 70 75 80

Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln

85

90

95

Trp Met His Gly Cys Glu Leu Gly Pro Asp Gly Arg Phe Leu Arg Gly

100

105

110

Tyr Glu Gln Phe Ala Tyr Asp Gly Lys Asp Tyr Leu Thr Leu Asn Glu

115

120

125

Asp Leu Arg Ser Trp Thr Ala Val Asp Thr Ala Ala Gln Ile Ser Glu

130

135

140

Gln Lys Ser Asn Asp Ala Ser Glu Ala Glu His Gln Arg Ala Tyr Leu

145

150

155

160

Glu Asp Thr Cys Val Glu Trp Leu His Lys Tyr Leu Glu Lys Gly Lys

165

170

175

Glu Thr Leu Leu His Leu Glu Pro Pro Lys Thr His Val Thr His His

180

185

190

Pro Ile Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe

195

200

205

Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His

210

215

220

Thr Gln Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr

225

230

235

240

Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg

245

250

255

Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu

260

265

270

Arg Trp Lys Pro Ala Ser Gln Pro Thr Ile Pro Ile Val Gly Ile Ile

275

280

285

Ala Gly Leu Val Leu Leu Gly Ser Val Val Ser Gly Ala Val Val Ala

290

295

300

Ala Val Ile Trp Arg Lys Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr

305

310

315

320

Ser Lys Ala Glu Trp Ser Asp Ser Ala Gln Gly Ser Glu Ser His Ser

325

330

335

Leu

<210> 4

<211> 476

<212> PRT

<213> homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(476)

<400> 4

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Ser Leu Ser

1 5 10 15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg

20 25 30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser

35 40 45

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu

50 55 60

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp

65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp

85 90 95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile

100

105

110

Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser His Ser Leu

130

135

140

Lys Tyr Phe His Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg

145

150

155

160

Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp

165

170

175

Asn Asp Ala Ala Ser Pro Arg Met Val Pro Arg Ala Pro Trp Met Glu

180

185

190

Gln Glu Gly Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala Arg Asp

195 200 205

Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly Tyr Tyr

210 215 220

Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Trp Met His Gly Cys

225 230 235 240

Glu Leu Gly Pro Asp Arg Arg Phe Leu Arg Gly Tyr Glu Gln Phe Ala

245 250 255

Tyr Asp Gly Lys Asp Tyr Leu Thr Leu Asn Glu Asp Leu Arg Ser Trp

260 265 270

Thr Ala Val Asp Thr Ala Ala Gln Ile Ser Glu Gln Lys Ser Asn Asp

275 280 285

Ala Ser Glu Ala Glu His Gln Arg Ala Tyr Leu Glu Asp Thr Cys Val

290 295 300

Glu Trp Leu His Lys Tyr Leu Glu Lys Gly Lys Glu Thr Leu Leu His

305 310 315 320

Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser Asp His

325 330 335

Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile

340 345 350

Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu

355 360 365

Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala

370 375 380

Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val

385 390 395 400

Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala

405

410

415

Ser Gln Pro Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu

420

425

430

Leu Gly Ser Val Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg

435

440

445

Lys Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp

450

455

460

Ser Asp Ser Ala Gln Gly Ser Glu Ser His Ser Leu

465

470

475

<210> 5

<211> 476

<212> PRT

<213> homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(476)

<400> 5

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Ser Leu Ser

1 5 10 15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg

20 25 30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser

35 40 45

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu

50 55 60

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp

65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp

85

90

95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile

100

105

110

Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Ser His Ser Leu

130

135

140

Lys Tyr Phe His Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg

145

150

155

160

Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp

165

170

175

Asn Asp Ala Ala Ser Pro Arg Met Val Pro Arg Ala Pro Trp Met Glu

180

185

190

Gln Glu Gly Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala Arg Asp

195 200 205

Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly Tyr Tyr

210 215 220

Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Trp Met His Gly Cys

225 230 235 240

Glu Leu Gly Pro Asp Gly Arg Phe Leu Arg Gly Tyr Glu Gln Phe Ala

245 250 255

Tyr Asp Gly Lys Asp Tyr Leu Thr Leu Asn Glu Asp Leu Arg Ser Trp

260 265 270

Thr Ala Val Asp Thr Ala Ala Gln Ile Ser Glu Gln Lys Ser Asn Asp

275 280 285

Ala Ser Glu Ala Glu His Gln Arg Ala Tyr Leu Glu Asp Thr Cys Val

290

295

300

Glu Trp Leu His Lys Tyr Leu Glu Lys Gly Lys Glu Thr Leu Leu His

305

310

315

320

Leu Glu Pro Pro Lys Thr His Val Thr His His Pro Ile Ser Asp His

325

330

335

Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile

340

345

350

Thr Leu Thr Trp Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu

355

360

365

Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala

370

375

380

Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val

385

390

395

400

Gln His Glu Gly Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala

405

410

415

Ser Gln Pro Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu

420

425

430

Leu Gly Ser Val Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg

435

440

445

Lys Lys Ser Ser Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp

450

455

460

Ser Asp Ser Ala Gln Gly Ser Glu Ser His Ser Leu

465

470

475

<210> 6

<211> 1428

<212> DNA

<213> homo sapiens

<220>

<221> gene

<222> (1)..(1428)

<400> 6

atgtctcgct ccgtggcctt agctgtgctc gcgctactct ctctttctgg cctggaggct 60

atccagcgta ctcaaagat tcaggtttac tcacgtcatc cagcagagaa tggaaagtca 120

aatttcctga attgctatgt gtctgggttt catccatccg acattgaagt tgacttactg 180

aagaatggag agagaattga aaaagtggag cattcagact tgtctttcag caaggactgg 240

tctttctatc tctgtacta cactgaattc acccccactg aaaaagatga gtatgcctgc 300

cggtgaacc atgtgacttt gtcacagccc aagatagtta agtgggatcg agacatgggt 360

ggtagcggtt ctggtggtgg cggtagtggc ggcggaggaa gcggtggtgg cggttccggt 420

tccactcct tgaagtatct ccacacttcc gtgtcccggc ccggccgcgg ggagccccgc 480

ttcatctctg tgggctacgt ggacgacacc cagttcgtgc gcttcgacaa cgacgccgcg 540

agtcagagga tggtagccgc ggcgccgtgg atggagcagg aggggtcaga gtattgggac 600

cgggagacac ggagcgccag ggacaccgca cagattttcc gagtgaacct gcggacgctg 660

cgcggtact acaatcagag cgaggccggt tctcacacc tgcatggat gcatggctgc 720

gagctggggc ccgacaggcg cttcctccgc gggtatgaac agttcgcta cgacggcaag 780

gattatctca ccctgaatga ggacctgcg tcctggaccg cggtggacac ggcggctcag 840

atctccgagc aaaagtcaaa tgatgcctt gaggcggagc accagagagc ctacctgga 900

gacacatgcg tggagtggct ccacaaatac ctggagaagg ggaaggagac gctgcttcac 960

ctggagcccc caaagacaca cgtgactcac caccatct ctgacctga ggccaccctg 1020

aggtgctggg ccctgggctt ctaccctcg gagatcacac tgacctggca gcaggatggg 1080

gagggccata ccagagacac ggagctcgtg gagaccaggc ctgcaggga tggaaccttc 1140

cagaagtggg cagctgtggt ggtgccttct ggagaggagc agagatacac gtgcatgtg 1200

cagcatgagg ggctaccga gccgctacc ctgagatgga agccggcttc ccagcccacc 1260

atccccatcg tgggcatcat tgctggcctg gttctccttg gatctgtgt ccttgagct 1320

gtggttgctg ctgtgatatg gaggaagaag agctcagtg ggaaaggagg gagctactct 1380

aaggctgagt ggagcgacag tgcccagggg tctgagtctc acagcttg 1428

<210> 7

<211> 1428

<212> DNA

<213> homo sapiens

<220>

<221> gene

<222> (1)..(1428)

<400> 7

atgtctcgct ccgtggcctt agctgtgctc gcgctactct ctctttctgg cctggaggct 60

atccagcgta ctcaaagat tcaggtttac tcacgtcatc cagcagagaa tggaaagtca 120

aatttcctga attgctatgt gtctgggttt catccatccg acattgaagt tgacttactg 180

aagaatggag agagaattga aaaagtgag cattcagact tgtctttcag caaggactgg 240

tctttctatc tctgtacta cactgaattc acccccactg aaaaagatga gtatgcctgc 300

cggtgaacc atgtgacttt gtcacagccc aagatagtta agtgggatcg agacatgggt 360

ggtggcgggt ctggtggtgg cggtagtggc ggcggaggaa gcggtggtgg cggttccggt 420

tcccactcct tgaagtattt ccacacttcc gtgtcccggc ccggccgagg ggagccccgc 480

ttcatctctg tgggctacgt ggacgacacc cagttcgtgc gcttcgacaa cgacgccgag 540

agtccgagga tggcgccgag ggcgccgtgg atggagcagg aggggtcaga gtattgggac 600

cgggagacac ggagcgccag ggacaccgca cagattttcc gagtgaacct gcggacgctg 660

cgcggtact acaatcagag cgaggccggt tctcacacc tgacgtgat gcatggctgc 720

gagctggggc ccgacgggag cttctccgc gggatgaac agttcgcta cgacggcaag 780

gattatctca ccctgaatga ggacctgagc tctggaccg cggaggacac ggcggctcag 840

atctccgagc aaaagtcaaa tgatgcctt gaggcggagc accagagagc ctacctgaa 900

gacacatgag tggagtggct ccacaaatac ctggagaagg ggaaggagac gctgcttcac 960

ctggagcccc caaagacaca cgtgactcac caccatct ctgacctga ggccaccctg 1020

aggtgctggg ccctgggctt ctacctgag gagatcacac tgacctgga gcaggatggg 1080

gagggccata ccagagacac ggagctcgtg gagaccaggc ctgcaggga tggaaccttc 1140

cagaagtggg cagctgtggt ggtgccttct ggagaggagc agagatacac gtgcatgtg 1200

cagcatgagg ggctacccga gcccgtcacc ctgagatgga agccggcttc ccagcccacc 1260

atcccatcg tgggcatcat tgctggcctg gttctccttg gatctgtggt ctctggagct 1320

gtggttgctg ctgtgatatg gaggaagaag agctcagggtg ggaaaggagg gagctactct 1380

aaggctgagt ggagcgacag tgcccagggg tctgagtctc acagcttg 1428

<210> 8

<211> 376

<212> PRT

<213> herpes simplex virus

<220>

<221> PEPTIDE

<222> (1)..(376)

<400> 8

Met Ala Ser Tyr Pro Gly His Gln His Ala Ser Ala Phe Asp Gln Ala

1 5 10 15

Ala Arg Ser Arg Gly His Ser Asn Arg Arg Thr Ala Leu Arg Pro Arg

20

25

30

Arg Gln Gln Glu Ala Thr Glu Val Arg Pro Glu Gln Lys Met Pro Thr

35

40

45

Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr

50

55

60

Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr

65

70

75

80

Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu Gly Ala Ser Glu Thr

85

90

95

Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile

100

105

110

Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met

115 120 125

Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Ile Gly

130 135 140

Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile

145 150 155 160

Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg

165 170 175

Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala

180 185 190

Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu

195 200 205

Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly

210 215 220

Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly

225 230 235 240

Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Cys Gly Gly Ser Trp Arg

245 250 255

Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala

260 265 270

Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu

275 280 285

Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu

290 295 300

Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu Arg

305 310 315 320

Ser Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala Gly Cys

325

330

335

Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln Thr His Val

340

345

350

Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu Ala Arg Thr Phe

355

360

365

Ala Arg Glu Met Gly Glu Ala Asn

370

375

<210> 9

<211> 1128

<212> DNA

<213> herpes simplex virus

<220>

<221> gene

<222> (1)..(1128)

<400> 9

atggcttctt accctggaca ccagcatgct tctgccttg accaggctgc cagatccagg 60

ggccactcca acaggagaac tgcctaaga cccagaagac agcaggaagc cactgaggtg 120

aggcctgagc agaagatgcc aacctgctg aggggtgaca ttgatggacc tcatggcatg 180

ggcaagacca ccaccactca actgctggtg gcactgggct ccagggatga catttgttat 240

gtgcctgagc caatgaccta ctggagagtg ctaggagcct ctgagacat tgccaacatc 300

tacaccacc agcacaggct ggaccaggga gaaatctctg ctggagatgc tgctgtggtg 360

atgacctctg cccagatcac aatgggaatg ccctatgctg tgactgatgc tttctggct 420

cctcacattg gaggagaggc tggctcttct catgccctc cacctgccct gaccctgatc 480

tttgacagac acccattgc agccctgctg tgctaccag cagcaaggta cctcatgggc 540

tccatgacc cacaggctgt gctggctttt gtggccctga tccctcaac cctcctggc 600

accaacattg ttctgggagc actgcctgaa gacagacaca ttgacaggct ggcaaagagg 660

cagagacctg gagagagact ggacctggcc atgctggctg caatcagaag ggtgtatgga 720

ctgctggcaa aactgtgag atacctccag tgtggaggct cttggagaga ggactgggga 780

cagctctctg gaacagcagt gccccctcaa ggagctgagc cccagtccaa tgctggtcca 840

agaccccaca ttggggacac cctgttcacc ctgttcagag cccctgagct gctggctccc 900

aatggagacc tgtacaatgt gttgcctgg gctctggatg ttctagccaa gaggctgagg 960

tccatgcatg tgttcatcct ggactatgac cagtcccctg ctggatgcag agatgctctg 1020

ctgcaactaa cctctggcat ggtgcagacc catgtgacca cccctggcag catccccacc 1080

atctgtgacc tagccagaac cttgccagg gagatgggag aggccaac 1128