SEQUENCE LISTING

<110> THE UNITED STATES OF AMERICA, as represented by the
Secretary, Department of Health
GlobeImmune, Inc.
Palena, Claudia
Guo, Zhimin
Apelian, David
Schlom, Jeffrey

<120> Yeast-Brachyury Immunotherapeutic Compositions for Cancer

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<150> 61/453,656
<151> 2011-03-17

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Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser

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Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Asn

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Asp His Lys Asp Val Met Glu Glu Pro Gly Asp Cys Gln Gln Pro Gly

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Tyr Ser Gln Trp Gly Trp Leu Val Pro Gly Ala Gly Thr Leu Cys Pro

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Pro Ala Ser Ser His Pro Gln Phe Gly Gly Ser Leu Ser Leu Pro Ser

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Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
115 120 125

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
130 135 140

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
145 150 155 160

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly

165 170 175

Asp Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe

180 185 190

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile

195 200 205

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser

210 215 220

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly

225 230 235 240

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro

245 250 255

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser

260 265 270

Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser

275 280 285

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser

290 295 300

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp

305 310 315 320

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His

325 330 335

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser

340 345 350

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Thr

355 360 365

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr

370 375 380

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu

385 390 395 400

Tyr Glu Gly Ala Ala Ala Ala Thr Asn Ile Val Asp Ser Gln Tyr Asp

405 410 415

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

420 425 430

Pro Ser Met

435

<210> 7

<211> 1357

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<220>

<221> CDS

<222> (10)..(1347)

<400> 7

gaattccgc atg gcc gat gaa gct ccg agc tcc cct ggc acc gag agc gcg 51

Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala

1 5 10

gga aag agc ctg cag tac cga gtg gac cac ctg ctg agc gcc gtg gag 99

Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu

15 20 25 30

aat gag ctg cag gcg ggc agc gag aag ggc gac ccc aca gag cgc gaa 147

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

35 40 45

ctg cgc gtg ggc ctg gag gag agc gag ctg tgg ctg cgc ttc aag gag 195

Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu

50 55 60

ctc acc aat gag atg atc gtg acc aag aac ggc agg agg atg ttt ccg 243

Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro

65 70 75

gtg ctg aag gtg aac gtg tct ggc ctg gac ccc aac gcc atg tac tcc 291

Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser

80 85 90

ttc ctg ctg gac ttc gtg gcg gcg gac aac cac cgc tgg aag tac gtg 339

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

95 100 105 110

aac ggg gaa tgg gtg ccg ggg ggc aag ccg gag ccg cag gcg ccc agc 387

Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser

115 120 125

tgc gtc tac atc cac ccc gac tcg ccc aac ttc ggg gcc cac tgg atg 435

Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met

130 135 140

aag gct ccc gtc tcc ttc agc aaa gtc aag ctc acc aac aag ctc aac 483

Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn

145 150 155

gga ggg ggc cag atc atg ctg aac tcc ttg cat aag tat gag cct cga 531
Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg
160 165 170

atc cac ata gtg aga gtt ggg gat cca cag cgc atg atc acc agc cac 579
Ile His Ile Val Arg Val Gly Asp Pro Gln Arg Met Ile Thr Ser His
175 180 185 190

tgc ttc cct gag acc cag ttc ata gcg gtg act gct tat cag aac gag 627
Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu
195 200 205

gag atc aca gct ctt aaa att aag tac aat cca ttt gca aaa gct ttc 675
Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe
210 215 220

ctt gat gca aag gaa aga agt gat cac aaa gag atg atg gag gaa ccc 723
Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro
225 230 235

gga gac agc cag caa cct ggg tac tcc caa tgg ggg tgg ctt ctt cct 771
Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro
240 245 250

gga acc agc acc ctg tgt cca cct gca aat cct cat cct cag ttt gga 819
Gly Thr Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly
255 260 265 270

ggt gcc ctc tcc ctc ccc tcc acg cac agc tgt gac agg tac cca acc 867

Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr

275 280 285

ctg agg agc cac cgg tcc tca ccc tac ccc agc ccc tat gct cat cgg 915

Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg

290 295 300

aac aat tct cca acc tat tct gac aac tca cct gca tgt tta tcc atg 963

Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met

305 310 315

ctg caa tcc cat gac aat tgg tcc agc ctt gga atg cct gcc cat ccc 1011

Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro

320 325 330

agc atg ctc ccc gtg agc cac aat gcc agc cca cct acc agc tcc agt 1059

Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser

335 340 345 350

cag tac ccc agc ctg tgg tct gtg agc aac ggc gcc gtc acc ccg ggc 1107

Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly

355 360 365

tcc cag gca gca gcc gtg acc aac ggg ctg ggg gcc cag ttc ttc cgg 1155

Ser Gln Ala Ala Ala Val Thr Asn Gly Leu Gly Ala Gln Phe Phe Arg

370 375 380

ggc tcc ccc gcg cac tac aca ccc ctc acc cat ccg gtc tcg gca ccc 1203

Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro

385 390 395

tct tcc tcg gga tcc cca ctg tac gaa ggg gcg gcc gcg gcc aca aac 1251

Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asn

400 405 410

atc gtg gac agc cag tac gac gcc gca gcc caa ggc cgc ctc ata gcc 1299

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

415 420 425 430

tca tgg aca cct gtg tcg cca cct tcc atg cat cac cat cac cat cac 1347

Ser Trp Thr Pro Val Ser Pro Pro Ser Met His His His His His His

435 440 445

tgagactagt 1357

<210> 8

<211> 446

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 8

Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys

1 5 10 15

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

20 25 30

Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg

35 40 45

Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr

50 55 60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu

65 70 75 80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu

85 90 95

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

100 105 110

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val

115 120 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala

130 135 140

Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly

145 150 155 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
165 170 175

Ile Val Arg Val Gly Asp Pro Gln Arg Met Ile Thr Ser His Cys Phe
180 185 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
195 200 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp
210 215 220

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

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr
245 250 255

Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala
260 265 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg

275 280 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn

290 295 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln

305 310 315 320

Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met

325 330 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr

340 345 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln

355 360 365

Ala Ala Ala Val Thr Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser

370 375 380

Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser

385 390 395 400

Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asn Ile Val

405 410 415

Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp

420 425 430

Thr Pro Val Ser Pro Pro Ser Met His His His His His His

435 440 445

<210> 9

<211> 1360

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<220>

<221> CDS

<222> (10)..(1353)

<400> 9

gaattccgc atg gcc gat gaa gct ccg agc tcg ccg ggc aca gag agc gca 51

Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala

1 5 10

ggg aag agc ctg cag tac cga gtg gac cac ctg ctc agc gcc gtg gag 99

Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu

15 20 25 30

agc gag ctg cag gcg ggc agc gag aag gga gac ccc acc gaa cgc gaa 147

Ser Glu Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu

35 40 45

ctg cga gtg ggc ctg gag gag agc gag ctg tgg ctg cgc ttc aag gag 195

Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu

50 55 60

cta act aac gag atg att gtg acc aag aac ggc agg agg atg ttc ccg 243

Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro

65 70 75

gtg ctg aag gta aat gtg tca ggc ctg gac ccc aat gcc atg tac tct 291

Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser

80 85 90

ttc ttg ctg gac ttc gtg acg gct gac aac cac cgc tgg aaa tat gtg 339

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

95 100 105 110

aac ggg gag tgg gta cct ggg ggc aaa cca gag cct cag gcg ccc agc 387

Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser

115 120 125

tgc gtc tac atc cac cca gac tcg ccc aat ttt ggg gcc cac tgg atg 435

Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met

130 135 140

aag gcg cct gtg tct ttc agc aaa gtc aaa ctc acc aac aag ctc aat 483

Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn

145 150 155

gga ggg gga cag atc atg tta aac tcc ttg cat aag tat gaa cct cgg 531

Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg

160 165 170

att cac atc gtg aga gtt ggg ggc ccg caa cgc atg atc acc agc cac 579

Ile His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His

175 180 185 190

tgc ttt ccc gag acc cag ttc ata gct gtg act gcc tac cag aat gag 627

Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu

195 200 205

gag att aca gcc ctt aaa att aaa tac aac cca ttt gct aaa gcc ttc 675

Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe

210 215 220

ctt gat gcc aaa gaa aga aac gac cac aaa gat gta atg gag gaa ccg 723

Leu Asp Ala Lys Glu Arg Asn Asp His Lys Asp Val Met Glu Glu Pro

225 230 235

ggg gac tgc cag cag ccg ggg tat tcc caa tgg ggg tgg ctt gtt cct 771

Gly Asp Cys Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Val Pro

240 245 250

ggt gct ggc acc ctc tgc ccg cct gcc agc tcc cac cct cag ttt gga 819

Gly Ala Gly Thr Leu Cys Pro Pro Ala Ser Ser His Pro Gln Phe Gly

255 260 265 270

ggc tcg ctc tct ctc ccc tcc aca cac ggc tgt gag agg tac cca gct 867
Gly Ser Leu Ser Leu Pro Ser Thr His Gly Cys Glu Arg Tyr Pro Ala
275 280 285

cta agg aac cac cgg tca tcg ccc tac ccc agc ccc tat gct cat cgg 915
Leu Arg Asn His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg
290 295 300

aac agc tct cca acc tac gcg gac aat tca tct gct tgt ctg tcc atg 963
Asn Ser Ser Pro Thr Tyr Ala Asp Asn Ser Ser Ala Cys Leu Ser Met
305 310 315

ctg cag tcc cat gat aac tgg tct agc ctc gga gtg cct ggc cac acc 1011
Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Val Pro Gly His Thr
320 325 330

agc atg ctg cct gtg agt cat aac gcc agc cca cct act ggc tct agc 1059
Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Gly Ser Ser
335 340 345 350

cag tat ccc agt ctc tgg tct gtg agc aat ggt acc atc acc cca ggc 1107
Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Thr Ile Thr Pro Gly
355 360 365

tcc cag aca gct ggg gtg tcc aac ggg ctg gga gct cag ttc ttt cga 1155
Ser Gln Thr Ala Gly Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg
370 375 380

ggc tcc cct gca cat tac aca cca ctg aca cac acg gtc tca gct gcc 1203

Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Thr Val Ser Ala Ala

385 390 395

acg tcc tcg tct tct ggt tct ccg atg tat gaa ggg gct gct aca gtc 1251

Thr Ser Ser Ser Ser Gly Ser Pro Met Tyr Glu Gly Ala Ala Thr Val

400 405 410

aca gac att tct gac agc cag tat gac acg gcc caa agc ctc ctc ata 1299

Thr Asp Ile Ser Asp Ser Gln Tyr Asp Thr Ala Gln Ser Leu Leu Ile

415 420 425 430

gcc tcg tgg aca cct gtg tca ccc cca tct atg cat cac cat cac cat 1347

Ala Ser Trp Thr Pro Val Ser Pro Pro Ser Met His His His His His

435 440 445

cac tga gactagt 1360

His

<210> 10

<211> 447

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 10

Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys

1 5 10 15

Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Ser Glu
20 25 30

Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg
35 40 45

Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
50 55 60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65 70 75 80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu
85 90 95

Leu Asp Phe Val Thr Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly
100 105 110

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
115 120 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala

130 135 140

Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly

145 150 155 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His

165 170 175

Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe

180 185 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile

195 200 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp

210 215 220

Ala Lys Glu Arg Asn Asp His Lys Asp Val Met Glu Glu Pro Gly Asp

225 230 235 240

Cys Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Val Pro Gly Ala

245 250 255

Gly Thr Leu Cys Pro Pro Ala Ser Ser His Pro Gln Phe Gly Gly Ser

260 265 270

Leu Ser Leu Pro Ser Thr His Gly Cys Glu Arg Tyr Pro Ala Leu Arg

275 280 285

Asn His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Ser

290 295 300

Ser Pro Thr Tyr Ala Asp Asn Ser Ser Ala Cys Leu Ser Met Leu Gln

305 310 315 320

Ser His Asp Asn Trp Ser Ser Leu Gly Val Pro Gly His Thr Ser Met

325 330 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Gly Ser Ser Gln Tyr

340 345 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Thr Ile Thr Pro Gly Ser Gln

355 360 365

Thr Ala Gly Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser

370 375 380

Pro Ala His Tyr Thr Pro Leu Thr His Thr Val Ser Ala Ala Thr Ser

385 390 395 400

Ser Ser Ser Gly Ser Pro Met Tyr Glu Gly Ala Ala Thr Val Thr Asp

405 410 415

Ile Ser Asp Ser Gln Tyr Asp Thr Ala Gln Ser Leu Leu Ile Ala Ser

420 425 430

Trp Thr Pro Val Ser Pro Pro Ser Met His His His His His His

435 440 445

<210> 11

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Synthetic Peptide

<400> 11

Met Ala Asp Glu Ala Pro

1 5

<210> 12

<211> 9

<212> PRT

<213> Homo sapiens

<400> 12

Trp Leu Leu Pro Gly Thr Ser Thr Leu

1 5

<210> 13

<211> 9

<212> PRT

<213> Homo sapiens

<400> 13

Trp Leu Leu Pro Gly Thr Ser Thr Val

1 5

<210> 14

<211> 9

<212> PRT

<213> Homo sapiens

<400> 14

Ser Gln Tyr Pro Ser Leu Trp Ser Val

1 5

<210> 15

<211> 9

<212> PRT

<213> Homo sapiens

<400> 15

Arg Leu Ile Ala Ser Trp Thr Pro Val

1 5

<210> 16

<211> 10

<212> PRT

<213> Homo sapiens

<400> 16

Ala Met Tyr Ser Phe Leu Leu Asp Phe Val

1 5 10

<210> 17

<211> 1305

<212> DNA

<213> Artificial

<220>

<223> Synthetic Construct

<220>

<221> CDS

<222> (1)..(1305)

<400> 17

atg agc tcc cct ggc acc gag agc gcg gga aag agc ctg cag tac cga 48

Met Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg

1 5 10 15

gtg gac cac ctg ctg agc gcc gtg gag aat gag ctg cag gcg ggc agc 96

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

20 25 30

gag aag ggc gac ccc aca gag cgc gaa ctg cgc gtg ggc ctg gag gag 144

Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu

35 40 45

agc gag ctg tgg ctg cgc ttc aag gag ctc acc aat gag atg atc gtg 192

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val

50 55 60

acc aag aac ggc agg agg atg ttt ccg gtg ctg aag gtg aac gtg tct 240

Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser

65 70 75 80

ggc ctg gac ccc aac gcc atg tac tcc ttc ctg ctg gac ttc gtg gcg 288

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala

85 90 95

gcg gac aac cac cgc tgg aag tac gtg aac ggg gaa tgg gtg ccg ggg 336

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly

100 105 110

ggc aag ccg gag ccg cag gcg ccc agc tgc gtc tac atc cac ccc gac 384

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp

115 120 125

tcg ccc aac ttc ggg gcc cac tgg atg aag gct ccc gtc tcc ttc agc 432

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser

130 135 140

aaa gtc aag ctc acc aac aag ctc aac gga ggg ggc cag atc atg ctg 480

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu

145 150 155 160

aac tcc ttg cat aag tat gag cct cga atc cac ata gtg aga gtt ggg 528

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly

165 170 175

gat cca cag cgc atg atc acc agc cac tgc ttc cct gag acc cag ttc 576

Asp Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe

180 185 190

ata gcg gtg act gct tat cag aac gag gag atc aca gct ctt aaa att 624

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile

195 200 205

aag tac aat cca ttt gca aaa gct ttc ctt gat gca aag gaa aga agt 672

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser

210 215 220

gat cac aaa gag atg atg gag gaa ccc gga gac agc cag caa cct ggg 720
Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
225 230 235 240

tac tcc caa tgg ggg tgg ctt ctt cct gga acc agc acc gtg tgt cca 768
Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro
245 250 255

cct gca aat cct cat cct cag ttt gga ggt gcc ctc tcc ctc ccc tcc 816
Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
260 265 270

acg cac agc tgt gac agg tac cca acc ctg agg agc cac cgg tcc tca 864
Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
275 280 285

ccc tac ccc agc ccc tat gct cat cgg aac aat tct cca acc tat tct 912
Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
290 295 300

gac aac tca cct gca tgt tta tcc atg ctg caa tcc cat gac aat tgg 960
Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
305 310 315 320

tcc agc ctt gga atg cct gcc cat ccc agc atg ctc ccc gtg agc cac 1008
Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
325 330 335

aat gcc agc cca cct acc agc tcc agt cag tac ccc agc ctg tgg tct 1056

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser

340 345 350

gtg agc aac ggc gcc gtc acc ccg ggc tcc cag gca gca gcc gtg acc 1104

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Thr

355 360 365

aac ggg ctg ggg gcc cag ttc ttc cgg ggc tcc ccc gcg cac tac aca 1152

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr

370 375 380

ccc ctc acc cat ccg gtc tcg gca ccc tct tcc tcg gga tcc cca ctg 1200

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu

385 390 395 400

tac gaa ggg gcg gcc gcg gcc aca aac atc gtg gac agc cag tac gac 1248

Tyr Glu Gly Ala Ala Ala Ala Thr Asn Ile Val Asp Ser Gln Tyr Asp

405 410 415

gcc gca gcc caa ggc cgc ctc ata gcc tca tgg aca cct gtg tcg cca 1296

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

420 425 430

cct tcc atg 1305

Pro Ser Met

435

<210> 18

<211> 435

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 18

Met Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg
1 5 10 15

Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
20 25 30

Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu
35 40 45

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
50 55 60

Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
65 70 75 80

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
85 90 95

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly

100 105 110

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp

115 120 125

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser

130 135 140

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu

145 150 155 160

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly

165 170 175

Asp Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe

180 185 190

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile

195 200 205

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser

210 215 220

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly

225 230 235 240

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro

245 250 255

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser

260 265 270

Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser

275 280 285

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser

290 295 300

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp

305 310 315 320

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His

325 330 335

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser

340 345 350

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Thr

355 360 365

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr

370 375 380

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu

385 390 395 400

Tyr Glu Gly Ala Ala Ala Ala Thr Asn Ile Val Asp Ser Gln Tyr Asp

405 410 415

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

420 425 430

Pro Ser Met

435

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Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala

1 5 10

gga aag agc ctg cag tac cga gtg gac cac ctg ctg agc gcc gtg gag 99

Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu

15 20 25 30

aat gag ctg cag gcg ggc agc gag aag ggc gac ccc aca gag cgc gaa 147

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

35 40 45

ctg cgc gtg ggc ctg gag gag agc gag ctg tgg ctg cgc ttc aag gag 195

Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu

50 55 60

ctc acc aat gag atg atc gtg acc aag aac ggc agg agg atg ttt ccg 243

Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro

65 70 75

gtg ctg aag gtg aac gtg tct ggc ctg gac ccc aac gcc atg tac tcc 291

Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser

80 85 90

ttc ctg ctg gac ttc gtg gcg gcg gac aac cac cgc tgg aag tac gtg 339
Phe Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val
95 100 105 110

aac ggg gaa tgg gtg ccg ggg ggc aag ccg gag ccg cag gcg ccc agc 387
Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser
115 120 125

tgc gtc tac atc cac ccc gac tcg ccc aac ttc ggg gcc cac tgg atg 435
Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met
130 135 140

aag gct ccc gtc tcc ttc agc aaa gtc aag ctc acc aac aag ctc aac 483
Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn
145 150 155

gga ggg ggc cag atc atg ctg aac tcc ttg cat aag tat gag cct cga 531
Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg
160 165 170

atc cac ata gtg aga gtt ggg gat cca cag cgc atg atc acc agc cac 579
Ile His Ile Val Arg Val Gly Asp Pro Gln Arg Met Ile Thr Ser His
175 180 185 190

tgc ttc cct gag acc cag ttc ata gcg gtg act gct tat cag aac gag 627
Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu
195 200 205

gag atc aca gct ctt aaa att aag tac aat cca ttt gca aaa gct ttc 675

Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe

210 215 220

ctt gat gca aag gaa aga agt gat cac aaa gag atg atg gag gaa ccc 723

Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro

225 230 235

gga gac agc cag caa cct ggg tac tcc caa tgg ggg tgg ctt ctt cct 771

Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro

240 245 250

gga acc agc acc gtg tgt cca cct gca aat cct cat cct cag ttt gga 819

Gly Thr Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly

255 260 265 270

ggt gcc ctc tcc ctc ccc tcc acg cac agc tgt gac agg tac cca acc 867

Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr

275 280 285

ctg agg agc cac cgg tcc tca ccc tac ccc agc ccc tat gct cat cgg 915

Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg

290 295 300

aac aat tct cca acc tat tct gac aac tca cct gca tgt tta tcc atg 963

Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met

305 310 315

ctg caa tcc cat gac aat tgg tcc agc ctt gga atg cct gcc cat ccc 1011

Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro

320 325 330

agc atg ctc ccc gtg agc cac aat gcc agc cca cct acc agc tcc agt 1059

Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser

335 340 345 350

cag tac ccc agc ctg tgg tct gtg agc aac ggc gcc gtc acc ccg ggc 1107

Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly

355 360 365

tcc cag gca gca gcc gtg acc aac ggg ctg ggg gcc cag ttc ttc cgg 1155

Ser Gln Ala Ala Ala Val Thr Asn Gly Leu Gly Ala Gln Phe Phe Arg

370 375 380

ggc tcc ccc gcg cac tac aca ccc ctc acc cat ccg gtc tcg gca ccc 1203

Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro

385 390 395

tct tcc tcg gga tcc cca ctg tac gaa ggg gcg gcc gcg gcc aca aac 1251

Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asn

400 405 410

atc gtg gac agc cag tac gac gcc gca gcc caa ggc cgc ctc ata gcc 1299

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

415 420 425 430

tca tgg aca cct gtg tcg cca cct tcc atg cat cac cat cac cat cac 1347

Ser Trp Thr Pro Val Ser Pro Pro Ser Met His His His His His His

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tga gactagtccc gggcggccgc 1370

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Met Ala Asp Glu Ala Pro Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys
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Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu
20 25 30

Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg
35 40 45

Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
50 55 60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65 70 75 80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu

85 90 95

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

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
115 120 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala
130 135 140

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

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
165 170 175

Ile Val Arg Val Gly Asp Pro Gln Arg Met Ile Thr Ser His Cys Phe
180 185 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
195 200 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp

210 215 220

Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp

225 230 235 240

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr

245 250 255

Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala

260 265 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg

275 280 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn

290 295 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln

305 310 315 320

Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met

325 330 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr

340 345 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln

355 360 365

Ala Ala Ala Val Thr Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser

370 375 380

Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser

385 390 395 400

Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asn Ile Val

405 410 415

Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp

420 425 430

Thr Pro Val Ser Pro Pro Ser Met His His His His His His

435 440 445