

SEQUENCE LISTING

<110> Astellas Pharma Inc.
RIKEN

<120> alpha-GalCer concentration on aAVC cell for treatment cancer

<130> A20025A00

<150> JP 2019-217712

<151> 2019-12-02

<160> 6

<170> PatentIn version 3.5

<210> 1

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic nucleic acid encoding human WT1

<220>

<221> CDS

<222> (1)..(1554)

<400> 1

atg cag gac cct gcc agc aca tgt gtg cct gag cct gcc agc cag cac	48
Met Gln Asp Pro Ala Ser Thr Cys Val Pro Glu Pro Ala Ser Gln His	
1 5 10 15	

acc ctg aga tct ggc cct gga tgc ctg cag cag cct gaa cag cag ggc	96
Thr Leu Arg Ser Gly Pro Gly Cys Leu Gln Gln Pro Glu Gln Gln Gly	
20 25 30	

gtg cgc gat cct ggc gga att tgg gcc aaa ctg gga gcc gcc gaa gcc	144
Val Arg Asp Pro Gly Gly Ile Trp Ala Lys Leu Gly Ala Ala Glu Ala	
35 40 45	

agc gct gaa aga ctg cag ggc aga aga agc aga ggc gcc agc gga tct	192
Ser Ala Glu Arg Leu Gln Gly Arg Arg Ser Arg Gly Ala Ser Gly Ser	
50 55 60	

gag ccc cag cag atg gga tct gac gtg cgg gac ctg aat gcc ctg ctg	240
Glu Pro Gln Gln Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu	
65 70 75 80	

cct gct gtg cct tct ctg ggc gga ggc gga gga tgt gct ctg cct gtg	288
Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu Pro Val	
85 90 95	

tct ggc gct gct cag tgg gct ccc gtg ctg gat ttt gct cct cct ggc Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Gly	336
100 105 110	
gct tct gcc tac ggc tct ctg gga gga cct gct cct cca cca gct cca Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala Pro	384
115 120 125	
cct cca ccc cct cca cca ccc cca cac agc ttc atc aag cag gaa cct Pro Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu Pro	432
130 135 140	
agc tgg ggc gga gcc gag cct cac gag gaa cag tgt ctg agc gcc ttc Ser Trp Gly Gly Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala Phe	480
145 150 155 160	
acc gtg cac ttc agc ggc cag ttt acc ggc aca gcc ggc gct tgt aga Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg	528
165 170 175	
tac ggc cct ttt ggc cca cct ccc cca agc cag gca tct agc gga cag Tyr Gly Pro Phe Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser Gly Gln	576
180 185 190	
gcc aga atg ttc ccc aac gcc ccc tac ctg cct agc tgc ctg gaa agc Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu Ser	624
195 200 205	
cag ccc gcc atc aga aac cag ggc tac agc acc gtg acc ttc gac ggc Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp Gly	672
210 215 220	
aca cct agc tac ggc cac acc cct tct cat cac gcc gcc cag ttc ccc Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln Phe Pro	720
225 230 235 240	
aat cac tcc ttc aag cac gag gac ccc atg ggc cag cag gga agc ctg Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu	768
245 250 255	
gga gag cag cag tac agc gtg ccc cct cct gtg tac ggc tgt cac acc Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr	816
260 265 270	
cct acc gat agc tgc aca ggc agc cag gct ctg ctg ctg aga acc ccc Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro	864
275 280 285	
tac agc agc gac aac ctg tac cag atg acc agc cag ctg gaa tgc atg Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met	912
290 295 300	
acc tgg aac cag atg aac ctg ggc gcc acc ctg aaa ggc gtg gcc gct Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly Val Ala Ala	960

305	310	315	320	
gga tct agc agc tcc gtg aag tgg aca gag ggc cag agc aac cac agc				1008
Gly Ser Ser Ser Ser Val Lys Trp Thr Glu Gly Gln Ser Asn His Ser	325	330	335	
acc ggc tac gag tcc gac aac cac acc acc cct atc ctg tgc gga gcc				1056
Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala	340	345	350	
cag tac aga atc cac acc cac ggc gtg ttc cgg gga atc cag gat gtg				1104
Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val	355	360	365	
cgg aga gtg cct ggc gtg gcc cct aca ctc gtg cgc tct gcc tct gag				1152
Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu	370	375	380	
aca agc gag aag cgg ccc ttc atg tgc gcc tac ccc ggc tgc aac aag				1200
Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Pro Gly Cys Asn Lys	385	390	400	
cgg tac ttc aag ctg agc cat ctg cag atg cac agc aga aag cac acc				1248
Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His Thr	405	410	415	
ggc gag aag ccc tac cag tgc gac ttc aag gac tgc gag cgg cgg ttc				1296
Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe	420	425	430	
agc aga tcc gac cag ctg aag aga cac cag cgg cgg cac aca ggc gtg				1344
Ser Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val	435	440	445	
aaa cct ttc cag tgc aag acc tgc cag cgg aag ttc tcc aga agc gac				1392
Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp	450	455	460	
cac ctg aaa acc cac acc cgg acc cac acc ggc aag acc tcc gag aag				1440
His Leu Lys Thr His Thr Arg Thr His Thr Gly Lys Thr Ser Glu Lys	465	470	475	
cca ttc agc tgc cgg tgg ccc agc tgc cag aag aag ttt gcc aga tct				1488
Pro Phe Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser	485	490	495	
gac gag ctc gtg cgg cac cac aac atg cac cag cgg aac atg acc aaa				1536
Asp Glu Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys	500	505	510	
ctg cag ctg gct ctc tga				1554
Leu Gln Leu Ala Leu	515			

<210> 2
 <211> 517
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 2

Met Gln Asp Pro Ala Ser Thr Cys Val Pro Glu Pro Ala Ser Gln His
 1 5 10 15

Thr Leu Arg Ser Gly Pro Gly Cys Leu Gln Gln Pro Glu Gln Gln Gly
 20 25 30

Val Arg Asp Pro Gly Gly Ile Trp Ala Lys Leu Gly Ala Ala Glu Ala
 35 40 45

Ser Ala Glu Arg Leu Gln Gly Arg Arg Ser Arg Gly Ala Ser Gly Ser
 50 55 60

Glu Pro Gln Gln Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu Leu
 65 70 75 80

Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Gly Cys Ala Leu Pro Val
 85 90 95

Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro Gly
 100 105 110

Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala Pro
 115 120 125

Pro Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu Pro
 130 135 140

Ser Trp Gly Gly Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala Phe
 145 150 155 160

Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys Arg
 165 170 175

Tyr Gly Pro Phe Gly Pro Pro Pro Pro Ser Gln Ala Ser Ser Gly Gln
 180 185 190

Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu Ser
 195 200 205

Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp Gly
 210 215 220

Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln Phe Pro
 225 230 235 240

Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser Leu
 245 250 255

Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His Thr
 260 265 270

Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr Pro
 275 280 285

Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys Met
 290 295 300

Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly Val Ala Ala
 305 310 315 320

Gly Ser Ser Ser Ser Val Lys Trp Thr Glu Gly Gln Ser Asn His Ser
 325 330 335

Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala
 340 345 350

Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val
 355 360 365

Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu
 370 375 380

Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Pro Gly Cys Asn Lys

385 390 395 400
 Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His Thr
 405 410 415
 Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe
 420 425 430
 Ser Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val
 435 440 445
 Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp
 450 455 460
 His Leu Lys Thr His Thr Arg Thr His Thr Gly Lys Thr Ser Glu Lys
 465 470 475 480
 Pro Phe Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser
 485 490 495
 Asp Glu Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys
 500 505 510
 Leu Gln Leu Ala Leu
 515

<210> 3
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic nucleic acid encoding human CD1d

<220>
 <221> CDS
 <222> (1)..(1008)

<400> 3
 atg ggc tgc ctg ctg ttt ctg ctg ctg tgg gcc ctg ctg cag gcc tgg 48
 Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
 1 5 10 15
 gga tct gct gaa gtg ccc cag aga ctg ttc ccc ctg cgg tgc ctg cag 96

Gly	Ser	Ala	Glu	Val	Pro	Gln	Arg	Leu	Phe	Pro	Leu	Arg	Cys	Leu	Gln		
			20					25					30				
atc	agc	agc	ttc	gcc	aac	agc	agc	tgg	acc	aga	acc	gat	ggc	ctg	gcc		144
Ile	Ser	Ser	Phe	Ala	Asn	Ser	Ser	Trp	Thr	Arg	Thr	Asp	Gly	Leu	Ala		
		35					40					45					
tgg	ctg	gga	gag	ctg	cag	aca	cac	agc	tgg	tcc	aac	gac	agc	gac	acc		192
Trp	Leu	Gly	Glu	Leu	Gln	Thr	His	Ser	Trp	Ser	Asn	Asp	Ser	Asp	Thr		
	50					55					60						
gtg	cgg	agc	ctg	aag	cct	tgg	agc	cag	ggc	acc	ttt	agc	gac	cag	cag		240
Val	Arg	Ser	Leu	Lys	Pro	Trp	Ser	Gln	Gly	Thr	Phe	Ser	Asp	Gln	Gln		
65					70				75					80			
tgg	gag	aca	ctg	cag	cac	atc	ttc	cgg	gtg	tac	aga	agc	agc	ttc	acc		288
Trp	Glu	Thr	Leu	Gln	His	Ile	Phe	Arg	Val	Tyr	Arg	Ser	Ser	Phe	Thr		
			85					90						95			
cgg	gac	gtg	aaa	gaa	ttt	gcc	aag	atg	ctg	cgg	ctg	agc	tac	ccc	ctg		336
Arg	Asp	Val	Lys	Glu	Phe	Ala	Lys	Met	Leu	Arg	Leu	Ser	Tyr	Pro	Leu		
			100					105					110				
gaa	ctg	cag	gtg	tcc	gcc	ggc	tgt	gaa	gtg	cac	cct	ggc	aac	gcc	agc		384
Glu	Leu	Gln	Val	Ser	Ala	Gly	Cys	Glu	Val	His	Pro	Gly	Asn	Ala	Ser		
		115				120						125					
aac	aac	ttc	ttc	cac	gtg	gcc	ttc	cag	ggc	aag	gac	ata	ctg	agc	ttt		432
Asn	Asn	Phe	Phe	His	Val	Ala	Phe	Gln	Gly	Lys	Asp	Ile	Leu	Ser	Phe		
		130				135					140						
cag	ggc	acc	agc	tgg	gag	ccc	aca	cag	gaa	gct	cca	ctg	tgg	gtc	aac		480
Gln	Gly	Thr	Ser	Trp	Glu	Pro	Thr	Gln	Glu	Ala	Pro	Leu	Trp	Val	Asn		
145					150				155						160		
ctg	gcc	atc	cag	gtg	ctg	aac	cag	gac	aag	tgg	acc	cgg	gaa	acc	gtg		528
Leu	Ala	Ile	Gln	Val	Leu	Asn	Gln	Asp	Lys	Trp	Thr	Arg	Glu	Thr	Val		
			165					170						175			
cag	tgg	ctg	ctg	aac	ggc	acc	tgt	ccc	cag	ttt	gtg	tcc	ggc	ctg	ctg		576
Gln	Trp	Leu	Leu	Asn	Gly	Thr	Cys	Pro	Gln	Phe	Val	Ser	Gly	Leu	Leu		
			180				185						190				
gaa	agc	ggc	aag	agc	gag	ctg	aag	aaa	caa	gtg	aag	ccc	aaa	gcc	tgg		624
Glu	Ser	Gly	Lys	Ser	Glu	Leu	Lys	Lys	Gln	Val	Lys	Pro	Lys	Ala	Trp		
		195				200						205					
ctg	agc	aga	ggc	cct	tct	cct	gga	cct	gga	cgg	ctg	ctg	ctc	gtg	tgt		672
Leu	Ser	Arg	Gly	Pro	Ser	Pro	Gly	Pro	Gly	Arg	Leu	Leu	Leu	Val	Cys		
		210				215					220						
cac	gtg	tcc	ggc	ttc	tac	ccc	aag	ccc	gtg	tgg	gtc	aag	tgg	atg	cgg		720
His	Val	Ser	Gly	Phe	Tyr	Pro	Lys	Pro	Val	Trp	Val	Lys	Trp	Met	Arg		
225					230				235						240		

gga gaa cag gaa cag cag ggc acc cag cct ggc gac atc ctg cct aac 768
 Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
 245 250 255

gcc gac gag aca tgg tat ctg cgg gcc acc ctg gat gtg gtg gct ggc 816
 Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
 260 265 270

gaa gca gcc ggc ctg tcc tgt aga gtg aag cac agc agc ctg gaa gga 864
 Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
 275 280 285

cag gac atc gtg ctg tac tgg ggc ggc agc tac acc agc atg gga ctg 912
 Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
 290 295 300

att gct ctg gcc gtg ctg gcc tgt ctg ctg ttt ctg ctg atc gtg gga 960
 Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
 305 310 315 320

ttc acc agc cgg ttc aag cgg cag acc agc tac cag ggc gtg ctc tga 1008
 Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
 325 330 335

<210> 4
 <211> 335
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 4

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
 1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
 20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
 35 40 45

Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr
 50 55 60

Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
 65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
85 90 95

Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu
100 105 110

Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser
115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
130 135 140

Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
145 150 155 160

Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val
165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
180 185 190

Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
195 200 205

Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
210 215 220

His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg
225 230 235 240

Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
245 250 255

Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
260 265 270

Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
275 280 285

Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
 290 295 300

Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
 305 310 315 320

Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
 325 330 335

<210> 5
 <211> 1011
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic nucleic acid encoding mouse CD1d

<220>
 <221> CDS
 <222> (1)..(1011)

<400> 5
 atg aga tac ctg ccc tgg ctg ctg ctg tgg gcc ttc ctc cag gtg tgg 48
 Met Arg Tyr Leu Pro Trp Leu Leu Leu Trp Ala Phe Leu Gln Val Trp
 1 5 10 15

gga cag tct gag gcc cag cag aag aac tac acc ttc cgg tgc ctg cag 96
 Gly Gln Ser Glu Ala Gln Gln Lys Asn Tyr Thr Phe Arg Cys Leu Gln
 20 25 30

atg agc agc ttc gcc aac aga agc tgg tcc cgg acc gac agc gtc gtg 144
 Met Ser Ser Phe Ala Asn Arg Ser Trp Ser Arg Thr Asp Ser Val Val
 35 40 45

tgg ctg gga gat ctg cag acc cac aga tgg tcc aac gac agc gcc acc 192
 Trp Leu Gly Asp Leu Gln Thr His Arg Trp Ser Asn Asp Ser Ala Thr
 50 55 60

atc agc ttc acc aag ccc tgg tcc cag ggc aag ctg agc aac cag cag 240
 Ile Ser Phe Thr Lys Pro Trp Ser Gln Gly Lys Leu Ser Asn Gln Gln
 65 70 75 80

tgg gag aag ctg cag cac atg ttc cag gtg tac cgg gtg tcc ttc acc 288
 Trp Glu Lys Leu Gln His Met Phe Gln Val Tyr Arg Val Ser Phe Thr
 85 90 95

cgg gac atc cag gaa ctc gtg aag atg atg agc ccc aaa gag gac tac 336
 Arg Asp Ile Gln Glu Leu Val Lys Met Met Ser Pro Lys Glu Asp Tyr
 100 105 110

ccc atc gag atc cag ctg agc gcc ggc tgc gag atg tac cct ggc aat	384
Pro Ile Glu Ile Gln Leu Ser Ala Gly Cys Glu Met Tyr Pro Gly Asn	
115 120 125	
gcc agc gag agc ttc ctg cac gtg gcc ttc cag ggc aaa tac gtc gtg	432
Ala Ser Glu Ser Phe Leu His Val Ala Phe Gln Gly Lys Tyr Val Val	
130 135 140	
cgg ttc tgg ggc acc agc tgg cag aca gtg cct ggc gct cct agc tgg	480
Arg Phe Trp Gly Thr Ser Trp Gln Thr Val Pro Gly Ala Pro Ser Trp	
145 150 155 160	
ctg gac ctg cct atc aag gtg ctg aac gcc gac cag ggc aca agc gcc	528
Leu Asp Leu Pro Ile Lys Val Leu Asn Ala Asp Gln Gly Thr Ser Ala	
165 170 175	
aca gtg cag atg ctg ctg aac gac aca tgc ccc ctg ttc gtg cgg gga	576
Thr Val Gln Met Leu Leu Asn Asp Thr Cys Pro Leu Phe Val Arg Gly	
180 185 190	
ctg ctg gaa gcc ggc aag agc gac ctg gaa aag cag gaa aag ccc gtg	624
Leu Leu Glu Ala Gly Lys Ser Asp Leu Glu Lys Gln Glu Lys Pro Val	
195 200 205	
gcc tgg ctg agc agc gtg cca tct tct gcc gat ggc cac aga cag ctc	672
Ala Trp Leu Ser Ser Val Pro Ser Ser Ala Asp Gly His Arg Gln Leu	
210 215 220	
gtg tgc cac gtg tcc ggc ttc tac ccc aag ccc gtg tgg gtc atg tgg	720
Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met Trp	
225 230 235 240	
atg cgg ggc gac cag gaa cag cag ggc aca cac aga ggc gac ttt ctg	768
Met Arg Gly Asp Gln Glu Gln Gln Gly Thr His Arg Gly Asp Phe Leu	
245 250 255	
ccc aac gcc gac gag aca tgg tat ctg caa gcc acc ctg gac gtg gaa	816
Pro Asn Ala Asp Glu Thr Trp Tyr Leu Gln Ala Thr Leu Asp Val Glu	
260 265 270	
gct ggc gag gaa gct gga ctg gcc tgc aga gtg aag cac agc tct ctg	864
Ala Gly Glu Glu Ala Gly Leu Ala Cys Arg Val Lys His Ser Ser Leu	
275 280 285	
ggc ggc cag gac atc atc ctg tac tgg gat gcc aga cag gcc cca gtg	912
Gly Gly Gln Asp Ile Ile Leu Tyr Trp Asp Ala Arg Gln Ala Pro Val	
290 295 300	
ggc ctg atc gtg ttc atc gtg ctg atc atg ctg gtg gtc gtg ggc gcc	960
Gly Leu Ile Val Phe Ile Val Leu Ile Met Leu Val Val Val Gly Ala	
305 310 315 320	
gtg gtg tac tac atc tgg cgg aga aga agc gcc tac cag gat atc aga	1008
Val Val Tyr Tyr Ile Trp Arg Arg Arg Ser Ala Tyr Gln Asp Ile Arg	

325 330 335

tga 1011

<210> 6
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

Met Arg Tyr Leu Pro Trp Leu Leu Leu Trp Ala Phe Leu Gln Val Trp
 1 5 10 15

Gly Gln Ser Glu Ala Gln Gln Lys Asn Tyr Thr Phe Arg Cys Leu Gln
 20 25 30

Met Ser Ser Phe Ala Asn Arg Ser Trp Ser Arg Thr Asp Ser Val Val
 35 40 45

Trp Leu Gly Asp Leu Gln Thr His Arg Trp Ser Asn Asp Ser Ala Thr
 50 55 60

Ile Ser Phe Thr Lys Pro Trp Ser Gln Gly Lys Leu Ser Asn Gln Gln
 65 70 75 80

Trp Glu Lys Leu Gln His Met Phe Gln Val Tyr Arg Val Ser Phe Thr
 85 90 95

Arg Asp Ile Gln Glu Leu Val Lys Met Met Ser Pro Lys Glu Asp Tyr
 100 105 110

Pro Ile Glu Ile Gln Leu Ser Ala Gly Cys Glu Met Tyr Pro Gly Asn
 115 120 125

Ala Ser Glu Ser Phe Leu His Val Ala Phe Gln Gly Lys Tyr Val Val
 130 135 140

Arg Phe Trp Gly Thr Ser Trp Gln Thr Val Pro Gly Ala Pro Ser Trp
 145 150 155 160

Leu Asp Leu Pro Ile Lys Val Leu Asn Ala Asp Gln Gly Thr Ser Ala
 165 170 175

Thr Val Gln Met Leu Leu Asn Asp Thr Cys Pro Leu Phe Val Arg Gly
 180 185 190

Leu Leu Glu Ala Gly Lys Ser Asp Leu Glu Lys Gln Glu Lys Pro Val
 195 200 205

Ala Trp Leu Ser Ser Val Pro Ser Ser Ala Asp Gly His Arg Gln Leu
 210 215 220

Val Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Met Trp
 225 230 235 240

Met Arg Gly Asp Gln Glu Gln Gln Gly Thr His Arg Gly Asp Phe Leu
 245 250 255

Pro Asn Ala Asp Glu Thr Trp Tyr Leu Gln Ala Thr Leu Asp Val Glu
 260 265 270

Ala Gly Glu Glu Ala Gly Leu Ala Cys Arg Val Lys His Ser Ser Leu
 275 280 285

Gly Gly Gln Asp Ile Ile Leu Tyr Trp Asp Ala Arg Gln Ala Pro Val
 290 295 300

Gly Leu Ile Val Phe Ile Val Leu Ile Met Leu Val Val Val Gly Ala
 305 310 315 320

Val Val Tyr Tyr Ile Trp Arg Arg Arg Ser Ala Tyr Gln Asp Ile Arg
 325 330 335