

SEQUENCE LISTING

<110> Astellas Pharma Inc.
 <120> Novel anti-human Tie2 antibody
 <130> A15017A00
 <150> JP2014-145135
 <151> 2014-07-15
 <160> 23
 <170> PatentIn version 3.5
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 <211> 2037
 <212> DNA
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 <223> H-chain of anti-human Tie2 antibody

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 <222> (1).. (2037)

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gct atg cac tgg gtg cga cag gcc cct ggc aag gga ctg gaa tgg gtg	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
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Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val	
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aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac acc ctg tac	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
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gct aag gac atc cgg gaa cag ctg gtg gaa gat gcc ttc gac atc tgg	336
Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp	
100 105 110	

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Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys		
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Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
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Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
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Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
225 230 235 240

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
245 250 255

Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
260 265 270

Glu Trp Val Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala
275 280 285

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
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290

295

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Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
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Tyr Tyr Cys Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe
 325 330 335

Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 340 345 350

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 355 360 365

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
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Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 385 390 395 400

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 405 410 415

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 420 425 430

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
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Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
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Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
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 485 490 495

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
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Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
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Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
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Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
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Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
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Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
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Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
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Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
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Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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<222> (1).. (657)

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His	Arg	Tyr	Asn 35	Tyr	Leu	Asp	Trp 40	Tyr	Gln	Gln	Lys	Pro 45	Gly	Lys	Ala	
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Pro	Lys 50	Leu	Leu	Ile	Tyr	Leu 55	Gly	Ser	Asn	Arg	Ala 60	Ser	Gly	Val	Pro	
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Ser 65	Arg	Phe	Ser	Gly	Ser 70	Gly	Ser	Gly	Thr	Asp 75	Phe	Thr	Leu	Thr 80	Ile	
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Ser	Ser	Val	Gln 85	Pro	Glu	Asp	Phe	Ala	Thr 90	Tyr	Tyr	Cys	Met	Gln 95	Thr	
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Leu	Gln	Thr	Pro 100	Leu	Thr	Phe	Gly	Gln 105	Gly	Thr	Lys	Val	Glu 110	Ile	Lys	
cgt	acg	gtg	gct	gca	cca	tot	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	384
Arg	Thr	Val 115	Ala	Ala	Pro	Ser	Val 120	Phe	Ile	Phe	Pro	Pro 125	Ser	Asp	Glu	
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Gln 130	Leu	Lys	Ser	Gly	Thr	Ala 135	Ser	Val	Val	Cys	Leu 140	Leu	Asn	Asn	Phe	
tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	480
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Ser	Gly	Asn	Ser	Gln 165	Glu	Ser	Val	Thr	Glu 170	Gln	Asp	Ser	Lys	Asp 175	Ser	
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Thr	Tyr	Ser	Leu 180	Ser	Ser	Thr	Leu	Thr 185	Leu	Ser	Lys	Ala	Asp 190	Tyr	Glu	
aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tgc	624
Lys	His	Lys 195	Val	Tyr	Ala	Cys	Glu 200	Val	Thr	His	Gln	Gly 205	Leu	Ser	Ser	
ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt						657
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35 40 45

Pro Lys Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Val Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Met Gln Thr
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
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Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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<210> 5
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 <212> DNA
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 <223> H-chain of anti-human Tie2 antibody

<220>
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 <222> (1).. (2037)

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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 gct atg cac tgg gtg cga cag gcc cct ggc aag gga ctg gaa tgg gtg 144
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gcc ggc atc tcc tgg aac tcc ggc tct atc gtg tac gcc gac tcc gtg 192
 Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val
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 aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac acc ctg tac 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg tac tac tgc 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gct aag gac atc cgg gaa cag ctg gtg gaa gat gcc ttc gac atc tgg 336
 Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
 100 105 110
 ggc cag ggc acc ctc gtg acc gtg tcc tct gct tct acc aag ggc ccc 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 tcc gtg ttc cct ctg gcc cct tcc agc aag tct acc tct ggc ggc aca 432
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

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gtg ccc tcc agc tct ctg ggc acc cag acc tac atc tgc aac gtg aac Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 195 200 205	624
cac aag ccc tcc aac acc aag gtg gac aag aag gtg gaa ccc aag tcc His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 210 215 220	672
tgc ggc agc gag gtg cag ctg gtg gaa agt ggg gga ggc ctg gtg cag Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 225 230 235 240	720
cca ggt gga agc ctg aga ctg agc tgc gcc gct tct ggc ttt acc ttt Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 245 250 255	768
gat gat tat gcc atg cat tgg gtg cgc cag gct cca ggg aaa ggc ctg Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 260 265 270	816
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act ctg tac ctg cag atg aat agc ctg cgc gct gag gat aca gct gtg Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 305 310 315 320	960
tat tac tgt gcc aag gat att cgc gag cag ctg gtg gaa gat gct ttt Tyr Tyr Cys Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe 325 330 335	1008
gat att tgg ggg cag ggt aca ctc gtg aca gtg tct agc gcc tcc acc Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr 340 345 350	1056
aag ggc cca agc gtg ttc cca ctg gct ccc agc tcc aag agc acc tcc Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser 355 360 365	1104

ggt gga act gct gcc ctg ggc tgt ctc gtg aaa gat tat ttt cct gag Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu 370 375 380	1152
cct gtg act gtg tcc tgg aat agc ggc gct ctg acc agc gga gtg cat Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His 385 390 395 400	1200
acc ttt cca gcc gtg ctg cag agc agc ggc ctg tat agc ctg tcc agc Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser 405 410 415	1248
gtc gtg acc gtg cct tcc tct agc ctg gga aca cag aca tat atc tgt Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys 420 425 430	1296
aat gtg aat cat aag ccc agt aat acc aaa gtg gat aag aaa gtg gaa Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu 435 440 445	1344
cct aag agc tgc gac aag acc cac acc tgt ccc cct tgt cct gcc cct Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 450 455 460	1392
gaa gct gct ggc ggc cct tct gtg ttt ctg ttc ccc cca aag cct aag Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys 465 470 475 480	1440
gac acc ctg atg gcc tcc cgg acc ccc gaa gtg acc tgc gtg gtg gtg Asp Thr Leu Met Ala Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 485 490 495	1488
gat gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 500 505 510	1536
ggc gtg gaa gtg cac aac gcc aag acc aag cct aga gag gaa cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 515 520 525	1584
aac tcc acc tac cgg gtg gtg tcc gtg ctg aca gtg ctg cat cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 530 535 540	1632
tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 545 550 555 560	1680
ccc gcc tcc atc gaa aag acc atc tcc aag gcc aag ggc cag ccc cgg Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 565 570 575	1728
gaa ccc cag gtg tac aca ctg ccc cct agc agg gac gag ctg acc aag Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 580 585 590	1776
aac cag gtg tcc ctg acc tgt ctc gtg aag ggc ttc tac ccc tcc gat	1824

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 595 600 605

atc gcc gtg gaa tgg gag tcc aac ggc cag cct gag aac aac tat aag 1872
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 610 615 620

acc acc ccc cct gtg ctg gac tcc gac ggc tca ttc ttt ctg tac tcc 1920
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 625 630 635 640

aag ctg acc gtg gac aag tcc cgg tgg cag cag ggc aac gtg ttc tcc 1968
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 645 650 655

tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc cag aag tcc 2016
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 660 665 670

ctg tcc ctg agc ccc ggc aaa 2037
 Leu Ser Leu Ser Pro Gly Lys
 675

<210> 6
 <211> 679
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
225 230 235 240

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
245 250 255

Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
260 265 270

Glu Trp Val Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala
275 280 285

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
290 295 300

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
305 310 315 320

Tyr Tyr Cys Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe
325 330 335

Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
340 345 350

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
355 360 365

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
370 375 380

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
385 390 395 400

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
405 410 415

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
420 425 430

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
435 440 445

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
450 455 460

Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
465 470 475 480

Asp Thr Leu Met Ala Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
485 490 495

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
500 505 510

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
515 520 525

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
530 535 540

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

545 550 555 560
 Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 565 570 575
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 580 585 590
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 595 600 605
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 610 615 620
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 625 630 635 640
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 645 650 655
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 660 665 670
 Leu Ser Leu Ser Pro Gly Lys
 675

<210> 7
 <211> 2037
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> H-chain of anti-human Tie2 antibody

<220>
 <221> CDS
 <222> (1).. (2037)

<400> 7
 gag gtg cag ctg gtg gaa tcc ggc gga ggc ctg gtg cag cct ggc ggc 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tct ctg aga ctg tcc tgt gcc gcc tcc ggc ttc acc ttc gac gac tac 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

gcc atg cac tgg gtc cga cag gcc cct ggc aag ggc ctg gaa tgg gtg Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	144
gcc ggc atc tcc tgg aac tcc ggc tcc atc gtg tac gcc gac tcc gtg Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val 50 55 60	192
aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac acc ctg tac Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80	240
ctg cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg tac tac tgc Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
gcc aag gac atc aga gag cag ctg gtc gag gac gcc ttc gac atc tgg Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp 100 105 110	336
ggc cag ggc acc ctg gtc acc gtg tcc tca gcc tcc acc aag ggc cca Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro 115 120 125	384
tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr 130 135 140	432
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 145 150 155 160	480
gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Ser Gly Val His Thr Phe Pro 165 170 175	528
gct gtc cta cag tcc tca gga ctc tac tcc ott agt agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Ser Leu Ser Ser Val Val Thr 180 185 190	576
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 195 200 205	624
cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 210 215 220	672
tgt gga tcc gag gtg cag ctg gtg gaa tcc ggc gga ggc ctg gtg cag Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 225 230 235 240	720
cct ggc ggc tct ctg aga ctg tcc tgt gcc gcc tcc ggc ttc acc ttc Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 245 250 255	768
gac gac tac gcc atg cac tgg gtc cga cag gcc cct ggc aag ggc ctg	816

Asp	Asp	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
			260					265					270			
gaa	tgg	gtg	gcc	ggc	atc	tcc	tgg	aac	tcc	ggc	tcc	atc	gtg	tac	gcc	864
Glu	Trp	Val	Ala	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Ile	Val	Tyr	Ala	
		275					280					285				
gac	tcc	gtg	aag	ggc	cgg	ttc	acc	atc	tcc	cgg	gac	aac	tcc	aag	aac	912
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
	290					295					300					
acc	ctg	tac	ctg	cag	atg	aac	tcc	ctg	cgg	gcc	gag	gac	acc	gcc	gtg	960
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
305					310					315					320	
tac	tac	tgc	gcc	aag	gac	atc	aga	gag	cag	ctg	gtc	gag	gac	gcc	ttc	1008
Tyr	Tyr	Cys	Ala	Lys	Asp	Ile	Arg	Glu	Gln	Leu	Val	Glu	Asp	Ala	Phe	
				325					330					335		
gac	atc	tgg	ggc	cag	ggc	acc	ctg	gtc	acc	gtg	tcc	tca	gcc	tcc	acc	1056
Asp	Ile	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	
			340					345					350			
aag	ggc	cca	tgc	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	1104
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
		355					360					365				
ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	1152
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	
		370				375					380					
ccg	gtg	acg	gtg	tgc	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	1200
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	
385					390					395					400	
acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctt	agt	agc	1248
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
				405					410					415		
gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	1296
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	
			420					425					430			
aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	1344
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
		435					440					445				
ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	1392
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
		450				455					460					
gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	1440
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
465					470					475					480	
gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	1488
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	

485	490	495	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 500 505 510			1536
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 515 520 525			1584
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 530 535 540			1632
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 545 550 555 560			1680
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 565 570 575			1728
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 580 585 590			1776
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 595 600 605			1824
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 610 615 620			1872
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 625 630 635 640			1920
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 645 650 655			1968
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 660 665 670			2016
ctc tcc ctg tct ccg ggt aaa Leu Ser Leu Ser Pro Gly Lys 675			2037

<210> 8
 <211> 679
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 8

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
20

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
450 455 460

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
465 470 475 480

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
485 490 495

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
500 505 510

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
515 520 525

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
530 535 540

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
545 550 555 560

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
565 570 575

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
580 585 590

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
595 600 605

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
610 615 620

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
625 630 635 640

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
645 650 655

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
660 665 670

Leu Ser Leu Ser Pro Gly Lys
675

<210> 9
<211> 2028
<212> DNA
<213> Artificial Sequence

<220>
<223> H-chain of anti-human Tie2 antibody

<220>
<221> CDS
<222> (1).. (2028)

<400> 9	
gag gtg cag ctg gtg gaa tcc ggc gga ggc ctg gtg cag cct ggc ggc	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
tct ctg aga ctg tcc tgt gcc gcc tcc ggc ttc acc ttc gac gac tac	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20 25 30	
gcc atg cac tgg gtc cga cag gcc cct ggc aag ggc ctg gaa tgg gtg	144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
gcc ggc atc tcc tgg aac tcc ggc tcc atc gtg tac gcc gac tcc gtg	192
Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac acc ctg tac	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg tac tac tgc	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcc aag gac atc aga gag cag ctg gtc gag gac gcc ttc gac atc tgg	336
Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp	
100 105 110	
ggc cag ggc acc ctg gtc acc gtg tcc tca gcc tcc acc aag ggc cca	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
115 120 125	
tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca	432
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	
130 135 140	
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg	480
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	

145	150	155	160	
gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 165 170 175				528
gct gtc cta cag tcc tca gga ctc tac tcc ctt agt agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 180 185 190				576
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 195 200 205				624
cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 210 215 220				672
tgt gga tcc gag gtg cag ctg gtg gaa tcc ggc gga ggc ctg gtg cag Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln 225 230 235 240				720
cct ggc ggc tct ctg aga ctg tcc tgt gcc gcc tcc ggc ttc acc ttc Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe 245 250 255				768
gac gac tac gcc atg cac tgg gtc cga cag gcc cct ggc aag ggc ctg Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 260 265 270				816
gaa tgg gtg gcc ggc atc tcc tgg aac tcc ggc tcc atc gtg tac gcc Glu Trp Val Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala 275 280 285				864
gac tcc gtg aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn 290 295 300				912
acc ctg tac ctg cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val 305 310 315 320				960
tac tac tgc gcc aag gac atc aga gag cag ctg gtc gag gac gcc ttc Tyr Tyr Cys Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe 325 330 335				1008
gac atc tgg ggc cag ggc acc ctg gtc acc gtg tcc tca gcc agc acc Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr 340 345 350				1056
aag ggg ccc tct gtg ttt ccc ctt gcc cct tgc agt agg tct acc agc Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser 355 360 365				1104
gaa agt act gcc gcc ctt ggc tgt ctg gtg aaa gat tat ttt cct gaa Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu 370 375 380				1152

cct Pro 385	gtc Val	acc Thr	gtg Val	tcc Ser	tgg Trp 390	aac Asn	tcc Ser	ggg Gly	gct Ala	ttg Leu 395	act Thr	tct Ser	ggc Gly	gtt Val	cat His 400	1200
act Thr	ttt Phe	cct Pro	gca Ala	gtc Val 405	ctg Leu	caa Gln	agt Ser	tct Ser	ggc Gly 410	ctg Leu	tac Tyr	agc Ser	ctt Leu	agc Ser 415	tcc Ser	1248
gtg Val	gta Val	act Thr	gtg Val 420	cct Pro	tcc Ser	tct Ser	tct Ser	ctg Leu 425	ggg Gly	acc Thr	aaa Lys	acc Thr	tat Tyr 430	acc Thr	tgc Cys	1296
aat Asn	gtg Val	gac Asp 435	cac His	aaa Lys	cct Pro	tct Ser	aat Asn 440	act Thr	aag Lys	gtc Val	gac Asp	aag Lys 445	agg Arg	gtg Val	gag Glu	1344
tct Ser	aag Lys 450	tac Tyr	gga Gly	cca Pro	cct Pro	tgt Cys 455	cct Pro	cca Pro	tgc Cys	ccc Pro	gcc Ala 460	ccc Pro	gag Glu	ttc Phe	gag Glu	1392
ggc Gly 465	ggg Gly	cct Pro	agt Ser	gtg Val 470	ttc Phe	ctg Leu	ttc Phe	cct Pro	cca Pro	aag Lys 475	ccc Pro	aag Lys	gac Asp	acc Thr	ttg Leu 480	1440
atg Met	ata Ile	agc Ser	agg Arg	act Thr 485	cct Pro	gag Glu	gtg Val	aca Thr	tgt Cys 490	gtg Val	gtt Val	gta Val	gac Asp	gtc Val 495	tct Ser	1488
cag Gln	gag Glu	gat Asp	ccc Pro 500	gaa Glu	gtg Val	cag Gln	ttt Phe	aat Asn 505	tgg Trp	tac Tyr	gtg Val	gat Asp	gga Gly 510	gtc Val	gag Glu	1536
gtg Val	cac His	aac Asn 515	gcc Ala	aaa Lys	acc Thr	aaa Lys	ccc Pro 520	cgc Arg	gag Glu	gag Glu	caa Gln	ttc Phe 525	aac Asn	tcc Ser	acc Thr	1584
tat Tyr 530	cgc Arg	gtg Val	gtg Val	tct Ser	gtc Val	ctg Leu 535	acc Thr	gtc Val	ctg Leu	cac His	caa Gln 540	gat Asp	tgg Trp	ctg Leu	aac Asn	1632
gga Gly 545	aaa Lys	gaa Glu	tat Tyr	aag Lys	tgt Cys 550	aaa Lys	gta Val	agc Ser	aat Asn	aag Lys 555	ggc Gly	ctg Leu	cct Pro	tca Ser	tcc Ser 560	1680
att Ile	gag Glu	aag Lys	aca Thr	atc Ile 565	agc Ser	aag Lys	gca Ala	aag Lys	ggc Gly 570	cag Gln	cct Pro	aga Arg	gaa Glu	ccc Pro 575	caa Gln	1728
gtg Val	tac Tyr	acc Thr	ctc Leu 580	cca Pro	ccc Pro	tct Ser	cag Gln	gag Glu 585	gaa Glu	atg Met	acc Thr	aag Lys	aat Asn 590	cag Gln	gtt Val	1776
agc Ser	ctt Leu	act Thr 595	tgt Cys	ctc Leu	gta Val	aag Lys	ggg Gly 600	ttc Phe	tac Tyr	cct Pro	agc Ser	gac Asp 605	att Ile	gct Ala	gtc Val	1824

gag tgg gaa agc aat gga cag cct gag aat aac tat aaa acc act ccc Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 610 615 620	1872
cca gtg ott gac tca gat ggc tct ttt ttc ott tac tcc cgc ttg aca Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr 625 630 635 640	1920
gtc gac aag agt aga tgg caa gag ggg aac gtg ttc agc tgc agt gtt Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val 645 650 655	1968
atg cac gag gca ctc cat aac cat tat act cag aaa tcc ttg agc ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 660 665 670	2016
tcc ctt gga aag Ser Leu Gly Lys 675	2028

<210> 10
 <211> 676
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
225 230 235 240

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
245 250 255

Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
260 265 270

Glu Trp Val Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala
275 280 285

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
290 295 300

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
305 310 315 320

Tyr Tyr Cys Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe
325 330 335

Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
340 345 350

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
355 360 365

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
370 375 380

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
385 390 395 400

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
405 410 415

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
420 425 430

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
435 440 445

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
450 455 460

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
465 470 475 480

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
485 490 495

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
500 505 510

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
515 520 525

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
530 535 540

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
545 550 555 560

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
565 570 575

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
580 585 590

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
595 600 605

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
610 615 620

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
625 630 635 640

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
645 650 655

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
660 665 670

Ser Leu Gly Lys
675

<210> 11
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> H-chain of anti-human Tie2 antibody

<220>
<221> CDS
<222> (1).. (1356)

<400> 11
gag gtg cag ctg gtg gaa tcc ggc gga ggc ctg gtg cag cct ggc ggc 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tct ctg aga ctg tcc tgt gcc gcc tcc ggc ttc acc ttc gac gac tac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

gcc atg cac tgg gtc cga cag gcc cct ggc aag ggc ctg gaa tgg gtg 144
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gcc ggc atc tcc tgg aac tcc ggc tcc atc gtg tac gcc gac tcc gtg Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val 50 55 60	192
aag ggc cgg ttc acc atc tcc cgg gac aac tcc aag aac acc ctg tac Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80	240
ctg cag atg aac tcc ctg cgg gcc gag gac acc gcc gtg tac tac tgc Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	288
gcc aag gac atc aga gag cag ctg gtc gag gac gcc ttc gac atc tgg Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp 100 105 110	336
ggc cag ggc acc ctg gtc acc gtg tcc tca gcc tcc acc aag ggc cca Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro 115 120 125	384
tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr 130 135 140	432
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 145 150 155 160	480
gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 165 170 175	528
gct gtc cta cag tcc tca gga ctc tac tcc ctt agt agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 180 185 190	576
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 195 200 205	624
cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser 210 215 220	672
tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 225 230 235 240	720
ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 245 250 255	768
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 260 265 270	816

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 275 280 285	864
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 290 295 300	912
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 305 310 315 320	960
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 325 330 335	1008
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 340 345 350	1056
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 355 360 365	1104
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 370 375 380	1152
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 385 390 395 400	1200
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 405 410 415	1248
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 420 425 430	1296
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 435 440 445	1344
tct ccg ggt aaa Ser Pro Gly Lys 450	1356

<210> 12
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Ile Arg Glu Gln Leu Val Glu Asp Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
290 295 300

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 13

Glu Pro Lys Ser Cys Gly Ser
1 5

<210> 14
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 14

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Ser
1 5 10

<210> 15
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 15

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser
20

<210> 16
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 16

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

<210> 17

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 17

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
35 40

<210> 18

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> linker

<400> 18

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
35 40 45

Gly Gly Gly Ser
50

<210> 19
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 19

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
35 40 45

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

<210> 20
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 20

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Ser Pro Arg Ser
1 5 10 15

Pro Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro
20 25 30

Glu Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Glu
35 40 45

Pro Lys Ser Ser Asp Thr Pro Pro Pro Ser Pro Arg Ser Pro Gly Ser
50 55 60

<210> 21
<211> 3369
<212> DNA

<213> Homo sapiens

<400> 21

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tctctcacct gcattgcctc tgggtggcgc ccccatgagc ccatcaccat aggaaggagc	180
tttgaagcct taatgaacca gcaccaggat ccgctggaag ttactcaaga tgtgaccaga	240
gaatgggcta aaaaagttgt ttggaagaga gaaaaggcta gtaagatcaa tggtgcttat	300
ttctgtgaag ggcgagttcg aggagaggca atcaggatac gaaccatgaa gatgcgtcaa	360
caagcttcct tcctaccagc tactttaact atgactgtgg acaagggaga taacgtgaac	420
atatctttca aaaaggtatt gactaaagaa gaagatgcag tgatttaca aaatggttcc	480
ttcatccatt cagtgcctcg gcatgaagta cctgatattc tagaagtaca cctgcctcat	540
gctcagcccc aggatgctgg agtgtactcg gccagggtata taggaggaaa cctcttcacc	600
tcggccttca ccaggctgat agtcgggaga tgtgaagccc agaagtgggg acctgaatgc	660
aacctctct gtactgcttg tatgaacaat ggtgtctgcc atgaagatac tggagaatgc	720
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ggcagaactt gtaaagaaag gtgcagtgga caagagggat gcaagtctta tgtgttctgt	840
ctccctgacc cctatgggtg ttctgtgcc acaggctgga agggctctgca gtgcaatgaa	900
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gagatgtgtg atcgcttcca aggatgtctc tgctctccag gatggcaggg gctccagtgt	1020
gagagagaag gcataccgag gatgacocca aagatagtgg atttgccaga tcatatagaa	1080
gtaaacagtg gtaaatttaa tcccatttgc aaagcttctg gctggccgct acctactaat	1140
gaagaaatga ccctggtgaa gccggatggg acagtgtctc atccaaaaga cttaaccat	1200
acggatcatt tctcagtagc catattcacc atccaccgga tcctcccccc tgactcagga	1260
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cttctataca aaccogttaa tcactatgag gcttggaac atattcaagt gacaaatgag	1500
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ctacttaaca acttacatcc cagggagcag tacgtggtcc gagctagagt caacaccaag	1860
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aactgtgatg atgaggtgta tgatctaata agacaatgct ggccgggagaa gccttatgag	3240
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gaagcggcc

3369

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> thrombin cleavage site

<400> 22

Leu Val Pro Arg Gly Ser
1 5

<210> 23
<211> 231
<212> PRT
<213> Homo sapiens

<400> 23

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
1 5 10 15

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65 70 75 80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
100 105 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
130 135 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
145 150 155 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
210 215 220

Leu Ser Leu Ser Pro Gly Lys
225 230