

Sequence Listing

<110> Biotheus (Suzhou) Co., Ltd.

<120> COMBINED EXPRESSION OF A CHIMERIC CD3 FUSION PROTEIN AND AN ANTI-CD3-BASED BISPECIFIC T CELL ACTIVATING ELEMENT

<130> 374629

<150> CN201910866695.4

<151> 2019-09-12

<160> 76

<170> SIPOSequenceListing 1.0

<210> 1

<211> 66

<212> DNA

<213> Homo sapiens

<220>

<223> GM-CSFRsp

<400> 1

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atcccc 66

<210> 2

<211> 22

<212> PRT

<213> Homo sapiens

<220>

<223> GM-CSFRsp

<400> 2

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15
Ala Phe Leu Leu Ile Pro
20

<210> 3

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<223> CD3eECD

<400> 3
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accaccgtga tcctgacctg ccctcagtac cccggctccg agatcctgtg gcagcacaac 120
gataagaaca tcggcggaga cgaggacgac aagaacatcg gaagtgcga ggaccacctg 180
agcctgaagg aattcagcga actggagcag agcggctatt acgtctgcta cccagagga 240
agcaaaccag aggacgcaa cttctatctg tacctgagag ccagagtgtg cgagaactgc 300
atggaaatgg ac 312

<210> 4
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<223> CD3eECD

<400> 4
Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1 5 10 15
Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
20 25 30
Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
35 40 45
Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
50 55 60
Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65 70 75 80
Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
85 90 95
Cys Glu Asn Cys Met Glu Met Asp
100

<210> 5
<211> 135
<212> DNA
<213> Homo sapiens

<220>
<223> CD8Hinge

<400> 5
acaaccaccc ccgccccag accccaacc cctgctccta ccattgccag ccagccactg 60
tcctgaggc ccgaagcctg cagaccagca gccggcggag ccgtgcacac cagaggactg 120
gacttcgcct gcgac 135

<210> 6
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<223> CD8Hinge

<400> 6
Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15
Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30
Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 7
<211> 72
<212> DNA
<213> Homo sapiens

<220>
<223> CD8TM

<400> 7
atctacatct gggccccct ggccgggacc tgcggagtgc tgctgctgag cctggtgatt 60
actctgtact gt 72

<210> 8
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<223> CD8TM

<400> 8
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15
Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 9
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<223> 4-1BBcostimulatorydomain

<400> 9
aagaggggaa gaaagaaact gctgtatatc ttcaagcagc cctttatgag acccgtgcag 60
accacccagg aggaggacgg ctgctcctgt agattccccg aggaggagga gggcggctgc 120
gagctg 126

<210> 10
 <211> 42
 <212> PRT
 <213> Homo sapiens

<220>
 <223> 4-1BBcostimulatorydomain

<400> 10
 Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
 1 5 10 15
 Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 20 25 30
 Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 35 40

<210> 11
 <211> 336
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CD3z

<400> 11
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 tacaacgagc tgaacctggg cagaagagag gagtatgacg tgctggacaa gagaagagga 120
 agagaccccg agatgggagg aaagccaaga agaaagaacc cccaggaggg cctgtacaat 180
 gagctgcaga aggacaagat ggcagaggca tatagcgaga tcggaatgaa gggagagaga 240
 agaagaggaa agggacacga cggactgtac cagggcctga gcacagctac aaaggacaca 300
 tacgacgcac tgcacatgca ggcactgcca ccaaga 336

<210> 12
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD3z

<400> 12
 Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
 1 5 10 15
 Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 20 25 30
 Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 35 40 45
 Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 50 55 60
 Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
 65 70 75 80

Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala
				85					90					95	
Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg
			100					105					110		

<210> 13
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> FLAG

<400> 13
 gactacaagg acgatgacga caag 24

<210> 14
 <211> 8
 <212> PRT
 <213> artificial sequence

<220>
 <223> FLAG

<400> 14
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 15
 <211> 1074
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD3e-BBζ

<400> 15
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 atccccgacg gcaacgagga gatggggcggc atcacccaga cccctacaa ggtgtccatc 120
 tccggcacca ccgtgatcct gacctgccct cagtaccccg gctccgagat cctgtggcag 180
 cacaacgata agaacatcgg cggagacgag gacgacaaga acatcggaag tgacgaggac 240
 cacctgagcc tgaaggaatt cagcgaactg gagcagagcg gctattacgt ctgctacccc 300
 agaggaagca aaccagagga cgccaacttc tatctgtacc tgagagccag agtgtgagcag 360
 aactgcatgg aaatggacac aaccaccccc gcccccagac ccccaacccc tgctcctacc 420
 attgccagcc agccactgtc cctgaggccc gaagcctgca gaccagcagc cggcggagcc 480
 gtgcacacca gaggactgga cttgcctgac gacatctaca tctgggcccc cctggcgggg 540
 acctgcggag tgctgctgct gagcctggtg attactctgt actgtaagag gggaagaaag 600
 aaactgctgt atatcttcaa gcagcccttt atgagaccg tgacagaccac ccaggaggag 660
 gacggctgct cctgtagatt ccccaggagg gagggggcg gctgagagct gagagtgaag 720
 ttctccagga gcgccgacgc ccccgccctac cagcaggggac agaaccagct gtacaacgag 780
 ctgaacctgg gcagaagaga ggagtatgac gtgctggaca agagaagagg aagagacccc 840

gagatgggag gaaagccaag aagaaagaac ccccaggagg gcctgtacaa tgagctgcag	900
aaggacaaga tggcagaggc atatagcgag atcggaatga agggagagag aagaagagga	960
aagggacacg acggactgta ccagggcctg agcacagcta caaaggacac atacgacgca	1020
ctgcacatgc aggcaactgcc accaagagac tacaaggacg atgacgacaa gtaa	1074

<210> 16
 <211> 357
 <212> PRT
 <213> artificial sequence

<220>
 <223> CD3e-BBζ

<400> 16

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	
Ala	Phe	Leu	Leu	Ile	Pro	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr
			20					25					30		
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr
		35					40					45			
Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys
	50					55					60				
Asn	Ile	Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp
65				70					75					80	
His	Leu	Ser	Leu	Lys	Glu	Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr
			85					90					95		
Val	Cys	Tyr	Pro	Arg	Gly	Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu
			100					105					110		
Tyr	Leu	Arg	Ala	Arg	Val	Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Thr	Thr
	115						120					125			
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln
	130					135					140				
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala
145				150					155						160
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala
			165					170						175	
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Ser	Leu	Val	Ile	Thr	
		180					185					190			
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln
	195					200					205				
Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser
	210				215						220				
Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys
225				230						235					240
Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln
			245					250						255	
Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu
		260					265						270		
Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg
	275					280						285			
Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met
	290				295						300				
Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly

305		310		315		320
Lys	Gly	His	Asp	Gly	Leu	Tyr
				325		
Thr	Tyr	Asp	Ala	Leu	His	Met
				340		
Asp	Asp	Asp	Asp	Lys		
				355		

<210> 17
 <211> 351
 <212> DNA
 <213> artificial sequence

<220>
 <223> CAIXVHH

<400> 17	
caggtgcagc tgcaggagtc tggcggcggc ctggtgcagc ctggaggatc tctgagactg	60
agctgcgccg cctccggcaa cagcgctaac atcttttcct ttgcttccgt ggcctggtat	120
aggcaggccc cagggaagca gagagagctg gtggccgtca ttacatccgc cggcggcaca	180
aagtactccg actctgtgaa gggaagattc accattagcc gggacaatgc caagaacacc	240
attctgctgc agatgaactc actgaaacct gaggataccg ccgtgtatta ttgtaacgtg	300
gactacctgc aggactactg ggggcagggc acccaggtga cagtgagcag c	351

<210> 18
 <211> 117
 <212> PRT
 <213> llama Antibody

<220>
 <223> CAIXVHH

<400> 18	
Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn Ser Ala Asn Ile Phe	
20 25 30	
Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg	
35 40 45	
Glu Leu Val Ala Val Ile Thr Ser Ala Gly Gly Thr Lys Tyr Ser Asp	
50 55 60	
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr	
65 70 75 80	
Ile Leu Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr	
85 90 95	
Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr Trp Gly Gln Gly Thr Gln	
100 105 110	
Val Thr Val Ser Ser	
115	

<210> 19
 <211> 729

<212> DNA
<213> Mouse Antibody

<220>
<223> L2K scFv

<400> 19
gatatcaagc tgcagcagag cggagccgag ctggccaggc ctggagctag cgtgaagatg 60
agctgcaaaa ccagcggcta cacattcacc agatacacca tgcattgggt gaagcagaga 120
cccggacagg gactggagtg gattggatac attaacccca gtcgaggcta caccaactac 180
aaccagaagt tcaaagacaa agccaccctg accaccgaca aaagcagcag caccgcatat 240
atgcagctga gctctctgac cagcgaggac agcgccgtgt actactgcgc cagatactac 300
gacgaccact actgcctgga ctactggggc cagggaacca ccctgacagt gtctagcgtg 360
gagggcggat ctggcggctc aggcggaagc ggaggaggcg gaggagtgga cgatatccag 420
ctgaccaga gtcccccat catgagtga agtcccggcg aaaaagtga catgacctgt 480
agagcttctt ctagtgtgag ttatatgaac tggtagcagc agaagagcgg gaccagcccc 540
aaaagatgga tctacgacac cagcaaggtg gccagcggcg tgccctaccg gttcagcgga 600
tctggcagcg gaacctcata cagcctgact atcagcagca tggaagcaga agacgccgca 660
acctactact gccagcagtg gagctctaac ccactgacct tcggcgctgg caccaagctg 720
gagctgaag 729

<210> 20
<211> 243
<212> PRT
<213> Mouse Antibody

<220>
<223> L2K scFv

<400> 20
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
115 120 125
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
130 135 140
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
145 150 155 160
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
165 170 175

Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
			180					185					190		
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser
		195					200					205			
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
	210					215					220				
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu
225					230					235					240
Glu	Leu	Lys													

<210> 21
 <211> 1164
 <212> DNA
 <213> artificial sequence

<220>
 <223> 1st-CAIX-BiTA

<400> 21

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agactgagct	gcgccgcctc	cggcaacagc	gctaacatct	tttcctttgc	ttccgtggcc	180
tggtataggc	aggccccagg	gaagcagaga	gagctggtgg	ccgtcattac	atccgccggc	240
ggcacaaagt	actccgactc	tgtgaaggga	agattcacca	ttagccggga	caatgccaaag	300
aacaccattc	tgctgcagat	gaactcactg	aaacctgagg	ataccgccgt	gtattattgt	360
aacgtggact	acctgcagga	ctactggggg	cagggcaccc	aggtgacagt	gagcagcggc	420
ggcggcgga	gcgatatcaa	gctgcagcag	agcggagccg	agctggccag	gcctggagct	480
agcgtgaaga	tgagctgcaa	aaccagcggc	tacacattca	ccagatacac	catgcattgg	540
gtgaagcaga	gacccggaca	gggactggag	tggattggat	acattaaccc	cagtcgaggc	600
tacaccaact	acaaccagaa	gttcaaagac	aaagccaccc	tgaccaccga	caaaagcagc	660
agcaccgcat	atatgcagct	gagctctctg	accagcgagg	acagcgccgt	gtactactgc	720
gccagatact	acgacgacca	ctactgcctg	gactactggg	gccagggaac	caccctgaca	780
gtgtctagcg	tggagggcgg	atctggcggc	tcaggcgga	gcggaggagg	cggaggagtg	840
gacgatatcc	agctgaccca	gagtcgccgc	atcatgagtg	caagtcccgg	cgaaaaagtg	900
accatgacct	gtagagcttc	ttctagtgtg	agttatatga	actggtacca	gcagaagagc	960
gggaccagcc	ccaaaagatg	gatctacgac	accagcaagg	tggccagcgg	cgtgccctac	1020
cggttcagcg	gatctggcag	cggaaacctca	tacagcctga	ctatcagcag	catggaagca	1080
gaagacgccg	caacctacta	ctgccagcag	tggagctcta	accactgac	cttcggcgct	1140
ggcaccaagc	tggagctgaa	gtaa				1164

<210> 22
 <211> 387
 <212> PRT
 <213> artificial sequence

<220>
 <223> 1st-CAIX-BiTA

<400> 22

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	

Ala Phe Leu Leu Ile Pro Gln Val Gln Leu Gln Glu Ser Gly Gly Gly
 20 25 30
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
 35 40 45
 Asn Ser Ala Asn Ile Phe Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln
 50 55 60
 Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Val Ile Thr Ser Ala Gly
 65 70 75 80
 Gly Thr Lys Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
 85 90 95
 Asp Asn Ala Lys Asn Thr Ile Leu Leu Gln Met Asn Ser Leu Lys Pro
 100 105 110
 Glu Asp Thr Ala Val Tyr Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr
 115 120 125
 Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 130 135 140
 Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
 165 170 175
 Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 195 200 205
 Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 225 230 235 240
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 245 250 255
 Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly
 260 265 270
 Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser
 275 280 285
 Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys
 290 295 300
 Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser
 305 310 315 320
 Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser
 325 330 335
 Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
 340 345 350
 Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
 355 360 365
 Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 370 375 380
 Glu Leu Lys
 385

<210> 23

<211> 54

<212> DNA

<213> Thoseaasigna virus

<220>

<223> T2A

<400> 23

gagggcagag gaagcctgct gacatgcgga gacgtggagg agaaccagg accc

54

<210> 24

<211> 18

<212> PRT

<213> Thoseaasigna virus

<220>

<223> T2A

<400> 24

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro

1

5

10

15

Gly Pro

<210> 25

<211> 2298

<212> DNA

<213> artificial sequence

<220>

<223> 1st-CAIX-CAB

<400> 25

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tccggcacca	ccgtgatcct	gacctgccct	cagtaccccc	gctccgagat	cctgtggcag	180
cacaacgata	agaacatcgg	cggagacgag	gacgacaaga	acatcggaag	tgacgaggac	240
cacctgagcc	tgaaggaatt	cagcgaactg	gagcagagcg	gctattacgt	ctgctacccc	300
agaggaaagca	aaccagagga	cgccaacttc	tatctgtacc	tgagagccag	agtgtgcgag	360
aactgcatgg	aaatggacac	aaccaccccc	gccccagac	ccccaacccc	tgctcctacc	420
attgccagcc	agccactgtc	cctgaggccc	gaagcctgca	gaccagcagc	cggcggagcc	480
gtgcacacca	gaggactgga	cttcgcctgc	gacatctaca	tctgggcccc	cctggccggg	540
acctgcggag	tgctgctgct	gagcctggtg	attactctgt	actgtaagag	gggaagaaag	600
aaactgctgt	atatcttcaa	gcagcccttt	atgagaccgc	tgagaccac	ccaggaggag	660
gacggctgct	cctgtagatt	ccccgaggag	gaggagggcg	gctgcgagct	gagagtgaag	720
ttctccagga	gcgccgacgc	ccccgcctac	cagcagggac	agaaccagct	gtacaacgag	780
ctgaacctgg	gcagaagaga	ggagtatgac	gtgctggaca	agagaagagg	aagagacccc	840
gagatgggag	gaaagccaag	aagaaagaac	ccccaggagg	gcctgtacaa	tgagctgcag	900
aaggacaaga	tggcagaggc	atatagcgag	atcggaatga	agggagagag	aagaagagga	960
aaggggacacg	acggactgta	ccagggcctg	agcacagcta	caaaggacac	atacgacgca	1020
ctgcacatgc	aggcactgcc	accaagagac	tacaaggacg	atgacgacaa	gggaagcgga	1080
gagggcagag	gaagcctgct	gacatgcgga	gacgtggagg	agaaccagg	acccatgctg	1140
ctgctggtga	cctccctgct	gctgtgcgag	ctgccccacc	ccgctttcct	gctgatcccc	1200
caggtgcagc	tgacaggatc	tggcggcggc	ctggtgcagc	ctggaggatc	tctgagactg	1260
agctgcgccg	cctccggcaa	cagcgctaac	atcttttcct	ttgctttcgt	ggcctggtat	1320

aggcaggccc	caggaagca	gagagagctg	gtggccgtca	ttacatccgc	cggcggcaca	1380
aagtactccg	actctgtgaa	gggaagattc	accattagcc	gggacaatgc	caagaacacc	1440
attctgctgc	agatgaactc	actgaaacct	gaggataccg	ccgtgtatta	ttgtaacgtg	1500
gactacctgc	aggactactg	ggggcagggc	accaggtga	cagtgagcag	cggcggcggc	1560
ggaagcgata	tcaagctgca	gcagagcgga	gccgagctgg	ccaggcctgg	agctagcgtg	1620
aagatgagct	gcaaaaccag	cggctacaca	ttcaccagat	acaccatgca	ttgggtgaag	1680
cagagacccg	gacagggact	ggagtggatt	ggatacatta	accccagtcg	aggctacacc	1740
aactacaacc	agaagttcaa	agacaaagcc	accctgacca	ccgacaaaag	cagcagcacc	1800
gcataatgct	agctgagctc	tctgaccagc	gaggacagcg	ccgtgtacta	ctgcgccaga	1860
tactacgacg	accactactg	cctggactac	tggggccagg	gaaccaccct	gacagtgtct	1920
agcgtggagg	gcggatctgg	cggctcaggc	ggaagcggag	ggagcggagg	agtggacgat	1980
atccagctga	cccagagtcc	cgccatcatg	agtgcaagtc	ccggcgaaaa	agtgaccatg	2040
acctgtagag	cttcttctag	tgtgagttat	atgaactggt	accagcagaa	gagcgggacc	2100
agccccaaaa	gatggatcta	cgacaccagc	aaggtggcca	gcggcgtgcc	ctaccggttc	2160
agcggatctg	gcagcggaac	ctcatacagc	ctgactatca	gcagcatgga	agcagaagac	2220
gccgcaacct	actactgcc	gcagtggagc	tctaaccac	tgaccttcgg	cgctggcacc	2280
aagctggagc	tgaagtaa					2298

<210> 26
 <211> 765
 <212> PRT
 <213> artificial sequence

<220>
 <223> 1st-CAIX-CAB

<400> 26

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
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Ala	Phe	Leu	Leu	Ile	Pro	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr
			20					25					30		
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr
			35				40					45			
Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys
	50					55					60				
Asn	Ile	Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp
65				70					75					80	
His	Leu	Ser	Leu	Lys	Glu	Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr
			85					90					95		
Val	Cys	Tyr	Pro	Arg	Gly	Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu
			100					105					110		
Tyr	Leu	Arg	Ala	Arg	Val	Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Thr	Thr
		115					120					125			
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln
	130					135					140				
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala
145				150					155					160	
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala
			165					170						175	
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr
		180					185						190		
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln
		195					200					205			

Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser		
	210					215					220						
Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys		
225				230						235					240		
Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln		
				245					250					255			
Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu		
		260					265						270				
Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg		
	275					280						285					
Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met		
290						295					300						
Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly		
305					310					315					320		
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp		
				325					330					335			
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys		
			340					345					350				
Asp	Asp	Asp	Asp	Lys	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr		
	355					360						365					
Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu	Leu	Leu	Val	Thr		
370						375					380						
Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe	Leu	Leu	Ile	Pro		
385				390					395						400		
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly		
			405					410						415			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asn	Ser	Ala	Asn	Ile	Phe		
			420					425				430					
Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg		
	435					440					445						
Glu	Leu	Val	Ala	Val	Ile	Thr	Ser	Ala	Gly	Gly	Thr	Lys	Tyr	Ser	Asp		
450					455						460						
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr		
465				470					475						480		
Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr		
			485					490						495			
Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln		
		500						505				510					
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	Leu	Gln	Gln		
	515					520					525						
Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys		
530					535					540							
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys		
545				550					555						560		
Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser		
			565					570						575			
Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu		
			580					585					590				
Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu		
	595						600					605					
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Asp	Asp		
610					615					620							
His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser		
625					630					635					640		

Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 645 650 655
 Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
 660 665 670
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
 675 680 685
 Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg
 690 695 700
 Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe
 705 710 715 720
 Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met
 725 730 735
 Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn
 740 745 750
 Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 755 760 765

<210> 27
 <211> 45
 <212> DNA
 <213> artificial sequence

<220>
 <223> Linker

<400> 27
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45

<210> 28
 <211> 15
 <212> PRT
 <213> artificial sequence

<220>
 <223> Linker

<400> 28
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 29
 <211> 555
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CD3e

<400> 29
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 accaccgtgatcctgacatgccctcagtatccaggaagcgagatcctgtggcagcacaaac

60
 120

gacaaaaaca	tcggcgggga	cgaggacgac	aaaaacattg	gcagcgacga	ggaccacctg	180
agcctgaagg	aattcagcga	actggagcag	agcggatact	acgtgtgcta	ccccagagga	240
agcaagcccg	aggacgcaa	cttctacctg	tacctgagag	ccagagtctg	cgagaactgt	300
atggagatgg	acgtgatgag	cgtggccaca	attgtgatcg	tggacatctg	catcaccggc	360
ggactgctgc	tgctggtcta	ctactggagc	aaaaacagaa	aagccaaggc	caagcccgtg	420
acaagaggag	ccggcgccgg	aggaagacag	agaggccaga	acaaggagcg	gccccccccc	480
gtgcctaacc	ctgattacga	gcccatacaga	aagggccaga	gagacctgta	cagcggcctg	540
aaccagagaa	gaatc					555

<210> 30
 <211> 185
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD3e

<400> 30

Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr	Gln	Thr	Pro	Tyr	Lys	Val
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Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr	Cys	Pro	Gln	Tyr	Pro	Gly
		20					25					30			
Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys	Asn	Ile	Gly	Gly	Asp	Glu
	35				40						45				
Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp	His	Leu	Ser	Leu	Lys	Glu
	50				55					60					
Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr	Val	Cys	Tyr	Pro	Arg	Gly
65					70					75					80
Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu	Tyr	Leu	Arg	Ala	Arg	Val
			85					90						95	
Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Val	Met	Ser	Val	Ala	Thr	Ile	Val
		100						105					110		
Ile	Val	Asp	Ile	Cys	Ile	Thr	Gly	Gly	Leu	Leu	Leu	Leu	Val	Tyr	Tyr
		115					120						125		
Trp	Ser	Lys	Asn	Arg	Lys	Ala	Lys	Ala	Lys	Pro	Val	Thr	Arg	Gly	Ala
	130					135					140				
Gly	Ala	Gly	Gly	Arg	Gln	Arg	Gly	Gln	Asn	Lys	Glu	Arg	Pro	Pro	Pro
145					150					155					160
Val	Pro	Asn	Pro	Asp	Tyr	Glu	Pro	Ile	Arg	Lys	Gly	Gln	Arg	Asp	Leu
			165					170						175	
Tyr	Ser	Gly	Leu	Asn	Gln	Arg	Arg	Ile							
			180					185							

<210> 31
 <211> 1020
 <212> DNA
 <213> artificial sequence

<220>
 <223> CAIX-TRuC

<400> 31

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agactgagct	gcgccgcctc	cggcaacagc	gctaacatct	tttcctttgc	ttccgtggcc	180
tggtataggc	aggccccagg	gaagcagaga	gagctggtgg	ccgtcattac	atccgccggc	240
ggcacaaagt	actccgactc	tgtgaaggga	agattcacca	ttagccggga	caatgccaaag	300
aacaccattc	tgctgcagat	gaactcactg	aaacctgagg	ataccgccgt	gtattattgt	360
aacgtggact	acctgcagga	ctactggggg	cagggcaccc	aggtgacagt	gagcagcggc	420
ggcggcgga	gcggaggagg	aggatctggc	ggcggaggaa	gcgatggaaa	cgaggagatg	480
gggggaatta	cacagacacc	ttacaaggtg	agtatcagcg	gcaccaccgt	gatacctgaca	540
tgccctcagt	atccaggaag	cgagatcctg	tggcagcaca	acgacaaaaa	catcggcggg	600
gacgaggacg	acaaaaacat	tggcagcgac	gaggaccacc	tgagcctgaa	ggaattcagc	660
gaactggagc	agagcggata	ctacgtgtgc	taccccagag	gaagcaagcc	cgaggacgcc	720
aacttctacc	tgtacctgag	agccagagtc	tgcgagaact	gtatggagat	ggacgtgatg	780
agcgtggcca	caattgtgat	cgtggacatc	tgcatacccg	gcggactgct	gctgctggtc	840
tactactgga	gcaaaaacag	aaaagccaag	gccaagcccc	tgacaagagg	agccggcggc	900
ggaggaagac	agagaggcca	gaacaaggag	cggccccccc	ccgtgcctaa	ccctgattac	960
gagcccatca	gaaagggcca	gagagacctg	tacagcggcc	tgaaccagag	aagaatctaa	1020

<210> 32
 <211> 339
 <212> PRT
 <213> artificial sequence

<220>
 <223> CAIX-TRuC

<400> 32

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
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Ala	Phe	Leu	Leu	Ile	Pro	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly
			20					25					30		
Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly
		35					40				45				
Asn	Ser	Ala	Asn	Ile	Phe	Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln
	50					55					60				
Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Val	Ile	Thr	Ser	Ala	Gly
65					70				75					80	
Gly	Thr	Lys	Tyr	Ser	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg
			85					90						95	
Asp	Asn	Ala	Lys	Asn	Thr	Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro
		100					105						110		
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr
	115						120					125			
Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Gly	Asn	Glu	Glu	Met
145					150				155					160	
Gly	Gly	Ile	Thr	Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr
			165					170						175	
Val	Ile	Leu	Thr	Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln
	180						185						190		
His	Asn	Asp	Lys	Asn	Ile	Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly
	195					200						205			

Ser Asp Glu Asp His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln
210 215 220
Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala
225 230 235 240
Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu
245 250 255
Met Asp Val Met Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile
260 265 270
Thr Gly Gly Leu Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys
275 280 285
Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln
290 295 300
Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr
305 310 315 320
Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln
325 330 335
Arg Arg Ile

<210> 33
<211> 639
<212> DNA
<213> Homo sapiens

<220>
<223> TruncatedERBB2

<400> 33
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tgcgtgaact gcagccagtt cctccgcggt caggaatgcg tcgaagaatg ccgggttctg 180
cagggactgc ccagagaata cgtaaagcc agacactgcc tgccctgcca cccgaatgt 240
cagccccaga acggctccgt cacctgtttc ggccccgagg cagaccaatg cgtggcctgc 300
gtcactaca aggaccccc cttctgcgtg gcccggtgcc cttccggcgt gaagcccgc 360
ctctcctaca tgcccatttg gaagttcccc gatgaggaag gcgcctgcca gccctgtccc 420
atcaactgca cccactcctg cgttgacctg gacgacaagg gctgtcccgc cgaacagaga 480
gccagcccc tcacctctat catctccgcc gtggtgggca ttctgctggt cgtggtcctg 540
ggcgttggtg tcggcatcct gatcaaaaga agacaacaaa agatcagaaa gtacaccatg 600
cggcgctcc tggactacaa ggacgatgat gataagtaa 639

<210> 34
<211> 212
<212> PRT
<213> Homo sapiens

<220>
<223> TruncatedERBB2

<400> 34
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1 5 10 15
Ala Phe Leu Leu Ile Pro Ala Cys His Gln Leu Cys Ala Arg Gly His

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Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	
		35					40					45				
Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	
	50					55					60					
Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	
65				70						75					80	
Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	Ala	Asp	Gln	
			85						90					95		
Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	
		100						105					110			
Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	
	115						120						125			
Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	
	130					135						140				
His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	Gly	Cys	Pro	Ala	Glu	Gln	Arg	
145				150						155					160	
Ala	Ser	Pro	Leu	Thr	Ser	Ile	Ile	Ser	Ala	Val	Val	Gly	Ile	Leu	Leu	
			165						170					175		
Val	Val	Val	Leu	Gly	Val	Val	Phe	Gly	Ile	Leu	Ile	Lys	Arg	Arg	Gln	
		180						185					190			
Gln	Lys	Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	Leu	Leu	Asp	Tyr	Lys	Asp	
	195						200					205				
Asp	Asp	Asp	Lys													
	210															

<210> 35
 <211> 18
 <212> DNA
 <213> artificial sequence

<220>
 <223> 6×His

<400> 35
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18

<210> 36
 <211> 6
 <212> PRT
 <213> artificial sequence

<220>
 <223> 6×His

<400> 36
 His His His His His His
 1 5

<210> 37
 <211> 1881
 <212> DNA

<213> artificial sequence

<220>

<223> CAIX-BiTA

<400> 37

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agactgagct	gcgccgcctc	cggcaacagc	gctaacatct	tttcctttgc	ttccgtggcc	180
tggtataggc	aggccccagg	gaagcagaga	gagctggtgg	ccgtcattac	atccgccggc	240
ggcacaaagt	actccgactc	tgtgaaggga	agattcacca	ttagccggga	caatgccaaag	300
aacaccattc	tgctgcagat	gaactcactg	aaacctgagg	ataccgccgt	gtattattgt	360
aacgtggact	acctgcagga	ctactggggg	cagggcaccc	aggtgacagt	gagcagcggc	420
ggcggcgga	gcatatcaa	gctgcagcag	agcggagccg	agctggccag	gcctggagct	480
agcgtgaaga	tgagctgcaa	aaccagcggc	tacacattca	ccagatacac	catgcattgg	540
gtgaagcaga	gacccggaca	gggactggag	tggattggat	acattaaccc	cagtcgaggc	600
tacaccaact	acaaccagaa	gttcaaagac	aaagccaccc	tgaccaccga	caaaagcagc	660
agcaccgcat	atatgcagct	gagctctctg	accagcgagg	acagcgccgt	gtactactgc	720
gccagatact	acgacgacca	ctactgcctg	gactactggg	gccagggaac	cacctgaca	780
gtgtctagcg	tggagggcgg	atctggcggc	tcaggcgga	gcggaggagg	cggaggagt	840
gacgatatcc	agctgacca	gagtcgcc	atcatgagt	caagtcccg	cgaaaaagt	900
accatgacct	gtagagcttc	ttctagtgtg	agttatatga	actggtacca	gcagaagagc	960
gggaccagcc	ccaaaagatg	gatctacgac	accagcaagg	tggccagcgg	cgtgccctac	1020
cggttcagcg	gatctggcag	cggaaacctca	tacagcctga	ctatcagcag	catggaagca	1080
gaagacgccg	caacctacta	ctgccagcag	tggagctcta	acccactgac	cttcggcgct	1140
ggcaccaagc	tggagctgaa	gcaccaccac	caccatcacg	gcagcggcga	aggcagaggc	1200
agcctcctga	catgcggcga	cgtcgaagaa	aaccccgcc	ccatgctgct	cctcgtcacc	1260
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gtcacctgtt	tcggccccga	ggcagaccaa	tgcgtggcct	gcgctcacta	caaggacccc	1560
cccttctg	tggcccggtg	cccttcggc	gtgaagccc	acctctccta	catgcccatt	1620
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tgcgttgacc	tggacgacaa	gggctgtccc	gccgaacaga	gagccagccc	cctcacctct	1740
atcatctccg	ccgtggtggg	cattctgctg	gtcgtggtcc	tggcggttgt	gttcggcatc	1800
ctgatcaaaa	gaagacaaca	aaagatcaga	aagtacacca	tgcggcgcct	cctggactac	1860
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<210> 38

<211> 626

<212> PRT

<213> artificial sequence

<220>

<223> CAIX-BiTA

<400> 38

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

Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly
		35					40					45			
Asn	Ser	Ala	Asn	Ile	Phe	Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln
	50					55					60				
Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Val	Ile	Thr	Ser	Ala	Gly
65					70					75					80
Gly	Thr	Lys	Tyr	Ser	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg
				85					90					95	
Asp	Asn	Ala	Lys	Asn	Thr	Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro
			100				105						110		
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr
		115					120					125			
Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
						135					140				
Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala
145					150					155					160
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
				165					170					175	
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
			180					185					190		
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
		195					200					205			
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210					215					220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
225					230				235						240
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly
				245				250						255	
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly
			260					265					270		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser
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Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys
	290					295					300				
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser
305					310					315					320
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser
				325					330					335	
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser
			340				345					350			
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys
		355				360						365			
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu
						375					380				
Glu	Leu	Lys	His	His	His	His	His	His	Gly	Ser	Gly	Glu	Gly	Arg	Gly
385					390					395					400
Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu
				405					410					415	
Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe
			420					425					430		
Leu	Leu	Ile	Pro	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp
		435					440					445			
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	450					455					460				

Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu
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 Tyr Val Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro
 485 490 495
 Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val
 500 505 510
 Ala Cys Ala His Tyr Lys Asp Pro Phe Cys Val Ala Arg Cys Pro
 515 520 525
 Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
 530 535 540
 Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser
 545 550 555 560
 Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser
 565 570 575
 Pro Leu Thr Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
 580 585 590
 Val Leu Gly Val Val Phe Gly Ile Leu Ile Lys Arg Arg Gln Gln Lys
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 Ile Arg Lys Tyr Thr Met Arg Arg Leu Leu Asp Tyr Lys Asp Asp Asp
 610 615 620
 Asp Lys
 625

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 <211> 2316
 <212> DNA
 <213> artificial sequence

<220>
 <223> CAIX-CAB

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 cacaacgata agaacatcgg cggagacgag gacgacaaga acatcggaag tgacgaggac 240
 cacctgagcc tgaaggaatt cagcgaactg gagcagagcg gctattacgt ctgctacccc 300
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 attgccagcc agccactgtc cctgaggccc gaagcctgca gaccagcagc cggcggagcc 480
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 aaactgctgt atatcttcaa gcagcccttt atgagaccg tgcagaccac ccaggaggag 660
 gacggctgct cctgtagatt ccccaggag gagggggcg gctgcgagct gagagtgaag 720
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gactacctgc	aggactactg	ggggcagggc	accaggtga	cagtgagcag	cggcggcggc	1560
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gcataatatgc	agctgagctc	tctgaccagc	gaggacagcg	ccgtgtacta	ctgcgccaga	1860
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agcggatctg	gcagcggaac	ctcatacagc	ctgactatca	gcagcatgga	agcagaagac	2220
gccgcaacct	actactgcca	gcagtggagc	tctaaccac	tgaccttcgg	cgctggcacc	2280
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<210> 40
 <211> 771
 <212> PRT
 <213> artificial sequence

<220>
 <223> CAIX-CAB

<400> 40

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			20					25					30		
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr
			35				40					45			
Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys
	50					55					60				
Asn	Ile	Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp
65				70					75					80	
His	Leu	Ser	Leu	Lys	Glu	Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr
			85					90					95		
Val	Cys	Tyr	Pro	Arg	Gly	Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu
			100					105					110		
Tyr	Leu	Arg	Ala	Arg	Val	Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Thr	Thr
		115					120					125			
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln
	130					135						140			
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala
145				150					155					160	
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala
			165					170					175		
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Ser	Leu	Val	Ile	Thr	
		180					185					190			
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln

		195					200					205				
Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	
	210					215					220					
Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	
225					230					235					240	
Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	
				245					250					255		
Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	
			260					265					270			
Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	
		275					280					285				
Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	
	290					295					300					
Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	
305					310					315					320	
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	
				325					330					335		
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys	
			340					345					350			
Asp	Asp	Asp	Asp	Lys	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	
		355					360					365				
Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu	Leu	Leu	Val	Thr	
	370					375					380					
Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe	Leu	Leu	Ile	Pro	
385					390					395					400	
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
				405					410					415		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asn	Ser	Ala	Asn	Ile	Phe	
			420					425					430			
Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	
		435					440					445				
Glu	Leu	Val	Ala	Val	Ile	Thr	Ser	Ala	Gly	Gly	Thr	Lys	Tyr	Ser	Asp	
	450					455					460					
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	
465					470					475					480	
Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	
				485					490					495		
Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	
			500					505					510			
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	Leu	Gln	Gln	
		515					520					525				
Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	
	530					535					540					
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys	
545					550					555						

625					630					635					640
Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly
				645					650					655	
Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala
			660					665					670		
Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val
		675					680					685			
Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg
	690					695					700				
Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe
705					710					715					720
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met
			725					730					735		
Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn
			740					745					750		
Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	His	His	His
		755					760					765			
His	His	His													
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<210> 41
 <211> 987
 <212> DNA
 <213> artificial sequence

<220>
 <223> CAIX-ζ

<400> 41	
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accacccccg	480
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agcctggtga	660
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gagatcggaa	900
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gattacaagg	987

<210> 42
 <211> 328
 <212> PRT
 <213> artificial sequence

<220>

<223> CAIX-ζ

<400> 42

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Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45
Asn Ser Ala Asn Ile Phe Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln
50 55 60
Ala Pro Gly Lys Gln Arg Glu Leu Val Ala Val Ile Thr Ser Ala Gly
65 70 75 80
Gly Thr Lys Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
85 90 95
Asp Asn Ala Lys Asn Thr Ile Leu Leu Gln Met Asn Ser Leu Lys Pro
100 105 110
Glu Asp Thr Ala Val Tyr Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr
115 120 125
Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser Thr Thr Thr Pro Ala
130 135 140
Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
145 150 155 160
Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
165 170 175
Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
180 185 190
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
195 200 205
Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
210 215 220
Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
225 230 235 240
Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
245 250 255
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
260 265 270
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
275 280 285
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
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Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 43

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<223> CD8L

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<210> 44
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> CD8L

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<210> 45
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> CAIX-BBζ

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ctgagctgctg ctgcctccgg caactccgcc aacattttct ccttcgcctc cgtggcctgg 180
tacaggcagg cccaggcaa gcagagagag ctggtggcag tcattacatc cgccggcggc 240
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<210> 46
<211> 369
<212> PRT

<223> CAIX-BBζ

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<211> 1101
<212> DNA
<213> artificial sequence

<220>
<223> CAIX-28ζ

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gtggactacc tgcaggacta ctggggccag ggcaccaggg tgaccgtgtc cagcgccatc 420
gagggtgatgt accccccccc ctacctggat aacgagaaga gtaatggcac cattatccat 480
gtgaagggca agcacctgtg ccccagccct ctgttccccg gccctagcaa acccttctgg 540
gtgctggtgg tcgtgggcgg cgtcctggct tgctactccc tgctggtgac cgtggccttt 600
atcatcttct gggtgaggtc caagcgtcc aggctgctgc acagcgatta catgaacatg 660
acccccagga gaccaggccc caccggaag cactaccagc cctatgcccc ccccgcgac 720
ttcgtgcttt atagaagcag agtcaagttc tccgcagcgc ccgacgcccc cgcataccag 780
caggacaga accagctgta caacgaactg aacctgggccc ggagagagga atacgacgtg 840
ctggataaga gaagaggaag ggaccccgag atgggaggaa aaccaagaag aaagaaccca 900
caggagggcc tgtacaatga gctgcagaaa gacaagatgg cagaggcata tagcgagatc 960
ggaatgaagg gagagagaag aagaggaaaag ggacacgacg gactgtacca gggactgagc 1020
acagctacaa aggacacata cgacgccctg cacatgcagg cactgccacc cagagactat 1080
aaggacgacg acgacaaata a 1101

<210> 48
<211> 366
<212> PRT
<213> artificial sequence

<220>
<223> CAIX-28ζ

<400> 48
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15
His Ala Ala Arg Pro Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu
20 25 30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asn
35 40 45
Ser Ala Asn Ile Phe Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln Ala
50 55 60
Pro Gly Lys Gln Arg Glu Leu Val Ala Val Ile Thr Ser Ala Gly Gly
65 70 75 80
Thr Lys Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
85 90 95

Asn	Ala	Lys	Asn	Thr	Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu
			100					105					110		
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr	Trp
		115					120					125			
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ile	Glu	Val	Met	Tyr
		130				135					140				
Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His
145					150					155					160
Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser
				165					170					175	
Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr
			180					185					190		
Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys
			195				200						205		
Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg
			210			215					220				
Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp
225					230					235					240
Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala
				245					250					255	
Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu
			260					265						270	
Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp
			275				280					285			
Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu
			290			295					300				
Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile
305					310					315					320
Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr
				325					330					335	
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met
			340					345					350		
Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys		
		355					360					365			

<210> 49
 <211> 2700
 <212> DNA
 <213> artificial sequence

<220>
 <223> HER2-CAB

<400> 49	
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gatgggcggc	
atcaccacga	
ccccctacaa	
ggtgtccatc	
tccggcacca	180
ccgtgaccta	
gacctgccct	
cagtaccccc	
gctccgagat	
cctgtggcag	
cacaacgata	240
agaacatcgg	
cggagacgag	
gacgacaaga	
acatcggaag	
tgacgaggac	
cacctgagcc	300
tgaaggaatt	
cagcgaactg	
gagcagagcg	
gctattacgt	
ctgctacccc	
agaggaagca	360
aaccagagga	
cgccaacttc	
tatctgtacc	
tgagagccag	
agtgtgcgag	
aactgcatgg	420
aaatggacac	
aaccaccccc	
gccccagac	
cccccaaccc	
tgctcctacc	
attgccagcc	480
agccactgtc	
cctgaggccc	
gaagcctgca	
gaccagcagc	
cggcggagcc	
gtgcacacca	540
gaggactgga	
cttcgcctgc	
gacatctaca	
tctgggcccc	
cctggccggg	

acctgctggag	tgctgctgct	gagcctggtg	attactctgt	actgtaagag	gggaagaaag	600
aaactgctgt	atatcttcaa	gcagcccttt	atgagaccgc	tgagaccac	ccaggaggag	660
gacggctgct	cctgtagatt	ccccgaggag	gaggagggcg	gctgagagct	gagagtgaag	720
ttctccagga	gcgccgacgc	ccccgcctac	cagcagggac	agaaccagct	gtacaacgag	780
ctgaacctgg	gcagaagaga	ggagtatgac	gtgctggaca	agagaagagg	aagagacccc	840
gagatgggag	gaaagccaag	aagaaagaac	ccccaggagg	gcctgtacaa	tgagctgcag	900
aaggacaaga	tggcagaggc	atatagcgag	atcggaatga	agggagagag	aagaagagga	960
aagggacacg	acggactgta	ccagggcctg	agcacagcta	caaaggacac	atacgacgca	1020
ctgcacatgc	aggcactgcc	accaagagac	tacaaggacg	atgacgacaa	gggaagcgga	1080
gagggcagag	gaagcctgct	gacatgcgga	gacgtggagg	agaaccagg	acccatgctg	1140
ctgctggtga	cctcccctgct	gctgtgagag	ctgccccacc	ccgctttcct	gctgatcccc	1200
gacatccaga	tgaccagtc	cccctcctcc	ctgtccgcct	ccgtgggaga	ccgcgtgacc	1260
atcacctgcc	gcgcctccca	ggacgtgaac	accgccgtcg	cctggtacca	gcagaagccc	1320
ggcaaagccc	ccaaactgct	gatctactcc	gcctcattcc	tgtatagcgg	cgtgccctcc	1380
agattctccg	gcagcagaag	cggcaccgac	ttcaccctga	ctatcagcag	cctgcagccc	1440
gaagacttcg	ccacctacta	ctgccagcag	cactacacca	cccccccccac	cttcggccag	1500
ggcacaaaag	tggagatcaa	gggcagcacc	agcggcagcg	gaaaaccggg	cagcggcgag	1560
ggatctacca	aaggcgaggt	ccagctggtg	gagagcggcg	gaggcctggt	gcagccagga	1620
ggaagcctga	gactgagctg	tgccgcaagc	ggattcaata	tcaaggatac	atacattcat	1680
tgggtgagac	aggcaccggg	aaaaggcctg	gagtgggtgg	ctagaattta	cccaaccaac	1740
ggatacacc	ggtacgccga	tagcgtgaag	ggcagattca	ccattagcgc	cgacaccagc	1800
aagaacacag	cctacctgca	gatgaacagc	ctgagagccg	aggacaccgc	agtgtactac	1860
tgacagagat	ggggagggga	cggattctac	gccatggact	actggggaca	gggcaccctg	1920
gtgacagtga	gcagcggcgg	cggcggaagc	gacattaagc	tgacagagag	tggcgccgag	1980
ctggcaagac	ccggagccag	tgtgaagatg	agctgcaaga	ctagcggcta	caccttcacc	2040
agatatacaa	tgcatgggtg	gaaacagaga	cccggccagg	gactggagtg	gattggatac	2100
attaaccca	gcagaggcta	caccaactac	aaccagaagt	tcaaggacaa	ggcaaccctg	2160
accacagaca	aaagcagcag	cacagcctac	atgcagctga	gcagcctgac	cagcaggagc	2220
agcgccgtgt	actactgtgc	cagatactac	gacgaccact	actgcctgga	ctactggggc	2280
cagggaaacca	cactgaccgt	gtccagcgtg	gagggcggat	caggcggcag	cggaggaagc	2340
ggaggaagtg	ggggcgtgga	cgacatccag	ctgacacaga	gtcccgtat	catgagcgca	2400
agtcccggtg	agaaggtgac	aatgacctgc	agagctagct	caagcgtgag	ctatatgaat	2460
tggtaccagc	agaaaagcgg	caccagcccc	aaaagatgga	tctacgacac	ctcaaaggtg	2520
gccagcggag	tgccctacag	attcagcgga	tcaggaagcg	gaacatcata	cagcctgact	2580
atctccagca	tggaggctga	agacgccgca	acctactact	gtcagcagtg	gagctctaac	2640
cccctgacct	tcggcgccgg	caccaagctg	gagctgaagc	accaccacca	ccatcactaa	2700

<210> 50

<211> 899

<212> PRT

<213> artificial sequence

<220>

<223> HER2-CAB

<400> 50

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
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Ala	Phe	Leu	Leu	Ile	Pro	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr
			20					25					30		
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr
		35					40					45			
Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys

50	55	60
Asn Ile Gly Gly Asp Glu	Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp	
65	70	75
His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr		80
	85	90
Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu		95
	100	105
Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Thr Thr		110
	115	120
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln		125
	130	135
Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala		140
145	150	155
Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala		160
	165	170
Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr		175
	180	185
Leu Tyr Cys Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln		190
	195	200
Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser		205
	210	215
Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys		220
225	230	235
Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln		240
	245	250
Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu		255
	260	265
Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg		270
	275	280
Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met		285
	290	295
Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly		300
305	310	315
Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp		320
	325	330
Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Asp Tyr Lys		335
	340	345
Asp Asp Asp Asp Lys Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr		350
	355	360
Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Leu Leu Leu Val Thr		365
	370	375
Ser Leu Leu Leu Cys Glu Leu Pro His Pro Ala Phe Leu Leu Ile Pro		380
385	390	395
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly		400
	405	410
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala		415
	420	425
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile		430
	435	440
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly		445
	450	455
Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro		460
465	470	475
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro		480

				485				490					495		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly	Ser	Thr	Ser	Gly
			500					505					510		
Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	Glu	Val	Gln
		515					520					525			
Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg
	530					535					540				
Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	Ile	His
545					550					555					560
Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile
				565					570						
Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg
			580					585					590		
Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met
		595					600					605			
Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp
	610					615					620				
Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
625					630					635					640
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Lys	Leu	Gln	Gln
				645					650					655	
Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys
			660					665					670		
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr	Thr	Met	His	Trp	Val	Lys
		675					680					685			
Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Ser
						695					700				
Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu
705					710					715					720
Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu
				725					730					735	
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Tyr	Asp	Asp
			740					745					750		
His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser
		755					760					765			
Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Ser	Gly
		770				775					780				
Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala
785					790					795					800
Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val
				805					810					815	
Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg
			820					825					830		
Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe
		835					840								

<210> 51
 <211> 1350
 <212> DNA
 <213> artificial sequence

<220>
 <223> HER2-ζ

<400> 51
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 cccgacatcc agatgaccga gagccccagc agcctgagcg ccagcgtggg cgaccgcgtg 120
 accatcacct gccgcgccag ccaggacgtg aacaccgccg tggcctggta ccagcagaag 180
 cccggcaagg cccccaagct gctgatctac agcgccagct tcctgtacag cggcgtgccc 240
 agccgcttca gcggcagccg cagcggcacc gacttcaccc tgaccatcag cagcctgcag 300
 cccgaggact tcgccaccta ctactgccag cagcactaca ccaccccccc cacttcgggc 360
 cagggcacca aggtggagat caagggcagc accagcggca gcggcaagcc cggcagcggc 420
 gagggcagca ccaagggcga ggtgcagctg gtggagagcg gcggcggcct ggtgcagccc 480
 ggcgggcagcc tgcgcctgag ctgcgccgcc agcggcttca acatcaagga cacctacatc 540
 cactgggtgc gccaggcccc cggcaagggc ctggagtggg tggcccgcac ctaccccacc 600
 aacggctaca cccgctacgc cgacagcgtg aagggccgct tcaccatcag cgccgacacc 660
 agcaagaaca ccgcctacct gcagatgaac agcctgcgcg ccgaggacac cgccgtgtac 720
 tactgcagcc gctggggcgg cgacggcttc tacgccatgg actactgggg ccagggcacc 780
 ctggtgaccg tgagcagcac gcgtaccacc acccccgcac caagaccccc caccagca 840
 ccaacctcgc ccagccagcc cctgagcctg agaccgaag cctgcagacc cgccgccgga 900
 ggagcagtgcc acaccagagg cctggacttc gcctgcgaca tctacatctg ggccccctg 960
 gccggcacct gcggagtgcct gctgctgagc ctggtgatca ccctgtattg tagagtgaag 1020
 ttttctagaa gcgcagatgc tcccgcctat cagcagggcc agaaccagct gtacaacgaa 1080
 ctgaacctgg gcaggagaga agagtacgac gtgctggaca aaagaagagg cagagacccc 1140
 gagatgggag ggaagcccag aagaaagaac cccagaggag gcctgtacaa cgagctgcag 1200
 aaagacaaga tggcagaggc atacagcgag atcggaatga agggagagag aagaagagga 1260
 aagggacacg acggactgta ccagggcctg agcacagcta caaaggacac atacgacgcc 1320
 ctgcacatgc aggcctgcc cccaagataa 1350

<210> 52
 <211> 449
 <212> PRT
 <213> artificial sequence

<220>
 <223> HER2-ζ

<400> 52
 Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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 His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
 20 25 30
 Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
 35 40 45
 Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 50 55 60
 Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro
 65 70 75 80

Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				85					90					95	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His
			100					105					110		
Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
		115					120					125			
Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr
	130					135					140				
Lys	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro
145					150					155					160
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys
				165					170					175	
Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
			180					185					190		
Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp
		195					200					205			
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr
	210					215					220				
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
225					230					235					240
Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp
				245					250					255	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Thr	Arg	Thr	Thr	Thr	Pro
			260					265					270		
Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu
		275					280					285			
Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His
	290					295					300				
Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu
305					310					315					320
Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr
				325					330					335	
Cys	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln
			340					345					350		
Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu
		355					360					365			
Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly
	370					375					380				
Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln
385					390					395					400
Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu
			405						410					415	
Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr
			420					425					430		
Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro
		435					440					445			

Arg

<210> 53
 <211> 1101
 <212> DNA
 <213> artificial sequence

<220>

<223> HER2-BBZ

<400> 53

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ctgagctgcg	ctgcctccgg	caactccgcc	aacattttct	ccttcgcctc	cgtggcctgg	180
tacaggcagg	ccccaggcaa	gcagagagag	ctggtggcag	tcattacatc	cgccggcggc	240
accaagtaca	gcgacagcgt	gaagggacgg	ttcactatct	ccagagacaa	tgccaagaac	300
acaatcctgc	tgcagatgaa	cagcctgaag	cctgaggaca	ccgcagtgtg	ttactgtaac	360
gtggactacc	tgcaggacta	ctggggccag	ggcaccaggg	tgaccgtgtc	cagcgccatc	420
gaggtgatgt	accccccccc	ctacctggat	aacgagaaga	gtaatggcac	cattatccat	480
gtgaagggca	agcacctgtg	ccccagccct	ctgttccccg	gccctagcaa	acccttctgg	540
gtgctgggtg	tcgtgggctg	cgtcctggct	tgctactccc	tgctgggtgac	cgtggccttt	600
atcatcttct	gggtgaggtc	caagcgctcc	aggctgctgc	acagcgatta	catgaacatg	660
acccccagga	gaccaggccc	caccggaag	cactaccagc	cctatgcccc	ccccgcgcac	720
ttcgtgcttt	atagaagcag	agtcaagttc	tcccgagcgc	ccgacgcccc	cgcataccag	780
cagggacaga	accagctgta	caacgaactg	aacctgggccc	ggagagagga	atacgacgtg	840
ctggataaga	gaagaggaag	ggaccccgag	atgggaggaa	aaccaagaag	aaagaaccca	900
caggagggcc	tgtacaatga	gctgcagaaa	gacaagatgg	cagaggcata	tagcgagatc	960
ggaatgaagg	gagagagaag	aagaggaaaag	ggacacgacg	gactgtacca	gggactgagc	1020
acagctacaa	aggacacata	cgacgccctg	cacatgcagg	cactgccacc	cagagactat	1080
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<210> 54

<211> 366

<212> PRT

<213> artificial sequence

<220>

<223> HER2-BBZ

<400> 54

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu
			20					25					30		
Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asn
			35				40					45			
Ser	Ala	Asn	Ile	Phe	Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln	Ala
			50				55				60				
Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala	Val	Ile	Thr	Ser	Ala	Gly	Gly
65					70					75				80	
Thr	Lys	Tyr	Ser	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp
				85					90					95	
Asn	Ala	Lys	Asn	Thr	Ile	Leu	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu
			100					105					110		
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr	Trp
			115				120					125			
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ile	Glu	Val	Met	Tyr
			130				135				140				
Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys	Ser	Asn	Gly	Thr	Ile	Ile	His

145					150					155				160	
Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser	Pro	Leu	Phe	Pro	Gly	Pro	Ser
				165					170					175	
Lys	Pro	Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr
			180					185					190		
Ser	Leu	Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val	Arg	Ser	Lys
		195				200					205				
Arg	Ser	Arg	Leu	Leu	His	Ser	Asp	Tyr	Met	Asn	Met	Thr	Pro	Arg	Arg
	210					215				220					
Pro	Gly	Pro	Thr	Arg	Lys	His	Tyr	Gln	Pro	Tyr	Ala	Pro	Pro	Arg	Asp
225				230						235					240
Phe	Ala	Ala	Tyr	Arg	Ser	Arg	Val	Lys	Phe	Ser	Arg	Ser	Ala	Asp	Ala
			245					250						255	
Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu
			260					265					270		
Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg	Arg	Gly	Arg	Asp
		275				280					285				
Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro	Gln	Glu	Gly	Leu
	290					295				300					
Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala	Tyr	Ser	Glu	Ile
305				310					315						320
Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr
			325					330					335		
Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp	Ala	Leu	His	Met
		340						345				350			
Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys		
	355					360						365			

<210> 55
 <211> 1485
 <212> DNA
 <213> artificial sequence

<220>
 <223> HER2-28ζ

<400> 55	
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cccgacatcc agatgaccga gtccccagc agcctgagcg ccagcgtggg agacagggtg	120
accatcacct gtagagcctc ccaggacgtc aacaccgccg tcgcctggta ccagcagaaa	180
ccaggcaagg ccccaaact gctgatctac tccgccagct tcctgtatag tggcgtgccc	240
tcccgattca gcggcagcag aagcggaacc gacttcaccc tgactatcag cagcctgcag	300
cccgaggatt tcgccaccta ctactgccag cagcactaca ccaccccccc cacattcggc	360
cagggcacia aggtggaaat caagggtcc acctccggct ccggcaaacc cggtacaggc	420
gaaggctcta ccaaaggcga ggtccagctg gtcgagagcg gcggaggcct ggtgcagcca	480
ggaggaagcc tgagactgag ctgtgccgcc agcggattca atatcaaaga cacctacatc	540
cattgggtga gacaggcacc cggaaaaggg ctggagtggg tggctagaat ctaccccacc	600
aacggataca cccgctacgc cgacagcgtg aagggccgct tcaccatcag cgccgacacc	660
agcaagaaca ccgcctacct gcagatgaac agcctgagag ccaggacac cgccgtgtac	720
tactgcagca gatggggagg agacggattc tacgccatgg actactgggg acagggcacc	780
ctggtgacag tgagcagcgc catcgaggtg atgtaccctc cccctacct ggacaacgag	840
aagagcaacg gcaccatcat tcacgtcaag ggaaagcacc tgtgccccag cccctgttc	900
cccgacatt ccaagccctt ctgggtcctg gtggtggtcg gcggcgtgct ggcttgctac	960

agcctgctgg	tgaccgtcgc	ctttatcatt	ttctgggtga	gatccaagag	atccgcctg	1020
ctgcacagcg	actacatgaa	catgaccccc	agaagaccgc	gccccaccgc	caagcactac	1080
cagccttatg	ccccccccc	cgacttcgcc	gcttatagaa	gcagagtga	gttctccgc	1140
agcgccgacg	cccccgctta	ccagcaggga	cagaaccagc	tgtacaacga	actgaacctg	1200
ggccgcagag	aagaatatga	cgtgctggat	aagagaagag	gaagagacc	cgagatggga	1260
ggaaaaccaa	gaagaaagaa	cccacaggag	ggcctgtaca	atgagctgca	gaaagacaag	1320
atggcagagg	catatagcga	gatcggaatg	aagggagaga	gaagaagagg	aaagggacac	1380
gacggactgt	accagggact	gagcacagct	acaaaggaca	catacgacgc	cctgcacatg	1440
caggcactgc	caccagaga	ctataaggac	gacgacgaca	aataa		1485

<210> 56
 <211> 494
 <212> PRT
 <213> artificial sequence

<220>
 <223> HER2-28Z

<400> 56

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		
His	Ala	Ala	Arg	Pro	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu
			20				25					30			
Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln
		35				40					45				
Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala
	50					55					60				
Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val	Pro
65				70					75						80
Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
			85					90					95		
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His
			100					105					110		
Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
		115					120					125			
Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr
	130					135					140				
Lys	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro
145				150					155						160
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys
			165					170					175		
Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
			180					185					190		
Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp
	195					200						205			
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr
	210					215					220				
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
225				230						235					240
Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp
			245					250					255		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ile	Glu	Val	Met	Tyr	
			260					265				270			

<400> 58
Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
1 5 10 15

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 20 25 30
 Leu Phe Pro Gly Pro Ser Lys Pro
 35 40

<210> 59
 <211> 81
 <212> DNA
 <213> artificial sequence

<220>
 <223> CD28TM

<400> 59
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 gcctttatca ttttctgggt g 81

<210> 60
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD28TM

<400> 60
 Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1 5 10 15
 Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 20 25

<210> 61
 <211> 123
 <212> DNA
 <213> Homo sapiens

<220>
 <223> CD28costimulatorydomain

<400> 61
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 ggccccaccc gcaagcacta ccagccttat gccccccccc gcgacttcgc cgcttataga 120
 agc 123

<210> 62
 <211> 41
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CD28costimulatorydomain

<400> 62

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15
Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30
Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 63

<211> 2235

<212> DNA

<213> artificial sequence

<220>

<223> HER2-BiTA

<400> 63

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gtgaccatca	cctgccgcgc	ctcccaggac	gtgaacaccg	ccgtcgctg	gtaccagcag	180
aagcccgga	aagccccaa	actgctgac	tactccgcct	cattcctgta	tagcggcgtg	240
ccctccagat	tctccggcag	cagaagcggc	accgacttca	ccctgactat	cagcagcctg	300
cagcccgaag	acttcgccac	ctactactgc	cagcagcact	acaccacccc	ccccaccttc	360
ggccagggca	caaaagtgga	gatcaagggc	agcaccagcg	gcagcggaaa	accgggcagc	420
ggcgagggat	ctaccaaagg	cgaggtccag	ctgggtggaga	gcggcggagg	cctgggtgcag	480
ccaggaggaa	gcctgagact	gagctgtgcc	gcaagcggat	tcaatatcaa	ggatacatat	540
attcattggg	tgagacaggc	acccggaaaa	ggcctggagt	gggtggctag	aattttacca	600
accaacggat	acaccgggta	cgccgatagc	gtgaagggca	gattcaccat	tagcgccgac	660
accagcaaga	acacagccta	cctgcagatg	aacagcctga	gagccgagga	caccgcagtg	720
tactactgca	gcagatgggg	aggggacgga	ttctacgcca	tggactactg	gggacagggc	780
accctgggtg	cagtgcagcag	cggcggcggc	ggaagcgaca	ttaagctgca	gcagagtggc	840
gccgagctgg	caagaccggg	agccagtgtg	aagatgagct	gcaagactag	cggctacacc	900
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ggatacatat	acccagcag	aggctacacc	aactacaacc	agaagttcaa	ggacaaggca	1020
accctgacca	cagacaaaag	cagcagcaca	gcctacatgc	agctgagcag	cctgaccagc	1080
gaggacagcg	ccgtgtacta	ctgtgccaga	tactacgacg	accactactg	cctggactac	1140
tggggccagg	gaaccacact	gaccgtgtcc	agcgtggagg	gcggatcagg	cggcagcgga	1200
ggaagcggag	gaagtggggg	cgtggacgac	atccagctga	cacagagtcc	cgctatcatg	1260
agcgcaagtc	ccggcgagaa	ggtgacaatg	acctgcagag	ctagctcaag	cgtgagctat	1320
atgaattggg	accagcagaa	aagcggcacc	agccccaaaa	gatggatcta	cgacacctca	1380
aagggtggcca	gcggagtgcc	ctacagattc	agcggatcag	gaagcggaac	atcatacagc	1440
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tctaaccccc	tgaccttcgg	cgccggcacc	aagctggagc	tgaagcacca	ccaccaccat	1560
cacggcagcg	gcgaaggcag	aggcagcctg	ctgacctgcg	gcgacgtcga	ggaaaacccc	1620
ggccccatgc	tgctgctggg	cacctccctg	ctgctgtgcg	aactgcccc	ccccgccttt	1680
ctgctgattc	ctgatggcaa	cgaggagatg	ggcggcatca	cacagacccc	ctacaaagtg	1740
tccatctccg	gcaccaccgt	gatcctgacc	tgccccaggt	accccggtc	cgagatcctg	1800
tggcagcaca	acgacaagaa	cattggcgga	gacgaggacg	acaaaaacat	cggaagcgac	1860
gaggaccacc	tgagcctgaa	ggaattcagc	gaactggagc	agtcaggcta	ctacgtctgc	1920
tacccaagag	gaagcaaacc	agaggacgcc	aacttctatc	tgtacctgag	agccagagtc	1980
tgcgagaact	gcatggagat	ggacacaacc	acccccgcc	ccagaccccc	taccctgct	2040

cctaccattg ccagccagcc actgtccctg aggcccgaag cctgcagacc agcagccggc	2100
ggagccgtgc acaccagagg actggacttc gcctgtgaca tctacatctg ggccccctg	2160
gccgggacct gcggagtgtct gctgctgagc ctggtgatta ctctgtactg cgattacaag	2220
gatgatgacg acaaa	2235

<210> 64
 <211> 745
 <212> PRT
 <213> artificial sequence

<220>
 <223> HER2-BiTA

<400> 64

Met	Leu	Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro
1				5					10					15	
Ala	Phe	Leu	Leu	Ile	Pro	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser
			20					25					30		
Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser
		35				40					45				
Gln	Asp	Val	Asn	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
	50					55					60				
Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Phe	Leu	Tyr	Ser	Gly	Val
65					70					75					80
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
			85						90					95	
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
			100					105					110		
His	Tyr	Thr	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile
	115						120					125			
Lys	Gly	Ser	Thr	Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser
	130					135					140				
Thr	Lys	Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
145					150					155					160
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile
			165						170					175	
Lys	Asp	Thr	Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
	180							185					190		
Glu	Trp	Val	Ala	Arg	Ile	Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala
	195					200					205				
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn
	210					215					220				
Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val
225					230					235					240
Tyr	Tyr	Cys	Ser	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr
			245						250					255	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
			260					265					270		
Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala
	275						280					285			
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
	290					295					300				
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile

305					310					315					320	
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	
				325					330					335		
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
				340					345					350		
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
				355					360					365		
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	
				370					375					380		
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly	
				385					390					395		
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser	
				405					410					415		
Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	
				420					425					430		
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	
				435					440					445		
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	
				450					455					460		
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	
				465					470					475		
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
				485					490					495		
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	
				500					505					510		
Glu	Leu	Lys	His	His	His	His	His	His	Gly	Ser	Gly	Glu	Gly	Arg	Gly	
				515					520					525		
Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu	
				530					535					540		
Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe	
				545					550					555		
Leu	Leu	Ile	Pro	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr	Gln	Thr	
				565					570					575		
Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr	Cys	Pro	
				580					585					590		
Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys	Asn	Ile	
				595					600					605		
Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp	His	Leu	
				610					615					620		
Ser	Leu	Lys	Glu	Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr	Val	Cys	
				625					630					635		
Tyr	Pro	Arg	Gly	Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu	Tyr	Leu	
				645					650					655		
Arg	Ala	Arg	Val	Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Thr	Thr	Thr	Pro	
				660					665					670		
Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	
				675					680					685		
Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	
				690					695					700		
Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	
				705					710					715		
Ala	Gly	Thr	Cys	Gly	Val											

<210> 65
 <211> 735
 <212> DNA
 <213> Humanized Mouse Antibody

<220>
 <223> TrastuzumabscFv

<400> 65
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 ggcaaggccc ccaagctgct gatctacagc gccagcttcc tgtacagcgg cgtgcccagc 180
 cgcttcagcg gcagccgcag cggcaccgac ttaccctga ccatcagcag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag cactacacca cccccccac cttcgccag 300
 ggaccaagg tggagatcaa gggcagcacc agcggcagcg gcaagcccgg cagcggcgag 360
 ggagcacca agggcgaggt gcagctggtg gagagcggcg gcggcctggt gcagcccggc 420
 ggagcctgc gcctgagctg cgccgccagc ggcttcaaca tcaaggacac ctacatccac 480
 tgggtgcgcc agggccccgg caagggcctg gagggtgggg cccgcattca cccaccaaac 540
 ggctacacc gctacgccga cagcgtgaag ggccgcttca ccatcagcgc cgacaccagc 600
 aagaacaccg cctacctgca gatgaacagc ctgcgcgccg aggacaccgc cgtgtactac 660
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<210> 66
 <211> 245
 <212> PRT
 <213> Humanized Mouse Antibody

<220>
 <223> TrastuzumabscFv

<400> 66
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 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Ser Thr Ser Gly
 100 105 110
 Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Gln
 115 120 125
 Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 130 135 140

Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	Ile	His
145					150					155					160
Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Arg	Ile
			165						170						175
Tyr	Pro	Thr	Asn	Gly	Tyr	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg
			180					185					190		
Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met
		195					200					205			
Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ser	Arg	Trp
	210					215					220				
Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
225					230					235					240
Val	Thr	Val	Ser	Ser											
				245											

<210> 67
 <211> 2700
 <212> DNA
 <213> artificial sequence

<220>
 <223> HER2-CABR

<400> 67

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aagcccgga	aagccccaa	actgctgac	tactccgcct	cattcctgta	tagcggcgtg	240
ccctccagat	tctccggcag	cagaagcggc	accgacttca	ccctgactat	cagcagcctg	300
cagcccgaag	acttcgccac	ctactactgc	cagcagcact	acaccacccc	ccccaccttc	360
ggccagggca	caaaagtgga	gatcaagggc	agcaccagcg	gcagcggaaa	accgggcagc	420
ggcgagggat	ctaccaaagg	cgaggtccag	ctgggtggaga	gcggcggagg	cctgggtgcag	480
ccaggaggaa	gcctgagact	gagctgtgcc	gcaagcggat	tcaatatcaa	ggatacatac	540
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accaacggat	acaccggta	cgccgatagc	gtgaagggca	gattcaccat	tagcgccgac	660
accagcaaga	acacagccta	cctgcagatg	aacagcctga	gagccgagga	caccgcagtg	720
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gccgagctgg	caagaccggg	agccagtgtg	aagatgagct	gcaagactag	cggctacacc	900
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ggatacatta	accccagcag	aggctacacc	aactacaacc	agaagttcaa	ggacaaggca	1020
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gaggacagcg	ccgtgtacta	ctgtgccaga	tactacgacg	accactactg	cctggactac	1140
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cacggatctg	gggaggggag	aggaagcctg	ctgacatgtg	gagacgtgga	ggagaaccct	1620
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gaggaccacc	tgagcctgaa	ggaatttagc	gaactggagc	agagcggata	ctacgtgtgc	1920
taccccagag	gaagcaaacc	agaggacgca	aacttctacc	tgtacctgag	agccagagtc	1980
tgcgagaact	gcatggagat	ggacacaacc	acccccgcac	caagaccccc	caccctgct	2040
ccaaccattg	ccagccagcc	cctgtccctg	agacccgagg	cctgcagacc	agccgccgga	2100
ggagcagtgc	acacaagagg	actggacttc	gcctgtgaca	tctacatctg	ggccccctg	2160
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aacgagctga	acctgggcag	acgggaagag	tatgacgtgc	tggataagag	aagaggaaga	2460
gaccagaga	tgggagggaa	gccaagaaga	aagaaccccc	aggagggcct	gtacaacgag	2520
ctgcagaaag	acaagatggc	agaggcatac	agcgagatcg	gaatgaaggg	agagagaaga	2580
agaggaaagg	gacacgacgg	actgtaccag	ggcctgagca	cagctacaaa	ggacacatac	2640
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<210> 68
 <211> 899
 <212> PRT
 <213> artificial sequence

<220>
 <223> HER2-CABR

<400> 68
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 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
 130 135 140
 Thr Lys Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 145 150 155 160
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile
 165 170 175
 Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 180 185 190
 Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala
 195 200 205
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn

210	215	220
Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val		
225	230	235
Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr		240
	245	250
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser		255
	260	265
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala		270
	275	280
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr		285
	290	295
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile		300
305	310	315
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe		320
	325	330
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr		335
	340	345
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys		350
	355	360
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly		365
370	375	380
Thr Thr Leu Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly		385
385	390	395
Gly Ser Gly Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser		400
	405	410
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys		415
	420	425
Arg Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser		430
	435	440
Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser		445
450	455	460
Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser		465
465	470	475
Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys		480
	485	490
Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu		495
	500	505
Glu Leu Lys His His His His His Gly Ser Gly Glu Gly Arg Gly		510
	515	520
Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Leu		525
	530	535
Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro Ala Phe		540
545	550	555
Leu Leu Ile Pro Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr		560
	565	570
Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro		575
	580	585
Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile		590
	595	600
Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu		605
	610	615
Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys		620
625	630	635
Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu		640

<213> Humanized llama Antibody

<220>

<223> HumanizedCAIXVHH

<400> 70

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Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Asn Ser Ala Asn Ile Phe
20          25          30
Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu
35          40          45
Glu Leu Val Ser Val Ile Thr Ser Ala Gly Gly Thr Lys Tyr Ser Asp
50          55          60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
65          70          75          80
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85          90          95
Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr Trp Gly Gln Gly Thr Leu
100          105          110
Val Thr Val Ser Ser
115
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<210> 71

<211> 1881

<212> DNA

<213> artificial sequence

<220>

<223> hCAIX-BiTA

<400> 71

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agactgagct gtagcgctc cggcaacagc gccaatatct tctcctttgc ttccgtggcc      180
tggtataggc agggccccgg gaagggcctg gagctggtgt cagtcattac atccgccggc      240
ggcaccaagt acagcgacag cgtgaaaggc cggttcacca tcagcagaga caatagcaag      300
aacacactgt acctgcagat gaatagcctg agagccgagg acaccgccgt gtattactgc      360
aacgtggact acctgcagga ctactggggc cagggcaccc tggtgaccgt gagcagcggc      420
ggaggcggaa gcgacatcaa gctgcagcag tccggagccg aactggctag gcccggcgca      480
agtgtgaaga tgagctgcaa gacctcaggc tacacattta ccagatatac aatgcattgg      540
gtgaagcaga gacccggcca gggactggag tggattggat acattaacc cagcagaggc      600
tataccaact acaaccagaa attcaaagac aaggccaccc tgaccacaga caaaagcagc      660
agcaccgcat atatgcagct gagcagcctg acaagcgagg acagcgccgt gtactactgc      720
gccagatact acgacgacca ctactgcctg gactactggg gacaggggaa cacactgacc      780
gtgagtagcg tggagggcgg atcaggcggc agcggaggaa gcgagggaag tgggggggtg      840
gacgacatcc agctgacaca gagccccgcc atcatgagcg caagccccgg cgagaagggtg      900
accatgacct gcagagctag ctcaagcgtg agctacatga actggtacca gcagaagagc      960
ggcaccagcc caaaaagatg gatctatgac accagcaagg tggccagcgg agtgccctac     1020
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gaagacgcag ccacatacta ctgccagcag tggagctcta accccctgac attcggcgca     1140
ggcaccaagc tggaactgaa gcaccaccac caccatcacg gcagcggcga aggaagaggc     1200
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ttcctccgcg	gtcaggaatg	cgtcgaagaa	tgccgggttc	tgcagggact	gcccagagaa	1440
tacgttaacg	ccagacactg	cctgccctgc	caccccgaat	gtcagcccca	gaacggctcc	1500
gtcacctgtt	tcggccccga	ggcagaccaa	tgcgtggcct	gcgctcacta	caaggacccc	1560
cccttctgcg	tggcccgttg	cccttcgggc	gtgaagcccg	acctctccta	catgcccatt	1620
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tgcgttgacc	tggacgacaa	gggctgtccc	gccgaacaga	gagccagccc	cctcacctct	1740
atcatctccg	ccgtggtggg	cattctgctg	gtcgtggtcc	tgggcgttgt	gttcggcatc	1800
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<210> 72
 <211> 626
 <212> PRT
 <213> artificial sequence

<220>
 <223> hCAIX-BiTA

<400> 72

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			20					25					30		
Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ser	Ala	Ser	Gly
		35					40				45				
Asn	Ser	Ala	Asn	Ile	Phe	Ser	Phe	Ala	Ser	Val	Ala	Trp	Tyr	Arg	Gln
	50					55					60				
Ala	Pro	Gly	Lys	Gly	Leu	Glu	Leu	Val	Ser	Val	Ile	Thr	Ser	Ala	Gly
65				70					75					80	
Gly	Thr	Lys	Tyr	Ser	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg
			85					90						95	
Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala
			100					105					110		
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Asn	Val	Asp	Tyr	Leu	Gln	Asp	Tyr
		115					120				125				
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
	130				135						140				
Asp	Ile	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Ala	Arg	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Met	Ser	Cys	Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Arg	Tyr
			165					170						175	
Thr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		180						185					190		
Gly	Tyr	Ile	Asn	Pro	Ser	Arg	Gly	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe
	195						200					205			
Lys	Asp	Lys	Ala	Thr	Leu	Thr	Thr	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
	210				215						220				
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
225				230					235					240	
Ala	Arg	Tyr	Tyr	Asp	Asp	His	Tyr	Cys	Leu	Asp	Tyr	Trp	Gly	Gln	Gly

				245				250					255				
Thr	Thr	Leu	Thr	Val	Ser	Ser	Val	Glu	Gly	Gly	Ser	Gly	Gly	Ser	Gly		
			260					265					270				
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser		
		275					280					285					
Pro	Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys		
		290				295					300						
Arg	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser		
305					310					315					320		
Gly	Thr	Ser	Pro	Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser		
			325						330					335			
Gly	Val	Pro	Tyr	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser		
		340					345						350				
Leu	Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys		
		355				360						365					
Gln	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu		
		370				375					380						
Glu	Leu	Lys	His	His	His	His	His	His	Gly	Ser	Gly	Glu	Gly	Arg	Gly		
385					390					395					400		
Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu		
				405					410					415			
Leu	Leu	Val	Thr	Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe		
		420					425					430					
Leu	Leu	Ile	Pro	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp		
		435				440					445						
Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly		
		450				455				460							
Gln	Glu	Cys	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu		
465					470					475					480		
Tyr	Val	Asn	Ala	Arg	His	Cys	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro		
				485					490					495			
Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val		
		500						505					510				
Ala	Cys	Ala	His	Tyr	Lys	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro		
		515					520					525					
Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro		
		530				535					540						
Asp	Glu	Glu	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser		
545					550					555					560		
Cys	Val	Asp	Leu	Asp	Asp	Lys	Gly	Cys	Pro	Ala	Glu	Gln	Arg	Ala	Ser		
				565					570					575			
Pro	Leu	Thr	Ser	Ile	Ile	Ser	Ala	Val	Val	Gly	Ile	Leu	Leu	Val	Val		
		580						585					590				
Val	Leu	Gly	Val	Val	Phe	Gly	Ile	Leu	Ile	Lys	Arg	Arg	Gln	Gln	Lys		
		595				600						605					
Ile	Arg	Lys	Tyr	Thr	Met	Arg	Arg	Leu	Leu	Asp	Tyr	Lys	Asp	Asp	Asp		
	610					615					620						
Asp	Lys																
625																	

<210> 73

<211> 2316

<212> DNA

<213> artificial sequence

<220>

<223> hCAIX-CAB

<400> 73

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tccggcacca	ccgtgatcct	gacctgccct	cagtaccccg	gctccgagat	cctgtggcag	180
cacaacgata	agaacatcgg	cggagacgag	gacgacaaga	acatcggaag	tgacgaggac	240
cacctgagcc	tgaaggaatt	cagcgaactg	gagcagagcg	gctattacgt	ctgctacccc	300
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aactgcatgg	aaatggacac	aaccaccccc	gccccagac	ccccaacccc	tgctcctacc	420
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gacggctgct	cctgtagatt	ccccgaggag	gaggagggcg	gctgcgagct	gagagtgaag	720
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aagggacacg	acggactgta	ccagggcctg	agcacagcta	caaaggacac	atacgacgca	1020
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gccgcaacat	actactgcc	gcagtggagc	tctaattccac	tgacattcgg	cgcaggcacc	2280
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<210> 74

<211> 771

<212> PRT

<213> artificial sequence

<220>

<223> hCAIX-CAB

<400> 74

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		20					25					30			
Gln	Thr	Pro	Tyr	Lys	Val	Ser	Ile	Ser	Gly	Thr	Thr	Val	Ile	Leu	Thr
	35					40					45				
Cys	Pro	Gln	Tyr	Pro	Gly	Ser	Glu	Ile	Leu	Trp	Gln	His	Asn	Asp	Lys
50					55					60					
Asn	Ile	Gly	Gly	Asp	Glu	Asp	Asp	Lys	Asn	Ile	Gly	Ser	Asp	Glu	Asp
65				70					75					80	
His	Leu	Ser	Leu	Lys	Glu	Phe	Ser	Glu	Leu	Glu	Gln	Ser	Gly	Tyr	Tyr
				85				90						95	
Val	Cys	Tyr	Pro	Arg	Gly	Ser	Lys	Pro	Glu	Asp	Ala	Asn	Phe	Tyr	Leu
			100					105					110		
Tyr	Leu	Arg	Ala	Arg	Val	Cys	Glu	Asn	Cys	Met	Glu	Met	Asp	Thr	Thr
	115						120					125			
Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln
	130					135					140				
Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala
145				150					155						160
Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala
			165					170						175	
Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr
		180					185						190		
Leu	Tyr	Cys	Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln
	195						200					205			
Pro	Phe	Met	Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser
	210					215					220				
Cys	Arg	Phe	Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys
225				230						235					240
Phe	Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln
			245						250					255	
Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu
		260					265						270		
Asp	Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg
	275					280						285			
Lys	Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met
	290					295					300				
Ala	Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly
305				310						315					320
Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp
			325					330						335	
Thr	Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys
		340						345					350		
Asp	Asp	Asp	Asp	Lys	Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr
	355					360						365			
Cys	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Leu	Leu	Leu	Val	Thr
	370					375					380				
Ser	Leu	Leu	Leu	Cys	Glu	Leu	Pro	His	Pro	Ala	Phe	Leu	Leu	Ile	Pro
385				390						395					400
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
			405					410						415	

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Asn Ser Ala Asn Ile Phe
 420 425 430
 Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu
 435 440 445
 Glu Leu Val Ser Val Ile Thr Ser Ala Gly Gly Thr Lys Tyr Ser Asp
 450 455 460
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 465 470 475 480
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 485 490 495
 Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr Trp Gly Gln Gly Thr Leu
 500 505 510
 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln
 515 520 525
 Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys
 530 535 540
 Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys
 545 550 555 560
 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser
 565 570 575
 Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu
 580 585 590
 Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
 595 600 605
 Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp
 610 615 620
 His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 625 630 635 640
 Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
 645 650 655
 Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
 660 665 670
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
 675 680 685
 Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg
 690 695 700
 Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe
 705 710 715 720
 Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met
 725 730 735
 Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn
 740 745 750
 Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys His His His
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 His His His
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<210> 75

<211> 1113

<212> DNA

<213> artificial sequence

<220>

<223> hCAIX-BBζ

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agactgagct gtagcgctc cggcaacagc gccaatatct tctcctttgc ttccgtggcc      180
tggtataggc aggccccgg gaagggcctg gagctggtgt cagtcattac atccgccggc      240
ggcaccaagt acagcgacag cgtgaaaggc cggttcacca tcagcagaga caatagcaag      300
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cccgaagagg aagaaggcgg gtgcgagctg agagtgaat tctctaggag cgccgacgcc      780
cccgcttacc agcagggaca gaaccagctg tacaacgagc tgaacctggg gagacgggag      840
gagtatgacg tgctggataa gagaagaggc agagaccccg agatgggagg aaaaccaaga      900
agaaagaacc cacaggaggg cctgtacaac gaactgcaga aggacaagat ggcagaggca      960
tacagcgaga tcggaatgaa gggagagaga agaagaggaa agggacacga cggactgtac     1020
cagggactga gcacagctac aaaggacaca tacgacgcac tgcacatgca ggcactgccca     1080
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<210> 76
<211> 370
<212> PRT
<213> artificial sequence

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<220>
<223> hCAIX-BBζ

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<400> 76
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20          25          30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly
35          40          45
Asn Ser Ala Asn Ile Phe Ser Phe Ala Ser Val Ala Trp Tyr Arg Gln
50          55          60
Ala Pro Gly Lys Gly Leu Glu Leu Val Ser Val Ile Thr Ser Ala Gly
65          70          75          80
Gly Thr Lys Tyr Ser Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
85          90          95
Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
100         105         110
Glu Asp Thr Ala Val Tyr Tyr Cys Asn Val Asp Tyr Leu Gln Asp Tyr
115         120         125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Thr Thr Thr Pro Ala
130         135         140
Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
145         150         155         160
Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr

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165																170																175															
Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala																																
180																185																190															
Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys																																
195																200																205															
Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met																																
210																215																220															
Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe																																
225																230																235															
Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu	Arg	Val	Lys	Phe	Ser	Arg																																
245																250																255															
Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu	Tyr	Asn																																
260																265																270															
Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp	Lys	Arg																																
275																280																285															
Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys	Asn	Pro																																
290																295																300															
Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu	Ala																																
305																310																315															
Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His																																
325																330																335															
Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr	Asp																																
340																345																350															
Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg	Asp	Tyr	Lys	Asp	Asp	Asp																																
355																360																365															
Asp	Lys															370																															