

SEQUENCE LISTING

<110> Jiangsu Hengrui Pharmaceuticals Co., Ltd.
Shanghai Hengrui Pharmaceutical Co., Ltd.

<120> ANTI-HER3 ANTIBODY AND ANTI-HER3 ANTIBODY-DRUG CONJUGATE AND MEDICAL USE THEREOF

<130> 721110CPCT

<150> CN202011097383.0

<151> 2020-10-14

<150> CN202111171200.X

<151> 2021-10-08

<160> 28

<170> SIPOSequenceListing 1.0

<210> 1

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<223> Amino acid sequence of HuMan ErbB3

<400> 1

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

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Gly	Pro	Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala			
			180					185					190					
Pro	Gln	Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys			
		195					200					205						
His	Asp	Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys			
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Phe	Ala	Cys	Arg	His	Phe	Asn	Asp	Ser	Gly	Ala	Cys	Val	Pro	Arg	Cys			
225					230					235					240			
Pro	Gln	Pro	Leu	Val	Tyr	Asn	Lys	Leu	Thr	Phe	Gln	Leu	Glu	Pro	Asn			
			245						250						255			
Pro	His	Thr	Lys	Tyr	Gln	Tyr	Gly	Gly	Val	Cys	Val	Ala	Ser	Cys	Pro			
			260					265							270			
His	Asn	Phe	Val	Val	Asp	Gln	Thr	Ser	Cys	Val	Arg	Ala	Cys	Pro	Pro			
		275					280					285						
Asp	Lys	Met	Glu	Val	Asp	Lys	Asn	Gly	Leu	Lys	Met	Cys	Glu	Pro	Cys			
	290					295					300							
Gly	Gly	Leu	Cys	Pro	Lys	Ala	Cys	Glu	Gly	Thr	Gly	Ser	Gly	Ser	Arg			
305					310					315					320			
Phe	Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Gly	Phe	Val	Asn	Cys	Thr			
			325						330						335			
Lys	Ile	Leu	Gly	Asn	Leu	Asp	Phe	Leu	Ile	Thr	Gly	Leu	Asn	Gly	Asp			
			340					345						350				
Pro	Trp	His	Lys	Ile	Pro	Ala	Leu	Asp	Pro	Glu	Lys	Leu	Asn	Val	Phe			
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Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Tyr	Leu	Asn	Ile	Gln	Ser	Trp	Pro			
	370					375					380							
Pro	His	Met	His	Asn	Phe	Ser	Val	Phe	Ser	Asn	Leu	Thr	Thr	Ile	Gly			
385					390					395					400			
Gly	Arg	Ser	Leu	Tyr	Asn	Arg	Gly	Phe	Ser	Leu	Leu	Ile	Met	Lys	Asn			
			405						410					415				
Leu	Asn	Val	Thr	Ser	Leu	Gly	Phe	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Ala			
			420					425						430				
Gly	Arg	Ile	Tyr	Ile	Ser	Ala	Asn	Arg	Gln	Leu	Cys	Tyr	His	His	Ser			
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Leu	Asn	Trp	Thr	Lys	Val	Leu	Arg	Gly	Pro	Thr	Glu	Glu	Arg	Leu	Asp			
	450					455					460							
Ile	Lys	His	Asn	Arg	Pro	Arg	Arg	Asp	Cys	Val	Ala	Glu	Gly	Lys	Val			
465					470					475					480			
Cys	Asp	Pro	Leu	Cys	Ser	Ser	Gly	Gly	Cys	Trp	Gly	Pro	Gly	Pro	Gly			
			485						490					495				
Gln	Cys	Leu	Ser	Cys	Arg	Asn	Tyr	Ser	Arg	Gly	Gly	Val	Cys	Val	Thr			
			500					505					510					
His	Cys	Asn	Phe	Leu	Asn	Gly	Glu	Pro	Arg	Glu	Phe	Ala	His	Glu	Ala			
		515					520					525						
Glu	Cys	Phe	Ser	Cys	His	Pro	Glu	Cys	Gln	Pro	Met	Glu	Gly	Thr	Ala			
	530					535					540							
Thr	Cys	Asn	Gly	Ser	Gly	Ser	Asp	Thr	Cys	Ala	Gln	Cys	Ala	His	Phe			
545					550					555					560			
Arg	Asp	Gly	Pro	His	Cys	Val	Ser	Ser	Cys	Pro	His	Gly	Val	Leu	Gly			
			565						570					575				
Ala	Lys	Gly	Pro	Ile	Tyr	Lys	Tyr	Pro	Asp	Val	Gln	Asn	Glu	Cys	Arg			
			580					585					590					
Pro	Cys	His	Glu	Asn	Cys	Thr	Gln	Gly	Cys	Lys	Gly	Pro	Glu	Leu	Gln			

	595		600		605										
Asp	Cys	Leu	Gly	Gln	Thr	Leu	Val	Leu	Ile	Gly	Lys	Thr	His	Leu	Thr
	610						615					620			

<210> 2
 <211> 1872
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> gene
 <223> Nucleotide sequence of HuMan ErbB3

<400> 2

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atgggaaatc	tggagatcgt	gctgactggc	cataacgccg	atctgtcctt	tctgcagtgg	180
attagggaaag	tgactggcta	cgtgctggtc	gccatgaatg	agttttccac	tctgccactg	240
ccaaatctga	gagtgggtgag	gggcactcaa	gtgtacgacg	gcaagttcgc	cattttcgtc	300
atgctcaact	acaacacaaa	ctccagccac	gccctcagac	agctgagggt	cactcagctg	360
acagaaattc	tgtccggcgg	cgtctatatc	gagaaaaacg	ataaactgtg	ccacatggac	420
acaatcgatt	ggagggacat	cgtgagggat	agggatgccg	agatcggtgt	caaggataac	480
ggaaggagct	gtcctccttg	tcagtaggtc	tgcaagggaa	ggtgttgggg	acccggctcc	540
gaagactgcc	agacactgac	taagactatc	tgcgccctc	agtgcaatgg	acactgcttc	600
ggcccaaadc	caaaccagt	ctgccacgac	gaatgtgccg	gcggatgcag	cggaccacaa	660
gatacagact	gcttcgcttg	tagacacttc	aatgactccg	gcgcttggtg	gcctagggtg	720
ccacagccac	tcgtgtacaa	caagctcact	tttcagctcg	agcctaacc	tcacactaag	780
taccaatacg	gcggagtctg	cgtcgccagc	tgtcctcaca	acttcgtggt	ggatcagaca	840
agctgcgtga	gagcttgccc	tccagataaa	atggaggtgg	acaagaacgg	actgaagatg	900
tgtgagcctt	gcggcggtg	gtgtcctaaa	gcttgcgagg	gcactggctc	cggatctagg	960
ttccagactg	tcgactccag	caacatcgac	ggctttgtga	actgcactaa	gattctgggc	1020
aatctggact	ttctgatcac	tggcctcaac	ggcgatcctt	ggcacaagat	cccagctctg	1080
gacccagaaa	agctgaatgt	gtttaggaca	gtgagggaga	ttactggcta	cctcaacatc	1140
cagagctggc	ctccacacat	gcacaacttc	agcgtgttct	ccaatctgac	tacaatcggc	1200
ggcagatccc	tctataatag	gggcttctct	ctgctcatca	tgaagaatct	gaacgtcact	1260
tctctgggct	tcagatctct	gaaggagatc	tccgccggaa	ggatttacat	ctccgccaat	1320
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gaaaggctgg	acattaaaca	caataggcca	agaagggtgt	gcgtcgctga	gggcaaagt	1440
tgtgatcctc	tgtgtagctc	cggaggatgt	tggggaccgc	gccccggcca	gtgtctgagc	1500
tgtaggaatt	attctagggg	cggcgtgtgt	gtgacacact	gcaactttct	gaacggcgaa	1560
cctagggaat	tcgcccata	agccgagtgc	ttcagctgcc	accagagtg	tcagcctatg	1620
gagggcacag	ctacatgcaa	tggcagcgga	tccgacacat	gtgctcagtg	tgcccacttt	1680
agggatggac	ctcattgcgt	cagcagctgt	ccacacggcg	tgctgggagc	caagggccct	1740
atctacaagt	accagatgt	gcagaacgag	tgtaggcctt	gccacgagaa	ttgcacacaa	1800
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<210> 3
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of U3

<400> 3
 Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Glu Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Lys Trp Thr Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn

370		375		380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser				
385		390		400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg				
	405		410	415
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu				
	420		425	430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
	435		440	445

<210> 4
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of U3

<400> 4
Asp Ile Glu Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Ser Asn Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Asn Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 5
 <211> 330
 <212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<223> Heavy chain constant region of human IgG1

<400> 5

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

<210> 6

<211> 107

<212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Human kappa light chain constant region

<400> 6
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 20 25 30
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 7
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain variable region of HER3-29

<400> 7
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Gly Leu Pro Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 8

<211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain variable region of HER3-29

<400> 8
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1 5 10 15
 Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Gln His Val Gly Thr Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Thr Pro Lys Leu Leu Ile
 35 40 45
 Ser Gly Ala Ala Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly 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 Ser Tyr Asn Thr Pro Pro
 85 90 95
 Phe Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 9
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Chothia HCDR1

<400> 9
 Gly Phe Thr Phe Asp Asp Tyr
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Chothia HCDR2

<400> 10
 Ser Trp Asn Ser Gly Ser
 1 5

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Chothia HCDR3

<400> 11
Glu Gly Leu Pro Gly Leu Asp Tyr
1 5

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Chothia LCDR1

<400> 12
Arg Ala Ser Gln His Val Gly Thr Tyr Leu Asn
1 5 10

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

<220>
<221> DOMAIN
<223> Chothia LCDR2

<400> 13
Gly Ala Ala Asn Leu Gln Ser
1 5

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Chothia LCDR3

<400> 14

Gln Gln Ser Tyr Asn Thr Pro Pro Phe Ser
1 5 10

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT HCDR1

<400> 15
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT HCDR2

<400> 16
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT HCDR3

<400> 17
Ala Lys Glu Gly Leu Pro Gly Leu Asp Tyr
1 5 10

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT LCDR1

<400> 18
Gln His Val Gly Thr Tyr
1 5

<210> 19
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT LCDR2

<400> 19
Gly Ala Ala
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<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> IMGT LCDR3

<400> 20
Gln Gln Ser Tyr Asn Thr Pro Pro Phe Ser
1 5 10

<210> 21
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Kabat HCDR1

<400> 21
Asp Tyr Ala Met His
1 5

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Kabat HCDR2

<400> 22
Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 23
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Kabat HCDR3

<400> 23
Glu Gly Leu Pro Gly Leu Asp Tyr
1 5

<210> 24
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Kabat LCDR1

<400> 24
Arg Ala Ser Gln His Val Gly Thr Tyr Leu Asn
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> DOMAIN
<223> Kabat LCDR2

<400> 25
Gly Ala Ala Asn Leu Gln Ser
1 5

<210> 26
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> DOMAIN
 <223> Kabat LCDR3

<400> 26
 Gln Gln Ser Tyr Asn Thr Pro Pro Phe Ser
 1 5 10

<210> 27
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Heavy chain of HER3-29

<400> 27
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Gly Leu Pro Gly Leu Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220

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

<210> 28
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> CHAIN
 <223> Light chain of HER3-29

<400> 28
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1 5 10 15
 Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Gln His Val Gly Thr Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Thr Pro Lys Leu Leu Ile
 35 40 45
 Ser Gly Ala Ala Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly 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 Ser Tyr Asn Thr Pro Pro
 85 90 95
 Phe Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala

			100				105				110				
Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
		115					120					125			
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu
	130					135					140				
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser
145					150					155					160
Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
				165					170					175	
Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val
			180					185					190		
Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys
		195					200					205			
Ser	Phe	Asn	Arg	Gly	Glu	Cys									
	210					215									