

Sequence Listing

<110> CHIA TAI TIANQING PHARMACEUTICAL GROUP CO., LTD.

<120> BISPECIFIC ANTIBODY

<160> 53

<170> SIPOSequenceListing 1.0

<210> 1

<211> 103

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of MHCICαori

<400> 1

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

<210> 2

<211> 97

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of MHCICβori

<400> 2

```
Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu
1      5      10      15
Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro
20     25     30
```

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45
Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60
Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
65 70 75 80
Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp
85 90 95
Arg

<210> 3
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Optimized amino acid sequence of Ca

<400> 3
Gly Lys Glu Thr Leu Gln Arg Ala Asp Pro Pro Lys Thr His Val Thr
1 5 10 15
His His Pro Ile Ser Arg His Glu Ala Thr Leu Arg Cys Trp Ala Leu
20 25 30
Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Lys
35 40 45
Asp Gln Thr Gln Lys Thr Glu Leu Val Glu Thr Arg Pro Cys Gly Asp
50 55 60
Arg Thr Phe Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu
65 70 75 80
Gln Arg Tyr Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu
85 90 95
Thr Leu Arg Trp Glu Pro Ser
100

<210> 4
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> Optimized amino acid sequence of Cβ

<400> 4
Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Cys His Pro Ala Glu
1 5 10 15
Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro

		20					25					30			
Ser	Asp	Ile	Glu	Val	Asp	Leu	Leu	Lys	Asn	Gly	Glu	Arg	Ile	Glu	Lys
		35					40					45			
Val	Glu	His	Ser	Asp	Leu	Ser	Phe	Ser	Lys	Asp	Trp	Ser	Phe	Tyr	Leu
		50				55					60				
Leu	Tyr	Tyr	Thr	Arg	Phe	Thr	Pro	Thr	Glu	Lys	Asp	Glu	Tyr	Ala	Cys
65					70					75					80
Arg	Val	Asn	His	Val	Thr	Leu	Ser	Gln	Pro	Lys	Ile	Val	Lys	Trp	Asp
				85					90					95	
Arg Gly Pro															

<210> 5
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of another embodiment of C β

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

<210> 6
 <211> 448
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of polypeptide chain H1 of MHI383-1122-IgG4

<400> 6															
Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	Asn	Ser	Phe

Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
			420					425					430		
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly
		435					440					445			

<210> 7
 <211> 1344
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of polypeptide chain H1 of MHI383-1122-IgG4

<400> 7

gaggtgcagc	tgctggagag	cggaggagga	ctgggtgcagc	caggaggcag	cctgagactg	60
tcttgcgccg	tgtccggctt	cacctttaac	agcttcgcca	tgtcttgggt	gcgccaggct	120
cctggcaagg	gactggagtg	ggtgtctgcc	atctctggat	ccggaggagg	aacatactat	180
gctgactccg	tgaagggcag	gttcaccatc	tcccgggata	acagcaagaa	tacactgtac	240
ctgcagatga	attctctgag	ggccgaggac	accgccgtgt	acttttgtgc	taaggataag	300
atcctgtggt	tcggcgagcc	agtgtttgac	tactggggcc	agggcaccct	ggtgacagtg	360
tccagcgctt	ctacaaaggg	cccttccgtg	ttcccactgg	ctccttgctc	tcgctccaca	420
agcgagtcta	ccgccgtctt	gggctgtctg	gtgaaggact	acttccccga	gcctgtgacc	480
gtgtcttgga	attccggcgc	cctgacaagc	ggagtgcaca	cctttcctgc	tgtgctgcag	540
tcttccggcc	tgtactctct	gagctctgtg	gtgacagtgc	cttccagctc	tctgggcacc	600
aagacatata	cctgcaacgt	ggaccataag	ccatctaata	ccaagggtgga	taagagagtg	660
gagagcaagt	acggaccacc	atgccctcca	tgtcctgctc	cagagttcct	gggaggacca	720
tccgtgttcc	tgtttccacc	taagcctaag	gacacactga	tgatcagccg	gacaccagag	780
gtgacctgcg	tgggtggtgga	cgtgtctcag	gaggatcccg	agggtgcagt	caactggtac	840
gtggatggcg	tggaggtgca	caatgctaag	accaagccta	gagaggagca	gtttaattcc	900
acataccgcg	tggtagcgt	gctgaccgtg	ctgcatcagg	actggctgaa	cggcaaggag	960
tataagtgtg	aggtgtccaa	taagggcctg	ccatccagca	tcgagaagac	catcagcaag	1020
gccaaaggcc	agccaagaga	gccccagggtg	tacacactgc	caccctgcca	ggaggagatg	1080
accaagaacc	aggtgtccct	gtgggtgtctg	gtgaagggtc	tctatcccag	cgacatcgct	1140
gtggagtggg	agtctaattg	ccagcctgag	aacaattaca	agaccacacc	tccagtgcctg	1200
gacagcgatg	gctctttctt	tctgtattct	aggctgacag	tggataagtc	ccggtggcag	1260
gagggcaacg	tgttttcttg	ctccgtgatg	cacgaggccc	tgcacaatca	ttacaccagg	1320
aagagcctgt	ctctgtccct	gggc				1344

<210> 8
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of polypeptide chain L1 of MHI383-1122-IgG4

<400> 8

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

<210> 9
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of polypeptide chain L1 of MHI383-1122-IgG4

<400> 9	
gagatcgtgc	tgacccagtc
ctgtcctgca	gggcttccca
ggccaggctc	ccaggctgct
cgcttctctg	gatccggaag
gaggatttgc	ccgtgtacta
ggcacaaagg	tggagatcaa
tctgacgagc	agctgaagtc
ccacgcgagg	ccaaggtgca
gagtcctgtga	cagagcagga
ctgtctaagg	ccgattacga
ctgagcctgt	ctccaggaga
agctacctgg	cctggatatca
gccagcaaca	gagctaccgg
tttaccctga	caatctcttc
agatctaatt	ggccccctac
gccgctcctt	ccgtgttcat
tccgtgggtgt	gcctgctgaa
gataacgctc	tgcagtccgg
agcacctatt	ctctgtcttc
gtgtatgctt	gcgaggtgac
	acatcagggc
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600

ctgagctctc ccgtgaccaa gtccttcaac agaggcgagt gt

642

<210> 10

<211> 456

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of polypeptide chain H2 of MHI383-1122-IgG4

<400> 10

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

290		295		300
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His				
305		310		315
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys				
	325		330	
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln				
	340		345	
Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met				
	355		360	
Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro				
	370		375	
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn				
385		390		395
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu				
	405		410	
Val Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val				
	420		425	
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln				
	435		440	
Lys Ser Leu Ser Leu Ser Leu Gly			445	
450		455		

<210> 11

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of polypeptide chain H2 of MHI383-1122-IgG4

<400> 11

gaggtgcagc	tggtggagtc	tggaggagga	ctggtgcagc	caggaggaag	cctgaggctg	60
tcttgcgccg	cttccggcct	cacctttaac	acatacgcca	tgaattgggt	gagacaggct	120
cctggcaagg	gactggagtg	ggtggctagg	atccgggtcca	agtacaacaa	ttatgccacc	180
tactatgctg	acagcgtgaa	ggatagattc	accatcagcc	gcgacgattc	taagaacaca	240
gcctatctgc	agatgaacaa	tctgaagacc	gaggacacag	ctatgtacta	ttgcgtgagg	300
cacggcaact	tcggcaattc	ttacgtgtcc	tggtttgctt	attggggcca	gggcaccctg	360
gtgacagtgt	ccagcggcaa	ggagaccctg	cagagagctg	acccccctaa	gaccacagtg	420
acacaccatc	ccatctctag	acatgaggcc	acactgaggt	gctgggctct	gggcttctac	480
cctgccgaga	tcaccctgac	atggcagcgc	gacggcaagg	atcagaccca	gaagacagag	540
ctggtggaga	ccaggccttg	cggcgatcgg	acatttcaga	agtgggctgc	tgtggtggtg	600
ccatccggag	aggagcagag	gtatacctgt	cacgtgcagc	atgagggcct	gccaaagccc	660
ctgacactgc	ggtgggagcc	aagcgagagc	aagtacggac	caccttgccc	accatgtcca	720
gctcctgagt	tcctgggagg	accatccgtg	ttcctgtttc	ctccaaagcc	caaggacaca	780
ctgatgatct	ctcggacacc	agaggtgacc	tgctgtggtg	tggacgtgtc	ccaggaggat	840
cccagggtgc	agttcaactg	gtacgtggat	ggcgtggagg	tgcacaatgc	caagaccaag	900
cccagagagg	agcagtttaa	ttccacatac	cgcgtggtga	gcgtgctgac	cgtgctgcat	960
caggattggc	tgaacggcaa	ggagtataag	tgcaagggtga	gcaataaggg	cctgccttcc	1020

agcatcgaga	agaccatctc	taaggctaag	ggccagccta	gggagccaca	ggtgtgcaca	1080
ctgcccccta	gccaggagga	gatgaccaag	aaccaggtgt	ccctgagctg	tgccgtgaag	1140
ggcttctacc	ccagcgacat	cgctgtggag	tgggagtcta	atggccagcc	tgagaacaat	1200
tataagacca	caccacccgt	gctggacagc	gatggctctt	tctttctggt	gtctaggctg	1260
acagtggata	agtcccgggtg	gcaggagggc	aacgtgtttt	cttgttccgt	gatgcatgag	1320
gccctgcaca	atcattacac	ccagaagagc	ctgtctctgt	ccctgggctg	a	1371

<210> 12
 <211> 208
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of polypeptide chain L2 of MHI383-1122-IgG4

<400> 12

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

<210> 13
 <211> 624
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Nucleotide sequence of polypeptide chain L2 of MHI383-1122-IgG4

<400> 13

```
gagctggtgg tgacacagga gcctagcctg accacatctc caggcggcac cgtgacactg      60
acctgcagat ccagcaccgg cgccgtgacc acatccaact acgctaattg ggtgcagcag      120
aagccaggac aggctccaag gggactgatc ggaggaacaa acaagagggc tccaggaacc      180
cctgctcggg tctctggatc cctgctggga ggcaaggccg ctctgacaat caccggagtg      240
cagccagagg acgaggctga gtactattgt gctctgtggt atagcaatct gtgggtgttt      300
ggcggcggca caaagctgac cgtgctgac cagagaaccc ccaagatcca ggtgtacagc      360
tgccaccctg ccgagaacgg caagtctaac ttcctgaatt gttacgtgtc cggctttcat      420
ccttccgaca tcgagggtgga tctgctgaag aatggcgagc gcatcgagaa ggtggagcac      480
tccgacctgt ccttcagcaa ggattggagc ttttacctgc tgtactatac caggttcacc      540
ccaacagaga aggacgagta tgcttgccgg gtgaaccatg tgacactgtc tcagccaaag      600
atcgtgaagt gggatagggg cccc                                     624
```

<210> 14

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of polypeptide chain H3 of MHI383-1133-IgG4

<400> 14

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

Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr
 180 185 190
 Thr Arg Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn
 195 200 205
 His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Gly Pro
 210 215 220
 Glu Ser Lys Tyr Gly Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 225 230 235 240
 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 290 295 300
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 325 330 335
 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Cys Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Arg Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Leu Gly
 450

<210> 15
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of polypeptide chain H3 of MHI383-1133-IgG4

<400> 15
 gaggtgcagc tgggtggagtc tggaggagga ctggtgcagc caggaggaag cctgaggctg 60
 tcttgcgccg cttccggcctt cacctttaac acatacgcca tgaattgggt gagacaggct 120

cctggcaagg	gactggagtg	ggtggctagg	atccggtcca	agtacaacaa	ttatgccacc	180
tactatgctg	acagcgtgaa	ggatagattc	accatcagcc	gcgacgattc	taagaacaca	240
gcctatctgc	agatgaacaa	tctgaagacc	gaggacacag	ctatgtacta	ttgcgtgagg	300
cacggcaact	tcggcaattc	ttacgtgtcc	tggtttgctt	attggggcca	gggcaccctg	360
gtgacagtgt	ccagcatcca	gagaaccccc	aagatccagg	tgtacagctg	ccaccctgcc	420
gagaacggca	agtctaactt	cctgaattgt	tacgtgtccg	gctttcatcc	ttccgacatc	480
gaggtggatc	tgctgaagaa	tggcgagcgc	atcgagaagg	tggagcactc	cgacctgtcc	540
ttcagcaagg	attggagctt	ttacctgctg	tactatacca	ggttcacccc	aacagagaag	600
gacgagtatg	cttgccgggt	gaaccatgtg	acactgtctc	agccaaagat	cgtgaagtgg	660
gatagggggc	ccgagagcaa	gtacggacca	ccttgcccac	catgtccagc	tcctgagttc	720
ctgggaggac	catccgtgtt	cctgttttct	ccaaagccca	aggacacact	gatgatctct	780
cggacaccag	aggtgacctg	cgtggtggtg	gacgtgtccc	aggaggatcc	cgaggtgcag	840
ttcaactggt	acgtggatgg	cgtggagggtg	cacaatgcca	agaccaagcc	cagagaggag	900
cagtttaatt	ccacataaccg	cgtggtgagc	gtgctgaccg	tgctgcatca	ggattggctg	960
aacggcaagg	agtataagtg	caaggtgagc	aataagggcc	tgctttccag	catcgagaag	1020
accatctcta	aggctaaggg	ccagcctagg	gagccacagg	tgtgcacact	gccccctagc	1080
caggaggaga	tgaccaagaa	ccaggtgtcc	ctgagctgtg	ccgtgaaggg	cttctacccc	1140
agcgacatcg	ctgtggagtg	ggagtctaata	ggccagcctg	agaacaatta	taagaccaca	1200
ccaccctgtc	tggacagcga	tggctctttc	tttctggtgt	ctaggctgac	agtggataag	1260
tcccgggtggc	aggagggcaa	cgtgttttct	tgttccgtga	tgcatgaggc	cctgcacaat	1320
cattacaccc	agaagagcct	gtctctgtcc	ctgggctga			1359

<210> 16

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of polypeptide chain L3 of MHI383-1133-IgG4

<400> 16

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

130	135	140
Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Lys Asp Gln Thr		
145	150	155
Gln Lys Thr Glu Leu Val Glu Thr Arg Pro Cys Gly Asp Arg Thr Phe		
	165	170
Gln Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr		
	180	185
Thr Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg		
	195	200
Trp Glu Pro Ser		205
210		

<210> 17
 <211> 636
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of polypeptide chain L3 of MHI383-1133-IgG4

<400> 17	
gagctggtgg tgacacagga gcctagcctg accacatctc caggcggcac cgtgacactg	60
acctgcagat ccagcaccgg cgccgtgacc acatccaact acgctaattg ggtgcagcag	120
aagccaggac aggctccaag gggactgac ggaggaacaa acaagagggc tccaggaacc	180
cctgctcggt tctctggatc cctgctggga ggcaaggccg ctctgacaat caccggagtg	240
cagccagagg acgaggctga gtactattgt gctctgtggt atagcaatct gtgggtgttt	300
ggcggcggca caaagctgac cgtgctgggc aaggagaccc tgcagagagc tgacccccct	360
aagaccacg tgacacacca tcccatctct agacatgagg ccacactgag gtgctgggct	420
ctgggcttct accctgccga gatcaccttg acatggcagc gcgacggcaa ggatcagacc	480
cagaagacag agctggtgga gaccaggcct tgcggcgatc ggacatttca gaagtgggct	540
gctgtggtgg tgccatccgg agaggagcag aggtatacct gtcacgtgca gcatgagggc	600
ctgccaaagc ccctgacact gcggtgggag ccaagc	636

<210> 18
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of Hc of MHI383-ccff-IgG1

<400> 18
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Asn Ser Phe
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

		35				40					45				
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys
				85					90					95	
Ala	Lys	Asp	Lys	Ile	Leu	Trp	Phe	Gly	Glu	Pro	Val	Phe	Asp	Tyr	Trp
			100					105					110		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
			115				120					125			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
	130					135					140				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145					150					155					160
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				165					170					175	
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			180					185					190		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		195				200						205			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
	210					215					220				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala
225					230					235					240
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				245					250					255	
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			260					265					270		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
	275						280					285			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
	290					295					300				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
305					310					315					320
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				325					330					335	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			340					345					350		
Val	Tyr	Thr	Leu	Pro	Pro	Cys	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		355					360					365			
Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
	370					375					380				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
385					390					395					400
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
				405					410					415	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
			420					425					430		

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445
 Ser Pro Gly Lys
 450

<210> 19
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of Hc of MHI383-ccff-IgG1

<400> 19
 gaggtgcagc tgctggagag cggaggagga ctggtgcagc caggaggcag cctgagactg 60
 tcttgcgccg tgtccggcctt cacctttaac agcttcgccca tgtcttgggt gcgccaggct 120
 cctggcaagg gactggagtg ggtgtctgcc atctctggat ccggaggagg aacatactat 180
 gctgactccg tgaagggcag gttcaccatc tcccgggata acagcaagaa tacactgtac 240
 ctgcagatga attctctgag ggccgaggac accgccgtgt acttttgtgc taaggataag 300
 atcctgtggt tcggcgagcc agtgtttgac tactggggcc agggcaccct ggtgacagtg 360
 tccagcgctt ctaccaaggg accatccgtg ttcccactgg ctccatccag caagtccacc 420
 agcggaggaa cagccgctct gggatgcctg gtgaaggact acttcccaga gcccgtgaca 480
 gtgagctgga actctggcgc cctgaccagc ggagtgcaca catttccagc tgtgctgcag 540
 tcttccggcc tgtactctct gagctctgtg gtgaccgtgc cctccagctc tctgggcacc 600
 cagacatata tctgcaacgt gaatcacaag ccaagcaata caaagggtgga caagaagggtg 660
 gagcccaagt cttgtgataa gaccataca tgccccctt gtcctgctcc agaggctgct 720
 ggaggaccat ccgtgttcct gtttccacc aagcctaagg acaccctgat gatctccagg 780
 acccccgagg tgacatgcgt ggtggtggac gtgagccacg aggatcctga ggtgaagttt 840
 aactggtacg tggatggcgt ggagggtgcat aatgctaaga ccaagcctag ggaggagcag 900
 tacaacagca cctatcgggt ggtgtctgtg ctgacagtgc tgcaccagga ctggctgaac 960
 ggcaaggagt ataagtgtaa ggtgtctaata aaggccctgc ccgctcctat cgagaagacc 1020
 atctccaagg ccaagggcca gcctagagag ccacaggtgt acaccctgcc tccatgccgc 1080
 gacgagctga caaagaacca ggtgagcctg tgggtgtctgg tgaagggcctt ctatccttct 1140
 gatatcgctg tggagtggga gtccaatggc cagccagaga acaattacaa gaccacaccc 1200
 cctgtgctgg actccgatgg cagcttcttt ctgtattcca agctgaccgt ggataagagc 1260
 agatggcagc agggcaacgt gttttcttgt tccgtgatgc atgaggccct gcacaatcat 1320
 tatacacaga agagcctgtc tctgtcccca ggcaag 1356

<210> 20
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of Lc of MHI383-ccff-IgG1

<400> 20

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

<210> 21
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of Lc of MHI383-ccff-IgG1

<400> 21
 gagatcgtgc tgacccagtc tcctgccaca ctgagcctgt ctccaggaga gagggccacc 60
 ctgtcctgca gggcttccca gagcgtgtcc agctacctgg cctggtatca gcagaagcca 120
 ggccaggctc ccaggctgct gatctacgac gccagcaaca gagctaccgg catccccgct 180
 cgcttctctg gatccggaag cggcacagac tttaccctga caatctcttc cctggagcct 240
 gaggatttcg ccgtgtacta ttgtcagcag agatctaatt ggccccctac ctttggccag 300
 ggcacaaagg tggagatcaa gcgtacgggtg gccgctcctt ccgtgttcat ctttccaccc 360
 tctgacgagc agctgaagtc tggcaccgct tccgtgggtgt gcctgctgaa caacttctac 420
 ccacgcgagg ccaagggtgca gtggaagggtg gataacgctc tgcagtccgg caatagccag 480
 gagtctgtga cagagcagga ctccaaggat agcacctatt ctctgtcttc caccctgaca 540
 ctgtctaagg ccgattacga gaagcacaag gtgtatgctt gcgaggtgac acatcagggc 600

ctgagctctc ccgtgaccaa gtccttcaac agaggcgagt gt

642

<210> 22

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Hf of MHI383-ccff-IgG1

<400> 22

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

290	295	300
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr		
305	310	315
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val		320
	325	330
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala		335
	340	345
Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg		350
	355	360
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly		365
	370	375
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro		380
	385	390
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser		395
	405	410
Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln		415
	420	425
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg		430
	435	440
Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		445
	450	455
		460

<210> 23
 <211> 1380
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of Hf of MHI383-ccff-IgG1

<400> 23

gaggtgcagc	tggtggagtc	tggaggagga	ctggtgcagc	caggaggaag	cctgaggctg	60
tcttgcgccg	cttccggctt	cacctttaac	acatacgcca	tgaattgggt	gagacaggct	120
cctggcaagg	gactggagtg	ggtggctagg	atccgggtcca	agtacaacaa	ttatgccacc	180
tactatgctg	acagcgtgaa	ggatagattc	accatcagcc	gcgacgattc	taagaacaca	240
gcctatctgc	agatgaacaa	tctgaagacc	gaggacacag	ctatgtacta	ttgcgtgagg	300
cacggcaact	tcggcaattc	ttacgtgtcc	tggtttgctt	attggggcca	gggcaccctg	360
gtgacagtgt	ccagcggcaa	ggagaccctg	cagagagctg	acccccctaa	gaccacagtg	420
acacaccatc	ccatctctag	acatgaggcc	acactgaggt	gctgggctct	gggcttctac	480
cctgccgaga	tcaccctgac	atggcagcgc	gacggcaagg	atcagaccca	gaagacagag	540
ctggtggaga	ccaggccttg	cggcgatcgg	acatttcaga	agtgggctgc	tgtggtggtg	600
ccatccggag	aggagcagag	gtatacctgt	cacgtgcagc	atgagggcct	gccaaagccc	660
ctgacactgc	ggtgggagcc	aagcgagcca	aagtccagcg	acaagaccca	cacatgccca	720
ccttgtccag	ctccagaggc	tgctggagga	ccatccgtgt	tcctgtttcc	acccaagccc	780
aaggataccc	tgatgatctc	taggaccccc	gaggtgacat	gcgtgggtgt	ggacgtgtcc	840
cacgaggatc	ctgaggtgaa	gttcaactgg	tacgtggacg	gcgtggaggt	gcataatgcc	900
aagacaaagc	ccagggagga	gcagtacaac	tctacctatc	gggtgggtgtc	cgtgctgaca	960
gtgctgcatc	aggattggct	gaacggcaag	gagtataagt	gtaagggtgag	caataaggcc	1020

ctgcctgctc	caatcgagaa	gaccatctct	aaggctaagg	gccagcccag	agagcctcag	1080
gtgtgcaccc	tgcttccatc	ccgcgacgag	ctgacaaaga	accaggtgtc	tctgtcctgt	1140
gccgtgaagg	gctttttaccc	ttccgatatc	gctgtggagt	gggagagcaa	tggccagcca	1200
gagaacaatt	ataagaccac	accccctgtg	ctggactccg	atggcagctt	ctttctggtg	1260
agcaagctga	ccgtggacaa	gtctaggtgg	cagcagggca	acgtgttcag	ctgctctgtg	1320
atgcacgagg	ctctgcataa	taggttcacc	cagaagtccc	tgagcctgtc	tcccggcaag	1380

<210> 24
 <211> 208
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of Lf of MHI383-ccff-IgG1

<400> 24

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

<210> 25
 <211> 624
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Nucleotide sequence of Lf of MHI383-ccff-IgG1

<400> 25

```
gagctggtgg tgacacagga gcctagcctg accacatctc caggcggcac cgtgacactg      60
acctgcagat ccagcaccgg cgccgtgacc acatccaact acgctaattg ggtgcagcag      120
aagccaggac aggctccaag gggactgatc ggaggaacaa acaagagggc tccaggaacc      180
cctgctcggg tctctggatc cctgctggga ggcaaggccg ctctgacaat caccggagtg      240
cagccagagg acgaggctga gtactattgt gctctgtggt atagcaatct gtgggtgttt      300
ggcggcggca caaagctgac cgtgctgac cagagaaccc ccaagatcca ggtgtacagc      360
tgccaccctg ccgagaacgg caagtctaac ttcctgaatt gttacgtgtc cggctttcat      420
ccttccgaca tcgagggtga tctgctgaag aatggcgagc gcatcgagaa ggtggagcac      480
tccgacctgt ccttcagcaa ggattggagc ttttacctgc tgtactatac caggttcacc      540
ccaacagaga aggacgagta tgcttgccgg gtgaaccatg tgacactgtc tcagccaaag      600
atcgtgaagt gggatagggg cccc                                     624
```

<210> 26

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of heavy chain HZ5G11VH-CH1-IgG1

<400> 26

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

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 27
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of heavy chain HZ5G11VH-CH1-IgG1

<400> 27
 caaatcactc taaaggaaaag tgggtccaact ctggtgaaac ccacccagac cctgacactg 60
 acctgtaccg tgtctggctt tagcctgtct acctacggcg tgcactggat cagacagcct 120
 cctggcaagg ccctcgagtg gctgggagtg atctggcggg gcgtgaccac cgactataat 180
 gctgccttca tgtcccggct gaccatcacc aaggacaact ccaagaacca agtggtgctg 240

accatgaaca	acatggatcc	tgtggacaca	gctacctact	actgcgccag	actgggcttc	300
tacgccatgg	actactgggg	ccagggcacc	ctgggtcacag	tgtcctctgc	tagcacaaag	360
ggcccttccg	tgttcccact	ggctccctct	tccaagtcta	catccggagg	aaccgccgct	420
ctgggatgcc	tgggtgaagga	ttattttcca	gagcccgtga	ccgtgtcttg	gaactccggc	480
gccctgacaa	gcggagtgc	tacctttcct	gctgtgctgc	agagctctgg	cctgtattct	540
ctgtccagcg	tgggtgacagt	gccatcttcc	agcctgggca	cccagacata	catctgcaac	600
gtgaatcaca	agcctagcaa	taccaagggtg	gacaagaagg	tggagccaaa	gtcttgtgat	660
aagacccata	catgcccccc	ttgtcctgct	ccagagctgc	tgggaggacc	atccgtgttc	720
ctgtttccac	ccaagcccaa	ggacaccctg	atgatctccc	gcacaccaga	ggtgacctgc	780
gtgggtgggg	acgtgagcca	cgaggatccc	gaggtgaagt	ttaactggta	cgtggatggc	840
gtggagggtgc	ataatgctaa	gaccaagcca	agagaggagc	agtataacag	cacataccgc	900
gtgggtgtctg	tgctgaccgt	gctgcaccag	gactggctga	acggcaagga	gtacaagtgc	960
aaggtgtcta	ataaggccct	gcccgtctct	atcgagaaga	caatctccaa	ggccaagggc	1020
cagcctagggg	agccacaggt	gtataccctg	cctccatctc	gggacgagct	gacaaagaac	1080
caggtgtccc	tgacctgtct	ggtgaagggc	ttctacccca	gcgatatcgc	tgtggagtgg	1140
gagtctaattg	gccagcctga	gaacaattat	aagaccacac	cccctgtgct	ggacagcgat	1200
ggctctttct	ttctgtactc	taagctgaca	gtggataagt	ccaggtggca	gcagggaac	1260
gtgttttagct	gctctgtgat	gcatgaggct	ctgcacaatc	attacaccca	gaagtccctg	1320
agcctgtctc	ccggcaag					1338

<210> 28

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of light chain HZ5G11VL-IgK

<400> 28

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

145		150		155		160									
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
		165		170		175									
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		180		185		190									
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195		200		205									
Phe	Asn	Arg	Gly	Glu	Cys										
	210														

<210> 29
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of light chain HZ5G11VL-IgK

<400> 29	
gatatccaaa	tgactcaaag tccaagtagt ctgtccgctt ctgtcggcga cagagtgacc 60
atcacctgta	aggcctctca gtccgtgtcc aacgacgtgg cttggtacca gcagaagcct 120
ggcaaggctc	ctaagctgct gatctactac gccgccaacc ggtacaccgg cgtgcccgat 180
agattctccg	gctctggcta cggcaccgac ttacacctta caatctccag cctgcagcct 240
gaggatatcg	ccacctactt ctgccagcag gactacacct ctccatatac cttcggccaa 300
ggaacaaaac	tggaaatcaa gcgtacgggtg gccgctcctt ccgtgttcat ctttccccct 360
tccgatgagc	agctgaagag cggcacagct tctgtgggtg gcctgctgaa caacttctac 420
ccaagggagg	ccaaggtgca gtggaagggtg gacaacgctc tgcagagcgg caattctcag 480
gagtccgtga	ccgagcagga cagcaaggat tctacatatt ccctgtccag caccctgaca 540
ctgtccaagg	ccgattacga gaagcacaag gtgtatgctt gcgagggtgac ccatcagggc 600
ctgtcttccc	ccgtgacaaa gagctttaat agaggcgagt gt 642

<210> 30
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of heavy chain HZ5G11VH-Cα-IgG1

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

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

Pro Gly Lys
450

<210> 31
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence of heavy chain HZ5G11VH-C α -IgG1

<400> 31
caaatcactc taaaggaaag tgggtccaact ctggtgaaac ccacccagac cctgacactg 60
acctgtaccg tgtctggctt tagcctgtct acctacggcg tgcactggat cagacagcct 120
cctggcaagg ccctcgagtg gctgggagtg atctggcggg gcgtgaccac cgactataat 180
gctgccttca tgtcccggct gaccatcacc aaggacaact ccaagaacca agtgggtgctg 240
accatgaaca acatggatcc tgtggacaca gctacctact actgcgccag actgggcttc 300
tacgcatggg actactgggg ccagggcacc ctggtcacag tgtcctctgg caaggagacc 360
ctgcagagag ctgaccccc taagaccac gtgacacacc atcccatctc tagacatgag 420
gccacactga ggtgctgggc tctgggcttc taccctgccg agatcacctt gacatggcag 480
cgcgacggca aggatcagac ccagaagaca gagctgggtg agaccaggcc ttgcggcgat 540
cggacatttc agaagtgggc tgctgtggtg gtgccatccg gagaggagca gaggtatacc 600
tgtcacgtgc agcatgaggg cctgccaaag cccctgacac tgcggtggga gccaaagcgag 660
ccaaagtctt gtgataagac ccatacatgc ccccttgtc ctgctccaga gctgctggga 720
ggaccatccg tgttcctgtt tccacccaag cccaaggaca ccctgatgat ctcccgcaca 780
ccagagggtga cctgcgtggt ggtggacgtg agccacgagg atcccagggt gaagtttaac 840
tggtagctgg atggcgtgga ggtgcataat gctaagacca agccaagaga ggagcagtat 900
aacagcacat accgcgtggt gtctgtgctg accgtgctgc accaggactg gctgaacggc 960
aaggagtaca agtgcaagggt gtctaataag gccctgcccg ctcctatcga gaagacaatc 1020
tccaaggcca agggccagcc tagggagcca caggtgtata ccctgcctcc atctcgggac 1080
gagctgacaa agaaccagggt gtccctgacc tgtctggtga agggcttcta cccagcgat 1140
atcgctgtgg agtgggagtc taatggccag cctgagaaca attataagac cacacccctt 1200
gtgctggaca gcgatggctc tttctttctg tactctaagc tgacagtgga taagtccagg 1260
tggcagcagg gcaacgtgtt tagctgctct gtgatgcatg aggcctctgca caatcattac 1320
accagaagt ccctgagcct gtctcccggc aag 1353

<210> 32
<211> 206
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of light chain HZ5G11VL-C β

<400> 32
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

<210> 33

<211> 618

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of light chain HZ5G11VL-C β

<400> 33

gatatccaaa	tgactcaaag	tccaagtagt	ctgtccgctt	ctgtcggcga	cagagtgacc	60
atcacctgta	aggcctctca	gtccgtgtcc	aacgacgtgg	cttgggtacca	gcagaagcct	120
ggcaaggctc	ctaagctgct	gatctactac	gccgccaacc	ggtacaccgg	cgtgcccgat	180
agattctccg	gctctggcta	cggcaccgac	ttcaccttta	caatctccag	cctgcagcct	240
gaggatatcg	ccacctactt	ctgccagcag	gactacacct	ctccatatac	cttcggccaa	300
ggaacaaaac	tggaaatcaa	gatccagaga	acccccaaaga	tccagggtgta	cagctgccac	360
cctgccgaga	acggcaagtc	taacttcctg	aattgttacg	tgtccggctt	tcatacttcc	420
gacatcgagg	tggatctgct	gaagaatggc	gagcgcacgc	agaagggtgga	gcactccgac	480
ctgtccttca	gcaaggattg	gagcttttac	ctgctgtact	ataccagggt	cacccaaca	540
gagaaggacg	agtatgcttg	ccgggtgaac	catgtgacac	tgtctcagcc	aaagatcgtg	600
aagtgggata	ggggcccc					618

<210> 34

<211> 98

<212> PRT
<213> Artificial Sequence

<220>

<223> Wild type amino acid sequence of constant region CH1 of IgG1

<400> 34

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1			5					10					15		
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														

<210> 35

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild type amino acid sequence of constant region CL of IgK

<400> 35

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> 36

<211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of HZ5G11VL-IgK-S114A

<400> 36
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Ala Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Tyr Thr Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ala Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 37
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of HZ5G11VL-IgK-S114A

<400> 37
 gatatccaaa tgactcaaag tccaagtagt ctgtccgctt ctgtcggcga cagagtgacc

atcacctgta	aggcctctca	gtccgtgtcc	aacgacgtgg	cttggtacca	gcagaagcct	120
ggcaaggctc	ctaagctgct	gatctactac	gccgccaacc	ggtacaccgg	cgtgcccgat	180
agattctccg	gctctggcta	cggcaccgac	ttcaccttta	caatctccag	cctgcagcct	240
gaggatatcg	ccacctactt	ctgccagcag	gactacacct	ctccatatac	cttcggccaa	300
ggaacaaaac	tggaaatcaa	gcgtacgggtg	gccgctcctg	ccgtgttcat	ctttccccct	360
tccgatgagc	agctgaagag	cggcacagct	tctgtgggtg	gcctgctgaa	caacttctac	420
ccaagggagg	ccaaggtgca	gtggaagggtg	gacaacgctc	tgcagagcgg	caattctcag	480
gagtccgtga	ccgagcagga	cagcaaggat	tctacatatt	ccctgtccag	caccctgaca	540
ctgtccaagg	ccgattacga	gaagcacaag	gtgtatgctt	gcgagggtgac	ccatcagggc	600
ctgtcttccc	ccgtgacaaa	gagctttaat	agaggcgagt	gt		642

<210> 38
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of HZ5G11VL-IgK-F116A

<400> 38
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Ala Ala Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Tyr Thr Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Ala Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 39
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of HZ5G11VL-IgK-F116A

```

<400> 39
gatatccaaa tgactcaaag tccaagtagt ctgtccgctt ctgtcggcga cagagtgacc      60
atcacctgta aggcctctca gtccgtgtcc aacgacgtgg cttggtacca gcagaagcct      120
ggcaaggctc ctaagctgct gatctactac gccgccaacc ggtacaccgg cgtgcccgat      180
agattctccg gctctggcta cggcaccgac ttcaccttta caatctccag cctgcagcct      240
gaggatatcg ccacctactt ctgccagcag gactacacct ctccatatac cttcggccaa      300
ggaacaaaac tggaaatcaa gcgtacggtg gccgctcctt ccgtggccat ctttccccct      360
tccgatgagc agctgaagag cggcacagct tctgtggtgt gcctgctgaa caacttctac      420
ccaagggagg ccaagggtgca gtggaagggtg gacaacgctc tgcagagcgg caattctcag      480
gagtccgtga ccgagcagga cagcaaggat tctacatatt ccctgtccag caccctgaca      540
ctgtccaagg ccgattacga gaagcacaag gtgtatgctt gcgagggtgac ccatcagggc      600
ctgtcttccc ccgtgacaaa gagctttaat agaggcgagt gt                                642
  
```

<210> 40
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of HZ5G11VL-IgK-F118A

```

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

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

<210> 41
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of HZ5G11VL-IgK-F118A

<400> 41
 gatattccaaa tgactcaaaag tccaagtagt ctgtccgctt ctgtcggcga cagagtgacc 60
 atcacctgta aggcctctca gtccgtgtcc aacgacgtgg cttggtacca gcagaagcct 120
 ggcaaggctc ctaagctgct gatctactac gccgccaacc ggtacaccgg cgtgcccgat 180
 agattctccg gctctggcta cggcaccgac ttcaccttta caatctccag cctgcagcct 240
 gaggatatcg ccacctactt ctgccagcag gactacacct ctccatatac cttcggccaa 300
 ggaacaaaac tggaaatcaa gcgtacgggtg gccgctcctt ccgtgttcat cgctccccct 360
 tccgatgagc agctgaagag cggcacagct tctgtggtgt gcctgctgaa caacttctac 420
 ccaagggagg ccaagggtgca gtggaagggtg gacaacgctc tgcagagcgg caattctcag 480
 gagtccgtga ccgagcagga cagcaaggat tctacatatt ccctgtccag caccctgaca 540
 ctgtccaagg ccgattacga gaagcacaag gtgtatgctt gcgagggtgac ccatcagggc 600
 ctgtcttccc ccgtgacaaa gagctttaat agaggcgagt gt 642

<210> 42
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of HZ5G11VL-IgK-F118I

<400> 42
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Ser Asn Asp
 20 25 30

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

<210> 43

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of HZ5G11VL-IgK-F118I

<400> 43

gatatccaaa	tgactcaaag	tccaagtagt	ctgtccgctt	ctgtcggcga	cagagtgacc	60
atcacctgta	aggcctctca	gtccgtgtcc	aacgacgtgg	cttggtacca	gcagaagcct	120
ggcaaggctc	ctaagctgct	gatctactac	gccgccaacc	ggtacaccgg	cgtgcccgat	180
agattctccg	gctctggcta	cggcaccgac	ttcaccttta	caatctccag	cctgcagcct	240
gaggatatcg	ccacctactt	ctgccagcag	gactacacct	ctccatatac	cttcggccaa	300
ggaacaaaac	tggaaatcaa	gcgtacgggtg	gccgctcctt	ccgtgttcat	cattccccct	360
tccgatgagc	agctgaagag	cggcacagct	tctgtgggtgt	gcctgctgaa	caacttctac	420
ccaagggagg	ccaaggtgca	gtggaagggtg	gacaacgctc	tgcagagcgg	caattctcag	480
gagtccgtga	ccgagcagga	cagcaaggat	tctacatatt	ccctgtccag	caccctgaca	540
ctgtccaagg	ccgattacga	gaagcacaag	gtgtatgctt	gcgaggtgac	ccatcagggc	600
ctgtcttccc	ccgtgacaaa	gagctttaat	agaggcgagt	gt		642

<210> 44

<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of CL domain containing F118A

<400> 44
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Ala 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> 45
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of HZ14A9VH-CH1-IgG1

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

Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
130						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165						170						175
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
		180						185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
	195					200					205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215				220					
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
225				230					235						240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
			245					250							255
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
		260					265						270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
		275					280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305				310					315						320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
			325						330					335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
		340					345						350		
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu
	355					360						365			
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	370				375					380					
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
385				390					395						400
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
			405					410						415	
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
		420					425						430		
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
		435				440						445			
Gly	Lys														
450															

<210> 46
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of HZ14A9VL-IgK

<400> 46

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

<210> 47

<211> 455

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HZ14A9VH-C α -IgG1

<400> 47

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

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

450

455

<210> 48
 <211> 206
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of HZ14A9VL-C β

<400> 48
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Ser Tyr
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ile Gly
 50 55 60
 Ser Gly Ser Ser Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Tyr Ser Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ile Gln Arg Thr Pro
 100 105 110
 Lys Ile Gln Val Tyr Ser Cys His Pro Ala Glu Asn Gly Lys Ser Asn
 115 120 125
 Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu Val
 130 135 140
 Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser Asp
 145 150 155 160
 Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Arg
 165 170 175
 Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val
 180 185 190
 Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Gly Pro
 195 200 205

<210> 49
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of H2 of MHL147-3322-IgG1-wt/MHL147-3322-F118A

<400> 49
 Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
 1 5 10 15

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

				405					410					415			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
			420					425					430				
His	Glu	Ala	Leu	His	Asn	Arg	Phe	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
		435					440					445					
Pro	Gly	Lys															
	450																

<210> 50
 <211> 206
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of L2 of MHL147-3322-IgG1-wt/MHL147-3322-F118A

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

<210> 51
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of H3 of MHL147-3322-IgG1-wt/MHL147-3322-F118A

<400> 51

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

		355					360					365					
Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp		
	370					375					380						
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val		
385					390					395					400		
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp		
			405						410					415			
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His		
		420					425					430					
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro		
		435					440					445					
Gly	Lys																
	450																

<210> 52

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of L3 of MHL147-3322-F118A

<400> 52

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

Phe Asn Arg Gly Glu Cys
210

<210> 53
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of L3 of MHL147-3322-IgG1-wt

<400> 53
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Glu Asn Val Val Ser Tyr
20 25 30
Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg Phe Ile Gly
50 55 60
Ser Gly Ser Ser Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Ser Tyr Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210