

SEQUENCE LISTING

<110> SHANGHAI YAKE BIOTECHNOLOGY LTD.

<120> CD7-TARGETED ENGINEERED IMMUNE CELL, CHIMERIC ANTIGEN RECEPTOR, CD7 BLOCKING MOLECULE AND USE THEREOF

<130> DD12447P

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 69

<212> PRT

<213> Artificial sequence

<400> 1

Thr Thr Thr Pro Ala Pro Ala Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gly Pro Leu Ser Leu Ala Pro Gly Ala Cys Ala Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Ala Gly Leu Ala Pro Ala Cys Ala Ile Thr Ile
35 40 45

Thr Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr Leu Thr Cys
65

<210> 2

<211> 42

<212> PRT

<213> Artificial sequence

<400> 2

Leu Ala Gly Ala Leu Leu Leu Leu Thr Ile Pro Leu Gly Pro Pro Met
1 5 10 15

Ala Pro Val Gly Thr Thr Gly Gly Gly Ala Gly Cys Ser Cys Ala Pro
20 25 30

Pro Gly Gly Gly Gly Gly Gly Cys Gly Leu
35 40

<210> 3
<211> 107
<212> PRT
<213> Artificial sequence

<400> 3

Ile Gly Val Met Thr Pro Pro Pro Thr Leu Ala Ala Gly Leu Ser Ala
1 5 10 15

Gly Thr Ile Ile His Val Leu Gly Leu His Leu Cys Pro Ser Pro Leu
20 25 30

Pro Pro Gly Pro Ser Leu Pro Pro Thr Val Leu Val Val Val Gly Gly
35 40 45

Val Leu Ala Cys Thr Ser Leu Leu Val Thr Val Ala Pro Ile Ile Pro
50 55 60

Thr Val Ala Ser Leu Ala Ser Ala Leu Leu His Ser Ala Thr Met Ala
65 70 75 80

Met Thr Pro Ala Ala Pro Gly Pro Thr Ala Leu His Thr Gly Pro Thr
85 90 95

Ala Pro Pro Ala Ala Pro Ala Ala Thr Ala Ser
100 105

<210> 4
<211> 112
<212> PRT
<213> Artificial sequence

<400> 4

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

Gly Ala Gly Leu Thr Ala Gly Leu Ala Leu Gly Ala Ala Gly Gly Thr
20 25 30

Ala Val Leu Ala Leu Ala Ala Gly Ala Ala Pro Gly Met Gly Gly Leu
35 40 45

Pro Ala Ala Leu Ala Pro Gly Gly Gly Leu Thr Ala Gly Leu Gly Leu
50 55 60

Ala Leu Met Ala Gly Ala Thr Ser Gly Ile Gly Met Leu Gly Gly Ala
65 70 75 80

Ala Ala Gly Leu Gly His Ala Gly Leu Thr Gly Gly Leu Ser Thr Ala
85 90 95

Thr Leu Ala Thr Thr Ala Ala Leu His Met Gly Ala Leu Pro Pro Ala
100 105 110

<210> 5
<211> 145
<212> PRT
<213> Artificial sequence

<400> 5

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

Gly Thr Leu Leu Pro Leu Ala Ala Ser Leu Ser Ala Gly Ala Gly Gly
20 25 30

Thr Ala Ser Pro Ile Cys Thr Gly Gly Val Val Ser Val Ser Thr Gly
35 40 45

Gly Ala Thr Val Met Ser Cys Ala Ile Ser Ala Ala Pro Ser His Val
50 55 60

Ala Ile Leu Leu Ala Ala His Gly Gly Gly Ser Ala Ile Pro Ala Gly
65 70 75 80

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

Gly Gly Val Ala Gly Leu Val Ile Leu Gly Ala Ala Ala Ser His Ala
100 105 110

Gly Leu Thr Met Thr His Leu Val Gly His Gly Ala Ala Ala Ala Gly
115 120 125

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

Gly
145

<210> 6
<211> 4
<212> PRT
<213> Artificial sequence

<400> 6

Leu Ala Gly Leu
1

<210> 7
<211> 6
<212> PRT
<213> Artificial sequence

<400> 7

Ser Gly Leu Ala Gly Leu
1 5

<210> 8
<211> 240

<212> PRT
<213> Artificial sequence

<400> 8

Ala Ile Gly Met Thr Gly Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Ala Ala Val Thr Ile Ser Cys Ser Ala Ser Gly Gly Ile Ser Ala Thr
20 25 30

Leu Ala Thr Thr Gly Gly Leu Pro Ala Gly Thr Val Leu Leu Leu Ile
35 40 45

Thr Thr Thr Ser Ser Leu His Ser Gly Val Pro Ser Ala Pro Ser Gly
50 55 60

Ser Gly Ser Gly Thr Ala Thr Ser Leu Thr Ile Ser Ala Leu Gly Pro
65 70 75 80

Gly Ala Ile Ala Thr Thr Thr Cys Gly Gly Thr Ser Leu Leu Pro Thr
85 90 95

Thr Pro Gly Gly Gly Thr Leu Leu Gly Ile Leu Ala Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Val Gly Leu Val
115 120 125

Gly Ser Gly Gly Gly Leu Val Leu Pro Gly Gly Ser Leu Leu Leu Ser
130 135 140

Cys Ala Ala Ser Gly Leu Thr Pro Ser Ser Thr Ala Met Ser Thr Val
145 150 155 160

Ala Gly Thr Pro Gly Leu Ala Leu Gly Thr Val Ala Ser Ile Ser Ser
165 170 175

Gly Gly Pro Thr Thr Thr Pro Ala Ser Val Leu Gly Ala Pro Thr Ile

180	185	190
Ser Ala Ala Ala Ala Ala Ala	Ile Leu Thr Leu Gly Met Ser Ser Leu	
195	200	205
Ala Ser Gly Ala Thr Ala Met Thr Thr Cys Ala Ala Ala Gly Val Ala		
210	215	220
Gly Thr Leu Ala Val Thr Gly Ala Gly Thr Thr Val Thr Val Ser Ser		
225	230	235
		240

<210> 9
 <211> 1116
 <212> DNA
 <213> Artificial sequence

<400> 9	
atgcagacct gccccctggc attccctggc cacgtttccc aggcccttgg gaccctcctg	60
tttttggctg cctccttgag tgctcagaat gaaggctggg acagcccat ctgcacagag	120
ggggtagtct ctgtgtcttg gggcgagaac accgtcatgt cctgcaacat ctccaacgcc	180
ttctcccatg tcaacatcaa gctgcgtgcc caggggcagg agagcgccat cttcaatgag	240
gtggctccag gctacttctc ccgggacggc tggcagctcc aggttcaggg aggcgtggca	300
cagctgggtga tcaaaggcgc ccgggactcc catgctgggc tgtacatgtg gcacctcgtg	360
ggacaccaga gaaataacag acaagtcacg ctggaggttt caggtgcaga accccagtcc	420
gccccgaca ctggggcggc cgcaacaact accccagcac ctcgaccacc aacaccagca	480
cccactattg ctagtcagcc actgtcactg cgaccagaag catgccgacc tgcagctgga	540
ggcgctgtgc acaccgggg cctggacttt gcctgcgaca tctatatattg ggctcctctg	600
gcaggaacct gtggagtgtg gctgctgagc ctgggtcatca cactgtattg taagcgaggg	660
cggaagaaac tgctctacat tttaaacag ctttttatga gaccagtgc gacaactcag	720
gaggaagagg gctgctcctg taggttcca gaggaagagg aagggggatg cgagctgaga	780
gtgaagtca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	840
aagagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg	900

gaccctgaga tggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa 960
 ctgcagaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg 1020
 aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac 1080
 gacgcccttc acatgcaggc cctgccccct cgctaa 1116

<210> 10
 <211> 462
 <212> DNA
 <213> Artificial sequence

<400> 10
 atgcagacct gccccctggc attccctggc cacgtttccc aggcccttgg gaccctcctg 60
 tttttggctg cctccttgag tgctcagaat gaaggctggg acagccccat ctgcacagag 120
 ggggtagtct ctgtgtcttg gggcgagaac accgtcatgt cctgcaacat ctccaacgcc 180
 ttctcccatg tcaacatcaa gctgcgtgcc cacgggcagg agagcgccat cttcaatgag 240
 gtggctccag gctacttctc ccgggacggc tggcagctcc aggttcaggg aggcgtggca 300
 cagctgggtga tcaaaggcgc ccgggactcc catgctgggc tgtacatgtg gcacctcgtg 360
 ggacaccaga gaaataacag acaagtcacg ctggaggttt caggtgcaga accccagtcc 420
 gcccccgaca ctggggatat cagcgaaaag gacgagctgt aa 462

<210> 11
 <211> 810
 <212> DNA
 <213> Artificial sequence

<400> 11
 atggccttac cagtgaaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60
 ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
 accatcagtt gcagtgaag tcagggcatt agcaattatt taaactggta tcagcagaaa 180
 ccagatggaa ctgttaaact cctgatctat tacacatcaa gtttacctc aggagtccca 240
 tcaagggtca gtggcagtggt gtctgggaca gattattctc tcaccatcag caacctggaa 300
 cctgaagata ttgccactta ttattgtcag cagtatagca agcttccgta cacgttcgga 360

ggggggacca agctggaaat aaaacgtgga ggaggaggaa gcggaggagg aggatctgga 420
 ggaggcgggt ctgaggtgca gctggtcgaa tctggaggag gactggtgaa gccaggagga 480
 tctctgaaac tgagttgtgc cgcttcaggc ctgaccttct caagctacgc catgagctgg 540
 gtgcgacaga cacctgagaa gcggctggaa tgggtcgcta gcatctcctc tggcgggttc 600
 acatactatc cagactccgt gaaaggcaga ttactatct ctcgggataa cgcaagaaat 660
 attctgtacc tgcagatgag ttactgagg agcgaggaca ccgcaatgta ctattgtgcc 720
 agggacgaag tgcgcggcta tctggatgtc tggggagctg gcactaccgt caccgtctcc 780
 agcgatatca gcgaaaagga cgagctgtaa 810

<210> 12
 <211> 21
 <212> PRT
 <213> Artificial sequence

<400> 12

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
 1 5 10 15

His Ala Ala Ala Pro
 20

<210> 13
 <211> 22
 <212> PRT
 <213> Artificial sequence

<400> 13

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

Ala Pro Leu Leu Ile Pro
 20

<210> 14
 <211> 15

<212> PRT
<213> Artificial sequence

<400> 14

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 15
<211> 18
<212> PRT
<213> Artificial sequence

<400> 15

Gly Ser Thr Ser Gly Ser Gly Leu Pro Gly Ser Gly Gly Gly Ser Thr
1 5 10 15

Leu Gly

<210> 16
<211> 18
<212> PRT
<213> Artificial sequence

<400> 16

Gly Gly Ala Gly Ser Leu Leu Thr Cys Gly Ala Val Gly Gly Ala Pro
1 5 10 15

Gly Pro

<210> 17
<211> 24
<212> PRT
<213> Artificial sequence

<400> 17

Ala Pro Val Leu Gly Thr Leu Ala Pro Ala Leu Leu Leu Leu Ala Gly
1 5 10 15

Ala Val Gly Ser Ala Pro Gly Pro
20

<210> 18
<211> 1464
<212> DNA
<213> Artificial sequence

<400> 18
atggctctgc ccgtcaccgc tctgctgctg cctctggctc tgctgctgca cgccgcaaga 60
cccgacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
accatcagtt gcagtgaag tcagggcatt agcaattatt taaactggta tcagcagaaa 180
ccagatggaa ctgttaaact cctgatctat tacacatcaa gtttacactc aggagtccca 240
tcaaggttca gtggcagtgg gtctgggaca gattattctc tcaccatcag caacctggaa 300
cctgaagata ttgccactta ttattgtcag cagtatagca agcttccgta cacgttcgga 360
ggggggacca agctggaaat aaaacgtgga ggaggaggaa gcggaggagg aggatctgga 420
ggaggcgggt ctgaggtgca gctggtcgaa tctggaggag gactggtgaa gccaggagga 480
tctctgaaac tgagttgtgc cgcttcaggc ctgaccttct caagctacgc catgagctgg 540
gtgcgacaga cacctgagaa gcggctggaa tgggtcgcta gcattctctc tggcgggttc 600
acatactatc cagactccgt gaaaggcaga ttactatct ctcgggataa cgcaagaaat 660
attctgtacc tgcagatgag ttcactgagg agcgaggaca ccgcaatgta ctattgtgcc 720
agggacgaag tgcgcggtta tctggatgtc tggggagctg gcactaccgt caccgtctcc 780
agcgcgggcg caacaactac cccagcacct cgaccaccaa caccagcacc cactattgct 840
agtcagccac tgtcactgag accagaagca tgccgacctg cagctggagg cgctgtgcac 900
acccggggcc tggactttgc ctgcgacatc tatatttggg ctctctggc aggaacctgt 960
ggagtgtctg tctgagcct ggtcatcaca ctgtattgta agcgaggcg gaagaaactg 1020
ctctacattt tcaaacagcc ttttatgaga ccagtgcaga caactcagga ggaagacggc 1080
tgctcctgta ggttccaga ggaagaggaa gggggatgag agctgagagt gaagttcagc 1140
aggagcgag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat 1200

ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg 1260
gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat 1320
aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg 1380
cacgatggcc ttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac 1440
atgcaggccc tgccccctcg ctaa 1464

SEQUENCE LISTING

<110> SHANGHAI YAKE BIOTECHNOLOGY LTD.

<120> CD7-TARGETED ENGINEERED IMMUNE CELL, CHIMERIC ANTIGEN RECEPTOR,
CD7 BLOCKING MOLECULE AND USE THEREOF

<130> DD12447P

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> hinge and transmembrane domain

<400> 1

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

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

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr Leu Tyr Cys
65

<210> 2

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> 4-1BB

<400> 2

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met

1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
 20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 35 40

<210> 3
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hinge, transmembrane domain and intracellular co-stimulatory domain

<400> 3

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
 1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
 20 25 30

Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
 35 40 45

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
 50 55 60

Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
 65 70 75 80

Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
 85 90 95

Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 100 105

<210> 4
 <211> 112
 <212> PRT
 <213> Artificial sequence

<220>

<223> intracellular primary stimulatory domain

<400> 4

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 5

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> CD7-L extracellular domain

<400> 5

Met Gln Thr Cys Pro Leu Ala Phe Pro Gly His Val Ser Gln Ala Leu
1 5 10 15

Gly Thr Leu Leu Phe Leu Ala Ala Ser Leu Ser Ala Gln Asn Glu Gly
20 25 30

Trp Asp Ser Pro Ile Cys Thr Glu Gly Val Val Ser Val Ser Trp Gly
35 40 45

Glu Asn Thr Val Met Ser Cys Asn Ile Ser Asn Ala Phe Ser His Val
50 55 60

Asn Ile Lys Leu Arg Ala His Gly Gln Glu Ser Ala Ile Phe Asn Glu
65 70 75 80

Val Ala Pro Gly Tyr Phe Ser Arg Asp Gly Trp Gln Leu Gln Val Gln
85 90 95

Gly Gly Val Ala Gln Leu Val Ile Lys Gly Ala Arg Asp Ser His Ala
100 105 110

Gly Leu Tyr Met Trp His Leu Val Gly His Gln Arg Asn Asn Arg Gln
115 120 125

Val Thr Leu Glu Val Ser Gly Ala Glu Pro Gln Ser Ala Pro Asp Thr
130 135 140

Gly
145

<210> 6
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> endoplasmic reticulum retention domain

<400> 6

Lys Asp Glu Leu
1

<210> 7
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> endoplasmic reticulum retention domain

<400> 7

Ser Glu Lys Asp Glu Leu
1 5

<210> 8
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> TH69 scFv

<400> 8

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Lys Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val
115 120 125

Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser
130 135 140

Cys Ala Ala Ser Gly Leu Thr Phe Ser Ser Tyr Ala Met Ser Trp Val
145 150 155 160

Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala Ser Ile Ser Ser
165 170 175

Gly Gly Phe Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu Gln Met Ser Ser Leu
195 200 205

Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Asp Glu Val Arg
210 215 220

Gly Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
225 230 235 240

<210> 9
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> CD7BB-002

<400> 9
atgcagacct gccccctggc attccctggc cacgtttccc aggcccttgg gaccctcctg 60
tttttggtg cctccttgag tgctcagaat gaaggctggg acagcccat ctgcacagag 120
ggggtagtct ctgtgtcttg gggcgagaac accgtcatgt cctgcaacat ctccaacgcc 180
ttctcccatg tcaacatcaa gctgcgtgcc cacgggcagg agagcgccat cttcaatgag 240
gtggctccag gctacttctc ccgggacggc tggcagctcc aggttcaggg aggcgtggca 300
cagctggtga tcaaaggcgc ccgggactcc catgctgggc tgtacatgtg gcacctcgtg 360
ggacaccaga gaaataacag acaagtcacg ctggaggttt caggtgcaga accccagtcc 420
gccccgaca ctggggcggc cgcaacaact accccagcac ctcgaccacc aacaccagca 480
cccactattg ctagtcagcc actgtcactg cgaccagaag catgccgacc tgcagctgga 540
ggcgctgtgc acaccgggg cctggacttt gcctgcgaca tctatatattg ggctcctctg 600
gcaggaacct gtggagtgtc gctgctgagc ctgggtcatca cactgtattg taagcgaggg 660
cggaagaaac tgctctacat tttcaaacag ctttttatga gaccagtgc gacaactcag 720
gaggaagacg gctgctcctg taggttccca gaggaagagg aagggggatg cgagctgaga 780

gtgaagttca gcaggagcgc agacgcccc gcgtaccagc agggccagaa ccagctctat	840
aacgagctca atctaggacg aagagaggag tacgatgttt tggacaagag acgtggccgg	900
gaccctgaga tgggggggaaa gccgagaagg aagaaccctc aggaaggcct gtacaatgaa	960
ctgcagaaaag ataagatggc ggaggcctac agtgagattg ggatgaaagg cgagcgccgg	1020
aggggcaagg ggcacgatgg cctttaccag ggtctcagta cagccaccaa ggacacctac	1080
gacgcccttc acatgcaggc cctgccccct cgctaa	1116

<210> 10
 <211> 462
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD7-L-ER2.1

<400> 10	
atgcagacct gccccctggc attccctggc cacgtttccc aggcccttgg gaccctcctg	60
tttttggctg cctccttgag tgctcagaat gaaggctggg acagccccat ctgcacagag	120
ggggtagtct ctgtgtcttg gggcgagaac accgtcatgt cctgcaacat ctccaacgcc	180
ttctcccatg tcaacatcaa gctgcgtgcc cacgggcagg agagcgccat cttcaatgag	240
gtggctccag gctacttctc ccgggacggc tggcagctcc aggttcaggg aggcgtggca	300
cagctggtga tcaaaggcgc ccgggactcc catgctgggc tgtacatgtg gcacctcgtg	360
ggacaccaga gaaataacag acaagtcacg ctggaggttt caggtgcaga accccagtcc	420
gccccgaca ctggggatat cagcgaaaag gacgagctgt aa	462

<210> 11
 <211> 810
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TH69-ER2.1

<400> 11	
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg	60
ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc	120
accatcagtt gcagtgaag tcagggcatt agcaattatt taaactggta tcagcagaaa	180

ccagatggaa ctgttaaact cctgatctat tacacatcaa gtttacactc aggagtccca 240
tcaaggttca gtggcagtgg gtctgggaca gattattctc tcaccatcag caacctggaa 300
cctgaagata ttgccactta ttattgtcag cagtatagca agcttccgta cacgttcgga 360
ggggggacca agctggaaat aaaacgtgga ggaggaggaa gcggaggagg aggatctgga 420
ggaggcgggt ctgaggtgca gctggtcgaa tctggaggag gactggtgaa gccaggagga 480
tctctgaaac tgagttgtgc cgcttcaggc ctgaccttct caagctacgc catgagctgg 540
gtgcgacaga cacctgagaa gcggctggaa tgggtcgcta gcatctcctc tggcgggttc 600
acatactatc cagactccgt gaaaggcaga ttactatct ctcgggataa cgcaagaaat 660
attctgtacc tgcagatgag ttactgagg agcgaggaca ccgcaatgta ctattgtgcc 720
agggacgaag tgcgcggcta tctggatgtc tggggagctg gcactaccgt caccgtctcc 780
agcgatatca gcgaaaagga cgagctgtaa 810

<210> 12
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> signal peptide

<400> 12

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 13
<211> 22
<212> PRT
<213> Artificial sequence

<220>
<223> signal peptide

<400> 13

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

Ala Phe Leu Leu Ile Pro
20

<210> 14
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> connecting peptide

<400> 14

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 15
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> connecting peptide

<400> 15

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 16
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> T2A

<400> 16

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 17
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> F2A

<400> 17

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
1 5 10 15

Asp Val Glu Ser Asn Pro Gly Pro
20

<210> 18
<211> 1464
<212> DNA
<213> Artificial sequence

<220>
<223> TH69BB-002

<400> 18
atggctctgc ccgtcaccgc tctgctgctg cctctggctc tgctgctgca cgccgcaaga 60
cccgacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120
accatcagtt gcagtgaag tcagggcatt agcaattatt taaactggta tcagcagaaa 180
ccagatggaa ctgttaaact cctgatctat tacacatcaa gtttacactc aggagtccca 240
tcaaggttca gtggcagtgg gtctgggaca gattattctc tcaccatcag caacctggaa 300
cctgaagata ttgccactta ttattgtcag cagtatagca agcttccgta cacgttcgga 360
ggggggacca agctggaaat aaaacgtgga ggaggaggaa gcggaggagg aggatctgga 420
ggaggcgggt ctgagggtga gctggtcgaa tctggaggag gactggtgaa gccaggagga 480
tctctgaaac tgagttgtgc cgcttcaggc ctgaccttct caagctacgc catgagctgg 540
gtgcgacaga cacctgagaa gcggctggaa tgggtcgcta gcattctctc tggcgggttc 600
acatactatc cagactccgt gaaaggcaga ttactatct ctcgggataa cgcaagaaat 660
attctgtacc tgcagatgag ttactgagg agcaggaca ccgcaatgta ctattgtgcc 720
agggacgaag tgcgcggcta tctggatgtc tggggagctg gcactaccgt caccgtctcc 780

agcgcggccg caacaactac cccagcacct cgaccaccaa caccagcacc cactattgct	840
agtcagccac tgtcactgcg accagaagca tgccgacctg cagctggagg cgctgtgcac	900
acccggggcc tggactttgc ctgcgacatc tatatttggg ctcctctggc aggaacctgt	960
ggagtgtgctg tgctgagcct ggtcatcaca ctgtattgta agcgaggcg gaagaaactg	1020
ctctacattt tcaaacagcc ttttatgaga ccagtgcaga caactcagga ggaagacggc	1080
tgctcctgta ggttcccaga ggaagaggaa gggggatgcg agctgagagt gaagttcagc	1140
aggagcgcag acgccccgc gtaccagcag ggccagaacc agctctataa cgagctcaat	1200
ctaggacgaa gagaggagta cgatgttttg gacaagagac gtggccggga ccctgagatg	1260
gggggaaagc cgagaaggaa gaaccctcag gaaggcctgt acaatgaact gcagaaagat	1320
aagatggcgg aggcctacag tgagattggg atgaaaggcg agcgccggag gggcaagggg	1380
cacgatggcc ttaccaggg tctcagtaca gccaccaagg acacctacga cgcccttcac	1440
atgcaggccc tgccccctcg ctaa	1464