

SEQUENCE LISTING

<110> SHANGHAI GENBASE BIOTECHNOLOGY CO., LTD.

<120> ANTI-CLDN6 ANTIBODY AND USE THEREOF

<130> IEC210075PCT

<160> 33

<170> PatentIn version 3.5

<210> 1

<211> 116

<212> PRT

<213> artificial

<220>

<223> 15H2 heavy chain variable region

<400> 1

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

Ser	Leu	Ser	Leu	Thr	Cys	Ser	Val	Thr	Gly	Tyr	Ser	Ile	Thr	Ser	Gly
			20					25					30		

Tyr	Tyr	Trp	Asn	Trp	Ile	Arg	Gln	Phe	Pro	Gly	Asn	Lys	Leu	Glu	Trp
		35					40					45			

Met	Gly	Tyr	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Asn	Tyr	Asn	Pro	Ser	Leu
	50					55					60				

Lys	Asn	Arg	Phe	Ser	Ile	Ile	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Phe
65					70					75					80

Leu	Lys	Phe	Asn	Ser	Val	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys
			85						90					95	

Ala	Arg	Gly	Gly	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu
			100					105						110	

Thr Val Ser Ser
115

<210> 2
<211> 113
<212> PRT
<213> artificial

<220>
<223> 15H2 light chain variable region

<400> 2

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

Gln Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Thr
20 25 30

Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Val Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
85 90 95

His Tyr Asn Ala Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 3
<211> 9
<212> PRT
<213> artificial

<220>

<223> 15H2 HCDR1

<400> 3

Gly Tyr Ser Ile Thr Ser Gly Tyr Tyr
1 5

<210> 4

<211> 7

<212> PRT

<213> artificial

<220>

<223> 15H2 HCDR2

<400> 4

Ile Ser Tyr Asp Gly Ser Asn
1 5

<210> 5

<211> 9

<212> PRT

<213> artificial

<220>

<223> 15H2 HCDR3

<400> 5

Ala Arg Gly Gly Tyr Tyr Phe Asp Tyr
1 5

<210> 6

<211> 12

<212> PRT

<213> artificial

<220>

<223> 15H2 LCDR1

<400> 6

Gln Ser Leu Leu Asn Thr Asn Asn Gln Lys Asn Tyr
1 5 10

<210> 7
<211> 7
<212> PRT
<213> artificial

<220>
<223> 15H2 LCDR2

<400> 7

Phe Ala Ser Thr Arg Glu Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> artificial

<220>
<223> 15H2 LCDR3

<400> 8

Gln Gln His Tyr Asn Ala Pro Arg Thr
1 5

<210> 9
<211> 121
<212> PRT
<213> artificial

<220>
<223> 7008-03 heavy chain variable region

<400> 9

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 Ser Ile Tyr
20 25 30

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

Ala Thr Ile Ser Arg Asp Ala Ser Tyr Thr Tyr Phe Pro Asp Ser Val
 50 55 60

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

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

Val Arg Leu Gly Asp Asn Asp Arg Gly Tyr Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 10
 <211> 112
 <212> PRT
 <213> artificial

<220>
 <223> 7008-03 light chain variable region

<400> 10

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Val Val His Val
 20 25 30

Asn Ala Asn Thr Tyr Leu Glu Trp Tyr Gln Gln Arg Pro Gly Gln Ser
 35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 11
<211> 121
<212> PRT
<213> artificial

<220>
<223> 9H3 heavy chain variable region

<400> 11

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ser Pro Asp Arg Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Arg Asp Gly Ser Tyr Thr Tyr Phe Pro Asp Ser Val
50 55 60

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

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

Val Arg Leu Gly Asp Asn Asp Arg Gly Tyr Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 12
 <211> 112
 <212> PRT
 <213> artificial

<220>
 <223> 9H3 light chain variable region

<400> 12

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Val Val His Val
 20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95

Ser His Val Pro Arg Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys
 100 105 110

<210> 13
 <211> 8
 <212> PRT
 <213> artificial

<220>
 <223> 9H3 HCDR1

<400> 13

Gly Phe Thr Phe Ser Ile Tyr Gly
1 5

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

<220>
<223> 9H3 HCDR2

<400> 14

Ile Ser Arg Asp Gly Ser Tyr Thr
1 5

<210> 15
<211> 14
<212> PRT
<213> artificial

<220>
<223> 9H3 HCDR3

<400> 15

Val Arg Leu Gly Asp Asn Asp Arg Gly Tyr Ala Met Asp Tyr
1 5 10

<210> 16
<211> 11
<212> PRT
<213> artificial

<220>
<223> 9H3 LCDR1

<400> 16

Gln Ser Val Val His Val Asn Gly Asn Thr Tyr
1 5 10

<210> 17
<211> 7
<212> PRT
<213> artificial

<220>

<223> 9H3 LCDR2

<400> 17

Lys Val Ser Asn Arg Phe Pro
1 5

<210> 18

<211> 9

<212> PRT

<213> artificial

<220>

<223> 9H3 LCDR3

<400> 18

Phe Gln Gly Ser His Val Pro Arg Thr
1 5

<210> 19

<211> 116

<212> PRT

<213> artificial

<220>

<223> 7008-01 heavy chain variable region

<400> 19

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Tyr Ser Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 20
<211> 113
<212> PRT
<213> artificial

<220>
<223> 7008-01 light chain variable region

<400> 20

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Thr
20 25 30

Asn Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

His Tyr Asn Ala Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 21
<211> 330
<212> PRT
<213> artificial

<220>
<223> Human IgG1 heavy chain constant region

<400> 21

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 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 22
<211> 107
<212> PRT
<213> artificial

<220>
<223> Human ?? light chain constant region

<400> 22

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> 23
<211> 8
<212> PRT
<213> artificial

<220>
<223> 7008-03 HCDR2

<400> 23

Ile Ser Arg Asp Ala Ser Tyr Thr
1 5

<210> 24
<211> 11
<212> PRT
<213> artificial

<220>
<223> 7008-03 LCDR1

<400> 24

Gln Ser Val Val His Val Asn Ala Asn Thr Tyr
1 5 10

<210> 25
<211> 348
<212> DNA
<213> artificial

<220>
<223> Nucleic acid sequence encoding 15H2 heavy chain variable region

<400> 25
gatgtacagc ttcaggagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60
acctgctctg tcactggcta ctccatcacc agtgggttatt actggaactg gatccggcag 120
tttccaggaa acaaactgga atggatgggc tacataagct acgacggtag caataactac 180
aaccatctc tcaaaaatcg attctccatc attcgtgaca catctaagaa ccagtttttc 240
ctgaagttca attctgtgac tactgaggac acagctacat attactgcgc cagggggggg 300
tactactttg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 26
<211> 339
<212> DNA
<213> artificial

<220>
<223> Nucleic acid sequence encoding 15H2 light chain variable region

<400> 26
gacattgtga tgacacagtc tccatcctcc ctggctatgt cagtaggaca gaaggtcact 60

atgagctgca agtccagtca gaggcctttta aataactaaca atcaaaaagaa ctattttggcc	120
tggtaccagc agaaaccagg acagtctcct aaacttctgg tatactttgc atccactagg	180
gagtctgggg tccctgatcg cttcataggc agtggatctg ggacagattt cactcttacc	240
atcagcagtg tgcaggctga agacctggca gattacttct gtcaacaaca ttataacgct	300
cctcggacgt tcggtggagg caccaagctg gaaatcaaa	339

<210> 27
 <211> 363
 <212> DNA
 <213> artificial

<220>
 <223> Nucleic acid sequence encoding 9H3 heavy chain variable region

<400> 27	
gaggtgcagc tgggtggaatc tgggggagac ttagtgaagc ctggagggtc cctgaaactc	60
tcctgtgcag cctctggatt cactttcagt atctatggca tgtcttgggt tcgccagagt	120
ccagacagga ggctggaatg ggtcgcaacc attagtcgtg atggtagtta cacctacttt	180
ccagacagtg tgaaggggcg attcaccatc tccagagaca atgccaagaa caccctgtat	240
ttgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtgt aagactgggt	300
gataacgaca ggggctatgc tatggactac tgggggtcaag gaacttcagt caccgtctcc	360
tca	363

<210> 28
 <211> 336
 <212> DNA
 <213> artificial

<220>
 <223> Nucleic acid sequence encoding 9H3 light chain variable region

<400> 28	
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca gatctagtca gagtgttgta catgttaatg gaaacaccta tttagaatgg	120
tacctgcaga aaccaggcca gtctccaagg ctctgatct acaaagtttc caaccgttt	180

cctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaggatc	240
agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcct	300
cggacgttcg gtggaggcac caacctggaa atcaaa	336

<210> 29
 <211> 348
 <212> DNA
 <213> artificial

<220>
 <223> Nucleic acid sequence encoding 7008-01 heavy chain variable region

<400> 29	
caggtgcagc tgcaggagag cggccccgga ctggtgaagc cctcagagac actgagcctg	60
acatgcacag tgagcggcta ctccattaca agcggctact actggaactg gatcagacag	120
ccccccggca agggcctgga atggatgggc tatatctcct acagcggcag caacaactac	180
aaccccagcc tgaagaacag ggtgaccatc tctcgcgaca cctccaagaa ccagttctcc	240
ctgaagctga gtagcgtgac tgccgctgac accgccgtgt actattgcgc cagaggcggc	300
tactacttcg actactgggg ccagggcacc ctggtgaccg tgagcagc	348

<210> 30
 <211> 339
 <212> DNA
 <213> artificial

<220>
 <223> Nucleic acid sequence encoding 7008-01 light chain variable region

<400> 30	
gacattgtga tgaccagag ccccgactcc ctggccgtga gcctgggaga aagagccacc	60
atcaactgca agagcagcca gagcctgctg aacaccaaca accagaaaaa ctacctggcc	120
tggtaccagc agaaacccgg ccagcccccc aaactgctga tctacttcgc ctccaccgc	180
gagtcggcg tgctgatag attctccggc agcggcagcg gcaccgactt caccctgact	240
atcagcagcc tgagggtga ggacgtggcc gtgtacttct gccagcagca ttacaacgct	300
cccagaacct ttggaggagg caccaaggtg gaaatcaag	339

<210> 31
 <211> 363
 <212> DNA
 <213> artificial

<220>

<223> Nucleic acid sequence encoding 7008-03 heavy chain variable region

<400> 31
 gaggtgcagc tggtggagag cgggggggga ctggtgcagc caggaggaag cctgagactg 60
 agctgtgccg ccagcgggtt tacatttagc atttatggga tgcctgggt gagacaggcc 120
 cccggaaaag gactggagt ggtggctact atcagcagag acgctagcta cacctacttc 180
 cccgattccg tgaagggcag attcacaatc agcagagata acgctaagaa cagcctgtat 240
 ctgcagatga acagcctgcg ggccgaggac acagccgtgt attactgcgt gaggctgggc 300
 gacaacgata gaggatacgc catggactac tgggggcagg gaacactggt gaccgtgagc 360
 agc 363

<210> 32
 <211> 336
 <212> DNA
 <213> artificial

<220>

<223> Nucleic acid sequence encoding 7008-03 light chain variable region

<400> 32
 gacgtggtga tgaccagag cccctgagc ctgcccgtga ccctgggaca gcccgctagt 60
 atcagctgca gaagcagcca gagcgtggtg cacgtgaacg ccaacacata tctggagtgg 120
 tatcagcaga ggcctggaca gagccccaga ctgctgatct acaagtgag caacagattc 180
 ccaggcgtgc cagacagatt ctctggaagc ggcagcgga cagactttac cctgaagatc 240
 tccagagtgg aggccgagga cgtgggagtg tactactgct tccagggcag ccacgtgccc 300
 agaacattcg gcggcggcac caagtggag atcaaa 336

<210> 33
 <211> 7

<212> PRT
<213> artificial

<220>
<223> 7008-01 HCDR2

<400> 33

Ile Ser Tyr Ser Gly Ser Asn
1 5