

<110> Prestige BioPharma Pte. Ltd.
 <120> Novel CTHRC1-specific antibodies and the use thereof
 <130> OPA20050
 <150> KR 10-2019-0070048
 <151> 2019-06-13
 <160> 28
 <170> KoPatentIn 3.0
 <210> 1
 <211> 8
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> 4H5-VH-CDR1
 <400> 1
 Gly Tyr Ser Phe Thr Asp Tyr Ile
 1 5
 <210> 2
 <211> 8
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> 4H5-VH-CDR2
 <400> 2
 Ile Asn Pro Tyr Tyr Gly Ser Thr
 1 5
 <210> 3
 <211> 14
 <212> PRT
 <213> Artificial Sequence
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 <223> 4H5-VH-CDR3
 <400> 3
 Ala Arg Ser Gly Tyr Gly Tyr Asp Glu Ser Ala Met Asp Tyr
 1 5 10

<210> 4
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 4H5-VL-CDR1

<400> 4
Lys Ser Leu Leu Asn Ser Asp Gly Phe Thr Tyr
1 5 10

<210> 5
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 4H5-VL-CDR2

<400> 5
Leu Val Ser
1

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 4H5-VL-CDR3

<400> 6
Phe Gln Ser Asn Tyr Leu Pro Leu Thr
1 5

<210> 7
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> cCMAb45-Heavy chain

<400> 7
 Glu Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
 20 25 30
 Ile Met Leu Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Asn Pro Tyr Tyr Gly Ser Thr Ser Tyr Asn Leu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Tyr Gly Tyr Asp Glu Ser Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Ser Val Thr Val Ser Ser
 115 120

<210> 8
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cCMAB45-Heavy chain

<400> 8
 gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggccttc agtgaagata 60
 tcctgcaagg cttctgggta ttcattcact gactacatca tgctctgggt gaagcagagc 120
 catggaaaga gccttgagtg gattggaaat attaatcctt actatggtag tactagctac 180
 aatctgaagt tcaagggcaa ggccacattg actgtagaca aatcttccag cacagcctac 240
 atgcagctca acagtctgac atctgaggac tctgcagtct attactgtgc aagatcgggc 300
 tatggttacg acgagagtgc tatggactac tggggtcaag gaacctcagt caccgtctcc 360
 tca 363

<210> 9
 <211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> cCMAB45-Light chain

<400> 9
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser
20 25 30
Asp Gly Phe Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser 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 Leu Gly Val Tyr Tyr Cys Phe Gln Ser
85 90 95
Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 10
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> cCMAB45-Light chain

<400> 10
gatgttttga tgacccaaac tccactctct ctgcctgtca atattggaga tcaagcctct 60
atctcttgca agtctactaa gagtcttctg aatagtgatg gattcactta tttggactgg 120
tacctgcaga agccaggcca gtctccacag ctctaatat atttggtttc taatcgattt 180
tctggagttc cagacagggt cagtggcagt gggtcaggaa cagatttcac actcaagatc 240
agcagagtgg aggctgagga tttgggagtt tattattgct tccagagtaa ctatcttcct 300
ctcacgttcg gctcggggac aaagttggaa ataaaa 336

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

<220>
<223> 9E6-VH-CDR1

<400> 11
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 12
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E6-VH-CDR2

<400> 12
Ile Tyr Pro Ser Ser Gly Thr Thr
1 5

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E6-VH-CDR3

<400> 13
Thr Thr Glu Ser Tyr
1 5

<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E6-VL-CDR1

<400> 14
Gln Asn Ile Asn Val Trp
1 5

<210> 15
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E6-VL-CDR2

<400> 15
Lys Ala Ser
1

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 9E6-VL-CDR3

<400> 16
Gln Gln Gly Gln Ser Tyr Pro Leu Thr
1 5

<210> 17
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> cCMAb96-Heavy chain

<400> 17
Gln Val Gln Leu Gln Gln Pro Gly Ser Glu Leu Val Arg Pro Gly Ala
1 5 10 15

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

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Pro Ser Ser Gly Thr Thr Asn Tyr Asp Glu Lys Phe

50		55		60											
Lys	Asn	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ser	Thr	Thr	Ala	Tyr
65					70					75					80
Met	His	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Thr	Thr	Glu	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser
			100					105					110		

<210> 18
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cCMAB96-Heavy chain

<400> 18
 cagggtccaac tgcagcagcc tgggtctgag ctggtgaggc ctggagcttc agtgaagctg 60
 tcctgcaagg cttctggcta cacattcacc agctactgga tgcactgggt gaagcagagg 120
 cctggacaag gccttgagtg gattggaaat atttatccta gtagtggtac tactaactac 180
 gatgagaagt tcaagaacaa ggccacactg actgtagaca catcctccac cacagcctac 240
 atgcacctca gcagcctgac atctgaggac tctgcggtct attactgtac aacagagtct 300
 tactggggcc aaggcaccac tctcacagtc tcctca 336

<210> 19
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> cCMAB96-Light chain

<400> 19
 Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Asn Ile Pro Lys Leu Leu Ile
 35 40 45
 Tyr Lys Ala Ser Asn Leu His Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 20
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cCMAb96-Light chain

<400> 20
 gacattgtga tgacccagtc tccatccagt ctgtctgcat cccttggaga cacaattacc 60
 atcacttgcc atgccagtca gaacattaat gtttggttaa gctggtacca gcagaaacca 120
 ggaaatattc ctaaactatt gatctataag gttccaact tgcacacagg cgtcccatca 180
 aggttttagtg gcagtggatc tggaacaggt ttcacattaa ccatcagcag cctgcagcct 240
 gaagacattg ccacttacta ctgtcaacag ggtcaaagtt atcctctgac gttcggtgga 300
 ggcaccaagc tggaaatcaa a 321

<210> 21
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCMAb45-Heavy chain

<400> 21
 Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr

	20		25		30										
Ile	Ile	Leu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Ala	Ile	Asn	Pro	Tyr	Tyr	Gly	Ser	Thr	Val	Tyr	Gly	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Leu	Thr	Ile	Thr	Ala	Asp	Gly	Ser	Met	Ser	Thr	Ala	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	Ser	Gly	Tyr	Gly	Tyr	Asp	Glu	Ser	Ala	Met	Asp	Tyr	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
	115						120								

<210> 22
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hCMAb45-Heavy chain

<400> 22
 cagggtgcagc tgggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60
 tcctgcaagg cttctggtta ttcattcact gactacatca tattatgggt gcggcaggcg 120
 cctggacaag ggcttgagtg gatgggagca attaatcctt actatggtag tactgtgtac 180
 gggcagaagt tccagggcag actcaccatt accgcggacg ggtctatgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac actgcagtct attactgtgc aagatcgggc 300
 tatggttacg acgagagtgc tatggactac tgggggtcaag gaaccctagt caccgtctcc 360
 tca 363

<210> 23
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hCMAb45-Light chain

<400> 23
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser
 20 25 30
 Asp Gly Phe Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser 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 Ser
 85 90 95
 Asn Tyr Leu Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 24
 <211> 336
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> hCMAb45-Light chain

<400> 24
 gatattgtga tgaccagac tccactctcc ctgcccgtca cccctggaga gccggcctct 60
 atctcttgcc ggtctagtaa gagtcttctg aatagtgatg gattcactta tttggactgg 120
 tacctgcaga agccaggcca gtctccacag ctctaatat atttggtttc taatcgattt 180
 tctggagttc cagacagggtt cagtggcagt gggtcaggaa cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tgttggagtt tattattgct tccagagtaa ctatcttcct 300
 ctcacgttcg gccaggggac aaagttggaa ataaaa 336

<210> 25
 <211> 112
 <212> PRT

<213> Artificial Sequence

<220>

<223> hCMAb96-Heavy chain

<400> 25

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 Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Pro Ser Ser Gly Thr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Thr Thr Glu Ser Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

<210> 26

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> hCMAb96-Heavy chain

<400> 26

caggtccaac tggtagagtc tggggctgaa gtgaagaagc ctggggcttc agtgaaggtc 60

tcctgtaagg cttctggcta cacattcacc agctactgga tgcactgggt ccgtcaagct 120

ccgggacaag ggctggagtg gattggatat atttatccta gtagtggtac tactaactac 180

aacaaaaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gccccctgag atctgaggac acagcggctt attactgtac aacagagtct 300

tactggggcc aggaaccac tgtcaccgtc tcctca 336

<210> 27
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hCMAb96-Light chain

<400> 27
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Lys Ala Ser Asn Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Gly Gln Ser Tyr Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 28
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> hCMAb96-Light chain

<400> 28
gacattcaga tgacccagtc tccatccagt ctgtctgcat cccttggaga cacaattacc 60
atcacttgcc atgccagtca gaacattaat gtttggttag cctggtatca gcagaaacca 120
gggaaagccc ctaaactatt gatctataag gcttccaact tgcacagtgg cgtcccatca 180
aggtttagtg gcagtggatc tggaacagat ttcactctca ccatcagcag cctgcagcct 240
gaagacattg ccacttacta ctgtcaacag ggtcaaagtt atcctctgac gttcggccag 300

gggaccaagg tggaaatcaa a

321