

SEQUENCE LISTING

<110> AGENCY FOR SCIENCE, TECHNOLOGY AND RESEARCH
NATIONAL UNIVERSITY OF SINGAPORE

<120> A Serotype Cross-Reactive Dengue Antibody And Uses Thereof

<130> 9869SG3767

<150> SG10201502068V

<151> 2015-03-17

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<220>

<221> misc_feature

<223> Heavy chain variable region

<400> 1

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tcctgcaagg catctggata caccttcacc agcaactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagt gatgggggta atcaacccta ggggtggttag cacagccagc 180

gcacagaaat tccagggaag aatcaccatg accagggaaca cgtccacgag cacagtttac 240

atggaactga gcagcctgag atctgacgac acggccgtgt attactgtgc gagaggggga 300

agggcccttt tctatgatag ttacacgacc ccccgagacg gagggtcgtg gtggttcgac 360

ccctggggcc agggaagcct ggtcaccgtc tcctca 396

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<211> 324

<212> DNA

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<400> 2

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ttcacttgcc aggcgagcca ggacattagg aagtatttaa attggatatca gcagaaacca 120

gggaaagccc ctaaactcct aatctacgat gcatccaatt tgaaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatgttg caacatacta ctgtcaacag tttgatgatc tcccgatcac cttcggccag 300

gggacacgac tgcagattaa acga 324

<210> 3

<211> 8

<212> PRT

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<220>

<221> MISC_FEATURE

<223> CDRH1

<400> 3

Gly Tyr Thr Phe Thr Ser Asn Tyr

1 5

<210> 4

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<220>

<221> MISC_FEATURE

<223> CDRH2

<400> 4

Ile Asn Pro Arg Gly Gly Ser Thr
1 5

<210> 5

<211> 25

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic sequence

<220>

<221> MISC_FEATURE

<223> CDRH3

<400> 5

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg
1 5 10 15

Asp Gly Gly Ser Trp Trp Phe Asp Pro
20 25

<210> 6

<211> 6

<212> PRT

<213> Artificial sequence

<220>

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<221> MISC_FEATURE

<223> CDRL1

<400> 6

Gln Asp Ile Arg Lys Tyr
1 5

<210> 7

<211> 4
<212> PRT
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<220>
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<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 7

Asp Ala Ser Xaa
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<210> 8
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<212> PRT
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<220>
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<223> CDRL3

<400> 8

Gln Gln Phe Asp Asp Leu Pro Ile Thr
1 5

<210> 9
<211> 132
<212> PRT
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<220>
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<220>
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 <223> Heavy chain variable region

<400> 9

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

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

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

Gly Val Ile Asn Pro Arg Gly Gly Ser Thr Ala Ser Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Gly Gly Arg Ala Leu Phe Tyr Asp Ser Tyr Thr Thr Pro Arg
 100 105 110

Asp Gly Gly Ser Trp Trp Phe Asp Pro Trp Gly Gln Gly Ser Leu Val
 115 120 125

Thr Val Ser Ser
 130

<210> 10
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 <212> PRT
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<220>
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<220>
 <221> MISC_FEATURE
 <223> Light chain variable region

<400> 10

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

Asp Arg Val Thr Phe Thr Cys Gln Ala Ser Gln Asp Ile Arg Lys Tyr
 20 25 30

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

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

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

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

Thr Phe Gly Gln Gly Thr Arg Leu Gln Ile Lys
 100 105

<210> 11
 <211> 984
 <212> DNA
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<220>
 <223> Synthetic sequence

<220>
 <221> misc_feature
 <223> 3C H5L1 heavy chain constant region with LALA mutation

<400> 11
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tggaactcag gcgccctgac cagtggcgtg cacaccttcc cggctgtcct acagtcctca	180
ggactctact ccctcagtag tgtgggtgacc gtgccctcca gtagtttggg caccagacc	240
tacatctgca acgtgaatca caagcccagt aacaccaagg tggacaagag agttgagccc	300
aaatcttgtg acaaaaactca cacatgcccc ccgtgcccag cacctgaggc cgccggggga	360
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct	420
gaggtcacat gcgtgggtgt ggacgtgagt cacgaagacc ctgaggtcaa gttcaactgg	480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	540
agtacgtacc gtgtggtcag tgcctcacc gtcctgcacc aggactggct gaatggcaag	600
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	660
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag	720
atgaccaaga accaggtcag tctgacctgc ctgggtcaaag gcttctatcc cagtgacatc	780
gccgtggagt gggagagtaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	840
ctggactccg acggctcctt cttcctctac agtaagctca ccgtggacaa gagtaggtgg	900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	960
cagaagagtc tctccctgtc tccg	984

<210> 12
 <211> 328
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic sequence

<220>
 <221> MISC_FEATURE
 <223> 3C H5L1 heavy chain constant region with LALA mutation

<220>
 <221> MISC_FEATURE
 <222> (117)..(118)
 <223> LALA mutation

<400> 12

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

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

Pro Ala Pro Glu Ala Ala 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
 325