

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt
SEQUENCE LISTING

<110> Agency for Science, Technology and Research
Nanyang Technological University

<120> NANOCAPSULES CARRYING CHIKUNGUNYA-ASSOCIATED PEPTIDES

<130> 9869SG3613

<160> 26

<170> PatentIn version 3.5

<210> 1
<211> 54
<212> DNA
<213> Artificial

<220>
<223> E2EP3

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<212> DNA
<213> Artificial

<220>
<223> E2EP3 mutant

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<220>
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<220>
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<220>
<223> E2EP5 mutant

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

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<400> 6
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<210> 7
<211> 18
<212> PRT
<213> artificial

<220>
<223> E2EP3

<400> 7
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1 5 10 15

Ala His

<210> 8
<211> 18
<212> PRT
<213> artificial

<220>
<223> E2EP3 mutant

<400> 8
Ser Ile Lys Asp His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1 5 10 15

Ala His

<210> 9
<211> 18
<212> PRT
<213> Artificial

<220>
<223> E2EP4

<400> 9
Trp Gly Asn Asn Glu Pro Tyr Lys Tyr Trp Pro Gln Leu Ser Thr Asn
1 5 10 15

Gly Thr

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

<210> 10
<211> 18
<212> PRT
<213> artificial

<220>
<223> E2EP5

<400> 10

Leu Leu Ser Met Val Gly Met Ala Ala Gly Met Cys Met Cys Ala Arg
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Arg Arg

<210> 11
<211> 19
<212> PRT
<213> artificial

<220>
<223> E2EP5 mutant

<400> 11

Leu Leu Ser Met Val Gly Val Ala Val Gly Met Cys Met Cys Ala Arg
1 5 10 15

Arg Arg Lys

<210> 12
<211> 10
<212> PRT
<213> artificial

<220>
<223> E2EP3 CV

<400> 12

Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys
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<210> 13
<211> 525
<212> DNA
<213> artificial

<220>
<223> Mutated ferritin

<400> 13

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tactcagcat acctctacct ctccatggcc tcttacttcg actccatcgg gcttaagggc 120
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9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt
gactttgtca gtgagagggg agggagagtt aagctctacg ctgttgagga gccaccatct 240
gagtgggatt cgcctttggc agcctttgag cacgtttacg agcatgaggt aaatgttacg 300
aagagaattc acgagcttgt tgagatggca atgcaggaaa aggactttgc aacctacaac 360
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<210> 14
<211> 173
<212> PRT
<213> artificial

<220>
<223> Mutated ferritin

<400> 14

Met Ala Ser Ile Ser Glu Lys Met Val Glu Ala Leu Asn Arg Gln Ile
1 5 10 15

Asn Ala Glu Ile Tyr Ser Ala Tyr Leu Tyr Leu Ser Met Ala Ser Tyr
20 25 30

Phe Asp Ser Ile Gly Leu Lys Gly Phe Ser Asn Trp Met Arg Val Gln
35 40 45

Trp Gln Glu Glu Leu Met His Ala Met Lys Met Phe Asp Phe Val Ser
50 55 60

Glu Arg Gly Gly Arg Val Lys Leu Tyr Ala Val Glu Glu Pro Pro Ser
65 70 75 80

Glu Trp Asp Ser Pro Leu Ala Ala Phe Glu His Val Tyr Glu His Glu
85 90 95

Val Asn Val Thr Lys Arg Ile His Glu Leu Val Glu Met Ala Met Gln
100 105 110

Glu Lys Asp Phe Ala Thr Tyr Asn Phe Leu Gln Trp Tyr Val Ala Glu
115 120 125

Gln Val Glu Glu Glu Ala Ser Ala Leu Asp Ile Val Glu Lys Leu Arg
130 135 140

Leu Ile Gly Glu Asp Ala Ala Ala Leu Leu Phe Leu Asp Lys Glu Leu
145 150 155 160

Ser Leu Arg Gln Phe Thr Pro Pro Ala Glu Glu Glu Lys
165 170

<210> 15

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

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<211> 525
<212> DNA
<213> artificial

<220>
<223> wild type ferritin

<400> 15
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ttctcaaact ggatgagggg gcagtggcag gaggagctga tgcatgcgat gaagatgttt      180
gactttgtca gtgagagggg agggagagtt aagctctacg ctgttgagga gccaccatct      240
gagtgggatt cgcctttggc agcctttgag cacgtttacg agcatgaggt aaatgttacg      300
aagagaattc acgagcttgt tgagatggca atgcaggaaa aggactttgc aacctacaac      360
ttctgcagt ggtatgttgc ggagcagggt gaggaggaag cctctgccct cgacattgtg      420
gagaagctga ggttgattgg agaggacaaa agggctttgc ttttccttga taaggagctt      480
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<210> 16
<211> 173
<212> PRT
<213> artificial

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<220>
<223> wild type ferritin

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<400> 16

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Met Ala Ser Ile Ser Glu Lys Met Val Glu Ala Leu Asn Arg Gln Ile
1           5           10           15

```

```

Asn Ala Glu Ile Tyr Ser Ala Tyr Leu Tyr Leu Ser Met Ala Ser Tyr
20           25           30

```

```

Phe Asp Ser Ile Gly Leu Lys Gly Phe Ser Asn Trp Met Arg Val Gln
35           40           45

```

```

Trp Gln Glu Glu Leu Met His Ala Met Lys Met Phe Asp Phe Val Ser
50           55           60

```

```

Glu Arg Gly Gly Arg Val Lys Leu Tyr Ala Val Glu Glu Pro Pro Ser
65           70           75           80

```

```

Glu Trp Asp Ser Pro Leu Ala Ala Phe Glu His Val Tyr Glu His Glu
85           90           95

```

```

Val Asn Val Thr Lys Arg Ile His Glu Leu Val Glu Met Ala Met Gln
100          105          110

```

```

Glu Lys Asp Phe Ala Thr Tyr Asn Phe Leu Gln Trp Tyr Val Ala Glu
115          120          125

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9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

Gln Val Glu Glu Glu Ala Ser Ala Leu Asp Ile Val Glu Lys Leu Arg
130 135 140

Leu Ile Gly Glu Asp Lys Arg Ala Leu Leu Phe Leu Asp Lys Glu Leu
145 150 155 160

Ser Leu Arg Gln Phe Thr Pro Pro Ala Glu Glu Glu Lys
165 170

<210> 17
<211> 31
<212> DNA
<213> artificial

<220>
<223> Mutagenesis primer (forward)

<400> 17
gattggagag gacgcggcgg ctttgctttt c 31

<210> 18
<211> 31
<212> DNA
<213> artificial

<220>
<223> Mutagenesis primer (reverse)

<400> 18
gaaaagcaaa gccgccgcgt cctctccaat c 31

<210> 19
<211> 193
<212> PRT
<213> artificial

<220>
<223> CVAf

<400> 19

Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1 5 10 15

Ala His Ser Gly Gly Ala Ser Ile Ser Glu Lys Met Val Glu Ala Leu
20 25 30

Asn Arg Gln Ile Asn Ala Glu Ile Tyr Ser Ala Tyr Leu Tyr Leu Ser
35 40 45

Met Ala Ser Tyr Phe Asp Ser Ile Gly Leu Lys Gly Phe Ser Asn Trp
50 55 60

Met Arg Val Gln Trp Gln Glu Glu Leu Met His Ala Met Lys Met Phe
65 70 75 80

Asp Phe Val Ser Glu Arg Gly Gly Arg Val Lys Leu Tyr Ala Val Glu

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt
85 90 95

Glu Pro Pro Ser Glu Trp Asp Ser Pro Leu Ala Ala Phe Glu His Val
100 105 110

Tyr Glu His Glu Val Asn Val Thr Lys Arg Ile His Glu Leu Val Glu
115 120 125

Met Ala Met Gln Glu Lys Asp Phe Ala Thr Tyr Asn Phe Leu Gln Trp
130 135 140

Tyr Val Ala Glu Gln Val Glu Glu Glu Ala Ser Ala Leu Asp Ile Val
145 150 155 160

Glu Lys Leu Arg Leu Ile Gly Glu Asp Lys Arg Ala Leu Leu Phe Leu
165 170 175

Asp Lys Glu Leu Ser Leu Arg Gln Phe Thr Pro Pro Ala Glu Glu Glu
180 185 190

Lys

<210> 20
<211> 185
<212> PRT
<213> artificial

<220>
<223> CVcAf

<400> 20

Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ser Gly Gly Ala Ser Ile
1 5 10 15

Ser Glu Lys Met Val Glu Ala Leu Asn Arg Gln Ile Asn Ala Glu Ile
20 25 30

Tyr Ser Ala Tyr Leu Tyr Leu Ser Met Ala Ser Tyr Phe Asp Ser Ile
35 40 45

Gly Leu Lys Gly Phe Ser Asn Trp Met Arg Val Gln Trp Gln Glu Glu
50 55 60

Leu Met His Ala Met Lys Met Phe Asp Phe Val Ser Glu Arg Gly Gly
65 70 75 80

Arg Val Lys Leu Tyr Ala Val Glu Glu Pro Pro Ser Glu Trp Asp Ser
85 90 95

Pro Leu Ala Ala Phe Glu His Val Tyr Glu His Glu Val Asn Val Thr
100 105 110

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

Lys Arg Ile His Glu Leu Val Glu Met Ala Met Gln Glu Lys Asp Phe
115 120 125

Ala Thr Tyr Asn Phe Leu Gln Trp Tyr Val Ala Glu Gln Val Glu Glu
130 135 140

Glu Ala Ser Ala Leu Asp Ile Val Glu Lys Leu Arg Leu Ile Gly Glu
145 150 155 160

Asp Lys Arg Ala Leu Leu Phe Leu Asp Lys Glu Leu Ser Leu Arg Gln
165 170 175

Phe Thr Pro Pro Ala Glu Glu Glu Lys
180 185

<210> 21
<211> 250
<212> DNA
<213> Artificial sequence

<220>
<223> Sequencing result of theoretical DNA sequence of pCVAf after site-directed mutagenesis (top line; Figure 8)

<400> 21
gaggaagcct ctgccctcga cattgtggag aagctgaggt tgattggaga ggacgcggcg 60
gctttgcgga gaggacgcgg cggctttgct ggagaggacg cggcggcttt gcttttcatt 120
ggagaggacg cggcggcttt gcttttcctt gataaggagc tttctctcag gcagtttact 180
cctccagctg aggaggagaa gtaaggatcc ggatcgacga gagcagcgcg actggatctg 240
tcgcccgtct 250

<210> 22
<211> 129
<212> DNA
<213> Artificial sequence

<220>
<223> theoretical DNA sequence of pCVAf after site-directed mutagenesis (bottom line; Fig. 8)

<400> 22
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gctttgcttt tccttgataa ggagctttct ctcaggcagt ttactcctcc agctgaggag 120
gagaagtaa 129

<210> 23
<211> 600
<212> DNA
<213> Artificial sequence

<220>
<223> sequence alignment comparison for pCVAf-pET-11a (result)

<400> 23

9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

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catatgagca ccaaagataa ctttaatgtg tacaaagcaa cccgtccgta tctggcacat      60
agcgggtggtg ctagcatttc tgaaaaaatg gttgaggctt tgaacaggca gataaacgct     120
gaaatctact cagcatacct ctacctctcc atggcctctt acttcgactc catcgggctt     180
aagggtcttct caaactggat gaggggtgcag tggcaggagg agctgatgca tgcgatgaag     240
atgtttgact ttgtcagtga gaggggaggg agagttaagc tctacgctgt tgaggagcca     300
ccatctgagt gggattcgcc tttggcagcc tttgagcacg tttacgagca tgaggtaaata     360
gttacgaaga gaattcacga gcttgttgag atggcaatgc aggaaaagga ctttgcaacc     420
tacaacttcc tgcagtggta tgttgcggag caggttgagg aggaagcctc tgccctcgac     480
attgtggaga agctgagggtt gattggagag gacaaaaggg ctttgctttt ctttgataag     540
gagctttctc tcaggcagtt tactcctcca gctgaggagg agaagtaagg atccggatcg     600

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<210> 24
 <211> 594
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sequence alignment comparison for pCVAf-pET-11a (theoretical;
 Fig. 22)

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agcgggtggtg ctagcatttc tgaaaaaatg gttgaggctt tgaacaggca gataaacgct     120
gaaatctact cagcatacct ctacctctcc atggcctctt acttcgactc catcgggctt     180
aagggtcttct caaactggat gaggggtgcag tggcaggagg agctgatgca tgcgatgaag     240
atgtttgact ttgtcagtga gaggggaggg agagttaagc tctacgctgt tgaggagcca     300
ccatctgagt gggattcgcc tttggcagcc tttgagcacg tttacgagca tgaggtaaata     360
gttacgaaga gaattcacga gcttgttgag atggcaatgc aggaaaagga ctttgcaacc     420
tacaacttcc tgcagtggta tgttgcggag caggttgagg aggaagcctc tgccctcgac     480
attgtggaga agctgagggtt gattggagag gacaaaaggg ctttgctttt ctttgataag     540
gagctttctc tcaggcagtt tactcctcca gctgaggagg agaagtaagg atcc          594

```

<210> 25
 <211> 600
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sequence alignment comparison for pCVAf-pET-11a (results; Fig.
 23)

```

<400> 25
ctcgcaccca tatgagcacc aaagataact ttaatgtgta caaaagcggg ggtgctagca      60
tttctgaaaa aatgggttgag gctttgaaca ggcagataaa cgctgaaatc tactcagcat     120
acctctacct ctccatggcc tcttacttcg actccatcgg gcttaagggc ttctcaaact     180

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9869SG3612 includes SEQ from figures 8 22 and 23_ST25.txt

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ggatgaggggt gcagtggcag gaggagctga tgcattgcgat gaagatgttt gactttgtca      240
gtgagaggggg agggagagtt aagctctacg ctgttgagga gccaccatct gagtgggatt      300
cgccctttggc agccctttgag cacgtttacg agcatgaggt aaatgttacg aagagaattc      360
acgagcttgt tgagatggca atgcaggaaa aggactttgc aacctacaac ttcctgcagt      420
ggtatgttgc ggagcagggt gaggaggaag cctctgccct cgacattgtg gagaagctga      480
ggttgattgg agaggacaaa agggctttgc ttttccttga taaggagctt tctctcaggc      540
agtttactcc tccagctgag gaggagaagt aaggatccgg atcgacgaga gcagcgcgac      600

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<210> 26
 <211> 570
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sequence alignment comparison for pCVcAf-pET-11a (theoretical)

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<400> 26
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aaaatggttg aggctttgaa caggcagata aacgctgaaa tctactcagc atacctctac      120
ctctccatgg cctcttactt cgactccatc gggcttaagg gcttctcaaa ctggatgagg      180
gtgcagtggc aggaggagct gatgcatgcg atgaagatgt ttgactttgt cagtgagagg      240
ggagggagag ttaagctcta cgctgttgag gagccaccat ctgagtggga ttcgcctttg      300
gcagcctttg agcacgttta cgagcatgag gtaaatgtta cgaagagaat tcacgagctt      360
gttgagatgg caatgcagga aaaggacttt gcaacctaca acttcctgca gtggtatgtt      420
gcggagcagg ttgaggagga agcctctgcc ctcgacattg tggagaagct gaggttgatt      480
ggagaggaca aaagggcttt gcttttcctt gataaggagc tttctctcag gcagtttact      540
cctccagctg aggaggagaa gtaaggatcc

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