

SP100642WO_ST25.txt
SEQUENCE LISTING

<110> Agency for Science, Technology and Research
ImmunoSCAPE Pte. Ltd.

<120> High Yield Production and Use of Enzymatic-Exchangeable Peptide
Major Histocompatibility Complex Class I Single Chain Trimer
Tetramer

<130> SP100642WO

<150> SG10201904052S
<151> 2019-05-06

<160> 54

<170> PatentIn version 3.5

<210> 1
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Mellitin secretion leader

<400> 1

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15

Ser Tyr Ile Tyr Ala
20

<210> 2
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Enterokinase cleavable linker

<400> 2

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

Asp Asp Asp Lys Gly
20

<210> 3
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GS-Linker

<400> 3

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

Gly Gly Gly Ser
 20

<210> 4
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 <223> Peptide ligand 1

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Ala Val Phe Ala Ala Ala Ser Asp Ala Lys
 1 5 10

<210> 5
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<220>
 <223> Peptide ligand 2

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Ala Val Phe Asp Arg Lys Ser Asp Ala Lys
 1 5 10

<210> 6
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 <212> PRT
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<220>

<223> Peptide ligand 3

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Lys Ile Leu Gly Arg Val Phe Phe Val
1 5

<210> 7

<211> 9

<212> PRT

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<220>

<223> Peptide ligand 4

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Lys Leu Ala Glu Ala Ile Phe Lys Leu
1 5

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide ligand 5

<400> 8

Tyr Ala Glu Thr Ala Ala Phe Ala Tyr
1 5

<210> 9

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> beta-2 microglobulin

<400> 9

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu
1 5 10 15

SP100642W0_ST25.txt

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro
20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp
85 90 95

Arg Asp Met

<210> 10
<211> 273
<212> PRT
<213> Artificial Sequence

<220>
<223> A*11:01 Heavy chain

<400> 10

His Ser Met Arg Tyr Phe Tyr Thr Ser Val Ser Arg Pro Gly Arg Gly
1 5 10 15

Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val
20 25 30

Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro
35 40 45

Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn
50 55 60

Val Lys Ala Gln Ser Gln Thr Asp Arg Val Asp Leu Gly Thr Leu Arg
65 70 75 80

Gly Tyr Tyr Asn Gln Ser Glu Asp Gly Ser His Thr Ile Gln Ile Met
85 90 95

Tyr Gly Cys Asp Val Gly Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg
100 105 110

Gln Asp Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu
115 120 125

Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Ile Thr Lys Arg Lys
130 135 140

Trp Glu Ala Ala His Ala Ala Glu Gln Gln Arg Ala Tyr Leu Glu Gly
145 150 155 160

Arg Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr
165 170 175

Leu Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile
180 185 190

Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro
195 200 205

Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln
210 215 220

Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln
225 230 235 240

Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr
245 250 255

Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp
260 265 270

Glu

<210> 11
 <211> 273
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A*02:01 Heavy chain

<400> 11

His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly
 1 5 10 15

Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val
 20 25 30

Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro
 35 40 45

Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys
 50 55 60

Val Lys Ala His Ser Gln Thr His Arg Val Asp Leu Gly Thr Leu Arg
 65 70 75 80

Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser His Thr Val Gln Arg Met
 85 90 95

Tyr Gly Cys Asp Val Gly Ser Asp Trp Arg Phe Leu Arg Gly Tyr His
 100 105 110

Gln Tyr Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu
 115 120 125

Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Thr Thr Lys His Lys
 130 135 140

Trp Glu Ala Ala His Val Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly
 145 150 155 160

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Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr
165 170 175

Leu Gln Arg Thr Asp Ala Pro Lys Thr His Met Thr His His Ala Val
180 185 190

Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro
195 200 205

Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln
210 215 220

Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln
225 230 235 240

Lys Trp Ala Ala Val Val Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr
245 250 255

Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp
260 265 270

Glu

<210> 12
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> MHC-I heavy chain polypeptide

<400> 12

His Ser Met Arg Tyr Phe Phe Thr Ser Val Ser Arg Pro Gly Arg Gly
1 5 10 15

Glu Pro Arg Phe Ile Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val
20 25 30

Arg Phe Asp Ser Asp Ala Ala Ser Gln Lys Met Glu Pro Arg Ala Pro
35 40 45

SP100642W0_ST25.txt

Trp Ile Glu Gln Glu Gly Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn
50 55 60

Met Lys Ala His Ser Gln Thr Asp Arg Ala Asn Leu Gly Thr Leu Arg
65 70 75 80

Gly Tyr Tyr Asn Gln Ser Glu Asp Gly Ser His Thr Ile Gln Ile Met
85 90 95

Tyr Gly Cys Asp Val Gly Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg
100 105 110

Gln Asp Ala Tyr Asp Gly Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu
115 120 125

Arg Ser Trp Thr Ala Ala Asp Met Ala Ala Gln Ile Thr Lys Arg Lys
130 135 140

Trp Glu Ala Val His Ala Ala Glu Gln Arg Arg Val Tyr Leu Glu Gly
145 150 155 160

Arg Cys Val Asp Gly Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr
165 170 175

Leu Gln Arg Thr Asp Pro Pro Lys Thr His Met Thr His His Pro Ile
180 185 190

Ser Asp His Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro
195 200 205

Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln
210 215 220

Asp Thr Glu Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln
225 230 235 240

Lys Trp Ala Ala Val Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr
245 250 255

Cys His Val Gln His Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp
 260 265 270

Glu Leu

<210> 13
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BirA recognition site

<400> 13

Leu His His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg
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<210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His6x

<400> 14

His His His His His His
 1 5

<210> 15
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A*11:01-AVFAAASDAK

<400> 15

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15

SP100642W0_ST25.txt

Ser Tyr Ile Tyr Ala Ala Val Phe Ala Ala Ala Ser Asp Ala Lys Gly
20 25 30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Asp
35 40 45

Asp Asp Lys Gly Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg
50 55 60

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
65 70 75 80

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
85 90 95

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
100 105 110

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
115 120 125

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
130 135 140

Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Ser Met Arg Tyr
165 170 175

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

Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
195 200 205

Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu
210 215 220

SP100642W0_ST25.txt

Gly Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn Val Lys Ala Gln Ser
225 230 235 240

Gln Thr Asp Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln
245 250 255

Ser Glu Asp Gly Ser His Thr Ile Gln Ile Met Tyr Gly Cys Asp Val
260 265 270

Gly Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg Gln Asp Ala Tyr Asp
275 280 285

Gly Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala
290 295 300

Ala Asp Met Ala Ala Gln Ile Thr Lys Arg Lys Trp Glu Ala Ala His
305 310 315 320

Ala Ala Glu Gln Gln Arg Ala Tyr Leu Glu Gly Arg Cys Val Glu Trp
325 330 335

Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp
340 345 350

Pro Pro Lys Thr His Met Thr His His Pro Ile Ser Asp His Glu Ala
355 360 365

Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu
370 375 380

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
385 390 395 400

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
405 410 415

Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His
420 425 430

SP100642W0_ST25.txt

Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Gly Ser Leu
435 440 445

His His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg His His
450 455 460

His His His His
465

<210> 16
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> A*11:01-AVFDRKSDAK

<400> 16

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15

Ser Tyr Ile Tyr Ala Ala Val Phe Asp Arg Lys Ser Asp Ala Lys Gly
20 25 30

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Asp
35 40 45

Asp Asp Lys Gly Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg
50 55 60

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser
65 70 75 80

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu
85 90 95

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp
100 105 110

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp
115 120 125

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile
130 135 140

Val Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Ser Met Arg Tyr
165 170 175

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

Ala Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp
195 200 205

Ala Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu
210 215 220

Gly Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn Val Lys Ala Gln Ser
225 230 235 240

Gln Thr Asp Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln
245 250 255

Ser Glu Asp Gly Ser His Thr Ile Gln Ile Met Tyr Gly Cys Asp Val
260 265 270

Gly Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg Gln Asp Ala Tyr Asp
275 280 285

Gly Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala
290 295 300

Ala Asp Met Ala Ala Gln Ile Thr Lys Arg Lys Trp Glu Ala Ala His
305 310 315 320

Ala Ala Glu Gln Gln Arg Ala Tyr Leu Glu Gly Arg Cys Val Glu Trp
325 330 335

Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp
340 345 350

Pro Pro Lys Thr His Met Thr His His Pro Ile Ser Asp His Glu Ala
355 360 365

Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu
370 375 380

Thr Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val
385 390 395 400

Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val
405 410 415

Val Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His
420 425 430

Glu Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Gly Ser Leu
435 440 445

His His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg His His
450 455 460

His His His His
465

<210> 17
<211> 466
<212> PRT
<213> Artificial Sequence

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<223> A*02:01-KILGRVFFV

<400> 17

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15

SP100642W0_ST25.txt

Ser Tyr Ile Tyr Ala Lys Ile Leu Gly Arg Val Phe Phe Val Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Asp Asp
35 40 45

Asp Lys Gly Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His
50 55 60

Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
65 70 75 80

Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg
85 90 95

Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser
100 105 110

Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu
115 120 125

Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val
130 135 140

Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Ser Met Arg Tyr Phe
165 170 175

Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
180 185 190

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
195 200 205

Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
210 215 220

SP100642W0_ST25.txt

Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln
225 230 235 240

Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
245 250 255

Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly
260 265 270

Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
275 280 285

Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala
290 295 300

Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val
305 310 315 320

Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu
325 330 335

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala
340 345 350

Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr
355 360 365

Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr
370 375 380

Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
385 390 395 400

Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
405 410 415

Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
420 425 430

SP100642W0_ST25.txt

Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Gly Ser Leu His
435 440 445

His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg His His His
450 455 460

His His
465

<210> 18
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> A*02:01-KLAEAIFKL

<400> 18

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15

Ser Tyr Ile Tyr Ala Lys Leu Ala Glu Ala Ile Phe Lys Leu Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Asp Asp
35 40 45

Asp Lys Gly Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His
50 55 60

Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
65 70 75 80

Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg
85 90 95

Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser
100 105 110

Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu
115 120 125

SP100642W0_ST25.txt

Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val
130 135 140

Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Ser Met Arg Tyr Phe
165 170 175

Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
180 185 190

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
195 200 205

Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
210 215 220

Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln
225 230 235 240

Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
245 250 255

Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly
260 265 270

Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
275 280 285

Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala
290 295 300

Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val
305 310 315 320

Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu
325 330 335

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala
340 345 350

Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr
355 360 365

Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr
370 375 380

Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
385 390 395 400

Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
405 410 415

Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
420 425 430

Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Gly Ser Leu His
435 440 445

His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg His His His
450 455 460

His His His
465

<210> 19
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> A*01:01-YAETAAFAY

<400> 19

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15

SP100642W0_ST25.txt

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Asp Asp
35 40 45

Asp Lys Gly Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His
50 55 60

Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly
65 70 75 80

Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg
85 90 95

Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser
100 105 110

Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu
115 120 125

Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val
130 135 140

Lys Trp Asp Arg Asp Met Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Ser Met Arg Tyr Phe
165 170 175

Phe Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
180 185 190

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
195 200 205

Ala Ser Gln Lys Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
210 215 220

SP100642W0_ST25.txt

Pro Glu Tyr Trp Asp Gln Glu Thr Arg Asn Met Lys Ala His Ser Gln
225 230 235 240

Thr Asp Arg Ala Asn Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
245 250 255

Glu Asp Gly Ser His Thr Ile Gln Ile Met Tyr Gly Cys Asp Val Gly
260 265 270

Pro Asp Gly Arg Phe Leu Arg Gly Tyr Arg Gln Asp Ala Tyr Asp Gly
275 280 285

Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
290 295 300

Asp Met Ala Ala Gln Ile Thr Lys Arg Lys Trp Glu Ala Val His Ala
305 310 315 320

Ala Glu Gln Arg Arg Val Tyr Leu Glu Gly Arg Cys Val Asp Gly Leu
325 330 335

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Pro
340 345 350

Pro Lys Thr His Met Thr His His Pro Ile Ser Asp His Glu Ala Thr
355 360 365

Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
370 375 380

Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
385 390 395 400

Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
405 410 415

Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
420 425 430

SP100642W0_ST25.txt

Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Gly Ser Leu His
 435 440 445

His Ile Leu Asp Ala Gln Lys Met Val Trp Asn His Arg His His His
 450 455 460

His His His
 465

<210> 20
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mellitin nucleotide sequence 1

<400> 20
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 gcg 63

<210> 21
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Enterokinase cleavable linker

<400> 21
 ggtggagggtg gctctggagg cggcggctcc ggaggcgggtg gtagtgatga cgatgacaaa 60
 gga 63

<210> 22
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GS-Linker

<400> 22
 ggaggaggcgg gatcaggagg cggaggaagt ggtggtggag gttctggtgg tggcggtagt 60

<210> 23
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> AVFAAASDAK

 <400> 23
 gctgtattcg ctgcggcttc cgatgccaaa 30

 <210> 24
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> AVFDRKSDAK

 <400> 24
 gctgtattcg ataggaagtc cgatgccaaa 30

 <210> 25
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> KILGRVFFV

 <400> 25
 aaaattttgg gtagggtttt ttttgtg 27

 <210> 26
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> KLAEAIFKL

 <400> 26
 aagctcgcag aggcgatttt caaactg 27

 <210> 27
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> YAETAAFAY

<400> 27

tatgcagaaa cggcggcatt tgcttat

27

<210> 28

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 microglobulin

<400> 28

atccaaagaa ctccgaagat ccaagtgtac tctagacacc ctgctgaaaa tggtaaattcc 60

aacttcctca actgttacgt gagcgggttc caccgtctg atatagaggt tgacctctc 120

aagaatggcg aacgcatcga aaaggttgaa cactcagacc tctctttcag caaagattgg 180

agcttttatc ttttgtatta cactgagttt accccgacag agaaagacga atatgcatgc 240

agagtgaatc acgtgacgtt gtcgcagccg aaaatcgtga aatgggaccg cgatatg 297

<210> 29

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> A*11:01 Heavy chain

<400> 29

cattcgatgc gttacttcta cacgtcgggtg tctaggcccg gcagaggaga gccccgtttc 60

atagcggtag gttacgttga cgacacgcaa ttcgtgcgtt ttgactcgga cgccgcctca 120

caaagaatgg aaccccgcg cccctggatt gagcaagagg gacctgaata ctgggatcaa 180

gaaacgagga acgtgaaggc gcagtcgcaa actgataggg tcgatctggg aacccttagg 240

ggatattata accaaagcga agacggatct catactattc aaattatgta tggttgac 300

gttggtcccg atggccgctt tcttcgtgga tacaggcagg acgcgtacga cggaaaggat 360

tatattgcgt tgaatgaaga tcttaggtcg tggacagcgg cggacatggc cgctcaaattc 420

accaaagcga aatgggaagc cgcacacgcc gcagaacaac agcgcgctta tttggaaggc 480

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agatgtgtag agtggttgcg tcgttatctc gaaaacggta aagaaacact ccaacgcacc	540
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tgttgggcat tgggattcta tccggcagaa ataacgctca catggcagcg tgacggagag	660
gatcaaacgc aagatacgga acttgtggag acacgccctg cgggtgacgg aacctttcag	720
aagtgggcag cagttgtagt cccaagcggc gaggaacaac gctatacctg ccacgtacaa	780
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 <223> A*02:01 Heavy chain

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<220>
 <223> A*01:01 Heavy chain

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 <223> BirA recognition site

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<210> 33
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<212> DNA

<213> Artificial Sequence

<220>

<223> His6X

<400> 33

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18

<210> 34

<211> 1419

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<213> Artificial Sequence

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<223> A*11:01-AVFDRKSDAK nucleotide

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ttgtcgcagc cgaaaatcgt gaaatgggac cgcgatattg gaggaggcgg atcaggaggc 480

ggaggaagtg gtggtggagg ttctggtggt ggcggtagtc attcgatgcg ttacttctac 540

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cttaggtcgt ggacagcggc ggacatggcc gctcaaatca ccaaactgaa atgggaagcc 960

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 <223> A*11:01-AVFAAASDAK nucleotide

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 <213> Artificial Sequence

<220>
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<210> 37
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 <213> Artificial Sequence

<220>
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<210> 38

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<212> DNA

<213> Artificial Sequence

<220>

<223> A*01:01- YAETAAFAY nucleotide

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<220>
 <223> EBV peptide 1

<400> 39

Ile Val Thr Asp Phe Ser Val Ile Lys
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<210> 40
 <211> 9
 <212> PRT
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<220>
 <223> EBV peptide 2

<400> 40

Asn Thr Leu Glu Gln Thr Val Lys Lys
 1 5

<210> 41
 <211> 9
 <212> PRT
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<220>
 <223> CMV peptide

<400> 41

Asn Leu Val Pro Met Val Ala Thr Val
 1 5

<210> 42
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<220>
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<400> 42

Val Glu Thr Glu His Asp Thr Leu Leu Tyr
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<210> 43
 <211> 5
 <212> PRT
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<220>
 <223> Cleavable DDDDK peptide

<400> 43

Asp Asp Asp Asp Lys
1 5

<210> 44

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> GTSGSPIVNR

<400> 44

Gly Thr Ser Gly Ser Pro Ile Val Asn Arg
1 5 10

<210> 45

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> ATYGWNLVK

<400> 45

Ala Thr Tyr Gly Trp Asn Leu Val Lys
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<210> 46

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> SIIPSGPLK

<400> 46

Ser Ile Ile Pro Ser Gly Pro Leu Lys
1 5

<210> 47

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> RMVLASTTAK

<400> 47

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<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> KSMREEYRK

<400> 48

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<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> ATIGTAMYK

<400> 49

Ala	Thr	Ile	Gly	Thr	Ala	Met	Tyr	Lys
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<210> 50

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> SSCSSCPLSK

<400> 50

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> YVNVNMGLK

<400> 51

Tyr Val Asn Val Asn Met Gly Leu Lys
 1 5

<210> 52
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLDKGTCTL

<400> 52

Phe Leu Asp Lys Gly Thr Tyr Thr Leu
 1 5

<210> 53
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VLEETSVML

<400> 53

Val Leu Glu Glu Thr Ser Val Met Leu
 1 5

<210> 54
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLYALALLL

<400> 54

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1 5