

SEQUENCE LISTING

<110> HIROSHIMA UNIVERSITY

<120> Novel nuclease domain and use thereof

<130> NED0002W0

<150> JP2018-158710

<151> 2018-08-27

<160> 122

<170> PatentIn version 3.5

<210> 1

<211> 585

<212> PRT

<213> Bacillus sp. SGD-V-76

<400> 1

Met Ala Thr Lys Arg Val Val Arg Thr Phe Gly Trp Ile Gln Asn Pro
1 5 10 15

Gly Lys Phe Glu Asn Leu Lys Arg Thr Val Gln Val Phe Asp Glu Asn
20 25 30

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

Lys Asp Lys Asp Val Arg Thr Thr Leu Ile Ala Ala Met Asn Arg Leu
50 55 60

Glu Asn Tyr Tyr Ser Tyr Lys Glu Leu Val Gly Thr Gly Thr Ser Val
65 70 75 80

Arg Ala Gln Ala Pro Cys Asp Ala Ile Ile Gln Ala Ala Ile Gln Asp
85 90 95

Gln Gly Asn Lys Lys Gly Tyr Ile Asp Asn Trp Ser Ser Asp Gly Phe
100 105 110

Val Arg Trp Ala His Ala Leu Gly Phe Leu Glu Tyr Asn Ser Asp Lys
115 120 125

Asp Ser Phe Tyr Leu Thr Asp Ile Gly Leu Glu Tyr Ser Arg Ser Thr
130 135 140

Asp Asp Ser Leu Asn Glu Lys Ile Ile Leu Ile Glu Ala Leu Ser Ser
145 150 155 160

Tyr Pro Pro Ala Ile Arg Ile Leu Thr Leu Leu Glu Asn Gly Glu His
165 170 175

Leu Thr Lys Phe Asp Leu Gly Lys Gln Leu Gly Phe Ser Gly Glu Ser
180 185 190

Gly Phe Thr Ser Leu Pro Gln Asn Leu Phe Leu Asp Ala Leu Ala Asn
195 200 205

Ala Pro Ser Ser Pro Pro Thr Ile Lys Asn Ser Ile Arg Ser Asp Trp
210 215 220

Glu Gly Ser Ala Asp Lys Tyr Ala Arg Met Ile Ser Gly Trp Leu Val
225 230 235 240

Lys Met Gly Leu Val Ala Gln Gly Arg Lys Asn Phe Val Val Pro Thr
245 250 255

Val Gly Gly Ser Thr Arg Asn Glu Tyr Ile Ser His Ala Phe Lys Ile
260 265 270

Thr Lys Asp Gly Leu Asp Val Leu Arg Arg Ala Lys Gly Ala Ser Lys
275 280 285

His Val Arg Val Pro Lys Arg Val Tyr Trp Glu Met Phe Ala Thr Asn
290 295 300

Ile Asn Asp Arg Val Tyr Val Arg Thr Arg Arg Ala Tyr Thr Leu Tyr
305 310 315 320

Leu Leu Met Arg Ser Asn Thr Ala Leu Asn Thr Val Gln Leu Gln Val
325 330 335

Lys Leu Lys Ala Leu Gly Phe Glu Glu Leu Glu Glu Thr Ile Glu Asn
340 345 350

Asp Val Lys Gly Leu Ile Asn Ser Gly Ile Phe Ile Asn Val Thr Asn
355 360 365

Lys Gly Tyr His Phe Lys Asp Thr Ile Lys Pro Phe Glu Ile Pro Glu
370 375 380

Phe Gly Val Thr Glu Pro Leu Val Lys Gly Glu Met Glu Lys Lys Lys
385 390 395 400

Ser Asp Leu Arg His Lys Leu Lys His Val Pro His Glu Tyr Ile Glu
405 410 415

Leu Ile Glu Ile Ala Gln Asp Ser Lys Gln Asn Arg Leu Phe Glu Phe
420 425 430

Lys Val Val Glu Phe Leu Lys Glu Val Tyr Asp Tyr Asn Gly Lys His
435 440 445

Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Leu Tyr Thr Asn Gly Leu
450 455 460

Lys Thr Asp Tyr Gly Ile Ile Leu Asp Thr Lys Ala Tyr Lys Asp Gly
465 470 475 480

Tyr Ser Leu Pro Ile Ser Gln Ala Asp Glu Met Gln Arg Tyr Val Asp
485 490 495

Glu Asn Asn Asn Arg Asn Ala Ile Ile Asn Pro Asn Glu Trp Trp Lys
500 505 510

Val Tyr Pro Asn Ser Ile Leu Asp Phe Lys Phe Leu Phe Val Ser Gly
515 520 525

Phe Phe Lys Gly Asp Tyr Lys Lys Gln Leu Ala Arg Val Ser Asn Leu
530 535 540

Thr Lys Arg Lys Gly Ala Val Leu Ser Val Glu Gln Leu Leu Leu Gly

Gly Glu Lys Ile Lys Asp Gly Ser Leu Thr Leu Glu Asp Val Gly Asp

565 570 575

```
<210> 2
<211> 1758
<212> DNA
<213> Bacillus sp. SGD-V-76
```

ggaatttttta tcaatgtgac gaataaaggt tatcatttta aagatacaat taaaccattc	1140
gaaattcctg aatttggcgt aacagaacca ttagtaaagg gggaaatgga gaagaagaaa	1200
tccgatttgc gtcataagtt aaaacacgta ccgcatgaat atattgaact aatagaaatt	1260
gcacaggatt caaagcaaaa tcgtttgttc gaatttaaag tagttgagtt tttgaaagaa	1320
gtttatgatt ataatggaaa gcacctaggg gggagtcgaa aaccagatgg cgcactatat	1380
accaatgggt taaaaacaga ttatggaata attttagata ccaaagctta caaagatggt	1440
tatagtttac caatctcca ggcagatgaa atgcagcgtt atgtcgatga aaataataat	1500
agaaatgcta ttattaatcc taacgaatgg tggaaagtgt atcctaattc tatcttggac	1560
tttaaattct tattcgtaag tggttttttt aaaggtgact ataaaaaaca attagctcgt	1620
gtaagtaatc ttacaaagcg taaaggtgct gtcctaagcg tagagcaact attattggga	1680
ggggaaaaaa ttaaagatgg tagtttaaca ttagaagatg ttggtgacaa attcaataat	1740
gatgaaatta ttttctaa	1758

<210> 3
 <211> 579
 <212> PRT
 <213> Clostridium botulinum

<400> 3

Val	Glu	Ser	Leu	Arg	Leu	Ser	Asp	Ile	Thr	Ile	Arg	Thr	Phe	Gly	Trp
1			5					10						15	

Ile	Gln	Asn	Pro	Ser	Asp	Phe	Ser	Lys	Leu	Lys	Lys	Ile	Val	Gln	Leu
			20					25					30		

Phe	Asp	His	Thr	Ser	Ser	Ile	His	Val	Asp	Leu	Lys	Glu	Asn	Arg	Ile
		35					40					45			

Pro	Arg	Leu	Val	Glu	Lys	Asp	Asp	Gly	Arg	Asp	Arg	Phe	Ile	Glu	Ile
	50					55					60				

Leu	Asn	Arg	Ile	Pro	Leu	Lys	Ile	Lys	Tyr	Ile	Asp	Leu	Val	Gly	Thr
65					70				75					80	

Ser	Phe	Lys	Pro	Arg	Ser	Ser	Gly	Arg	Cys	Asn	Gly	Ile	Ala	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Met Ile Glu Gly Gln Gly Lys Ser Phe Thr Asp Asn Trp Thr Ala Asp
 100 105 110

Gly Phe Ile Arg Trp Ala His Ala Leu Gly Phe Ile Gln Tyr Asp Tyr
 115 120 125

Leu Glu Asp Glu Phe Ser Ile Thr Gln Ala Gly Phe Asp Phe Ser Arg
 130 135 140

Ser Ile Asn Asp Ser Glu Gly Glu Asn Glu Ile Leu Ile Glu Ala Met
 145 150 155 160

Leu Ser Tyr Pro Pro Ala Val Arg Val Leu Asp Leu Leu Ser Leu Gly
 165 170 175

Glu His Leu Thr Lys Phe Asp Ile Gly Lys Asn Leu Gly Phe Asn Gly
 180 185 190

Glu Ser Gly Phe Thr Ser Leu Pro Leu Asn Ile Met Leu Gln Thr Leu
 195 200 205

Ala Asp Asn Asp Leu Val Ser Glu Lys Thr Lys Ile Arg Gln Asp Trp
 210 215 220

Glu Gly Ser Ser Asp Lys Tyr Ser Arg Met Ile Ala Gly Trp Leu Ser
 225 230 235 240

Lys Leu Gly Leu Val Lys Lys Gly Lys Lys Tyr Phe Asp Val Asn Ile
 245 250 255

Gly Gly Ile Ile His Arg Glu Tyr Ile Ser His Ala Tyr Lys Ile Thr
 260 265 270

Gly Glu Gly Leu Lys Gln Leu Arg Arg Ala Lys Gly Thr Thr Ser Ala
 275 280 285

Arg Arg Ile Glu Lys Arg Val Cys Trp Glu Met Phe Ala Thr Lys Asn
 290 295 300

Leu Asp Arg Thr Tyr Ile Arg Thr Arg Arg Ala Tyr Ile Leu Lys Phe
305 310 315 320

Leu Glu Val Ser Ser Ser Leu Ile Thr Ile Glu Gln Ile Lys Thr Lys
325 330 335

Leu Leu Glu Lys Gly Tyr Asp Glu Thr Val Glu Thr Ile Lys Ser Asp
340 345 350

Ile Lys Gly Leu Ile Asn Ile Gly Leu Asn Ile Gln Glu Thr Thr Arg
355 360 365

Gly Tyr Ser Leu Lys Asp Ser Ile Asn Asp Phe Met Ile Pro Val Thr
370 375 380

Asp Leu Asn Gln Ile Val Lys Ser Ser Ile Glu Met Ser Lys Ala Asn
385 390 395 400

Met Arg Asp Asn Leu Gln Met Leu Pro His Asp Tyr Ile Glu Leu Ile
405 410 415

Glu Ile Ser Gln Asp Pro Tyr Gln Asn Arg Ile Phe Glu Met Lys Val
420 425 430

Met Asp Leu Phe Ile Asn Glu Tyr Gly Phe Ser Gly Ser His Leu Gly
435 440 445

Gly Ser Arg Lys Pro Asp Gly Ala Met Tyr Ala His Gly Phe Gly Val
450 455 460

Ile Val Asp Thr Lys Ala Tyr Lys Asp Gly Tyr Asn Leu Pro Ile Ser
465 470 475 480

Gln Ala Asp Glu Met Glu Arg Tyr Val Arg Glu Asn Ile Asp Arg Asn
485 490 495

Glu His Val Asn Ser Asn Arg Trp Trp Asn Ile Phe Pro Glu Asp Thr
500 505 510

Asn Glu Tyr Lys Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asn Phe
515 520 525

Glu Lys Gln Leu Glu Arg Ile Ser Ile Asp Thr Gly Val Gln Gly Gly
530 535 540

Ala Leu Ser Val Glu His Leu Leu Leu Gly Ala Glu Tyr Ile Lys Arg
545 550 555 560

Gly Ile Leu Thr Leu Tyr Asp Phe Lys Asn Ser Phe Leu Asn Lys Glu
565 570 575

Ile Gln Phe

<210> 4
<211> 1740
<212> DNA
<213> Clostridium botulinum

<400> 4
gtggaatcat taagattatc agacataaca attagaacat ttgggtggat tcagaatcct 60
agtgatttta gtaaattaaa aaaaatagtt cagttatttg atcatacatc atctattcat 120
gtggatttga aagaaaaccg cataccacgg ttagtggaga aagatgacgg acgtgatagg 180
tttattgaga tattaaatcg gattccgtta aagataaagt atattgattt agtaggaaca 240
tcatttaaac ctagaagtag tggtagatgt aatggaattg ctcaagcaat gattgaaggt 300
caaggtaaga gttttactga taattggaca gctgatgggt ttattaggtg ggctcatgca 360
cttggcttta tacaatatga ttatttagaa gatgagtttt caataacaca agcaggcttt 420
gatttttcaa ggtcaatcaa tgatagtga ggggaaaatg aaatattaat agaggcaatg 480
ttgtcttadc cacctgcagt tagagtttta gatttacttt ctttaggaga gcatcttaca 540
aaatttgata ttggaaaaaa tctgggcttc aatggcgaat caggatttac atctttacct 600
ttaaatatca tgcttcaaac attagcagac aatgatttag taagtgaaaa gactaaaatt 660
cgtcaggatt gggaagggtc ttctgataag tattcacgaa tgatagccgg ctggttatcg 720
aaacttgggtt tggttaaaaa gggaaaaaag tattttgatg taaatattgg aggaataatt 780

catagagaat atatctctca tgcatataaa attactggag aaggtttaaa acaactccgt	840
agggctaaag gaactacaag tgcaaggcgt atagaaaaac gggtttgctg ggaaatgttc	900
gccacaaaga atctagatag gacatatatt cgtacaagaa gagcttatat tttaaagttt	960
ttagaagttt caagcagctt aattactatt gagcaaatta agactaagtt attggaaaaa	1020
ggttatgacg aaacagtaga aactattaaa tctgatatta aggggttaat taacattgggt	1080
ttaaatattc aagaaaccac tcgagggttat tcattaaagg attcaattaa tgactttatg	1140
attccagtaa ccgacttaaa tcaaattggt aaaagtagta tagagatgtc taaagctaac	1200
atgagagaca atcttcagat gttgcctcat gattatattg agctaattga aatatcacia	1260
gatccatattc aaaatagaat atttgaaatg aaagttatgg atttatttat taatgagtat	1320
ggtttcagtg gttcgcactt aggtggaagt aggaaacctg atgggtgctat gtatgcacat	1380
ggttttggtg ttattgttga tacaaaagca tataaagatg ggtacaatct tcctataagt	1440
caagctgatg aaatggaacg atatgtaagg gaaaatattg atagaaatga acatgtgaac	1500
tcaaatagat ggtggaatat atttcccgaa gatacaaatg aatataagtt tttattcgta	1560
agtggtttct ttaaaggaaa ttttgagaaa caattagaaa ggataagtat agatactggt	1620
gtacaaggag gggctttaag tgttgaacat ttattattag gtgctgagta cataaaggag	1680
ggtattctta ctttatatga ttttaagaat agctttttaa ataaggaaat tcaattttaa	1740

<210> 5
 <211> 587
 <212> PRT
 <213> Clostridium sp. 7_2_43FAA

<400> 5

Met	Ile	Asn	Ile	Ile	Asp	Val	Asn	Asn	Lys	Thr	Ile	Arg	Thr	Phe	Gly
1			5						10					15	

Trp	Val	Gln	Asn	Pro	Ser	Asn	Phe	Glu	Ser	Leu	Lys	Lys	Val	Val	Ala
		20						25					30		

Ile	Phe	Asp	Asn	Thr	Ser	Lys	Thr	Tyr	Asn	Glu	Leu	Lys	Asp	Lys	Lys
	35						40					45			

Ile	Lys	Lys	Leu	Val	Asp	Glu	Arg	Asp	Gly	Gln	Lys	Glu	Leu	Leu	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Ala Leu Asn Ala Asn Pro Leu Lys Ile Lys Tyr Cys Asn Leu Val Gly
65 70 75 80

Thr Ser Phe Thr Pro Arg Ser Ser Ala Arg Cys Asn Gly Ile Val Gln
85 90 95

Ala Thr Val Lys Gly Gln Arg Lys Glu Phe Ile Asp Asp Trp Ser Ser
100 105 110

Asp Asn Phe Val Arg Trp Ala His Ala Leu Gly Phe Ile Lys Tyr Asn
115 120 125

Tyr Asp Thr Asp Thr Phe Glu Ile Thr Asp Val Gly Arg Lys Tyr Val
130 135 140

Gln Ser Glu Asp Asp Ser Asn Glu Glu Ser Thr Ile Leu Glu Glu Ala
145 150 155 160

Met Leu Ser Tyr Pro Pro Val Ala Arg Val Leu Thr Leu Leu Ser Asn
165 170 175

Gly Glu His Leu Thr Lys Tyr Glu Ile Gly Lys Lys Leu Gly Phe Val
180 185 190

Gly Glu Ala Gly Phe Thr Ser Leu Pro Leu Asn Val Leu Ile Met Thr
195 200 205

Leu Ala Thr Thr Asp Glu Pro Lys Glu Lys Asn Lys Ile Lys Thr Asp
210 215 220

Trp Asp Gly Ser Ser Asp Lys Tyr Ala Arg Met Ile Ser Gly Trp Leu
225 230 235 240

Val Lys Leu Gly Leu Leu Val Gln Arg Pro Lys Leu Val Thr Val Asp
245 250 255

Phe Gly Gly Glu Leu Tyr Ser Glu Thr Ile Gly His Ala Tyr Met Ile
260 265 270

Thr Asp Arg Gly Leu Lys Ala Val Arg Arg Leu Leu Gly Ile Asn Lys
275 280 285

Val Ala Arg Val Ser Lys Asn Val Phe Trp Glu Met Leu Ala Thr Lys
290 295 300

Gly Ile Asp Lys Asn Tyr Ile Arg Thr Arg Arg Ala Tyr Ile Leu Lys
305 310 315 320

Ile Leu Ile Glu Ser Asn Lys Val Leu Thr Leu Glu Asp Ile Lys Gly
325 330 335

Lys Leu Lys Leu Ala Ser Ile Asn Glu Ser Ile Asn Thr Ile Lys Asp
340 345 350

Asp Ile Asn Gly Leu Ile Asn Thr Gly Ile Asn Ile Lys Ser Glu Thr
355 360 365

Thr Gly Tyr Lys Ile Tyr Asp Ser Ile Asn Asp Phe Ile Ile Pro Lys
370 375 380

Thr Gly Asp Thr Glu Gly Ile Lys Ser Asn Ile Ser Leu Leu Lys Asp
385 390 395 400

Glu Leu Arg Gly Gln Ile Ser His Ile Ser His Glu Tyr Leu Ser Leu
405 410 415

Ile Asp Leu Ala Phe Asp Ser Lys Gln Asn Arg Leu Phe Glu Met Lys
420 425 430

Val Leu Glu Leu Leu Val Asn Glu Tyr Gly Phe Lys Gly Arg His Leu
435 440 445

Gly Gly Ser Arg Lys Pro Asp Gly Ile Val Tyr Ser Thr Thr Leu Glu
450 455 460

Asp Asn Phe Gly Ile Ile Val Asp Thr Lys Ala Tyr Ser Glu Gly Tyr
465 470 475 480

Ser Leu Pro Ile Ser Gln Ala Asp Glu Met Glu Arg Tyr Val Arg Glu
485 490 495

Asn Ser Asn Arg Asp Glu Glu Val Asn Pro Asn Lys Trp Trp Glu Asn
500 505 510

Phe Ser Glu Glu Val Lys Lys Tyr Tyr Phe Val Phe Ile Ser Gly Ser
515 520 525

Phe Lys Gly Lys Phe Glu Glu Gln Leu Arg Arg Leu Ser Met Thr Thr
530 535 540

Gly Val Asn Gly Ser Ala Val Asn Val Val Asn Leu Leu Leu Gly Ala
545 550 555 560

Glu Lys Ile Arg Ser Gly Glu Met Thr Ile Glu Glu Leu Glu Arg Ala
565 570 575

Met Phe Asn Asn Ser Glu Phe Ile Leu Lys Tyr
580 585

<210> 6
<211> 1764
<212> DNA
<213> Clostridium sp. 7_2_43FAA

<400> 6
atgattaaca taattgacgt aaataataaa actattagaa cttttggatg gggtcagaat 60
ccaagtaatt ttgaaagctt aaaaaaagtt gtagcaatat ttgataatac atcaaagaca 120
tataatgaat taaaagataa gaaaataaaa aagttagtag acgaaagaga tgggcaaaaa 180
gaactattaa atgcttttaa tgctaatacct ttaaagataa agtattgtaa tttagtaggg 240
acatctttta ctccacgaag ttctgcaaga tgtaatggaa tagtacaagc cacagtaaaa 300
ggacaaagaa aagagttcat agatgattgg tcatctgata actttgtaag atgggcacat 360
gctttaggct ttattaaata taattatgat acagatacat ttgagataac cgatgtagga 420
agaaagtatg tacagagtga agatgatagc aatgaggaaa gtacaatttt agaagaagca 480
atgttatcat atccaccagt agcaagggtt ttgacattgc tttccaatgg agaacattta 540

acaaaatatg aaataggtaa gaaattagga tttgtagggg aagctggttt tactagtttg	600
ccattgaatg tattaattat gacattagct actacagatg agccgaagga aaaaaataaa	660
attaaaacag actgggatgg gtcttctgat aaatatgcaa gaatgatttc tggttggtta	720
gtaaaattag gattattggg acaaagacct aaattgggta ctgtagattt tggtagtgaa	780
ttatatagcg aaacaatagg acatgcttat atgattacgg ataggggatt aaaagctgtt	840
agaagattat taggaataaa taaagttgcg agggtttcaa aaaatgtttt ttgggaaatg	900
cttgcaacaa aaggaataga taaaaattat ataagaactc gaagagcata tattttaaaa	960
atattaattg aatctaataa ggtattaact ttagaggata taaaaggaaa gttgaaatta	1020
gcgagtatta atgaatctat taatactatt aaagacgata ttaatggatt aattaatata	1080
ggtataaata ttaagagtga aacaactggg tataaaatat atgattcaat taatgatttt	1140
attataccta aaacaggaga tacagaggga ataaagagta atattagctt attaaaagat	1200
gaattaagag ggcaaataag tcatatttca catgagtatt tatcattaat agatttagca	1260
tttgatagta agcaaaatag gttatttgaa atgaaagttt tagagttgtt agttaatgag	1320
tatggattta aaggaaggca tctaggtgga agtagaaaac ctgatgggat agtttattca	1380
acaactttag aagataattt tggaataata gtagatacta aagcttattc agaagggtat	1440
agcttaccta taagtcaagc tgatgaaatg gagagatatg ttagagaaaa ctctaataka	1500
gatgaggaag taaaccctaa taagtgggtg gaaaactttt cagaagaagt caaaaagtat	1560
tattttgtat tcatatcagg ttcctttaag ggcaaatttg aagaacaatt aagaagattg	1620
agcatgacta ctgggggttaa cggttcagct gttaatgtag taaatttatt actaggagct	1680
gaaaaaataa ggtctggaga aatgactatt gaagaattag agagagctat gtttaataac	1740
tcggaattta tattgaagta ttaa	1764

<210> 7
 <211> 589
 <212> PRT
 <213> Clostridiales bacterium KA00134

<400> 7

Met	Ala	Glu	Arg	Thr	Leu	Gly	Trp	Ile	Gln	Asn	Pro	Ser	Ser	Phe	Glu
1				5				10						15	

Asn Leu Lys Asn Val Val Ser Val Phe Asp Lys Asn Thr Asp Ile Tyr
20 25 30

Lys Glu Ile Leu Asn Thr Lys Leu Pro Lys Leu Val Lys Asp Leu Asp
35 40 45

Leu Gln Asn Lys Leu Ile Ser Glu Met Lys Lys Asp Pro Leu Glu Met
50 55 60

Asp Tyr Val Leu Leu Lys Gly His Gly Ile Lys Ser Gly Gln Lys Arg
65 70 75 80

Ser Asp Ala Ala Cys Ser Gly Ile Val Gln Ala Ala Ile Thr Thr Gln
85 90 95

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

Trp Gly Ile Ser Ile Gly Leu Leu Asp Tyr Asp Thr Glu Asn Asp Thr
115 120 125

Val Ser Ile Thr Lys Leu Gly Glu Lys Phe Val Lys Ser Asn Ser Glu
130 135 140

Asp Ser Asp Lys Glu Ile Leu Ile Ser Ala Phe Leu Ser Tyr Pro Pro
145 150 155 160

Ala Val Arg Ile Leu Thr Leu Leu Glu Ser Gly Asp His Leu Thr Lys
165 170 175

Phe Glu Leu Gly Lys Gln Leu Gly Gly Leu Gly Glu Ala Gly Phe Thr
180 185 190

Ser Ile Pro Gln Asp Leu Tyr Ile Gln Ala Ile Glu Leu Ala Ser Glu
195 200 205

Thr Asp Lys Ala Ser Ile Arg Ser Asn Thr Glu Gly Ser Ala Asp Lys
210 215 220

Tyr Ala Arg Met Ile Ser Gly Trp Leu Ser Lys Val Gly Leu Val Gln
225 230 235 240

Arg Val Glu Lys Glu Val Ser Thr Lys Ile Gly Asn Val Glu Tyr Met
245 250 255

Val Asn Ile Gly His Ser Phe Arg Ile Thr Leu Asn Gly Ile Lys Glu
260 265 270

Leu Lys Arg Ala Arg Gly Leu Ser Ser Tyr Pro Lys Thr Asp Lys Ile
275 280 285

Val Tyr Trp Gln Met Leu Ala Thr Lys Gly Lys Asp Arg Asp Tyr Ile
290 295 300

Arg Asn Arg Arg Gly Tyr Ile Ile Lys Ala Ile Asn Asn Arg Glu Arg
305 310 315 320

Asn Leu Glu Gly Ile Lys Ala Tyr Leu Met Glu Asn Asn Ile Asp Glu
325 330 335

Ser Ile Thr Thr Ile Glu Asp Glu Leu Lys Val Leu Lys Ala Met Gly
340 345 350

Leu Ser Leu Lys His Ser Arg Asn Gly Tyr Val Ile Asp Asp Asn Ile
355 360 365

Ile Lys Leu Glu Ile Pro Arg Thr Lys Ile Ser Lys Thr Asn Ile Leu
370 375 380

Glu Leu Lys Asp Lys Val Arg Asp Lys Leu Lys Tyr Val Asp His Arg
385 390 395 400

Tyr Leu Ala Leu Ile Asp Leu Ala Tyr Asp Gly Thr Ala Asn Arg Asp
405 410 415

Phe Glu Ile Gln Thr Ile Asp Leu Leu Ile Asn Glu Leu Lys Phe Lys
420 425 430

Gly Val Arg Leu Gly Glu Ser Arg Lys Pro Asp Gly Ile Ile Ser Tyr

435	440	445
Asn Ile Asn Gly Val Ile Ile Asp Asn Lys Ala Tyr Ser Thr Gly Tyr		
450	455	460
Asn Leu Pro Ile Asn Gln Ala Asp Glu Met Ile Arg Tyr Ile Glu Glu		
465	470	475
Asn Gln Thr Arg Asp Glu Lys Ile Asn Ser Asn Lys Trp Trp Glu Ser		
485	490	495
Phe Asp Glu Lys Val Lys Asp Phe Asn Tyr Leu Phe Val Ser Ser Phe		
500	505	510
Phe Lys Gly Asn Phe Lys Asn Asn Leu Lys His Ile Ala Asn Arg Thr		
515	520	525
Gly Val Asn Gly Gly Ala Ile Asn Val Glu Asn Leu Leu Tyr Phe Ala		
530	535	540
Glu Glu Leu Lys Ala Gly Arg Ile Ser Tyr Leu Asp Ser Phe Lys Met		
545	550	555
Tyr Asn Asn Asp Glu Ile Tyr Leu Gly Asp Ile Ser Asp Tyr Ser Tyr		
565	570	575
Val Lys Phe Ala Ala Glu Glu Glu Gly Glu Tyr Leu Thr		
580	585	

<210> 8
 <211> 1770
 <212> DNA
 <213> Clostridiales bacterium KA00134

<400> 8	
atggcagaaa gaacattggg ttggatacaa aatccatcaa gttttgaaaa tttaaaaaat	60
gtagtttctg tttttgataa aaatactgat atatataagg aaatattaaa tactaaactt	120
cctaaattag taaaagattt agattttacaa aataaactca tttcagaaat gaaaaaagat	180
ccacttgaaa tggactatgt tttattaaaa ggatcatggta taaaatcagg tcagaaaaga	240

tccgatgcag cgtgtagtgg tattgttcaa gctgccatta caacacaagg cggtagggct	300
tatacagacg attggactgc tgatggattt ttaagatggg gaatatccat aggactttta	360
gattatgata cagaaaatga tacagtttct ataacaaaac taggagaaaa gtttgtaaaa	420
tctaattctg aagattcaga taaagaaata ctaatttcag cttttttgtc ataccaccca	480
gccgtaagaa ttttaacttt attggaaagt ggagaccatt taacaaaatt tgagcttggt	540
aagcaattag gtggacttgg agaagctggt ttacatcaa ttcctcaaga tttatatatt	600
caagcaatag aacttgcttc tgaaacagat aaagcaagta ttcgatcaaa cacagaggga	660
tcagctgata aatatgccag aatgatttca ggatggttat ctaaggttgg tttagttcaa	720
agagttgaaa aagaagtttc aacaaaaatt ggaaatgttg aatacatggt aaatataggt	780
cattccttta gaattacttt gaatggtata aaagaactta aaagagcaag gggattatct	840
tcatatccaa agactgataa aattgtttat tggcaaatgc tagcaaccaa gggtaaagat	900
agagattata ttagaaacag acgtggatat ataatacaag ctatcaacaa cagagaaaga	960
aatttagaag gcattaaggc ttatttaatg gaaaataata ttgatgaaag tattacaact	1020
atagaagacg aactaaaagt tcttaaagca atgggtcttt cacttaaaca tagtaggaat	1080
ggctatgtaa ttgatgataa cattataaaa ttagaaatac ctagaactaa gatttctaag	1140
acaaatatac tagaattaaa ggataaagta agagataaat taaaatatgt tgaccacaga	1200
tatcttgcgc taattgattt agcttatgac ggaactgcca atagagattt tgagattcaa	1260
acaatagacc ttttaattaa tgaacttaag tttaaagggg ttcgtctagg agaaagcaga	1320
aaaccagatg gaattatatt ttataatatt aatggcgtaa ttatagataa caaggcttat	1380
tctacgggtt ataacttacc aattaatcaa gcagatgaaa tgattagata tatcgaagaa	1440
aatcaaacta gagatgaaaa aataaattca aataaatggt gggaaagctt tgatgaaaaa	1500
gttaaggatt tcaactatth atttgatatc tctttcttta agggaaactt taagaataat	1560
ttgaaacata tagccaatag aactgggtgta aatgggtggag ctattaatgt agaaaattta	1620
ttatatthttg cagaagaatt aaaagctgga agaatatctt atcttgactc atttaaaatg	1680
tataacaatg atgaaatata tttaggagat attagtactc atagttatgt taaatttgct	1740
gcagaagaag aaggcgaata tttaacataa	1770

<210> 9
 <211> 38
 <212> DNA
 <213> Artificial

 <220>
 <223> ND1 substitution forward primer

 <400> 9
 gatgagatca tcttctaagg gcccttcgaa ggtaagcc 38

<210> 10
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> ND1 substitution reverse primer

 <400> 10
 ctctcccttt actaaagctc ttgccgcagc accc 34

<210> 11
 <211> 38
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2 substitution forward primer

 <400> 11
 aaggagattc agttctaagg gcccttcgaa ggtaagcc 38

<210> 12
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2 substitution reverse primer

 <400> 12
 actacttttta acaatagctc ttgccgcagc accc 34

<210> 13
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> ND3 substitution forward primer

 <400> 13
 aacagcgagt tcataataagg gcccttcgaa ggtaagcc 38

<210> 14
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> ND3 substitution reverse primer

 <400> 14
 gttactcttg attccagctc ttgccgcagc accc 34

<210> 15
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> ND4 substitution forward primer

 <400> 15
 gatgaaatct acctgtaagg gcccttcgaa ggtaagcc 38

<210> 16
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> ND4 substitution reverse primer

 <400> 16
 gtttgtcttg gagatagctc ttgccgcagc accc 34

<210> 17
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> forward primer for linker alteration, ZFN-FokI-GS-F

 <400> 17
 agaacacacg gatccctagt caaaagtgaa ctggaggaga agaaatctg 49

<210> 18
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for linker alteration, ZFN-GS-inverse-R

 <400> 18
 ggatccgtgt gttctctgggt gtctcacgag attg 34

 <210> 19
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for linker alteration, ZFN-ND1-GS-F

 <400> 19
 agaacacacg gatccttagt aaaggagag atggagaaga aaaagagc 48

 <210> 20
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for linker alteration, ZFN-GS-inverse-R

 <400> 20
 ggatccgtgt gttctctgggt gtctcacgag attg 34

 <210> 21
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for linker alteration, ZFN-ND2-GS-F

 <400> 21
 agaacacacg gatccattgt taaaagtagt attgagatgt ccaaggc 47

 <210> 22
 <211> 34
 <212> DNA

<213> Artificial

<220>

<223> reverse primer for linker alteration, ZFN-GS-inverse-R

<400> 22
ggatccgtgt gttctctggt gtctcacgag attg 34

<210> 23
<211> 51
<212> DNA
<213> Artificial

<220>

<223> forward primer for linker alteration, ZFN-FokI-RPGEKP-F

<400> 23
gacccgggga gaagccccta gtcaaaagtg aactggagga gaagaaatct g 51

<210> 24
<211> 44
<212> DNA
<213> Artificial

<220>

<223> reverse primer for linker alteration, ZFN-RPGEKP-R

<400> 24
gcttctcccc gggctctgtgt gttctctggt gtctcacgag attg 44

<210> 25
<211> 50
<212> DNA
<213> Artificial

<220>

<223> forward primer for linker alteration, ZFN-ND1-RPGEKP-F

<400> 25
gacccgggga gaagccctta gtaaaggag agatggagaa gaaaaagagc 50

<210> 26
<211> 44
<212> DNA
<213> Artificial

<220>

<223> reverse primer for linker alteration, ZFN-RPGEKP-R

<400> 26
 gcttctcccc gggctctgtgt gttctctggt gtctcacgag attg 44

<210> 27
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> forward primer for linker alteration, ZFN-ND2-RPGEKP-F

<400> 27
 gacccgggga gaagccatt gttaaaagta gtattgagat gtccaaggc 49

<210> 28
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <223> reverse primer for linker alteration, ZFN-RPGEKP-R

<400> 28
 gcttctcccc gggctctgtgt gttctctggt gtctcacgag attg 44

<210> 29
 <211> 55
 <212> DNA
 <213> Artificial

<220>
 <223> forward primer for linker alteration, ZFN-FokI-TGPGAAARA-F

<400> 29
 cccggggctg cggcaagagc tctagtcaaa agtgaactgg aggagaagaa atctg 55

<210> 30
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> reverse primer for linker alteration, ZFN-FokI-TGPGAAARA-R

<400> 30
 tgccgcagcc cgggacccg tgtgtgttct ctggtgtctc acgagattg 49

<210> 31

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

 <220>
 <223> forward primer for linker alteration, ZFN-ND1-TGPGAAARA-F

 <400> 31
 cccggggctg cggcaagagc tttagtaaag ggagagatgg agaagaaaaa gagc 54

 <210> 32
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for linker alteration, ZFN-FokI-TGPGAAARA-R

 <400> 32
 tgccgcagcc ccgggacccg tgtgtgttct ctggtgtctc acgagattg 49

 <210> 33
 <211> 53
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for linker alteration, ZFN-ND2-TGPGAAARA-F

 <400> 33
 cccggggctg cggcaagagc tattgttaaa agtagtattg agatgtccaa ggc 53

 <210> 34
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for linker alteration, ZFN-FokI-TGPGAAARA-R

 <400> 34
 tgccgcagcc ccgggacccg tgtgtgttct ctggtgtctc acgagattg 49

 <210> 35
 <211> 59
 <212> DNA
 <213> Artificial

 <220>

<223> forward primer for Sharkey mutation introduction in FokI-ND

<400> 35
aaggtaatgg aattttttat gaaagtttat ggatatagag gtgaacattt gggtggatc 59

<210> 36
<211> 57
<212> DNA
<213> Artificial

<220>
<223> reverse primer for Sharkey mutation introduction in FokI-ND

<400> 36
aaattccatt accttcattt caagaattct atcctgagta ggatttctgg caatttc 57

<210> 37
<211> 59
<212> DNA
<213> Artificial

<220>
<223> forward primer for Sharkey mutation introduction in ND1

<400> 37
ttaaggtagt ggaatttctg aaagaagtgt acgattacaa tggtagcat ctgggcggc 59

<210> 38
<211> 56
<212> DNA
<213> Artificial

<220>
<223> reverse primer for Sharkey mutation introduction in ND1

<400> 38
attccactac cttaaactcg aagagtctgt tctgcttggg gtcctgagca atttcg 56

<210> 39
<211> 30
<212> DNA
<213> Artificial

<220>
<223> forward primer for Sharkey mutation introduction in ND2

<400> 39
tccggggagc atctgggggg tagccggaag 30

<210> 40
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for Sharkey mutation introduction in ND2

 <400> 40
 cagatgctcc ccggagaagc catactcggt gatg 34

 <210> 41
 <211> 19
 <212> DNA
 <213> Artificial

 <220>
 <223> ZFA substitution forward primer

 <400> 41
 acgggtgctg cggcaagag 19

 <210> 42
 <211> 43
 <212> DNA
 <213> Artificial

 <220>
 <223> ZFA substitution reverse primer

 <400> 42
 aggtctctcg tggggtctag atttatcgtc gtcacacctg tag 43

 <210> 43
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for FokI-DDD mutation introduction

 <400> 43
 gaagaaaatc aaacacgaga caaacatatc aaccctaagc aatgggtggaa agtc 54

 <210> 44
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <223> reverse primer for FokI-DDD mutation introduction

 <400> 44
 tgtttgattt tcttcgacat agtcttgcac ttcacatgct tggccaattg 50

 <210> 45
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for ND1-DDD mutation introduction

 <400> 45
 cgacgaaaat aacaataggg acgcaatcat caaccctaag gagtggtgg 49

 <210> 46
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for ND1-DDD mutation introduction

 <400> 46
 ttgttatattt cgtcgacata gtcttgcac tcacggcct gagaaattg 49

 <210> 47
 <211> 49
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for ND2-DDD mutation introduction

 <400> 47
 tcaggagaga cattgacaga gacgagcacg tcaattctaa ccgctggtg 49

 <210> 48
 <211> 44
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for ND2-DDD mutation introduction

 <400> 48

caatgttctc cctgacgtag tcttccattt catcggcctg gctg 44

<210> 49
<211> 43
<212> DNA
<213> Artificial

<220>
<223> forward primer for FokI-RRR vector mutation introduction

<400> 49
ttaaattcgga tcactaattg taatggagct gttcttagtg tag 43

<210> 50
<211> 34
<212> DNA
<213> Artificial

<220>
<223> reverse primer for FokI-RRR vector mutation introduction

<400> 50
atttcccggg cttggccaat tggcagatta taac 34

<210> 51
<211> 38
<212> DNA
<213> Artificial

<220>
<223> forward primer for FokI-RRR insert mutation introduction

<400> 51
ccaagcccgg gaaatgcaac gatatgtcga agaaaatc 38

<210> 52
<211> 42
<212> DNA
<213> Artificial

<220>
<223> reverse primer for FokI-RRR insert mutation introduction

<400> 52
agtgatccga tttaatcgtg taagctgagc tttgtagttt cc 42

<210> 53
<211> 28

<212> DNA
 <213> Artificial

 <220>
 <223> forward primer for ND1-RRR vector mutation introduction

 <400> 53
 gtgtccagac tgaccaagcg caagggcg 28

 <210> 54
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for ND1-RRR vector mutation introduction

 <400> 54
 catctcccgg gcctgagaaa ttgggaggct gtag 34

 <210> 55
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for ND1-RRR insert mutation introduction

 <400> 55
 caggcccggg agatgcaaag atatgttgac gaaaataaca atagg 45

 <210> 56
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for ND1-RRR insert mutation introduction

 <400> 56
 ggtcagtcctg gacacccttg ccagctgttt cttg 34

 <210> 57
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for ND2-RRR vector mutation introduction

<400> 57
 atctcaaggg ataccggggt gcagggcg 28

<210> 58
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> reverse primer for ND2-RRR vector mutation introduction

<400> 58
 catttcccgg gcctggctga tggggagatt g 31

<210> 59
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <223> forward primer for ND2-RRR insert mutation introduction

<400> 59
 caggcccggg aaatggaaag gtacgtcagg gagaacattg 40

<210> 60
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <223> reverse primer for ND2-RRR insert mutation introduction

<400> 60
 ggtatccctt gagattcttt ccaactgttt ctcaaagttt cc 42

<210> 61
 <211> 17
 <212> DNA
 <213> Artificial

<220>
 <223> M13-F primer

<400> 61
 gtaaaacgac ggccagt 17

<210>	62	
<211>	24	
<212>	DNA	
<213>	Cricetulus griseus	
<400>	62	
	accatcttcc actctgaaga tgga	24
<210>	63	
<211>	24	
<212>	DNA	
<213>	Cricetulus griseus	
<400>	63	
	accatcttca agagagaaga tggc	24
<210>	64	
<211>	24	
<212>	DNA	
<213>	Cricetulus griseus	
<400>	64	
	accatcttcc ttgatgaaga tgcc	24
<210>	65	
<211>	24	
<212>	DNA	
<213>	Cricetulus griseus	
<400>	65	
	gtcaccttca agtctgaaga tggt	24
<210>	66	
<211>	24	
<212>	DNA	
<213>	Cricetulus griseus	
<400>	66	
	ttcaccttct taagtgaaga tggt	24
<210>	67	
<211>	195	
<212>	PRT	
<213>	Artificial	
<220>		
<223>	FokI-DDD amino acid sequence	

<400> 67

Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys
1 5 10 15

Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg
20 25 30

Asn Ser Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe
35 40 45

Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val
65 70 75 80

Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly
85 90 95

Gln Ala Asp Glu Met Gln Asp Tyr Val Glu Glu Asn Gln Thr Arg Asp
100 105 110

Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val
115 120 125

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr
130 135 140

Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala
145 150 155 160

Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala
165 170 175

Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu
180 185 190

Ile Asn Phe
195

<210> 68
<211> 195
<212> PRT
<213> Artificial

<220>
<223> FokI-RRR amino acid sequence

<400> 68

Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys
1 5 10 15

Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg
20 25 30

Asn Ser Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe
35 40 45

Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val
65 70 75 80

Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly
85 90 95

Gln Ala Arg Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn
100 105 110

Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val
115 120 125

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr
130 135 140

Lys Ala Gln Leu Thr Arg Leu Asn Arg Ile Thr Asn Cys Asn Gly Ala
145 150 155 160

Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala
165 170 175

Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu
180 185 190

Ile Asn Phe
195

<210> 69
<211> 195
<212> PRT
<213> Artificial

<220>
<223> ND1-DDD amino acid sequence

<400> 69

Leu Val Lys Gly Glu Met Glu Lys Lys Lys Ser Asp Leu Arg His Lys
1 5 10 15

Leu Lys His Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Gln
20 25 30

Asp Ser Lys Gln Asn Arg Leu Phe Glu Phe Lys Val Val Glu Phe Leu
35 40 45

Lys Glu Val Tyr Asp Tyr Asn Gly Lys His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Leu Tyr Thr Asn Gly Leu Lys Thr Asp Tyr Gly Ile
65 70 75 80

Ile Leu Asp Thr Lys Ala Tyr Lys Asp Gly Tyr Ser Leu Pro Ile Ser
85 90 95

Gln Ala Asp Glu Met Gln Asp Tyr Val Asp Glu Asn Asn Asn Arg Asp
100 105 110

Ala Ile Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Asn Ser Ile
115 120 125

Leu Asp Phe Lys Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asp Tyr

130

135

140

Lys Lys Gln Leu Ala Arg Val Ser Asn Leu Thr Lys Arg Lys Gly Ala
 145 150 155 160

Val Leu Ser Val Glu Gln Leu Leu Leu Gly Gly Glu Lys Ile Lys Asp
 165 170 175

Gly Ser Leu Thr Leu Glu Asp Val Gly Asp Lys Phe Asn Asn Asp Glu
 180 185 190

Ile Ile Phe
 195

<210> 70
 <211> 195
 <212> PRT
 <213> Artificial

<220>
 <223> ND1-RRR amino acid sequence

<400> 70

Leu Val Lys Gly Glu Met Glu Lys Lys Lys Ser Asp Leu Arg His Lys
 1 5 10 15

Leu Lys His Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Gln
 20 25 30

Asp Ser Lys Gln Asn Arg Leu Phe Glu Phe Lys Val Val Glu Phe Leu
 35 40 45

Lys Glu Val Tyr Asp Tyr Asn Gly Lys His Leu Gly Gly Ser Arg Lys
 50 55 60

Pro Asp Gly Ala Leu Tyr Thr Asn Gly Leu Lys Thr Asp Tyr Gly Ile
 65 70 75 80

Ile Leu Asp Thr Lys Ala Tyr Lys Asp Gly Tyr Ser Leu Pro Ile Ser
 85 90 95

Gln Ala Arg Glu Met Gln Arg Tyr Val Asp Glu Asn Asn Asn Arg Asn
100 105 110

Ala Ile Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Asn Ser Ile
115 120 125

Leu Asp Phe Lys Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asp Tyr
130 135 140

Lys Lys Gln Leu Ala Arg Val Ser Arg Leu Thr Lys Arg Lys Gly Ala
145 150 155 160

Val Leu Ser Val Glu Gln Leu Leu Leu Gly Gly Glu Lys Ile Lys Asp
165 170 175

Gly Ser Leu Thr Leu Glu Asp Val Gly Asp Lys Phe Asn Asn Asp Glu
180 185 190

Ile Ile Phe
195

<210> 71
<211> 191
<212> PRT
<213> Artificial

<220>
<223> ND2-DDD amino acid sequence

<400> 71

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

Leu Gln Met Leu Pro His Asp Tyr Ile Glu Leu Ile Glu Ile Ser Gln
20 25 30

Asp Pro Tyr Gln Asn Arg Ile Phe Glu Met Lys Val Met Asp Leu Phe
35 40 45

Ile Asn Glu Tyr Gly Phe Ser Gly Ser His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Met Tyr Ala His Gly Phe Gly Val Ile Val Asp Thr
65 70 75 80

Lys Ala Tyr Lys Asp Gly Tyr Asn Leu Pro Ile Ser Gln Ala Asp Glu
85 90 95

Met Glu Asp Tyr Val Arg Glu Asn Ile Asp Arg Asp Glu His Val Asn
100 105 110

Ser Asn Arg Trp Trp Asn Ile Phe Pro Glu Asp Thr Asn Glu Tyr Lys
115 120 125

Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asn Phe Glu Lys Gln Leu
130 135 140

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

Glu His Leu Leu Leu Gly Ala Glu Tyr Ile Lys Arg Gly Ile Leu Thr
165 170 175

Leu Tyr Asp Phe Lys Asn Ser Phe Leu Asn Lys Glu Ile Gln Phe
180 185 190

<210> 72
<211> 191
<212> PRT
<213> Artificial

<220>
<223> ND2-RRR amino acid sequence

<400> 72

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

Leu Gln Met Leu Pro His Asp Tyr Ile Glu Leu Ile Glu Ile Ser Gln
20 25 30

Asp Pro Tyr Gln Asn Arg Ile Phe Glu Met Lys Val Met Asp Leu Phe
35 40 45

Ile Asn Glu Tyr Gly Phe Ser Gly Ser His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Met Tyr Ala His Gly Phe Gly Val Ile Val Asp Thr
65 70 75 80

Lys Ala Tyr Lys Asp Gly Tyr Asn Leu Pro Ile Ser Gln Ala Arg Glu
85 90 95

Met Glu Arg Tyr Val Arg Glu Asn Ile Asp Arg Asn Glu His Val Asn
100 105 110

Ser Asn Arg Trp Trp Asn Ile Phe Pro Glu Asp Thr Asn Glu Tyr Lys
115 120 125

Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asn Phe Glu Lys Gln Leu
130 135 140

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

Glu His Leu Leu Leu Gly Ala Glu Tyr Ile Lys Arg Gly Ile Leu Thr
165 170 175

Leu Tyr Asp Phe Lys Asn Ser Phe Leu Asn Lys Glu Ile Gln Phe
180 185 190

<210> 73
<211> 195
<212> PRT
<213> Artificial

<220>
<223> FokI-S418P/K441E amino acid sequence

<400> 73

Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys
1 5 10 15

Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg

20

25

30

Asn Pro Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe
 35 40 45

Met Lys Val Tyr Gly Tyr Arg Gly Glu His Leu Gly Gly Ser Arg Lys
 50 55 60

Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val
 65 70 75 80

Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly
 85 90 95

Gln Ala Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn
 100 105 110

Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val
 115 120 125

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr
 130 135 140

Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala
 145 150 155 160

Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala
 165 170 175

Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu
 180 185 190

Ile Asn Phe
 195

<210> 74

<211> 195

<212> PRT

<213> Artificial

<220>

<223> ND1-S418P/K441E amino acid sequence

<400> 74

Leu Val Lys Gly Glu Met Glu Lys Lys Lys Ser Asp Leu Arg His Lys
1 5 10 15

Leu Lys His Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Gln
20 25 30

Asp Pro Lys Gln Asn Arg Leu Phe Glu Phe Lys Val Val Glu Phe Leu
35 40 45

Lys Glu Val Tyr Asp Tyr Asn Gly Glu His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Leu Tyr Thr Asn Gly Leu Lys Thr Asp Tyr Gly Ile
65 70 75 80

Ile Leu Asp Thr Lys Ala Tyr Lys Asp Gly Tyr Ser Leu Pro Ile Ser
85 90 95

Gln Ala Asp Glu Met Gln Arg Tyr Val Asp Glu Asn Asn Asn Arg Asn
100 105 110

Ala Ile Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Asn Ser Ile
115 120 125

Leu Asp Phe Lys Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asp Tyr
130 135 140

Lys Lys Gln Leu Ala Arg Val Ser Asn Leu Thr Lys Arg Lys Gly Ala
145 150 155 160

Val Leu Ser Val Glu Gln Leu Leu Leu Gly Gly Glu Lys Ile Lys Asp
165 170 175

Gly Ser Leu Thr Leu Glu Asp Val Gly Asp Lys Phe Asn Asn Asp Glu
180 185 190

Ile Ile Phe

195

<210> 75
<211> 191
<212> PRT
<213> Artificial

<220>
<223> ND2-S441E amino acid sequence

<400> 75

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

Leu Gln Met Leu Pro His Asp Tyr Ile Glu Leu Ile Glu Ile Ser Gln
20 25 30

Asp Pro Tyr Gln Asn Arg Ile Phe Glu Met Lys Val Met Asp Leu Phe
35 40 45

Ile Asn Glu Tyr Gly Phe Ser Gly Glu His Leu Gly Gly Ser Arg Lys
50 55 60

Pro Asp Gly Ala Met Tyr Ala His Gly Phe Gly Val Ile Val Asp Thr
65 70 75 80

Lys Ala Tyr Lys Asp Gly Tyr Asn Leu Pro Ile Ser Gln Ala Asp Glu
85 90 95

Met Glu Arg Tyr Val Arg Glu Asn Ile Asp Arg Asn Glu His Val Asn
100 105 110

Ser Asn Arg Trp Trp Asn Ile Phe Pro Glu Asp Thr Asn Glu Tyr Lys
115 120 125

Phe Leu Phe Val Ser Gly Phe Phe Lys Gly Asn Phe Glu Lys Gln Leu
130 135 140

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

Glu His Leu Leu Leu Gly Ala Glu Tyr Ile Lys Arg Gly Ile Leu Thr
165 170 175

Leu Tyr Asp Phe Lys Asn Ser Phe Leu Asn Lys Glu Ile Gln Phe
180 185 190

<210> 76
<211> 34
<212> DNA
<213> Artificial

<220>
<223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 76
cagccacccat cttccactct gaagatggac aggt 34

<210> 77
<211> 35
<212> DNA
<213> Artificial

<220>
<223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 77
cagccacccat cttccactct tgaagatgga caggt 35

<210> 78
<211> 38
<212> DNA
<213> Artificial

<220>
<223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 78
cagccacccat cttccactca ctctgaagat ggacaggt 38

<210> 79
<211> 34
<212> DNA
<213> Artificial

<220>
<223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 79

cagccaccat cttccactct gaagatggac aggt 34

<210> 80
<211> 35
<212> DNA
<213> Artificial

<220>
<223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 80
cagccaccat cttccaactc tgaagatgga caggt 35

<210> 81
<211> 36
<212> DNA
<213> Artificial

<220>
<223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 81
cagccaccat cttccactct ctgaagatgg acaggt 36

<210> 82
<211> 38
<212> DNA
<213> Artificial

<220>
<223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 82
cagccaccat cttccactca ctctgaagat ggacaggt 38

<210> 83
<211> 32
<212> DNA
<213> Artificial

<220>
<223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 83
cagccaccat cttcctctga agatggacag gt 32

<210> 84
<211> 25

<212> DNA
 <213> Artificial

 <220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

 <400> 84
 cagcccactc tgaagatgga caggt 25

 <210> 85
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

 <400> 85
 cagccaccat cttccactct gaagatggac aggt 34

 <210> 86
 <211> 35
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

 <400> 86
 cagccaccat cttccactct tgaagatgga caggt 35

 <210> 87
 <211> 36
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

 <400> 87
 cagccaccat cttccactct ctgaagatgg acaggt 36

 <210> 88
 <211> 32
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 88
 cagccacat cttcctctga agatggacag gt 32

<210> 89
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 89
 cagccacat ctttctgaag atggacaggt 30

<210> 90
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> ND3-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 90
 cagccacat cttccactct gaagatggac aggt 34

<210> 91
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> ND4-cleaved CH0-K1 ZFA36-ZFA36 target 1st site

<400> 91
 cagccacat cttccactct gaagatggac aggt 34

<210> 92
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 92
 accttaccat cttcaagaga gaagatggct taaa 34

<210> 93
 <211> 36
 <212> DNA
 <213> Artificial

 <220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 93
 accttaccat cttcaagaga gagaagatgg cttaaa 36

 <210> 94
 <211> 38
 <212> DNA
 <213> Artificial

 <220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 94
 accttaccat cttcaagaga gagagaagat ggcttaaa 38

 <210> 95
 <211> 39
 <212> DNA
 <213> Artificial

 <220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 95
 accttaccat cttcaagagg agagagaaga tggcttaaa 39

 <210> 96
 <211> 32
 <212> DNA
 <213> Artificial

 <220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 96
 accttaccat cttcaagaga agatggctta aa 32

 <210> 97
 <211> 268
 <212> DNA
 <213> Artificial

<220>
 <223> FokI-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 97
 accttaccat cttcaagagc atgaacacat caccattcat taccaaaaat aaaaaatctt 60
 actatgaaga gctcttggga atgggagtgt tagcctaatag agagaacaga cacttagcat 120
 attctaggcc ttaggatcag tcaccaccac caaaaaacaa acaaacaaaa aacttaacac 180
 atgttcatcc ccagttagtt taagtcaggg accaagtaag attcccattt tgcagtagaa 240
 tggatatcact taggtaagat ggcttaaa 268

<210> 98
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 98
 accttaccat cttcaagaga gaagatggct taaa 34

<210> 99
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 99
 accttaccat cttcaagaga gagaagatgg cttaaa 36

<210> 100
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 100
 accttaccat cttcaagaga gagagaagat ggcttaaa 38

<210> 101
 <211> 32

<212> DNA
 <213> Artificial

 <220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 101
 accttaccat cttcaataga agatggctta aa 32

<210> 102
 <211> 30
 <212> DNA
 <213> Artificial

 <220>
 <223> ND1-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 102
 accttaccat cttcaagagg atggcttaaa 30

<210> 103
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 103
 accttaccat cttcaagaga gaagatggct taaa 34

<210> 104
 <211> 35
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

 <400> 104
 accttaccat cttcaaagag agaagatggc ttaaa 35

<210> 105
 <211> 36
 <212> DNA
 <213> Artificial

 <220>
 <223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 105
accttaccat cttcaagaga gagaagatgg cttaaa 36

<210> 106
<211> 38
<212> DNA
<213> Artificial

<220>
<223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 106
accttaccat cttcaagaga gagagaagat ggcttaaa 38

<210> 107
<211> 105
<212> DNA
<213> Artificial

<220>
<223> ND2-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 107
accttaccat cttcaggtct tcctgggtgta gaatccctag tctttgggtgg tgtcatataa 60
gtcttttgtt gttgaatgca ttcttaagag agaagatggc ttaaa 105

<210> 108
<211> 34
<212> DNA
<213> Artificial

<220>
<223> ND3-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 108
accttaccat cttcaagaga gaagatggct taaa 34

<210> 109
<211> 36
<212> DNA
<213> Artificial

<220>
<223> ND3-cleaved CH0-K1 ZFA36-ZFA36 target 2nd site

<400> 109
accttaccat cttcaagaga gagaagatgg cttaaa 36

<210> 110
 <211> 32
 <212> DNA
 <213> Artificial

 <220>
 <223> ND3-cleaved CHO-K1 ZFA36-ZFA36 target 2nd site

 <400> 110
 accttaccat cttcaagaga agatggctta aa 32

 <210> 111
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <223> ND3-cleaved CHO-K1 ZFA36-ZFA36 target 2nd site

 <400> 111
 accttaccat cttcagttgg cttaaa 26

 <210> 112
 <211> 34
 <212> DNA
 <213> Artificial

 <220>
 <223> ND4-cleaved CHO-K1 ZFA36-ZFA36 target 2nd site

 <400> 112
 cagccaccat cttcaagaga gaagatggct taaa 34

 <210> 113
 <211> 30
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for vector amplification for ptTALE-ND
 substitution, ptTALEN-inverse-F

 <400> 113
 taataaatca gcctcgactg tgccttctag 30

 <210> 114
 <211> 22

<212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for vector amplification for ptTALE-ND
 substitution, NC-inverse-R_2

 <400> 114
 ctgggatctg atcaattccg gc 22

 <210> 115
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <223> forward primer for insert amplification for ptTALE-ND
 substitution, ND1-NC-F_v2

 <400> 115
 ttgatcagat cccagttagt aaaggagag atggagaaga aaaagagc 48

 <210> 116
 <211> 46
 <212> DNA
 <213> Artificial

 <220>
 <223> reverse primer for insert amplification for ptTALE-ND
 substitution, ND1-ptTALEN-R

 <400> 116
 gaggctgatt ttttagaaga tgatctcatc gttgttgaac ttatcc 46

 <210> 117
 <211> 50
 <212> DNA
 <213> Cricetulus griseus

 <400> 117
 tgcccagaag actccgccc atctcccaga aagcctcgac ttgcagatca 50

 <210> 118
 <211> 51
 <212> DNA
 <213> Cricetulus griseus

 <400> 118
 tgaaccaggc tatgacctag atttattttg tattcctaata cactatgtcg a 51

<210> 119
 <211> 318
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ZF(ZFA36A)-ND1 amino acid sequence

<400> 119

Met Gly His His His His His His Met Arg Leu Glu Pro Lys Lys Lys
 1 5 10 15

Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Arg
 20 25 30

Pro Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser
 35 40 45

Thr Ser Gly His Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys
 50 55 60

Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Thr Ser Gly Asn
 65 70 75 80

Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys
 85 90 95

Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu Val Arg His
 100 105 110

Gln Arg Thr His Thr Gly Ala Ala Ala Arg Ala Leu Val Lys Gly Glu
 115 120 125

Met Glu Lys Lys Lys Ser Asp Leu Arg His Lys Leu Lys His Val Pro
 130 135 140

His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Gln Asp Ser Lys Gln Asn
 145 150 155 160

Arg Leu Phe Glu Phe Lys Val Val Glu Phe Leu Lys Glu Val Tyr Asp

165

170

175

Tyr Asn Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Leu
 180 185 190

Tyr Thr Asn Gly Leu Lys Thr Asp Tyr Gly Ile Ile Leu Asp Thr Lys
 195 200 205

Ala Tyr Lys Asp Gly Tyr Ser Leu Pro Ile Ser Gln Ala Asp Glu Met
 210 215 220

Gln Arg Tyr Val Asp Glu Asn Asn Asn Arg Asn Ala Ile Ile Asn Pro
 225 230 235 240

Asn Glu Trp Trp Lys Val Tyr Pro Asn Ser Ile Leu Asp Phe Lys Phe
 245 250 255

Leu Phe Val Ser Gly Phe Phe Lys Gly Asp Tyr Lys Lys Gln Leu Ala
 260 265 270

Arg Val Ser Asn Leu Thr Lys Arg Lys Gly Ala Val Leu Ser Val Glu
 275 280 285

Gln Leu Leu Leu Gly Gly Glu Lys Ile Lys Asp Gly Ser Leu Thr Leu
 290 295 300

Glu Asp Val Gly Asp Lys Phe Asn Asn Asp Glu Ile Ile Phe
 305 310 315

<210> 120

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> ZF(ZFL1)-ND1 amino acid sequence

<400> 120

Met Gly His His His His His His Met Arg Leu Glu Pro Lys Lys Lys
 1 5 10 15

Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Arg
20 25 30

Pro His Glu Arg Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
35 40 45

Asp Arg Ser Asn Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
50 55 60

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Leu Arg His His
65 70 75 80

Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
85 90 95

Arg Ile Cys Met Arg Asn Phe Ser Gln Lys Ala Asn Leu Thr Arg His
100 105 110

Leu Arg Thr His Thr Gly Ala Ala Ala Arg Ala Leu Val Lys Gly Glu
115 120 125

Met Glu Lys Lys Lys Ser Asp Leu Arg His Lys Leu Lys His Val Pro
130 135 140

His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Gln Asp Ser Lys Gln Asn
145 150 155 160

Arg Leu Phe Glu Phe Lys Val Val Glu Phe Leu Lys Glu Val Tyr Asp
165 170 175

Tyr Asn Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Leu
180 185 190

Tyr Thr Asn Gly Leu Lys Thr Asp Tyr Gly Ile Ile Leu Asp Thr Lys
195 200 205

Ala Tyr Lys Asp Gly Tyr Ser Leu Pro Ile Ser Gln Ala Asp Glu Met
210 215 220

Gln Arg Tyr Val Asp Glu Asn Asn Asn Arg Asn Ala Ile Ile Asn Pro

Leu Val Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys
85 90 95

Pro Glu Cys Gly Lys Ser Phe Ser Gln Ser Ser Asn Leu Val Arg His
100 105 110

Gln Arg Thr His Thr Gly Ala Ala Ala Arg Ala Leu Val Lys Ser Glu
115 120 125

Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro
130 135 140

His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp
145 150 155 160

Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly
165 170 175

Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile
180 185 190

Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys
195 200 205

Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met
210 215 220

Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro
225 230 235 240

Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe
245 250 255

Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr
260 265 270

Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu
275 280 285

Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu

290

295

300

Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe
 305 310 315

<210> 122

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> ZF(ZFL1)-FokI amino acid sequence

<400> 122

Met Gly His His His His His His Met Arg Leu Glu Pro Lys Lys Lys
 1 5 10 15

Arg Lys Val Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ser Arg
 20 25 30

Pro His Glu Arg Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
 35 40 45

Asp Arg Ser Asn Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
 50 55 60

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Leu Arg His His
 65 70 75 80

Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
 85 90 95

Arg Ile Cys Met Arg Asn Phe Ser Gln Lys Ala Asn Leu Thr Arg His
 100 105 110

Leu Arg Thr His Thr Gly Ala Ala Ala Arg Ala Leu Val Lys Ser Glu
 115 120 125

Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val Pro
 130 135 140

His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln Asp
 145 150 155 160

Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr Gly
 165 170 175

Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala Ile
 180 185 190

Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr Lys
 195 200 205

Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu Met
 210 215 220

Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn Pro
 225 230 235 240

Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe Lys Phe
 245 250 255

Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala Gln Leu Thr
 260 265 270

Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val Leu Ser Val Glu
 275 280 285

Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala Gly Thr Leu Thr Leu
 290 295 300

Glu Glu Val Arg Arg Lys Phe Asn Asn Gly Glu Ile Asn Phe
 305 310 315