

SEQUENCE LISTING

<110> XIAMEN UNIVERSITY
XIAMEN INNOVAX BIOTECH CO., LTD.

<120> COMPLEX FOR INTRACELLULAR DELIVERY OF MOLECULES

<130> IEC190104PCT

<150> CN201910624609.9
<151> 2019-07-11

<160> 54

<170> PatentIn version 3.5

<210> 1
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<212> PRT
<213> Artificial sequence

<220>
<223> Furin recognition sequence-1

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<222> (2)..(2)
<223> X=any amino acid

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X=K or R

<400> 1

Arg Xaa Xaa Arg
1

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<223> X=any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> X=K or R

<400> 2

Arg Arg Xaa Xaa Arg

1 5

<210> 3

<211> 5

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<223> Furin recognition sequence-3

<400> 3

Arg Arg His Lys Arg

1 5

<210> 4

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Furin recognition sequence-4 (Ne)

<400> 4

Gln Ser Val Ala Ser Ser Arg Arg His Lys Arg Phe Ala Gly Val

1 5 10 15

<210> 5

<211> 45

<212> DNA

<213> Artificial sequence

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<223> Nucleic acid sequence encoding Ne

<400> 5

cagagcgttg caagcagccg tcgtcataaa cgttttgcag gtggtt

45

<210> 6
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<220>
<223> CTSL recognition sequence N

<400> 6

Asn	Asn	Thr	His	Asp	Leu	Val	Gly	Asp	Val	Arg	Leu	Ala	Gly	Val
1				5				10					15	

<210> 7
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding N

<400> 7
aacaacactc atgaccttgt cggatgatgtg agattagccg gagtt

45

<210> 8
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> INF7

<400> 8

Gly	Leu	Phe	Glu	Ala	Ile	Glu	Gly	Phe	Ile	Glu	Asn	Gly	Trp	Glu	Gly
1				5				10					15		

Met	Ile	Asp	Gly	Trp	Tyr	Gly
			20			

<210> 9
<211> 69
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding INF7

<400> 9

ggcctgttcg aagcaataga aggtttcata gaaaatgggtt gggaggggaat gatagacggt 60
 tggtacggt 69

<210> 10
 <211> 13
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Tat(48-60)

<400> 10

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
 1 5 10

<210> 11
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding Tat (48-60)

<400> 11
 ggccgtaaga agcggagaca gcgacgaaga ccgccgcag 39

<210> 12
 <211> 56
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fusion protein TIN

<400> 12

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Leu Phe
 1 5 10 15

Glu Ala Ile Glu Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Ile Asp
 20 25 30

Gly Trp Tyr Gly Gly Gly Gly Gly Ser Asn Asn Thr His Asp Leu Val
 35 40 45

Gly Asp Val Arg Leu Ala Gly Val
50 55

<210> 13
<211> 56
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<213> Artificial sequence

<220>
<223> Fusion protein TINE

<400> 13

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Leu Phe
1 5 10 15

Glu Ala Ile Glu Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Ile Asp
20 25 30

Gly Trp Tyr Gly Gly Gly Gly Gly Ser Gln Ser Val Ala Ser Ser Arg
35 40 45

Arg His Lys Arg Phe Ala Gly Val
50 55

<210> 14
<211> 76
<212> PRT
<213> Artificial sequence

<220>
<223> Fusion protein TINNe

<400> 14

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Leu Phe
1 5 10 15

Glu Ala Ile Glu Gly Phe Ile Glu Asn Gly Trp Glu Gly Met Ile Asp
20 25 30

Gly Trp Tyr Gly Gly Gly Gly Gly Ser Asn Asn Thr His Asp Leu Val
35 40 45

Gly Asp Val Arg Leu Ala Gly Val Gly Gly Gly Gly Ser Gln Ser Val

50

55

60

Ala Ser Ser Arg Arg His Lys Arg Phe Ala Gly Val
65 70 75

<210> 15
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> NLS

<400> 15

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 16
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> CTSL recognition sequence Na

<400> 16

Ala Arg Ala Tyr Gly Phe Arg Gly Pro Gly Pro Gln Leu Arg Arg Gly
1 5 10 15

Trp Arg Pro Ser Ser
20

<210> 17
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> CTSL recognition sequence Nb

<400> 17

Glu Glu Asp Asn Arg Asp Ser Ser Met Lys Leu Ser Phe Arg Ala Arg
1 5 10 15

Ala Tyr Gly Phe Arg Gly Pro Gly
20

<210> 18
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Furin recognition sequence Nc

<400> 18

Gly Thr Ser Gly Gly Arg Gln Arg Arg Glu Leu Asp Pro Met Asp Ile
1 5 10 15

Arg

<210> 19
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Furin recognition sequence Nd

<400> 19

Glu Asp Thr Asp Phe Ala Arg Lys Asn Lys Ile Leu Tyr Thr Gln Gln
1 5 10 15

Val His Gln Thr
20

<210> 20
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> CTSD identification sequence Nf

<400> 20

Lys Pro Ile Leu Phe Phe Arg Leu Lys
1 5

<210> 21
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Mutant N

<400> 21

Asn Asn Thr His Asp Leu Val Gly Asp Val Gly Leu Ala Gly Val
1 5 10 15

<210> 22
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Mutant Ne

<400> 22

Gln Ser Val Ala Ser Ser Arg Arg His Lys Gly Phe Ala Gly Val
1 5 10 15

<210> 23
<211> 228
<212> PRT
<213> Artificial sequence

<220>
<223> GFP(beta)1-10-NLS

<400> 23

Met Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Arg Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Ile Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Ser Phe Lys Asp Asp Gly Lys Tyr Lys Thr Arg Ala Val
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Thr Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

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

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Thr Val Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys His His His His His His Pro Lys Lys
210 215 220

Lys Arg Lys Val
225

<210> 24
<211> 687
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding GFP(beta)1-10-NLS

<400> 24
atgggcagca aaggagaaga acttttcact ggagttgtcc caattcttgt tgaattagat 60
ggtgatgtta atgggcacaa attttctgtc agaggagagg gtgaagggtga tgctacaatc 120
ggaaaactca cccttaaatt tatttgcact actggaaaac tacctgttcc atggccaaca 180
cttgtcacta ctctgaccta tgggtgttcaa tgcttttccc gttatccgga tcacatgaaa 240
aggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaacg cactatatct 300
ttcaaagatg acgggaaata caagacgcgt gctgtagtca agtttgaagg tgataccctt 360
gttaatcgta tcgagttaaa ggggtactgat tttaaagaag atggaaacat tctcggacac 420
aaactcgagt acaactttaa ctacacacat gtatacatca cggcagacaa acaaaagaat 480
ggaatcaaag ctaacttcac agttcgccac aacgttgaag atggttccgt tcaactagca 540
gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaaccat 600
tacctgtcga cacaaactgt cttttcgaaa gatcccaacg aaaagcacca ccaccaccac 660
cacccaaga agaagaggaa ggtgttaa 687

<210> 25
<211> 411
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding Histone-H3

<400> 25
atggctcgca ctaagcaaac tgctcggaag tctactgggtg gcaaggcgcc acgcaaacag 60
ttggccacta aggcagcccg caaaagcgct ccggccaccg gcggcggtgaa aaagccccac 120
cgctaccggc cgggcaccgt ggctctgcgc gagatccgcc gttatcagaa gtccactgaa 180
ctgcttattc gtaaactacc tttccagcgc ctggtgcgcg agattgcgca ggactttaaa 240
acagacctgc gtttccagag ctccgctgtg atggctctgc aggaggcgtg cgaggcctac 300
ttggtagggc tatttgagga cactaacctg tgcgccatcc acgccaagcg cgtcactatc 360
atgcccaagg acatccagct cgcccgccgc atccgcggag agagggcgtg a 411

<210> 26
<211> 47

<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding GFP(beta)11

<400> 26
cgggaccaca tgggtgctgca cgagtacgtg aacgccgccg gcatcac

47

<210> 27
<211> 98
<212> PRT
<213> Artificial sequence

<220>
<223> ZFP9-NLS

<400> 27

Val Ser Arg Pro Gly Glu Arg Pro Phe Gln Cys Arg Ile Cys Met Arg
1 5 10 15

Asn Phe Ser Asp Lys Thr Lys Leu Arg Val His Thr Arg Thr His Thr
20 25 30

Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Val
35 40 45

Arg His Asn Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro
50 55 60

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

Gln Arg His Leu Lys Thr His Leu Arg Gly Ser Pro Lys Lys Lys Arg
85 90 95

Lys Val

<210> 28
<211> 294
<212> DNA
<213> Artificial sequence

<220>

<223> Nucleic acid sequence encoding ZFP9-NLS

<400> 28

gtctctagac ccggggagcg ccccttccag tgtcgcat	60
tttgcgga cttttcggat	
aaaactaaat tgagagttca taccgtact cataccggtg	120
aaaaaccgtt tcagtgtcgg	
atctgtatgc gaaatttctc cgtagacat aatttgacta	180
gacatctacg tacgcacacc	
ggcgagaagc cattccaatg ccgaatatgc atgcgcaact	240
tcagtcaatc tacttctttg	
caaagacacc taaaaacca cctgagagga tcccccaaga	294
agaagcgtaa ggtg	

<210> 29

<211> 714

<212> DNA

<213> Artificial sequence

<220>

<223> Sequence encoding BFP

<400> 29

atggtgtcta agggcgaaga gctgattaag gagaacatgc	60
acatgaagct gtacatggag	
ggcaccgtgg acaaccatca cttcaagtgc acatccgagg	120
gcgaaggcaa gccctacgag	
ggcaccaga ccatgagaat caagggtggc gagggcggcc	180
ctctcccctt cgccttcgac	
atcctggcta ctagcttcct ctacggcagc aagaccttca	240
tcaaccacac ccagggcatc	
cccgaattct tcaagcagtc cttccctgag ggcttcacat	300
gggagagagt caccacatac	
gaagacgggg gcgtgctgac cgctaccag gacaccagcc	360
tccaggacgg ctgcctcatc	
tacaacgtca agatcagagg ggtgaacttc acatccaacg	420
gccctgtgat gcagaagaaa	
acactcggct gggaggcctt caccgagacg ctgtaccccg	480
ctgacggcgg cctggaaggc	
agaaacgaca tggccctgaa gctcgtgggc gggagccatc	540
tgatcgcaaa cgccaagacc	
acatatagat ccaagaaacc cgctaagaac ctcaagatgc	600
ctggcgtcta ctatgtggac	
tacagactgg aaagaatcaa ggaggccaac aacgagacct	660
acgtcgagca gcacgaggtg	
gcagtggcca gatactgcga cctccctagc aaactggggc	714
acaagcttaa ttga	

<210> 30

<211> 11

<212> DNA

<213> Artificial sequence

<220>

<223> ZFP9 binding site sequence

<400> 30

tgtatgatgga g

11

<210> 31

<211> 378

<212> PRT

<213> Artificial sequence

<220>

<223> Ppm1b

<400> 31

Met Gly Ala Phe Leu Asp Lys Pro Lys Thr Glu Lys His Asn Ala His
1 5 10 15

Gly Ala Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp
20 25 30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Val Gly Ile Pro His
35 40 45

Gly Leu Asp Asn Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
50 55 60

Ser Arg Val Ala Asn Tyr Cys Ser Thr His Leu Leu Glu His Ile Thr
65 70 75 80

Thr Asn Glu Asp Phe Arg Ala Ala Asp Lys Ser Gly Ser Ala Leu Glu
85 90 95

Pro Ser Val Glu Ser Val Lys Thr Gly Ile Arg Thr Gly Phe Leu Lys
100 105 110

Ile Asp Glu Tyr Met Arg Asn Phe Ser Asp Leu Arg Asn Gly Met Asp
115 120 125

Arg Ser Gly Ser Thr Ala Val Gly Val Met Val Ser Pro Thr His Met
130 135 140

Tyr Phe Ile Asn Cys Gly Asp Ser Arg Ala Val Leu Cys Arg Asn Gly
 145 150 155 160

Gln Val Cys Phe Ser Thr Gln Asp His Lys Pro Cys Asn Pro Val Glu
 165 170 175

Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val
 180 185 190

Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Tyr Asp Tyr Lys
 195 200 205

Cys Val Asp Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro
 210 215 220

Glu Val Tyr Glu Ile Val Arg Ala Glu Glu Asp Glu Phe Val Val Leu
 225 230 235 240

Ala Cys Asp Gly Ile Trp Asp Val Met Ser Asn Glu Glu Leu Cys Glu
 245 250 255

Phe Val Lys Ser Arg Leu Glu Val Ser Asp Asp Leu Glu Asn Val Cys
 260 265 270

Asn Trp Val Val Asp Thr Cys Leu His Lys Gly Ser Arg Asp Asn Met
 275 280 285

Ser Val Val Leu Val Cys Phe Ser Asn Ala Pro Lys Val Ser Glu Glu
 290 295 300

Ala Val Lys Arg Asp Ser Glu Leu Asp Lys His Leu Glu Ser Arg Val
 305 310 315 320

Glu Glu Ile Met Gln Lys Ser Gly Glu Glu Gly Met Pro Asp Leu Ala
 325 330 335

His Val Met Arg Ile Leu Ser Ala Glu Asn Ile Pro Asn Leu Pro Pro
 340 345 350

Gly Gly Gly Leu Ala Gly Lys Arg His Val Ile Glu Ala Val Tyr Ser
 355 360 365

Arg Leu Asn Pro His Lys Asp Asn Asp Gly
 370 375

<210> 32
 <211> 1134
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding Ppm1b

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 ggtctgcgtt atggcctgag cagtatgcaa ggatggagag tagaaatgga agatgcacac 120
 acagctgttg tgggtattcc tcacggcttg gacaactggc cgttttttgc agtttatgac 180
 ggtcatgctg gatcccgagt ggcaaattac tgttcaacac atctattaga acacatcacc 240
 accaatgaag acttcagggc agctgacaaa tcaggctctg ctctcgagcc ttcagtagaa 300
 agtgtgaaga ctggtatcag gactggcttt ttgaaaattg atgaatatat gcgtaacttc 360
 tcagacctga ggaacgggat ggacaggagc ggctcgactg cagtgggcgt gatggctctc 420
 cctacacaca tgtacttcat caactgtggg gactctcgag ctgttctgtg taggaacgga 480
 caggtctgct tttctacca ggatcacaaa ctttgtaatc cagtggagaa ggagcgcac 540
 caaacgcag gaggcagtgt gatgatccag cgtgtgaacg gctcactagc agtgtctcgg 600
 gctctggggg actatgacta caagtgtgtg gatggcaagg gccctacaga gcagcttggt 660
 tctccagagc ctgaggttta tgagattgtg agagcagaag aggatgagtt tgtcgtcttg 720
 gcctgtgatg ggatctggga tgtgatgagc aatgaggagc tctgtgagtt tgtaagtct 780
 aggcttgagg tgtcggacga cctggagaat gtgtgcaatt gggtagtgga cacttgttta 840
 cataagggaa gtcgagataa catgagtgtt gtattagttt gcttttcaaa tgccccaag 900
 gtctcagagg aagccgtgaa gagagattca gagttggata agcacttgga atcacgggtt 960
 gaagaaatca tgcagaagtc tggggaggaa ggaatgcctg atcttgccca tgtgatgcgc 1020
 attttgtctg cagaaaatat cccgaattta cctcccgggg gaggtctcgc tggcaagcgc 1080

catgttattg aagctgttta tagtagactt aatccacaca aagacaatga tggg

1134

<210> 33
<211> 1368
<212> PRT
<213> Artificial sequence

<220>
<223> Cas9-NLS

<400> 33

Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
1 5 10 15

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
20 25 30

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

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
50 55 60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65 70 75 80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
85 90 95

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

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175

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

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195 200 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp

370

375

380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
 385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
 405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
 420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
 435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
 450 455 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
 465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
 485 490 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
 500 505 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
 515 520 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
 530 535 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
 545 550 555 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
 565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
 580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
595 600 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp Ala Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155

Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly

1205	1210	1215
Glu Leu Gln Lys Gly Asn Glu	Leu Ala Leu Pro Ser	Lys Tyr Val
1220	1225	1230
Asn Phe Leu Tyr Leu Ala Ser	His Tyr Glu Lys Leu	Lys Gly Ser
1235	1240	1245
Pro Glu Asp Asn Glu Gln Lys	Gln Leu Phe Val Glu	Gln His Lys
1250	1255	1260
His Tyr Leu Asp Glu Ile Ile	Glu Gln Ile Ser Glu	Phe Ser Lys
1265	1270	1275
Arg Val Ile Leu Ala Asp Ala	Asn Leu Asp Lys Val	Leu Ser Ala
1280	1285	1290
Tyr Asn Lys His Arg Asp Lys	Pro Ile Arg Glu Gln	Ala Glu Asn
1295	1300	1305
Ile Ile His Leu Phe Thr Leu	Thr Asn Leu Gly Ala	Pro Ala Ala
1310	1315	1320
Phe Lys Tyr Phe Asp Thr Thr	Ile Asp Arg Lys Arg	Tyr Thr Ser
1325	1330	1335
Thr Lys Glu Val Leu Asp Ala	Thr Leu Ile His Gln	Ser Ile Thr
1340	1345	1350
Gly Leu Tyr Glu Thr Arg Ile	Asp Leu Ser Gln Leu	Gly Gly Asp
1355	1360	1365

<210> 34
 <211> 4125
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding Cas9-NLS

<400> 34
 atggataaga aataactcaat aggcttagat atcggcacaa atagcgtcgg atgggcggtg

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cacagtatca aaaaaaatct tataggggct cttttatttg acagtggaga gacagcggaa	180
gcgactcgtc tcaaacggac agctcgtaga aggtatacac gtcggaagaa tcgtatttgt	240
tatctacagg agattttttc aaatgagatg gcgaaagtag atgatagttt ctttcatcga	300
cttgaagagt cttttttggt ggaagaagac aagaagcatg aacgtcatcc tatttttgga	360
aatatagtag atgaagtgtc ttatcatgag aaatatccaa ctatctatca tctgcgaaaa	420
aaattggtag attctactga taaagcggat ttgcgcttaa tctatttggc cttagcgc	480
atgattaagt ttcgtggtca ttttttgatt gagggagatt taaatcctga taatagtgat	540
gtggacaaac tatttatcca gttggtacaa acctacaatc aattatttga agaaaaccct	600
attaacgcaa gtggagtaga tgctaaagcg attctttctg cacgattgag taaatcaaga	660
cgattagaaa atctcattgc tcagctcccc ggtgagaaga aaaatggctt atttgggaat	720
ctcattgctt tgtcattggg ttgacccct aattttaaat caaattttga tttggcagaa	780
gatgctaaat tacagctttc aaaagatact tacgatgatg atttagataa tttattggcg	840
caaattggag atcaatatgc tgatttgttt ttggcagcta agaatttatc agatgctatt	900
ttactttcag atatcctaag agtaaatact gaaataacta aggctcccct atcagcttca	960
atgattaaac gctacgatga acatcatcaa gacttgactc ttttaaaagc tttagttcga	1020
caacaacttc cagaaaagta taaagaaatc ttttttgatc aatcaaaaaa cggatatgca	1080
ggttatattg atggggggagc tagccaagaa gaattttata aatttatcaa accaatttta	1140
gaaaaaatgg atggtactga ggaattattg gtgaaactaa atcgtgaaga tttgctgcgc	1200
aagcaacgga cctttgacaa cggctctatt ccccatcaaa ttcacttggg tgagctgcat	1260
gctattttga gaagacaaga agacttttat ccatttttaa aagacaatcg tgagaagatt	1320
gaaaaaatct tgacttttcg aattccttat tatgttggtc cattggcgcg tggcaatagt	1380
cgttttgcat ggatgactcg gaagtctgaa gaaacaatta ccccatggaa ttttgaagaa	1440
gttgctgata aaggtgcttc agctcaatca tttattgaac gcatgacaaa ctttgataaa	1500
aatcttccaa atgaaaaagt actaccaaaa catagtttgc tttatgagta ttttacggtt	1560
tataacgaat tgacaaaggt caaatatgtt actgaaggaa tgcgaaaacc agcatttctt	1620

tcaggatgaac agaagaaagc cattgttgat ttactcttca aaacaaatcg aaaagtaacc	1680
gttaagcaat taaaagaaga ttatttcaaa aaaatagaat gttttgatag tgttgaaatt	1740
tcaggagtgtg aagatagatt taatgcttca ttaggtacct accatgattt gctaaaaatt	1800
attaaagata aagatTTTTT ggataatgaa gaaaatgaag atatcttaga ggatattgtt	1860
ttaacattga ccttatttga agatagggag atgattgagg aaagacttaa aacatatgct	1920
cacctctttg atgataaggt gatgaaacag cttaaacgtc gccgttatac tggttgggga	1980
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gtaaaagttg ttgatgaatt ggtcaaagta atggggcggc ataagccaga aaatatcgtt	2280
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gttgaaaata ctcaattgca aaatgaaaag ctctatctct attatctcca aaatggaaga	2460
gacatgtatg tggaccaaga attagatatt aatcgtttaa gtgattatga tgtcgatcac	2520
attgtttcac aaagtttcct taaagacgat tcaatagaca ataaggctctt aacgcgttct	2580
gataaaaatc gtggtaaatt ggataacgtt ccaagtgaag aagtagtcaa aaagatgaaa	2640
aactattgga gacaacttct aaacgccaag ttaatcactc aacgtaagtt tgataattta	2700
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aatatcatga acttcttcaa aacagaaatt acacttgcaa atggagagat tcgcaaacgc	3180
cctctaatacg aaactaatgg ggaaactgga gaaattgtct gggataaagg gcgagatttt	3240

gccacagtgc gcaaagtatt gtccatgccc caagtcaata ttgtcaagaa aacagaagta	3300
cagacaggcg gattctccaa ggagtcaatt ttaccaaaaa gaaattcgga caagcttatt	3360
gctcgtaaaa aagactggga tccaaaaaaa tatgggtggtt ttgatagtcc aacggtagct	3420
tattcagtcc tagtggttgc taagggtgga aaagggaat cgaagaagtt aaaatccgtt	3480
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caaaaaggaa atgagctggc tctgccaagc aaatatgtga attttttata tttagctagt	3720
cattatgaaa agttgaaggg tagtccagaa gataacgaac aaaaacaatt gtttgtggag	3780
cagcataagc attatttaga tgagattatt gagcaaatca gtgaattttc taagcgtgtt	3840
attttagcag atgccaattt agataaagtt cttagtgcac ataacaaaca tagagacaaa	3900
ccaatacgtg aacaagcaga aaatattatt catttattta cgttgacgaa tcttggagct	3960
cccgtgctt ttaaataattt tgatacaaca attgatcgta aacgatatac gtctacaaaa	4020
gaagtttttag atgccactct tatccatcaa tccatcactg gtctttatga aacacgcatt	4080
gatttgagtc agctaggagg tgaccccaag aagaagagga aggtg	4125

<210> 35
 <211> 672
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding dsRed

<400> 35	
gcctcctccg agaacgtcat caccgagttc atgcgcttca aggtgcgcat ggagggcacc	60
gtgaacggcc acgagttcga gatcgagggc gagggcgagg gccgccccta cgagggccac	120
aacaccgtga agctgaaggt gaccaagggc ggccccctgc ctttcgcctg ggacatcctg	180
tccccccagt tccagtacgg ctccaaggtg tacgtgaagc accccgccga catccccgac	240
tacaagaagc tgtccttccc cgagggttcc aagtgggagc gcgtgatgaa cttcgaggac	300
ggcggcgtgg cgaccgtgac ccaggactcc tccctgcagg acggctgctt catctacaag	360

gtgaagttca tcggcgtgaa cttccccctcc gacggccccg tgatgcagaa gaagaccatg	420
ggctgggagg cctccaccga gcgcctgtac ccccgcgacg gcgtgctgaa gggcgagacc	480
cacaaggccc tgaagctgaa ggacggcggc cactacctgg tggagttcaa gtccatctac	540
atggccaaga agcccgtgca gctgcccggc tactactacg tggacgcaa gctggacatc	600
acctcccaca acgaggacta caccatcgtg gagcagtagc agcgcaccga gggccgccac	660
cacctgttcc tg	672

<210> 36
 <211> 708
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding mCherry

<400> 36	
atggtgagca agggcgagga ggataacatg gccatcatca aggagttcat gcgcttcaag	60
gtgcacatgg agggctccgt gaacggccac gagttcgaga tcgagggcga gggcgagggc	120
cgcccctacg agggcaccca gaccgccaag ctgaaggtga ccaagggtgg ccccctgccc	180
ttgccttggg acatcctgtc ccctcagttc atgtacggct ccaaggccta cgtgaagcac	240
cccgccgaca tccccgacta cttgaagctg tccttccccg agggcttcaa gtgggagcgc	300
gtgatgaact tcgaggacgg cggcgtggtg accgtgaccc aggactcctc cctgcaggac	360
ggcgagttca tctacaaggt gaagctgcgc ggcaccaact tcccctccga cggccccgta	420
atgcagaaga agaccatggg ctgggaggcc tcctccgagc ggatgtaccc cgaggacggc	480
gccctgaagg gcgagatcaa gcagaggctg aagctgaagg acggcggcca ctacgacgct	540
gaggtcaaga ccacctaca ggccaagaag cccgtgcagc tgcccggcgc ctacaacgtc	600
aacatcaagt tggacatcac ctcccacaac gaggactaca ccatcgtgga acagtacgaa	660
cgcgccgagg gccgccactc caccggcggc atggacgagc tgtacaag	708

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>

<223> DNA sequence of the recognition site for sgRNA

<400> 37

cccaaaagga ggatcgtact tgg

23

<210> 38

<211> 23

<212> PRT

<213> Artificial sequence

<220>

<223> Influenza virus HA2

<400> 38

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
1 5 10 15

Met Ile Asp Gly Trp Tyr Gly
20

<210> 39

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> KALA

<400> 39

Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
1 5 10 15

Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
20 25 30

<210> 40

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> GALA

<400> 40

Trp Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala Glu His

1 5 10 15

Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 41
<211> 26
<212> PRT
<213> Artificial sequence

<220>
<223> Melittin

<400> 41

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu
1 5 10 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln
20 25

<210> 42
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Penetratin

<400> 42

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 43
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> HIV-TAT(47-57)

<400> 43

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 44
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> HIV-1 Rev(34-50)

<400> 44

Lys Gln Ala Ile Pro Val Ala Lys
1 5

<210> 45
<211> 34
<212> PRT
<213> Artificial sequence

<220>
<223> VP22

<400> 45

Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
1 5 10 15

Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
20 25 30

Val Glu

<210> 46
<211> 27
<212> PRT
<213> Artificial sequence

<220>
<223> Transportan

<400> 46

Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu
1 5 10 15

Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
20 25

<210> 47
 <211> 21
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Pep-1

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> ACETYLATION

<220>
 <221> MOD_RES
 <222> (21)..(21)
 <223> AMIDATION (-NH-CH2-CH2-SH)

<400> 47

Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
 1 5 10 15

Lys Lys Arg Lys Val
 20

<210> 48
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Pep-7

<400> 48

Ser Asp Leu Trp Glu Met Met Met Val Ser Leu Ala Cys Gln Tyr
 1 5 10 15

<210> 49
 <211> 29
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Leucine zipper NZ

<400> 49

Ala Leu Lys Lys Glu Leu Gln Ala Asn Lys Lys Glu Leu Ala Gln Leu
1 5 10 15

Lys Trp Glu Leu Gln Ala Leu Lys Lys Glu Leu Ala Gln
20 25

<210> 50

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> Leucine zipper CZ

<400> 50

Glu Gln Leu Glu Lys Lys Leu Gln Ala Leu Glu Lys Lys Leu Ala Gln
1 5 10 15

Leu Glu Trp Lys Asn Gln Ala Leu Glu Lys Lys Leu Ala Gln
20 25 30

<210> 51

<211> 87

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence encoding leucine zipper NZ

<400> 51

gcactgaaaa aagaactgca ggcaaataaa aaagaactgg cacagctgaa atgggaactg 60

caggcactga aaaaagaact ggcacag 87

<210> 52

<211> 90

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence encoding leucine zipper CZ

<400> 52

gaacagctgg aaaaaaaact gcaggcactg gaaaaaaaac tggcacagct ggaatggaaa 60

aatcaggcac tggaaaaaaa actggcacag

90

<210> 53
<211> 109
<212> PRT
<213> Artificial sequence

<220>
<223> TrxA amino acid sequence

<400> 53

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp
20 25 30

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
35 40 45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn
50 55 60

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

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala
100 105

<210> 54
<211> 327
<212> DNA
<213> Artificial sequence

<220>
<223> TrxA nucleic acid sequence

<400> 54

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gacggggcga tcctcgtcga tttctgggca gagtgggtgcg gtccgtgcaa aatgatcgcc 120

ccgattctgg atgaaatcgc tgacgaatat cagggcaaac tgaccgttgc aaaactgaac	180
atcgatcaaa accctggcac tgcgccgaaa tatggcatcc gtggtatccc gactctgctg	240
ctgttcaaaa acggtgaagt ggcggcaacc aaagtgggtg cactgtctaa aggtcagttg	300
aaagagttcc tcgacgctaa cctggcc	327