

pctca2016050403-seq1
SEQUENCE LISTING

<110> FELDAN BIO INC.
GUAY, David
DEL'GUIDICE, Thomas
LEPETIT-STOFFAES, Jean-Pascal

<120> POLYPEPTIDE-BASED SHUTTLE AGENTS FOR IMPROVING THE TRANSDUCTION
EFFICIENCY OF POLYPEPTIDE CARGOS TO THE CYTOSOL OF TARGET
EUKARYOTIC CELLS, USES THEREOF, METHODS AND KITS RELATING TO SAME

<130> 016995-0010

<140> Not yet assigned

<141> 2016-04-08

<150> US 62/145,760

<151> 2015-04-10

<150> US 62/246,892

<151> 2015-10-27

<160> 103

<170> PatentIn version 3.5

<210> 1

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> CM18

<400> 1

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
1 5 10 15

Thr Gly

<210> 2

<211> 189

<212> PRT

<213> Artificial sequence

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<220>

<223> Diphtheria toxin T domain (DT)

<400> 2

Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
1 5 10 15

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly Pro Ile
20 25 30

Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys
35 40 45

Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu His Pro
50 55 60

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

Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val Ile Asp
85 90 95

Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile
100 105 110

Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
115 120 125

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu
130 135 140

Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly
145 150 155 160

Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe Gln Val
165 170 175

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Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 180 185

<210> 3
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 <212> PRT
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<220>
 <223> GALA

<400> 3

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> 4
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 <212> PRT
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<220>
 <223> PEA

<400> 4

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

Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu Ala Ala
 20 25 30

Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg
 35 40 45

His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro
 50 55 60

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Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn
65 70 75 80

Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly
85 90 95

Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu
100 105 110

Ala Leu Thr
115

<210> 5
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<223> INF-7

<400> 5

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 Cys
20

<210> 6
<211> 26
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<213> Artificial sequence

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<223> LAH4

<400> 6

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

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Leu His Leu Ala Leu Ala Leu Lys Lys Ala
20 25

<210> 7
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<220>
<223> HGP

<400> 7

Leu Leu Gly Arg Arg Gly Trp Glu Val Leu Lys Tyr Trp Trp Asn Leu
1 5 10 15

Leu Gln Tyr Trp Ser Gln Glu Leu
20

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

<220>
<223> H5WYG

<400> 8

Gly Leu Phe His Ala Ile Ala His Phe Ile His Gly Gly Trp His Gly
1 5 10 15

Leu Ile His Gly Trp Tyr Gly
20

<210> 9
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<223> HA2

<400> 9

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> 10

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<223> EB1

<400> 10

Leu Ile Arg Leu Trp Ser His Leu Ile His Ile Trp Phe Gln Asn Arg
1 5 10 15

Arg Leu Lys Trp Lys Lys Lys
20

<210> 11

<211> 25

<212> PRT

<213> Artificial sequence

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<223> VSVG

<400> 11

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
1 5 10 15

Val Pro Ser Asn Tyr His Tyr Cys Pro
20 25

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

<220>
 <223> Pseudomonas toxin

<400> 12

Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu
 1 5 10 15

Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln
 20 25 30

Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu
 35 40 45

Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala
 50 55 60

Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu
 65 70 75 80

Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser
 85 90 95

Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala
 100 105 110

Asn Ala Asp
 115

<210> 13
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pctca2016050403-seq1

<223> Melittin

<400> 13

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	

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<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> KALA

<400> 14

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> 15

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> JST-1

<400> 15

Gly	Leu	Phe	Glu	Ala	Leu	Leu	Glu	Leu	Leu	Glu	Ser	Leu	Trp	Glu	Leu
1				5				10						15	

Leu	Leu	Glu	Ala
			20

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

<220>
 <223> SP

<400> 16

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 1 5 10 15

<210> 17
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 <212> PRT
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<220>
 <223> TAT

<400> 17

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

<210> 18
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Penetratin (Antennapedia)

<400> 18

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

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

<220>

pctca2016050403-seq1

<223> pVEC

<400> 19

Leu	Leu	Ile	Ile	Leu	Arg	Arg	Arg	Ile	Arg	Lys	Gln	Ala	His	Ala	His
1				5					10					15	

Ser Lys

<210> 20

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> M918

<400> 20

Met	Val	Thr	Val	Leu	Phe	Arg	Arg	Leu	Arg	Ile	Arg	Arg	Ala	Cys	Gly
1				5					10					15	

Pro	Pro	Arg	Val	Arg	Val
			20		

<210> 21

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> Pep-1

<400> 21

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	

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<210> 22
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 <223> Pep-2

<400> 22

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

Lys	Lys	Arg	Lys	Val
			20	

<210> 23
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<220>
 <223> Xentry

<400> 23

Leu	Cys	Leu	Arg	Pro	Val	Gly
1			5			

<210> 24
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 <223> Arginine stretch

<400> 24

Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
1			5					

<210> 25
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<212> PRT
<213> Artificial sequence

<220>
<223> Transportan

<400> 25

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

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

<210> 26
<211> 18
<212> PRT
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<220>
<223> SynB1

<400> 26

Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr
1 5 10 15

Gly Arg

<210> 27
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> SynB3

<400> 27

Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe
1 5 10

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<210> 28
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<212> PRT
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<220>
<223> E1a

<400> 28

Lys Arg Pro Arg Pro
1 5

<210> 29
<211> 7
<212> PRT
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<223> SV40 T-Ag

<400> 29

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 30
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<212> PRT
<213> Artificial sequence

<220>
<223> c-myc

<400> 30

Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

<210> 31
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pctca2016050403-seq1

<223> Op-T-NLS

<400> 31

Ser Ser Asp Asp Glu Ala Thr Ala Asp Ser Gln His Ala Ala Pro Pro
1 5 10 15

Lys Lys Lys Arg Lys Val
20

<210> 32

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Vp3

<400> 32

Lys Lys Lys Arg Lys
1 5

<210> 33

<211> 16

<212> PRT

<213> Artificial sequence

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<223> Nucleoplasmin

<400> 33

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1 5 10 15

<210> 34

<211> 10

<212> PRT

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<223> Histone 2B NLS

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<400> 34

Asp Gly Lys Lys Arg Lys Arg Ser Arg Lys
1 5 10

<210> 35

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> Xenopus N1

<400> 35

Val Arg Lys Lys Arg Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys
1 5 10 15

Asp Ala Lys Lys Ser Lys Gln Glu
20

<210> 36

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> PARP

<400> 36

Lys Arg Lys Gly Asp Glu Val Asp Gly Val Asp Glu Cys Ala Lys Lys
1 5 10 15

Ser Lys Lys

<210> 37

<211> 7

<212> PRT

<213> Artificial sequence

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pctca2016050403-seq1

<223> PDX-1

<400> 37

Arg Arg Met Lys Trp Lys Lys
1 5

<210> 38

<211> 7

<212> PRT

<213> Artificial sequence

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<223> QKI-5

<400> 38

Arg Val His Pro Tyr Gln Arg
1 5

<210> 39

<211> 24

<212> PRT

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<220>

<223> HCDA

<400> 39

Lys Arg Pro Ala Cys Thr Leu Lys Pro Glu Cys Val Gln Gln Leu Leu
1 5 10 15

Val Cys Ser Gln Glu Ala Lys Lys
20

<210> 40

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<212> PRT

<213> Artificial sequence

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<223> H2B

pctca2016050403-seq1

<400> 40

Gly Lys Lys Arg Ser Lys Ala
1 5

<210> 41

<211> 6

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<223> v-Rel

<400> 41

Lys Ala Lys Arg Gln Arg
1 5

<210> 42

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Amida

<400> 42

Arg Lys Arg Arg Arg
1 5

<210> 43

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> RanBP3

<400> 43

Pro Pro Val Lys Arg Glu Arg Thr Ser
1 5

pctca2016050403-seq1

<210> 44
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<223> Pho4p

<400> 44

Pro Tyr Leu Asn Lys Arg Lys Gly Lys Pro
1 5 10

<210> 45
<211> 9
<212> PRT
<213> Artificial sequence

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<223> LEF-1

<400> 45

Lys Lys Lys Lys Arg Lys Arg Glu Lys
1 5

<210> 46
<211> 9
<212> PRT
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<223> TCF-1

<400> 46

Lys Lys Lys Arg Arg Ser Arg Glu Lys
1 5

<210> 47
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<212> PRT
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<223> BDV-P

<400> 47

Pro Arg Pro Arg Lys Ile Pro Arg
1 5

<210> 48

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> TR2

<400> 48

Lys Asp Cys Val Ile Asn Lys His His Arg Asn Arg Cys Gln Tyr Cys
1 5 10 15

Arg Leu Gln Arg
20

<210> 49

<211> 5

<212> PRT

<213> Artificial sequence

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<223> SOX9

<400> 49

Pro Arg Arg Arg Lys
1 5

<210> 50

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Max

pctca2016050403-seq1

<400> 50

Pro Gln Ser Arg Lys Lys Leu Arg
1 5

<210> 51

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Mitochondrial signal sequence from Tim9

<400> 51

Asn Leu Val Glu Arg Cys Phe Thr Asp
1 5

<210> 52

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Mitochondrial signal sequence from Yeast cytochrome c oxidase subunit IV

<400> 52

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys
1 5 10

<210> 53

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> Mitochondrial signal sequence from 18S rRNA

<400> 53

Met Leu Ile Ser Arg Cys Lys Trp Ser Arg Phe Pro Gly Asn Gln Arg
1 5 10 15

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<223> Peroxisome signal sequence - PTS1

<400> 54

Ser Lys Leu
1

<210> 55
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Nucleolar signal sequence from BIRC5

<400> 55

Met Gln Arg Lys Pro Thr Ile Arg Arg Lys Asn Leu Arg Leu Arg Arg
1 5 10 15

Lys

<210> 56
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Nucleolar signal sequence from RECQL4

<400> 56

Lys Gln Ala Trp Lys Gln Lys Trp Arg Lys Lys
1 5 10

<210> 57

pctca2016050403-seq1

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

<220>
 <223> CM18-TAT

<400> 57

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
 1 5 10 15

Thr Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 20 25

<210> 58
 <211> 34
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CM18-Penetratin

<400> 58

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
 1 5 10 15

Thr Gly Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp
 20 25 30

Lys Lys

<210> 59
 <211> 36
 <212> PRT
 <213> Artificial sequence

<220>
 <223> His-CM18-TAT

<400> 59

pctca2016050403-seq1

Met His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly
1 5 10 15

Ala Val Leu Lys Val Leu Thr Thr Gly Tyr Gly Arg Lys Lys Arg Arg
20 25 30

Gln Arg Arg Arg
35

<210> 60

<211> 290

<212> PRT

<213> Artificial sequence

<220>

<223> GFP

<400> 60

Met His His His His His His Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Ala Ser Thr Gly Thr Gly Ile Arg Met Val Ser Lys Gly
20 25 30

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
35 40 45

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
50 55 60

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
65 70 75 80

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val
85 90 95

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe

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100

105

110

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 115 120 125

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

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 145 150 155 160

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His
 165 170 175

Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
 180 185 190

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 195 200 205

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 210 215 220

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 225 230 235 240

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 245 250 255

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Gly Ser Gly Gly Gly
 260 265 270

Ser Gly Gly Gly Ser Gly Trp Ile Arg Ala Ser Ser Gly Gly Arg Glu
 275 280 285

Ile Ser

290

<210> 61
 <211> 317
 <212> PRT
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<220>
 <223> TAT-GFP

<400> 61

Met His His His His His His Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

Ser Gly Gly Ala Ser Thr Gly Thr Gly Arg Lys Lys Arg Arg Gln Arg
 20 25 30

Arg Arg Pro Pro Gln Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 35 40 45

Gly Gly Thr Gly Ile Arg Met Val Ser Lys Gly Glu Glu Leu Phe Thr
 50 55 60

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 65 70 75 80

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 85 90 95

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 100 105 110

Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg
 115 120 125

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
 130 135 140

pctca2016050403-seq1

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
145 150 155 160

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

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
180 185 190

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
195 200 205

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
210 215 220

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
225 230 235 240

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
245 250 255

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
260 265 270

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
275 280 285

Asp Glu Leu Tyr Lys Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
290 295 300

Gly Trp Ile Arg Ala Ser Ser Gly Gly Arg Glu Ile Ser
305 310 315

<210> 62
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<212> PRT

pctca2016050403-seq1

<213> Artificial sequence

<220>

<223> GFP-NLS

<400> 62

Met His His His His His His Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Ala Ser Thr Gly Ile Arg Met Val Ser Lys Gly Glu Glu
20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
65 70 75 80

Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys
85 90 95

Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
115 120 125

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

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

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val

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165

170

175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 210 215 220

His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys Gly Gly Ser Gly Gly Gly Ser Gly
 260 265 270

Gly Gly Ser Gly Trp Ile Arg Ala Ser Ser Gly Gly Arg Ser Ser Asp
 275 280 285

Asp Glu Ala Thr Ala Asp Ser Gln His Ala Ala Pro Pro Lys Lys Lys
 290 295 300

Arg Lys Val Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 305 310 315 320

Gly Arg Gly Thr Glu Ile Ser
 325

<210> 63

<211> 14

<212> PRT

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pctca2016050403-seq1

<220>

<223> C(LLKK)3C

<400> 63

Cys Leu Leu Lys Lys Leu Leu Lys Lys Leu Leu Lys Lys Cys
1 5 10

<210> 64

<211> 14

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<223> G(LLKK)3G

<400> 64

Gly Leu Leu Lys Lys Leu Leu Lys Lys Leu Leu Lys Lys Gly
1 5 10

<210> 65

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> PTD4

<400> 65

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
1 5 10

<210> 66

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> TAT-CM18

<400> 66

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Cys Lys Trp Lys Leu

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1 5 10 15

Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly
20 25 30

<210> 67
<211> 42
<212> PRT
<213> Artificial Sequence

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<223> TAT-KALA

<400> 67

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Cys Trp Glu Ala Lys
1 5 10 15

Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His Leu Ala Lys Ala
20 25 30

Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
35 40

<210> 68
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> His-CM18-PTD4

<400> 68

His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
1 5 10 15

Val Leu Lys Val Leu Thr Thr Gly Tyr Ala Arg Ala Ala Ala Arg Gln
20 25 30

Ala Arg Ala

35

<210> 69
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-CM18-9Arg

<400> 69

His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
 1 5 10 15

Val Leu Lys Val Leu Thr Thr Gly Arg Arg Arg Arg Arg Arg Arg Arg
 20 25 30

Arg

<210> 70
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-CM18-Transportan

<400> 70

His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
 1 5 10 15

Val Leu Lys Val Leu Thr Thr Gly Gly Trp Thr Leu Asn Ser Ala Gly
 20 25 30

Tyr Leu Leu Lys Ile Asn Leu Lys Ala Leu Ala Ala Leu Ala Lys Lys
 35 40 45

Ile Leu

50

<210> 71
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-LAH4-PDT4

<400> 71

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

His Leu Ala His Leu Ala Leu His Leu Ala Leu Ala Leu Lys Lys Ala
 20 25 30

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
 35 40

<210> 72
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-C(LLKK)3C-PDT4

<400> 72

His His His His His His Cys Leu Leu Lys Lys Leu Leu Lys Lys Leu
 1 5 10 15

Leu Lys Lys Cys Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
 20 25 30

<210> 73
 <211> 324
 <212> PRT
 <213> Artificial Sequence

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<220>

<223> mCherry-NLS

<400> 73

Met His His His His His His Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Gly Ala Ser Thr Gly Ile Arg Met Val Ser Lys Cys Glu Glu
20 25 30

Asp Asn Met Ala Ile Ile Lys Glu Phe Met Arg Phe Lys Val His Met
35 40 45

Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu
50 55 60

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

Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Met
85 90 95

Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr
100 105 110

Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn
115 120 125

Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln
130 135 140

Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
145 150 155 160

Ser Asp Gly Gln Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
165 170 175

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

Gln Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
195 200 205

Thr Thr Tyr Lys Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Asn
210 215 220

Val Asn Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
225 230 235 240

Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Gly Met
245 250 255

Asp Glu Leu Tyr Lys Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
260 265 270

Gly Trp Ile Arg Ala Ser Ser Gly Gly Arg Ser Ser Asp Asp Glu Ala
275 280 285

Thr Ala Asp Ser Gln His Ala Ala Pro Pro Lys Lys Lys Arg Lys Val
290 295 300

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Arg Gly
305 310 315 320

Thr Glu Ile Ser

<210> 74
<211> 1414
<212> PRT
<213> Artificial Sequence

<220>
<223> Cas9-NLS

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<400> 74

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

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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 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

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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

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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

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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 His 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

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945		950		955		960
Lys	Leu	Val	Ser	Asp	Phe	Arg
				965		
				Lys	Asp	Phe
					970	
				Gln	Phe	Tyr
						Lys
						Val
						Arg
						975
Glu	Ile	Asn	Asn	Tyr	His	His
		980				
				Ala	His	Asp
					985	
				Ala	Tyr	Leu
						Asn
						Ala
						Val
						990
Val	Gly	Thr	Ala	Leu	Ile	Lys
						Lys
						1000
						Tyr
						Pro
						Lys
						Leu
						Glu
						1005
						Ser
						Glu
						Phe
Val	Tyr	Gly	Asp	Tyr	Lys	Val
	1010					1015
						Tyr
						Asp
						Val
						Arg
						Lys
						1020
						Met
						Ile
						Ala
Lys	Ser	Glu	Gln	Glu	Ile	Gly
	1025					1030
						Lys
						Ala
						Thr
						Ala
						Lys
						1035
						Tyr
						Phe
						Phe
Tyr	Ser	Asn	Ile	Met	Asn	Phe
	1040					1045
						Phe
						Lys
						Thr
						Glu
						Ile
						1050
						Thr
						Leu
						Ala
Asn	Gly	Glu	Ile	Arg	Lys	Arg
	1055					1060
						Pro
						Leu
						Ile
						Glu
						Thr
						1065
						Asn
						Gly
						Glu
Thr	Gly	Glu	Ile	Val	Trp	Asp
	1070					1075
						Lys
						Gly
						Arg
						Asp
						Phe
						1080
						Ala
						Thr
						Val
Arg	Lys	Val	Leu	Ser	Met	Pro
	1085					1090
						Gln
						Val
						Asn
						Ile
						Val
						1095
						Lys
						Lys
						Thr
Glu	Val	Gln	Thr	Gly	Gly	Phe
	1100					1105
						Ser
						Lys
						Glu
						Ser
						Ile
						1110
						Leu
						Pro
						Lys
Arg	Asn	Ser	Asp	Lys	Leu	Ile
	1115					1120
						Ala
						Arg
						Lys
						Lys
						Asp
						1125
						Trp
						Asp
						Pro
Lys	Lys	Tyr	Gly	Gly	Phe	Asp
						Ser
						Pro
						Thr
						Val
						Ala
						Tyr
						Ser
						Val

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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					

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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

Gly Gly Arg Ser Ser Asp Asp Glu Ala Thr Ala Asp Ser Gln His
1370 1375 1380

Ala Ala Pro Pro Lys Lys Lys Arg Lys Val Gly Gly Ser Gly Gly
1385 1390 1395

Gly Ser Gly Gly Gly Ser Gly Gly Gly Arg His His His His His
1400 1405 1410

His

<210> 75

<211> 42

<212> RNA

<213> Artificial Sequence

<220>

<223> crRNA (Example 13.3)

<400> 75

gaguccgagc agaagaagaa guuuuagagc uaugcuguuu ug

42

<210> 76

<211> 69

<212> RNA

<213> Artificial Sequence

pctca2016050403-seq1

<220>

<223> tracrRNA (Example 13.3)

<400> 76

aaacagcaua gcaaguuaaa auaaggcuag uccguuauca acuugaaaaa guggcaccga 60

gucggugcu 69

<210> 77

<211> 69

<212> RNA

<213> Artificial Sequence

<220>

<223> tracrRNA (Example 13.5)

<400> 77

aaacagcaua gcaaguuaaa auaaggcuag uccguuauca acuugaaaaa guggcaccga 60

gucggugcu 69

<210> 78

<211> 42

<212> RNA

<213> Artificial Sequence

<220>

<223> PPIB crRNA (Example 13.5)

<400> 78

guguauuuug accuacgaau guuuuagagc uaugcuguuu ug 42

<210> 79

<211> 74

<212> RNA

<213> Artificial Sequence

<220>

<223> PPIB tracrRNA (Example 13.5)

<400> 79

aacagcauag caaguuaaaa uaaggcuagu ccguuaucaa cuugaaaaaag uggcaccgag 60

ucggugcuuu uuuu 74

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<210> 80
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HOXB4-WT

<400> 80

Met His His His His His His Met Ala Met Ser Ser Phe Leu Ile Asn
 1 5 10 15

Ser Asn Tyr Val Asp Pro Lys Phe Pro Pro Cys Glu Glu Tyr Ser Gln
 20 25 30

Ser Asp Tyr Leu Pro Ser Asp His Ser Pro Gly Tyr Tyr Ala Gly Gly
 35 40 45

Gln Arg Arg Glu Ser Ser Phe Gln Pro Glu Ala Gly Phe Gly Arg Arg
 50 55 60

Ala Ala Cys Thr Val Gln Arg Tyr Pro Pro Pro Pro Pro Pro Pro Pro
 65 70 75 80

Pro Pro Gly Leu Ser Pro Arg Ala Pro Ala Pro Pro Pro Ala Gly Ala
 85 90 95

Leu Leu Pro Glu Pro Gly Gln Arg Cys Glu Ala Val Ser Ser Ser Pro
 100 105 110

Pro Pro Pro Pro Cys Ala Gln Asn Pro Leu His Pro Ser Pro Ser His
 115 120 125

Ser Ala Cys Lys Glu Pro Val Val Tyr Pro Trp Met Arg Lys Val His
 130 135 140

Val Ser Thr Val Asn Pro Asn Tyr Ala Gly Gly Glu Pro Lys Arg Ser

145 150 155 160

His Tyr Asn Arg Tyr Leu Thr Arg Arg Arg Arg Val Glu Ile Ala His
180 185 190

Ala Leu Cys Leu Ser Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg
195 200 205

Arg Met Lys Trp Lys Lys Asp His Lys Leu Pro Asn Thr Lys Ile Arg
210 215 220

Ser Gly Gly Ala Ala Gly Ser Ala Gly Gly Pro Pro Gly Arg Pro Asn
225 230 235 240

Gly Gly Pro Arg Ala Leu
245

<210>	81
<211>	17
<212>	PRT
<213>	Artificial Sequence

<220>
<223> His-PTD4

<400> 81

His His His His His His Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg
1 5 10 15

Ala

$\langle 210 \rangle$	82
$\langle 211 \rangle$	41
$\langle 212 \rangle$	PRT

pctca2016050403-seq1

<213> Artificial Sequence

<220>

<223> PTD4-KALA

<400> 82

Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala Trp Glu Ala Lys Leu
1 5 10 15

Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His Leu Ala Lys Ala Leu
20 25 30

Ala Lys Ala Leu Lys Ala Cys Glu Ala
35 40

<210> 83

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> 9Arg-KALA

<400> 83

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

Ala Leu Ala Lys Ala Leu Ala Lys His Leu Ala Lys Ala Leu Ala Lys
20 25 30

Ala Leu Lys Ala Cys Glu Ala
35

<210> 84

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Pep1-KALA

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<400> 84

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

Ala Leu Ala Lys His Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala
35 40 45

Cys Glu Ala
50

<210> 85

<211> 37

<212> PRT

<213> Artificial Sequence

<220>

<223> Xentry-KALA

<400> 85

Leu Cys Leu Arg Pro Val Gly Trp Glu Ala Lys Leu Ala Lys Ala Leu
1 5 10 15

Ala Lys Ala Leu Ala Lys His Leu Ala Lys Ala Leu Ala Lys Ala Leu
20 25 30

Lys Ala Cys Glu Ala
35

<210> 86

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> SynB3-KALA

pctca2016050403-seq1

<400> 86

Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe Trp Glu Ala Lys Leu Ala
1 5 10 15

Lys Ala Leu Ala Lys Ala Leu Ala Lys His Leu Ala Lys Ala Leu Ala
20 25 30

Lys Ala Leu Lys Ala Cys Glu Ala
35 40

<210> 87

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> VSVG-PTD4

<400> 87

Lys Phe Thr Ile Val Phe Pro His Asn Gln Lys Gly Asn Trp Lys Asn
1 5 10 15

Val Pro Ser Asn Tyr His Tyr Cys Pro Tyr Ala Arg Ala Ala Ala Arg
20 25 30

Gln Ala Arg Ala
35

<210> 88

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> EB1-PTD4

<400> 88

Leu Ile Arg Leu Trp Ser His Leu Ile His Ile Trp Phe Gln Asn Arg

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1 5 10 15

Arg Leu Lys Trp Lys Lys Lys Tyr Ala Arg Ala Ala Ala Arg Gln Ala
20 25 30

Arg Ala

<210> 89
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> JST-PTD4

<400> 89

Gly Leu Phe Glu Ala Leu Leu Glu Leu Leu Glu Ser Leu Trp Glu Leu
1 5 10 15

Leu Leu Glu Ala Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
20 25 30

<210> 90
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> CM18-PTD4

<400> 90

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
1 5 10 15

Thr Gly Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
20 25

<210> 91

pctca2016050403-seq1

<211> 35
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 6Cys-CM18-PTD4

<400> 91

Cys Cys Cys Cys Cys Cys Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
 1 5 10 15

Val Leu Lys Val Leu Thr Thr Gly Tyr Ala Arg Ala Ala Ala Arg Gln
 20 25 30

Ala Arg Ala
 35

<210> 92
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CM18-L1-PTD4

<400> 92

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
 1 5 10 15

Thr Gly Gly Gly Ser Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
 20 25 30

<210> 93
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CM18-L2-PTD4

<400> 93

pctca2016050403-seq1

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
1 5 10 15

Thr Gly Gly Gly Ser Gly Gly Gly Ser Tyr Ala Arg Ala Ala Ala Arg
20 25 30

Gln Ala Arg Ala
35

<210> 94
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CM18-L3-PTD4

<400> 94

Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr
1 5 10 15

Thr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Tyr Ala
20 25 30

Arg Ala Ala Ala Arg Gln Ala Arg Ala
35 40

<210> 95
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> His-CM18-TAT

<400> 95

His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
1 5 10 15

pctca2016050403-seq1

Val Leu Lys Val Leu Thr Thr Gly Tyr Gly Arg Lys Lys Arg Arg Gln
 20 25 30

Arg Arg Arg
 35

<210> 96
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-CM18-PTD4-6Cys

<400> 96

His His His His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala
 1 5 10 15

Val Leu Lys Val Leu Thr Thr Gly Tyr Ala Arg Ala Ala Ala Arg Gln
 20 25 30

Ala Arg Ala Cys Cys Cys Cys Cys Cys
 35 40

<210> 97
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3His-CM18-PTD4

<400> 97

His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly Ala Val Leu Lys
 1 5 10 15

Val Leu Thr Thr Gly Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
 20 25 30

pctca2016050403-seq1

<210> 98
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 12His-CM18-PTD4

<400> 98

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

Phe Lys Lys Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Tyr Ala
 20 25 30

Arg Ala Ala Ala Arg Gln Ala Arg Ala
 35 40

<210> 99
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HA-CM18-PTD4

<400> 99

His His His Ala His His His Lys Trp Lys Leu Phe Lys Lys Ile Gly
 1 5 10 15

Ala Val Leu Lys Val Leu Thr Thr Gly Tyr Ala Arg Ala Ala Ala Arg
 20 25 30

Gln Ala Arg Ala
 35

<210> 100
 <211> 38
 <212> PRT

pctca2016050403-seq1

<213> Artificial Sequence

<220>

<223> 3HA-CM18-PTD4

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