

UCSD097001WOSEQUENCELISTING

SEQUENCE LISTING

<110> The Regents of the University of California
Yeo, Gene
Nelles, David A.
Fang, Mark
Batra, Ranjan
Corbett, Kevin D.

<120> TRACKING AND MANIPULATING CELLULAR RNA
VIA NUCLEAR DELIVERY OF CRISPR/CAS9

<130> UCSD097.001wo

<150> 62/259014
<151> 2015-11-23

<160> 39

<170> FastSEQ for windows Version 4.0

<210> 1
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Guide sequence

<400> 1
ggacucccca gcagugaggg 20

<210> 2
<211> 20
<212> RNA
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<220>
<223> Guide sequence

<400> 2
ggacucccca gcaguguccc 20

<210> 3
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<220>
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<400> 3
ggacucccca gcucacuccc 20

<210> 4
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Guide sequence

<400> 4
ggacucccggu cgucacuccc 20

<210> 5

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<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> GAPDH mRNA 3'UTR

 <400> 5
 cacaagagga agagagagac cctcactgct ggggagtcc 39

 <210> 6
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Beta-actin mRNA 3'UTR

 <400> 6
 gaaggtgaca gcagtcggtt ggagcgagca tcccccaa 39

 <210> 7
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Gamma2 bacteriophage

 <400> 7
 gctcaatttt gacagcggtc atggcattcc acttatcac 39

 <210> 8
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PAMmer, beta-actin 3'UTR

 <400> 8
 mucmgcmucm camuggmgam ctmgcmugmu cmacmctmuc 40

 <210> 9
 <211> 114
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA, beta-actin 3'UTR

 <400> 9
 gtttggggga tgctcgctcc agtttaagag ctatgctgga aacagcatag caagttttaa 60
 taaggctagt ccgttatcaa cttgaaaaag tggcaccgag tcggtgcttt tttt 114

 <210> 10
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PAMmer, GAPDH 3'UTR

 <400> 10
 magmugmagm ggmccgmctm ctmctmucmc tmctmugmug 40

 <210> 11
 <211> 113

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA, GAPDH 3'UTR

 <400> 11
 ggactcccca gcagtgaggg gtttaagagc tatgctggaa acagcatagc aagtttaaatt 60
 aaggctagtc cgttatcaac ttgaaaaagt ggcaccgagt cggtgctttt ttt 113

 <210> 12
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PAMmer, gamma2 bacteriophage

 <400> 12
 matmgcmcam ugmugmgcm ugmucmaama amutmgamgc 40

 <210> 13
 <211> 113
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA, gamma2 bacteriophage

 <400> 13
 gtgataagtg gaatgccatg gtttaagagc tatgctggaa acagcatagc aagtttaaatt 60
 aaggctagtc cgttatcaac ttgaaaaagt ggcaccgagt cggtgctttt ttt 113

 <210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> GAPDH forward primer

 <400> 14
 aaggtgaagg tcggagtcaa c 21

 <210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> GAPDH reverse primer

 <400> 15
 ggggtcattg atggcaacaa ta 22

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Renilla luciferase forward primer

 <400> 16
 gtaacgctgc ctccagctac 20

 <210> 17
 <211> 20

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Renilla luciferase reverse primer

 <400> 17
 gtggcccaca aagatgattt 20

 <210> 18
 <211> 4
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA target

 <400> 18
 cctg 4

 <210> 19
 <211> 6
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA target

 <400> 19
 ggggcc 6

 <210> 20
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PAMmer, CAG repeat

 <400> 20
 mtgmctmgcm tgmtggmctm gcmtgmctmg cmtgmctmgc 40

 <210> 21
 <211> 114
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sgRNA, CAG repeat

 <400> 21
 gtgctgctgc tgctgctgct gguuuuagag cuaugcugga aacagcauag caaguuuuuaa 60
 uaaggcuagu ccguuuaucaa cuugaaaaag uggcaccgag ucggugcuuu uuuu 114

 <210> 22
 <211> 429
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> U6 promoter-2XBbsi-sgRNA scaffold

 <400> 22
 tgtacaaaaa agcaggcttt aaaggaacca attcagtcga ctggatccgg taccaaggctc 60
 gggcaggaag agggcctatt tcccatgatt ctttcatatt tgcataatag atacaaggct 120
 gttagagaga taattagaat taatttgact gtaaacacaa agatattagt acaaaatagc 180
 tgacgtagaa agtaataatt tcttgaggtag tttgcagttt taaaattatg ttttaaaatg 240
 gactatcata tgcttaccgt aacttgaaag tatttcgatt tcttggtttt atatatcttg 300

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tggaaggac gaaacaccgg gtcttcgaga agacctgttt aagagctatg ctggaaacag 360
 catagcaagt ttaaataagg ctagtccgtt atcaacttga aaaagtggca ccgagtcggt 420
 gcttttttt 429

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

<220>
 <223> CAG 10 probe

<400> 23
 cagcagcagc agcagcagca gcagcagcag

30

<210> 24
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Split Venus (N-terminal portion, residues 2-155)
 (I152L reduced background complementation mutant)

<400> 24
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Leu Thr Ala
 145 150

<210> 25
 <211> 172
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Split Venus (N-terminal portion, residues 2-173)

<400> 25
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 165 170

<210> 26

<211> 99

<212> PRT

<213> Artificial Sequence

<220>

<223> Split Venus (C-terminal portion, Feature of aa
 16-99 as residues 155-238)

<400> 26

Ala Cys Lys Ile Pro Asn Asp Leu Lys Gln Lys Val Met Asn His Asp
 1 5 10 15
 Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile
 20 25 30
 Glu Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 35 40 45
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
 50 55 60
 Gln Ser Lys Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 65 70 75 80
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
 85 90 95
 Leu Tyr Lys

<210> 27

<211> 183

<212> PRT

<213> Artificial Sequence

<220>

<223> PIN domain (from human SMG6)

<400> 27

Gln Met Glu Leu Glu Ile Arg Pro Leu Phe Leu Val Pro Asp Thr Asn
 1 5 10 15
 Gly Phe Ile Asp His Leu Ala Ser Leu Ala Arg Leu Leu Glu Ser Arg
 20 25 30
 Lys Tyr Ile Leu Val Val Pro Leu Ile Val Ile Asn Glu Leu Asp Gly
 35 40 45
 Leu Ala Lys Gly Gln Glu Thr Asp His Arg Ala Gly Gly Tyr Ala Arg
 50 55 60
 Val Val Gln Glu Lys Ala Arg Lys Ser Ile Glu Phe Leu Glu Gln Arg
 65 70 75 80
 Phe Glu Ser Arg Asp Ser Cys Leu Arg Ala Leu Thr Ser Arg Gly Asn
 85 90 95
 Glu Leu Glu Ser Ile Ala Phe Arg Ser Glu Asp Ile Thr Gly Gln Leu
 100 105 110
 Gly Asn Asn Asp Asp Leu Ile Leu Ser Cys Cys Leu His Tyr Cys Lys
 115 120 125
 Asp Lys Ala Lys Asp Phe Met Pro Ala Ser Lys Glu Glu Pro Ile Arg
 130 135 140
 Leu Leu Arg Glu Val Val Leu Leu Thr Asp Asp Arg Asn Leu Arg Val
 145 150 155 160
 Lys Ala Leu Thr Arg Asn Val Pro Val Arg Asp Ile Pro Ala Phe Leu

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Thr Trp Ala Gln Val Gly Ser
 165 170 175
 180

<210> 28
 <211> 418
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human RBFOX1

<400> 28
 Met Leu Ala Ser Gln Gly Val Leu Leu His Pro Tyr Gly Val Pro Met
 1 5 10 15
 Ile Val Pro Ala Ala Pro Tyr Leu Pro Gly Leu Ile Gln Gly Asn Gln
 20 25 30
 Glu Ala Ala Ala Pro Asp Thr Met Ala Gln Pro Tyr Ala Ser Ala
 35 40 45
 Gln Phe Ala Pro Pro Gln Asn Gly Ile Pro Ala Glu Tyr Thr Ala Pro
 50 55 60
 His Pro His Pro Ala Pro Glu Tyr Thr Gly Gln Thr Thr Val Pro Glu
 65 70 75 80
 His Thr Leu Asn Leu Tyr Pro Pro Ala Gln Thr His Ser Glu Gln Ser
 85 90 95
 Pro Ala Asp Thr Ser Ala Gln Thr Val Ser Gly Thr Ala Thr Gln Thr
 100 105 110
 Asp Asp Ala Ala Pro Thr Asp Gly Gln Pro Gln Thr Gln Pro Ser Glu
 115 120 125
 Asn Thr Glu Asn Lys Ser Gln Pro Lys Arg Leu His Val Ser Asn Ile
 130 135 140
 Pro Phe Arg Phe Arg Asp Pro Asp Leu Arg Gln Met Phe Gly Gln Phe
 145 150 155 160
 Gly Lys Ile Leu Asp Val Glu Ile Ile Phe Asn Glu Arg Gly Ser Lys
 165 170 175
 Gly Phe Gly Phe Val Thr Phe Glu Asn Ser Ala Asp Ala Asp Arg Ala
 180 185 190
 Arg Glu Lys Leu His Gly Thr Val Val Glu Gly Arg Lys Ile Glu Val
 195 200 205
 Asn Asn Ala Thr Ala Arg Val Met Thr Asn Lys Lys Thr Val Asn Pro
 210 215 220
 Tyr Thr Asn Gly Trp Lys Leu Asn Pro Val Val Gly Ala Val Tyr Ser
 225 230 235 240
 Pro Glu Phe Tyr Ala Gly Thr Val Leu Leu Cys Gln Ala Asn Gln Glu
 245 250 255
 Gly Ser Ser Met Tyr Ser Ala Pro Ser Ser Leu Val Tyr Thr Ser Ala
 260 265 270
 Met Pro Gly Phe Pro Tyr Pro Ala Ala Thr Ala Ala Tyr Arg
 275 280 285
 Gly Ala His Leu Arg Gly Arg Gly Arg Thr Val Tyr Asn Thr Phe Arg
 290 295 300
 Ala Ala Ala Pro Pro Pro Pro Ile Pro Ala Tyr Gly Gly Val Val Tyr
 305 310 315 320
 Gln Glu Pro Val Tyr Gly Asn Lys Leu Leu Gln Gly Gly Tyr Ala Ala
 325 330 335
 Tyr Arg Tyr Ala Gln Pro Thr Pro Ala Thr Ala Ala Tyr Ser Asp
 340 345 350
 Ser Tyr Gly Arg Val Tyr Ala Ala Asp Pro Tyr His His Ala Leu Ala
 355 360 365
 Pro Ala Pro Thr Tyr Gly Val Gly Ala Met Asn Ala Phe Ala Pro Leu
 370 375 380
 Thr Asp Ala Lys Thr Arg Ser His Ala Asp Asp Val Gly Leu Val Leu
 385 390 395 400
 Ser Ser Leu Gln Ala Ser Ile Tyr Arg Gly Gly Tyr Asn Arg Phe Ala
 405 410 415
 Pro Tyr

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<210> 29
 <211> 380
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human RBFOX2

<400> 29
 Met Glu Lys Lys Lys Met Val Thr Gln Gly Asn Gln Glu Pro Thr Thr
 1 5 10 15
 Thr Pro Asp Ala Met Val Gln Pro Phe Thr Thr Ile Pro Phe Pro Pro
 20 25 30
 Pro Pro Gln Asn Gly Ile Pro Thr Glu Tyr Gly Val Pro His Thr Gln
 35 40 45
 Asp Tyr Ala Gly Gln Thr Gly Glu His Asn Leu Thr Leu Tyr Gly Ser
 50 55 60
 Thr Gln Ala His Gly Glu Gln Ser Ser Asn Ser Pro Ser Thr Gln Asn
 65 70 75 80
 Gly Ser Leu Thr Thr Glu Gly Gly Ala Gln Thr Asp Gly Gln Gln Ser
 85 90 95
 Gln Thr Gln Ser Ser Glu Asn Ser Glu Ser Lys Ser Thr Pro Lys Arg
 100 105 110
 Leu His Val Ser Asn Ile Pro Phe Arg Phe Arg Asp Pro Asp Leu Arg
 115 120 125
 Gln Met Phe Gly Gln Phe Gly Lys Ile Leu Asp Val Glu Ile Ile Phe
 130 135 140
 Asn Glu Arg Gly Ser Lys Gly Phe Gly Phe Val Thr Phe Glu Asn Ser
 145 150 155 160
 Ala Asp Ala Asp Arg Ala Arg Glu Lys Leu His Gly Thr Val Val Glu
 165 170 175
 Gly Arg Lys Ile Glu Val Asn Asn Ala Thr Ala Arg Val Met Thr Asn
 180 185 190
 Lys Lys Met Val Thr Pro Tyr Ala Asn Gly Trp Lys Leu Ser Pro Val
 195 200 205
 Val Gly Ala Val Tyr Gly Pro Glu Leu Tyr Ala Ala Ser Ser Phe Gln
 210 215 220
 Ala Asp Val Ser Leu Gly Asn Asp Ala Ala Val Pro Leu Ser Gly Arg
 225 230 235 240
 Gly Gly Ile Asn Thr Tyr Ile Pro Leu Ile Ser Leu Pro Leu Val Pro
 245 250 255
 Gly Phe Pro Tyr Pro Thr Ala Ala Thr Thr Ala Ala Ala Phe Arg Gly
 260 265 270
 Ala His Leu Arg Gly Arg Gly Arg Thr Val Tyr Gly Ala Val Arg Ala
 275 280 285
 Val Pro Pro Thr Ala Ile Pro Ala Tyr Pro Gly Val Val Tyr Gln Asp
 290 295 300
 Gly Phe Tyr Gly Ala Asp Leu Tyr Gly Gly Tyr Ala Ala Tyr Arg Tyr
 305 310 315 320
 Ala Gln Pro Ala Thr Ala Thr Ala Ala Thr Ala Ala Ala Ala Ala
 325 330 335
 Ala Ala Tyr Ser Asp Gly Tyr Gly Arg Val Tyr Thr Ala Asp Pro Tyr
 340 345 350
 His Ala Leu Ala Pro Ala Ala Ser Tyr Gly Val Gly Ala Val Ala Ser
 355 360 365
 Leu Tyr Arg Gly Gly Tyr Ser Arg Phe Ala Pro Tyr
 370 375 380

<210> 30
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFP

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<400> 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 31

<211> 1382

<212> PRT

<213> Streptococcus pyogenes

<400> 31

Arg Thr Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn
 1 5 10 15
 Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys
 20 25 30
 Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn
 35 40 45
 Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr
 50 55 60
 Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg
 65 70 75 80
 Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp
 85 90 95
 Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp
 100 105 110
 Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val
 115 120 125
 Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu
 130 135 140
 Val Asp Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu
 145 150 155 160
 Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu
 165 170 175
 Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln
 180 185 190
 Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val
 195 200 205
 Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu
 210 215 220

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Glu	Asn	Leu	Ile	Ala	Gln	Leu	Pro	Gly	Glu	Lys	Lys	Asn	Gly	Leu	Phe
225					230					235					240
Gly	Asn	Leu	Ile	Ala	Leu	Ser	Leu	Gly	Leu	Thr	Pro	Asn	Phe	Lys	Ser
				245					250					255	
Asn	Phe	Asp	Leu	Ala	Glu	Asp	Ala	Lys	Leu	Gln	Leu	Ser	Lys	Asp	Thr
			260					265					270		
Tyr	Asp	Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile	Gly	Asp	Gln	Tyr
		275					280					285			
Ala	Asp	Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp	Ala	Ile	Leu	Leu
	290					295					300				
Ser	Asp	Ile	Leu	Arg	Val	Asn	Thr	Glu	Ile	Thr	Lys	Ala	Pro	Leu	Ser
305					310					315					320
Ala	Ser	Met	Ile	Lys	Arg	Tyr	Asp	Glu	His	His	Gln	Asp	Leu	Thr	Leu
				325					330					335	
Leu	Lys	Ala	Leu	Val	Arg	Gln	Gln	Leu	Pro	Glu	Lys	Tyr	Lys	Glu	Ile
			340					345					350		
Phe	Phe	Asp	Gln	Ser	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile	Asp	Gly	Gly
		355					360					365			
Ala	Ser	Gln	Glu	Glu	Phe	Tyr	Lys	Phe	Ile	Lys	Pro	Ile	Leu	Glu	Lys
	370					375					380				
Met	Asp	Gly	Thr	Glu	Glu	Leu	Leu	Val	Lys	Leu	Asn	Arg	Glu	Asp	Leu
385					390					395					400
Leu	Arg	Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro	His	Gln	Ile
				405					410					415	
His	Leu	Gly	Glu	Leu	His	Ala	Ile	Leu	Arg	Arg	Gln	Glu	Asp	Phe	Tyr
			420					425					430		
Pro	Phe	Leu	Lys	Asp	Asn	Arg	Glu	Lys	Ile	Glu	Lys	Ile	Leu	Thr	Phe
		435					440					445			
Arg	Ile	Pro	Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Asn	Ser	Arg	Phe
	450					455					460				
Ala	Trp	Met	Thr	Arg	Lys	Ser	Glu	Glu	Thr	Ile	Thr	Pro	Trp	Asn	Phe
465					470					475					480
Glu	Glu	Val	Val	Asp	Lys	Gly	Ala	Ser	Ala	Gln	Ser	Phe	Ile	Glu	Arg
				485					490					495	
Met	Thr	Asn	Phe	Asp	Lys	Asn	Leu	Pro	Asn	Glu	Lys	Val	Leu	Pro	Lys
			500					505					510		
His	Ser	Leu	Leu	Tyr	Glu	Tyr	Phe	Thr	Val	Tyr	Asn	Glu	Leu	Thr	Lys
		515					520					525			
Val	Lys	Tyr	Val	Thr	Glu	Gly	Met	Arg	Lys	Pro	Ala	Phe	Leu	Ser	Gly
	530					535					540				
Glu	Gln	Lys	Lys	Ala	Ile	Val	Asp	Leu	Leu	Phe	Lys	Thr	Asn	Arg	Lys
545					550					555					560
Val	Thr	Val	Lys	Gln	Leu	Lys	Glu	Asp	Tyr	Phe	Lys	Lys	Ile	Glu	Cys
				565					570					575	
Phe	Asp	Ser	Val	Glu	Ile	Ser	Gly	Val	Glu	Asp	Arg	Phe	Asn	Ala	Ser
			580					585					590		
Leu	Gly	Thr	Tyr	His	Asp	Leu	Leu	Lys	Ile	Ile	Lys	Asp	Lys	Asp	Phe
		595				600						605			
Leu	Asp	Asn	Glu	Glu	Asn	Glu	Asp	Ile	Leu	Glu	Asp	Ile	Val	Leu	Thr
	610					615					620				
Leu	Thr	Leu	Phe	Glu	Asp	Arg	Glu	Met	Ile	Glu	Glu	Arg	Leu	Lys	Thr
625					630					635					640
Tyr	Ala	His	Leu	Phe	Asp	Asp	Lys	Val	Met	Lys	Gln	Leu	Lys	Arg	Arg
				645					650					655	
Arg	Tyr	Thr	Gly	Trp	Gly	Arg	Leu	Ser	Arg	Lys	Leu	Ile	Asn	Gly	Ile
			660					665					670		
Arg	Asp	Lys	Gln	Ser	Gly	Lys	Thr	Ile	Leu	Asp	Phe	Leu	Lys	Ser	Asp
		675					680					685			
Gly	Phe	Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ser	Leu
	690					695					700				
Thr	Phe	Lys	Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val	Ser	Gly	Gln	Gly	Asp
705					710					715					720
Ser	Leu	His	Glu	His	Ile	Ala	Asn	Leu	Ala	Gly	Ser	Pro	Ala	Ile	Lys
				725					730					735	
Lys	Gly	Ile	Leu	Gln	Thr	Val	Lys	Val	Val	Asp	Glu	Leu	Val	Lys	Val
			740					745					750		
Met	Gly	Arg	His	Lys	Pro	Glu	Asn	Ile	Val	Ile	Glu	Met	Ala	Arg	Glu
		755					760					765			

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Asn	Gln	Thr	Thr	Gln	Lys	Gly	Gln	Lys	Asn	Ser	Arg	Glu	Arg	Met	Lys
770						775					780				
Arg	Ile	Glu	Glu	Gly	Ile	Lys	Glu	Leu	Gly	Ser	Gln	Ile	Leu	Lys	Glu
785					790					795					800
His	Pro	Val	Glu	Asn	Thr	Gln	Leu	Gln	Asn	Glu	Lys	Leu	Tyr	Leu	Tyr
				805					810					815	
Tyr	Leu	Gln	Asn	Gly	Arg	Asp	Met	Tyr	Val	Asp	Gln	Glu	Leu	Asp	Ile
			820					825					830		
Asn	Arg	Leu	Ser	Asp	Tyr	Asp	Val	Asp	Ala	Ile	Val	Pro	Gln	Ser	Phe
		835					840					845			
Leu	Lys	Asp	Asp	Ser	Ile	Asp	Asn	Lys	Val	Leu	Thr	Arg	Ser	Asp	Lys
		850				855					860				
Asn	Arg	Gly	Lys	Ser	Asp	Asn	Val	Pro	Ser	Glu	Glu	Val	Val	Lys	Lys
865					870					875					880
Met	Lys	Asn	Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	Leu	Ile	Thr	Gln
				885					890					895	
Arg	Lys	Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Ser	Glu
			900					905					910		
Leu	Asp	Lys	Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln
		915					920					925			
Ile	Thr	Lys	His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	Met	Asn	Thr	Lys
						935					940				
Tyr	Asp	Glu	Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	Val	Ile	Thr	Leu
945					950					955					960
Lys	Ser	Lys	Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	Gln	Phe	Tyr	Lys
				965					970					975	
Val	Arg	Glu	Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn
			980					985					990		
Ala	Val	Val	Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	Lys	Leu	Glu	Ser
		995					1000					1005			
Glu	Phe	Val	Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	Arg	Lys	Met	Ile
		1010				1015					1020				
Ala	Lys	Ser	Glu	Gln	Glu	Ile	Gly	Lys	Ala	Thr	Ala	Lys	Tyr	Phe	Phe
1025					1030					1035					1040
Tyr	Ser	Asn	Ile	Met	Asn	Phe	Phe	Lys	Thr	Glu	Ile	Thr	Leu	Ala	Asn
				1045					1050					1055	
Gly	Glu	Ile	Arg	Lys	Arg	Pro	Leu	Ile	Glu	Thr	Asn	Gly	Glu	Thr	Gly
			1060					1065					1070		
Glu	Ile	Val	Trp	Asp	Lys	Gly	Arg	Asp	Phe	Ala	Thr	Val	Arg	Lys	Val
		1075					1080					1085			
Leu	Ser	Met	Pro	Gln	Val	Asn	Ile	Val	Lys	Lys	Thr	Glu	Val	Gln	Thr
		1090				1095					1100				
Gly	Gly	Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	Arg	Asn	Ser	Asp	Lys
1105					1110					1115					1120
Leu	Ile	Ala	Arg	Lys	Lys	Asp	Trp	Asp	Pro	Lys	Lys	Tyr	Gly	Gly	Phe
				1125					1130					1135	
Asp	Ser	Pro	Thr	Val	Ala	Tyr	Ser	Val	Leu	Val	Val	Ala	Lys	Val	Glu
			1140					1145					1150		
Lys	Gly	Lys	Ser	Lys	Lys	Leu	Lys	Ser	Val	Lys	Glu	Leu	Leu	Gly	Ile
		1155					1160					1165			
Thr	Ile	Met	Glu	Arg	Ser	Ser	Phe	Glu	Lys	Asn	Pro	Ile	Asp	Phe	Leu
		1170				1175					1180				
Glu	Ala	Lys	Gly	Tyr	Lys	Glu	Val	Lys	Lys	Asp	Leu	Ile	Ile	Lys	Leu
1185					1190					1195					1200
Pro	Lys	Tyr	Ser	Leu	Phe	Glu	Leu	Glu	Asn	Gly	Arg	Lys	Arg	Met	Leu
				1205					1210					1215	
Ala	Ser	Ala	Gly	Glu	Leu	Gln	Lys	Gly	Asn	Glu	Leu	Ala	Leu	Pro	Ser
			1220					1225					1230		
Lys	Tyr	Val	Asn	Phe	Leu	Tyr	Leu	Ala	Ser	His	Tyr	Glu	Lys	Leu	Lys
		1235					1240					1245			
Gly	Ser	Pro	Glu	Asp	Asn	Glu	Gln	Lys	Gln	Leu	Phe	Val	Glu	Gln	His
		1250				1255					1260				
Lys	His	Tyr	Leu	Asp	Glu	Ile	Ile	Glu	Gln	Ile	Ser	Glu	Phe	Ser	Lys
1265					1270					1275					1280
Arg	Val	Ile	Leu	Ala	Asp	Ala	Asn	Leu	Asp	Lys	Val	Leu	Ser	Ala	Tyr
				1285					1290					1295	
Asn	Lys	His	Arg	Asp	Lys	Pro	Ile	Arg	Glu	Gln	Ala	Glu	Asn	Ile	Ile
			1300					1305					1310		

UCSD097001WOSEQUENCELISTING

His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr
 1315 1320 1325
 Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val
 1330 1335 1340
 Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr
 1345 1350 1355 1360
 Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp Ala Tyr Pro Tyr Asp Val
 1365 1370 1375
 Pro Asp Tyr Ala Ser Leu
 1380

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<211> 1641

<212> PRT

<213> Artificial Sequence

<220>

<223> dCas9-2xNLS-EGFP

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Arg Thr Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn
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 Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys
 20 25 30
 Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn
 35 40 45
 Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr
 50 55 60
 Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg
 65 70 75 80
 Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp
 85 90 95
 Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp
 100 105 110
 Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val
 115 120 125
 Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu
 130 135 140
 Val Asp Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu
 145 150 155 160
 Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu
 165 170 175
 Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln
 180 185 190
 Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val
 195 200 205
 Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu
 210 215 220
 Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe
 225 230 235 240
 Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser
 245 250 255
 Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr
 260 265 270
 Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr
 275 280 285
 Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu
 290 295 300
 Ser Asp Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser
 305 310 315 320
 Ala Ser Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu
 325 330 335
 Leu Lys Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile
 340 345 350
 Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly
 355 360 365
 Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys

UCSD097001WSEQUENCELISTING

370	Met	Asp	Gly	Thr	Glu	Glu	375	Leu	Leu	Val	Lys	Leu	380	Asn	Arg	Glu	Asp	Leu
385	Leu	Arg	Lys	Gln	Arg	Thr	390	Phe	Asp	Asn	Gly	Ser	395	Ile	Pro	His	Gln	Ile
				405	Leu	His	410	Ala	Ile	Leu	Arg	Arg	415	Gln	Glu	Asp	Phe	Tyr
			420	Asp	Asn	Arg	425	Glu	Lys	Ile	Glu	Lys	430	Ile	Leu	Thr	Phe	
	Pro	Phe	435	Tyr	Tyr	Val	440	Gly	Pro	Leu	Ala	Arg	445	Gly	Asn	Ser	Arg	Phe
	Arg	Ile	450	Met	Thr	Arg	455	Ser	Glu	Glu	Thr	Ile	460	Thr	Pro	Trp	Asn	Phe
465	Ala	Trp	470	Thr	Arg	Lys	475	Glu	Glu	Thr	Ile	Thr	480	Pro	Trp	Asn	Phe	
	Glu	Glu	485	Val	Val	Asp	490	Gly	Ala	Ser	Ala	Gln	495	Ser	Phe	Ile	Glu	Arg
	Met	Thr	500	Asn	Phe	Asp	505	Lys	Asn	Leu	Pro	Asn	510	Glu	Lys	Val	Leu	Pro
	His	Ser	515	Leu	Leu	Tyr	520	Glu	Tyr	Phe	Thr	Val	525	Tyr	Asn	Glu	Leu	Thr
	Val	Lys	530	Tyr	Val	Thr	535	Glu	Gly	Met	Arg	Lys	540	Pro	Ala	Phe	Leu	Ser
	Glu	Gln	545	Lys	Lys	Ala	550	Ile	Val	Asp	Leu	Leu	555	Phe	Lys	Thr	Asn	Arg
	Val	Thr	565	Val	Lys	Gln	570	Leu	Lys	Glu	Asp	Tyr	575	Phe	Lys	Lys	Ile	Glu
	Phe	Asp	580	Ser	Val	Glu	585	Ile	Ser	Gly	Val	Glu	590	Asp	Arg	Phe	Asn	Ala
	Leu	Gly	595	Thr	Tyr	His	600	Asp	Leu	Leu	Lys	Ile	605	Ile	Lys	Asp	Lys	Asp
	Leu	Asp	610	Asn	Glu	Glu	615	Asn	Glu	Asp	Ile	Leu	620	Glu	Asp	Ile	Val	Leu
	Leu	Thr	625	Leu	Phe	Glu	630	Asp	Arg	Glu	Met	Ile	635	Glu	Arg	Leu	Lys	Thr
	Tyr	Ala	645	His	Leu	Phe	650	Asp	Asp	Lys	Val	Met	655	Lys	Gln	Leu	Lys	Arg
	Arg	Tyr	660	Thr	Gly	Trp	665	Gly	Arg	Leu	Ser	Arg	670	Lys	Leu	Ile	Asn	Gly
	Arg	Asp	675	Lys	Gln	Ser	680	Lys	Gly	Lys	Thr	Ile	685	Leu	Asp	Phe	Leu	Ser
	Gly	Phe	690	Ala	Asn	Arg	695	Asn	Phe	Met	Gln	Leu	700	Ile	His	Asp	Asp	Ser
	Thr	Phe	705	Lys	Glu	Asp	710	Gln	Lys	Ala	Gln	Val	715	Ser	Gly	Gln	Gly	Asp
	Ser	Leu	725	His	Glu	His	730	Ile	Ala	Asn	Leu	Ala	735	Gly	Ser	Pro	Ala	Ile
	Lys	Gly	740	Ile	Leu	Gln	745	Thr	Val	Lys	Val	Val	750	Asp	Glu	Leu	Val	Lys
	Met	Gly	755	Arg	His	Lys	760	Pro	Glu	Asn	Ile	Val	765	Ile	Glu	Met	Ala	Arg
	Asn	Gln	770	Thr	Thr	Gln	775	Lys	Gly	Gln	Lys	Asn	780	Ser	Arg	Glu	Arg	Met
	Arg	Ile	785	Glu	Glu	Gly	790	Ile	Lys	Glu	Leu	Gly	795	Ser	Gln	Ile	Leu	Lys
	His	Pro	805	Val	Glu	Asn	810	Thr	Gln	Leu	Gln	Asn	815	Glu	Lys	Leu	Tyr	Leu
	Tyr	Leu	820	Gln	Asn	Gly	825	Arg	Asp	Met	Tyr	Val	830	Asp	Gln	Glu	Leu	Asp
	Asn	Arg	835	Leu	Ser	Asp	840	Tyr	Asp	Val	Asp	Ala	845	Ile	Val	Pro	Gln	Ser
	Leu	Lys	850	Asp	Asp	Ser	855	Ile	Asp	Asn	Lys	Val	860	Leu	Thr	Arg	Ser	Asp
	Asn	Arg	865	Gly	Lys	Ser	870	Asp	Asn	Val	Pro	Ser	875	Glu	Glu	Val	Val	Lys
	Met	Lys	885	Asn	Tyr	Trp	890	Arg	Gln	Leu	Leu	Asn	895	Ala	Lys	Leu	Ile	Thr
	Arg	Lys	900	Phe	Asp	Asn	905	Leu	Thr	Lys	Ala	Glu	910	Arg	Gly	Gly	Leu	Ser
	Leu	Asp	910	Lys	Ala	Gly		Phe	Ile	Lys	Arg	Gln		Leu	Val	Glu	Thr	Arg

UCSD097001WSEQUENCELISTING

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      915      920      925
Ile Thr Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys
930      935      940
Tyr Asp Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu
945      950      955      960
Lys Ser Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys
965      970      975
Val Arg Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn
980      985      990
Ala Val Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser
995      1000      1005
Glu Phe Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile
1010      1015      1020
Ala Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025      1030      1035      1040
Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala Asn
1045      1050      1055
Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu Thr Gly
1060      1065      1070
Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg Lys Val
1075      1080      1085
Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr
1090      1095      1100
Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys
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Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe
1125      1130      1135
Asp Ser Pro Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val Glu
1140      1145      1150
Lys Gly Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile
1155      1160      1165
Thr Ile Met Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp Phe Leu
1170      1175      1180
Glu Ala Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu
1185      1190      1195      1200
Pro Lys Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu
1205      1210      1215
Ala Ser Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser
1220      1225      1230
Lys Tyr Val Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys
1235      1240      1245
Gly Ser Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His
1250      1255      1260
Lys His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265      1270      1275      1280
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr
1285      1290      1295
Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile Ile
1300      1305      1310
His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr
1315      1320      1325
Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val
1330      1335      1340
Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr
1345      1350      1355      1360
Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp Ala Tyr Pro Tyr Asp Val
1365      1370      1375
Pro Asp Tyr Ala Ser Leu Gly Ser Gly Ser Pro Lys Lys Lys Arg Lys
1380      1385      1390
Val Glu Asp Pro Lys Lys Lys Arg Lys Val Asp Val Ser Lys Gly Glu
1395      1400      1405
Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
1410      1415      1420
Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
1425      1430      1435      1440
Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
1445      1450      1455
Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln

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UCSD097001WSEQUENCELISTING

1460 1465 1470
 Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
 1475 1480 1485
 Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
 1490 1495 1500
 Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
 1505 1510 1515 1520
 Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
 1525 1530 1535
 Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
 1540 1545 1550
 Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
 1555 1560 1565
 Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
 1570 1575 1580
 Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
 1585 1590 1595 1600
 Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
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 Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1635 1640

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 Lys Tyr Ile Leu Val Val Pro Leu Ile Val Ile Asn Glu Leu Asp Gly
 35 40 45
 Leu Ala Lys Gly Gln Glu Thr Asp His Arg Ala Gly Gly Tyr Ala Arg
 50 55 60
 Val Val Gln Glu Lys Ala Arg Lys Ser Ile Glu Phe Leu Glu Gln Arg
 65 70 75 80
 Phe Glu Ser Arg Asp Ser Cys Leu Arg Ala Leu Thr Ser Arg Gly Asn
 85 90 95
 Glu Leu Glu Ser Ile Ala Phe Arg Ser Glu Asp Ile Thr Gly Gln Leu
 100 105 110
 Gly Asn Asn Asp Asp Leu Ile Leu Ser Cys Cys Leu His Tyr Cys Lys
 115 120 125
 Asp Lys Ala Lys Asp Phe Met Pro Ala Ser Lys Glu Glu Pro Ile Arg
 130 135 140
 Leu Leu Arg Glu Val Val Leu Leu Thr Asp Asp Arg Asn Leu Arg Val
 145 150 155 160
 Lys Ala Leu Thr Arg Asn Val Pro Val Arg Asp Ile Pro Ala Phe Leu
 165 170 175
 Thr Trp Ala Gln Val Gly Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
 180 185 190
 Ser Ala Thr Pro Glu Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile
 195 200 205
 Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val
 210 215 220
 Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile
 225 230 235 240
 Lys Lys Asn Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala
 245 250 255
 Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Tyr Thr Arg Arg
 260 265 270

UCSD097001WSEQUENCELISTING

Lys	Asn	Arg	Ile	Cys	Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met	Ala
		275					280					285			
Lys	Val	Asp	Asp	Ser	Phe	Phe	His	Arg	Leu	Glu	Glu	Ser	Phe	Leu	Val
	290					295					300				
Glu	Glu	Asp	Lys	Lys	His	Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Ile	Val
305					310					315					320
Asp	Glu	Val	Ala	Tyr	His	Glu	Lys	Tyr	Pro	Thr	Ile	Tyr	His	Leu	Arg
				325					330					335	
Lys	Lys	Leu	Val	Asp	Ser	Thr	Asp	Lys	Ala	Asp	Leu	Arg	Leu	Ile	Tyr
			340					345					350		
Leu	Ala	Leu	Ala	His	Met	Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile	Glu
		355					360					365			
Gly	Asp	Leu	Asn	Pro	Asp	Asn	Ser	Asp	Val	Asp	Lys	Leu	Phe	Ile	Gln
	370					375					380				
Leu	Val	Gln	Thr	Tyr	Asn	Gln	Leu	Phe	Glu	Glu	Asn	Pro	Ile	Asn	Ala
385					390					395					400
Ser	Gly	Val	Asp	Ala	Lys	Ala	Ile	Leu	Ser	Ala	Arg	Leu	Ser	Lys	Ser
				405					410					415	
Arg	Arg	Leu	Glu	Asn	Leu	Ile	Ala	Gln	Leu	Pro	Gly	Glu	Lys	Lys	Asn
			420					425					430		
Gly	Leu	Phe	Gly	Asn	Leu	Ile	Ala	Leu	Ser	Leu	Gly	Leu	Thr	Pro	Asn
		435					440					445			
Phe	Lys	Ser	Asn	Phe	Asp	Leu	Ala	Glu	Asp	Ala	Lys	Leu	Gln	Leu	Ser
	450					455					460				
Lys	Asp	Thr	Tyr	Asp	Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile	Gly
465					470					475					480
Asp	Gln	Tyr	Ala	Asp	Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp	Ala
				485					490					495	
Ile	Leu	Leu	Ser	Asp	Ile	Leu	Arg	Val	Asn	Thr	Glu	Ile	Thr	Lys	Ala
			500					505					510		
Pro	Leu	Ser	Ala	Ser	Met	Ile	Lys	Arg	Tyr	Asp	Glu	His	His	Gln	Asp
		515					520					525			
Leu	Thr	Leu	Leu	Lys	Ala	Leu	Val	Arg	Gln	Gln	Leu	Pro	Glu	Lys	Tyr
	530					535					540				
Lys	Glu	Ile	Phe	Phe	Asp	Gln	Ser	Lys	Asn	Gly	Tyr	Ala	Gly	Tyr	Ile
545					550					555					560
Asp	Gly	Gly	Ala	Ser	Gln	Glu	Glu	Phe	Tyr	Lys	Phe	Ile	Lys	Pro	Ile
				565					570					575	
Leu	Glu	Lys	Met	Asp	Gly	Thr	Glu	Glu	Leu	Leu	Val	Lys	Leu	Asn	Arg
			580					585					590		
Glu	Asp	Leu	Leu	Arg	Lys	Gln	Arg	Thr	Phe	Asp	Asn	Gly	Ser	Ile	Pro
		595					600					605			
His	Gln	Ile	His	Leu	Gly	Glu	Leu	His	Ala	Ile	Leu	Arg	Arg	Gln	Glu
	610					615					620				
Asp	Phe	Tyr	Pro	Phe	Leu	Lys	Asp	Asn	Arg	Glu	Lys	Ile	Glu	Lys	Ile
625					630					635					640
Leu	Thr	Phe	Arg	Ile	Pro	Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Asn
				645					650					655	
Ser	Arg	Phe	Ala	Trp	Met	Thr	Arg	Lys	Ser	Glu	Glu	Thr	Ile	Thr	Pro
			660					665					670		
Trp	Asn	Phe	Glu	Glu	Val	Val	Asp	Lys	Gly	Ala	Ser	Ala	Gln	Ser	Phe
		675					680					685			
Ile	Glu	Arg	Met	Thr	Asn	Phe	Asp	Lys	Asn	Leu	Pro	Asn	Glu	Lys	Val
	690					695					700				
Leu	Pro	Lys	His	Ser	Leu	Leu	Tyr	Glu	Tyr	Phe	Thr	Val	Tyr	Asn	Glu
705					710					715					720
Leu	Thr	Lys	Val	Lys	Tyr	Val	Thr	Glu	Gly	Met	Arg	Lys	Pro	Ala	Phe
				725					730					735	
Leu	Ser	Gly	Glu	Gln	Lys	Lys	Ala	Ile	Val	Asp	Leu	Leu	Phe	Lys	Thr
			740					745					750		
Asn	Arg	Lys	Val	Thr	Val	Lys	Gln	Leu	Lys	Glu	Asp	Tyr	Phe	Lys	Lys
		755					760					765			
Ile	Glu	Cys	Phe	Asp	Ser	Val	Glu	Ile	Ser	Gly	Val	Glu	Asp	Arg	Phe
	770					775					780				
Asn	Ala	Ser	Leu	Gly	Thr	Tyr	His	Asp	Leu	Leu	Lys	Ile	Ile	Lys	Asp
785					790					795					800
Lys	Asp	Phe	Leu	Asp	Asn	Glu	Glu	Asn	Glu	Asp	Ile	Leu	Glu	Asp	Ile
				805					810					815	

UCSD097001WSEQUENCELISTING

Val	Leu	Thr	Leu	Thr	Leu	Phe	Glu	Asp	Arg	Glu	Met	Ile	Glu	Glu	Arg
			820					825					830		
Leu	Lys	Thr	Tyr	Ala	His	Leu	Phe	Asp	Asp	Lys	Val	Met	Lys	Gln	Leu
		835					840					845			
Lys	Arg	Arg	Arg	Tyr	Thr	Gly	Trp	Gly	Arg	Leu	Ser	Arg	Lys	Leu	Ile
	850					855					860				
Asn	Gly	Ile	Arg	Asp	Lys	Gln	Ser	Gly	Lys	Thr	Ile	Leu	Asp	Phe	Leu
865					870					875					880
Lys	Ser	Asp	Gly	Phe	Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp
				885					890					895	
Asp	Ser	Leu	Thr	Phe	Lys	Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val	Ser	Gly
			900					905					910		
Gln	Gly	Asp	Ser	Leu	His	Glu	His	Ile	Ala	Asn	Leu	Ala	Gly	Ser	Pro
		915					920					925			
Ala	Ile	Lys	Lys	Gly	Ile	Leu	Gln	Thr	Val	Lys	Val	Val	Asp	Glu	Leu
	930					935					940				
Val	Lys	Val	Met	Gly	Arg	His	Lys	Pro	Glu	Asn	Ile	Val	Ile	Glu	Met
945					950					955					960
Ala	Arg	Glu	Asn	Gln	Thr	Thr	Gln	Lys	Gly	Gln	Lys	Asn	Ser	Arg	Glu
				965					970					975	
Arg	Met	Lys	Arg	Ile	Glu	Glu	Gly	Ile	Lys	Glu	Leu	Gly	Ser	Gln	Ile
			980					985					990		
Leu	Lys	Glu	His	Pro	Val	Glu	Asn	Thr	Gln	Leu	Gln	Asn	Glu	Lys	Leu
		995					1000					1005			
Tyr	Leu	Tyr	Tyr	Leu	Gln	Asn	Gly	Arg	Asp	Met	Tyr	Val	Asp	Gln	Glu
	1010					1015					1020				
Leu	Asp	Ile	Asn	Arg	Leu	Ser	Asp	Tyr	Asp	Val	Asp	Ala	Ile	Val	Pro
1025					1030					1035					1040
Gln	Ser	Phe	Leu	Lys	Asp	Asp	Ser	Ile	Asp	Asn	Lys	Val	Leu	Thr	Arg
				1045					1050					1055	
Ser	Asp	Lys	Asn	Arg	Gly	Lys	Ser	Asp	Asn	Val	Pro	Ser	Glu	Glu	Val
			1060					1065					1070		
Val	Lys	Lys	Met	Lys	Asn	Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	Leu
		1075					1080					1085			
Ile	Thr	Gln	Arg	Lys	Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly
	1090					1095					1100				
Leu	Ser	Glu	Leu	Asp	Lys	Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu
1105					1110					1115					1120
Thr	Arg	Gln	Ile	Thr	Lys	His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	Met
				1125					1130					1135	
Asn	Thr	Lys	Tyr	Asp	Glu	Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	Val
			1140					1145					1150		
Ile	Thr	Leu	Lys	Ser	Lys	Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	Gln
		1155					1160					1165			
Phe	Tyr	Lys	Val	Arg	Glu	Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	Ala
	1170					1175					1180				
Tyr	Leu	Asn	Ala	Val	Val	Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	Lys
1185					1190					1195					1200
Leu	Glu	Ser	Glu	Phe	Val	Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	Arg
				1205					1210					1215	
Lys	Met	Ile	Ala	Lys	Ser	Glu	Gln	Glu	Ile	Gly	Lys	Ala	Thr	Ala	Lys
			1220					1225					1230		
Tyr	Phe	Phe	Tyr	Ser	Asn	Ile	Met	Asn	Phe	Phe	Lys	Thr	Glu	Ile	Thr
		1235					1240						1245		
Leu	Ala	Asn	Gly	Glu	Ile	Arg	Lys	Arg	Pro	Leu	Ile	Glu	Thr	Asn	Gly
	1250					1255					1260				
Glu	Thr	Gly	Glu	Ile	Val	Trp	Asp	Lys	Gly	Arg	Asp	Phe	Ala	Thr	Val
1265					1270					1275					1280
Arg	Lys	Val	Leu	Ser	Met	Pro	Gln	Val	Asn	Ile	Val	Lys	Lys	Thr	Glu
				1285					1290					1295	
Val	Gln	Thr	Gly	Gly	Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	Arg	Asn
			1300					1305					1310		
Ser	Asp	Lys	Leu	Ile	Ala	Arg	Lys	Lys	Asp	Trp	Asp	Pro	Lys	Lys	Tyr
		1315					1320					1325			
Gly	Gly	Phe	Asp	Ser	Pro	Thr	Val	Ala	Tyr	Ser	Val	Leu	Val	Val	Ala
	1330					1335					1340				
Lys	Val	Glu	Lys	Gly	Lys	Ser	Lys	Lys	Leu	Lys	Ser	Val	Lys	Glu	Leu
1345					1350					1355					1360

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Leu Gly Ile Thr Ile Met Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile
 1365 1370 1375
 Asp Phe Leu Glu Ala Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile
 1380 1385 1390
 Ile Lys Leu Pro Lys Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys
 1395 1400 1405
 Arg Met Leu Ala Ser Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala
 1410 1415 1420
 Leu Pro Ser Lys Tyr Val Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu
 1425 1430 1435 1440
 Lys Leu Lys Gly Ser Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val
 1445 1450 1455
 Glu Gln His Lys His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu
 1460 1465 1470
 Phe Ser Lys Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu
 1475 1480 1485
 Ser Ala Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu
 1490 1495 1500
 Asn Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
 1505 1510 1515 1520
 Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr
 1525 1530 1535
 Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu
 1540 1545 1550
 Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp Ala Tyr Pro
 1555 1560 1565
 Tyr Asp Val Pro Asp Tyr Ala Ser Leu Gly Ser Gly Ser Pro Lys Lys
 1570 1575 1580
 Lys Arg Lys Val Glu Asp Pro Lys Lys Lys Arg Lys Val Asp Val
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<210> 34

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<212> PRT

<213> Artificial Sequence

<220>

<223> Telomerase-binding protein EST1A encoded by SMG6
gene

<400> 34

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 Gly Ile Leu Ala Thr Leu Ala Pro Gln Ala Gly Ser Arg Glu Asn Met
 20 25 30
 Lys Glu Leu Lys Glu Ala Arg Pro Arg Lys Asp Asn Arg Arg Pro Asp
 35 40 45
 Leu Glu Ile Tyr Lys Pro Gly Leu Ser Arg Leu Arg Asn Lys Pro Lys
 50 55 60
 Ile Lys Glu Pro Pro Gly Ser Glu Glu Phe Lys Asp Glu Ile Val Asn
 65 70 75 80
 Asp Arg Asp Cys Ser Ala Val Glu Asn Gly Thr Gln Pro Val Lys Asp
 85 90 95
 Val Cys Lys Glu Leu Asn Asn Gln Glu Asn Gly Pro Ile Asp Pro
 100 105 110
 Glu Asn Asn Arg Gly Gln Glu Ser Phe Pro Arg Thr Ala Gly Gln Glu
 115 120 125
 Asp Arg Ser Leu Lys Ile Ile Lys Arg Thr Lys Lys Pro Asp Leu Gln
 130 135 140
 Ile Tyr Gln Pro Gly Arg Arg Leu Gln Thr Val Ser Lys Glu Ser Ala
 145 150 155 160
 Ser Arg Val Glu Glu Glu Glu Val Leu Asn Gln Val Glu Gln Leu Arg
 165 170 175
 Val Glu Glu Asp Glu Cys Arg Gly Asn Val Ala Lys Glu Glu Val Ala
 180 185 190
 Asn Lys Pro Asp Arg Ala Glu Ile Glu Lys Ser Pro Gly Gly Arg
 195 200 205

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Val	Gly	Ala	Ala	Lys	Gly	Glu	Lys	Gly	Lys	Arg	Met	Gly	Lys	Gly	Glu
	210					215					220				
Gly	Val	Arg	Glu	Thr	His	Asp	Asp	Pro	Ala	Arg	Gly	Arg	Pro	Gly	Ser
225					230					235					240
Ala	Lys	Arg	Tyr	Ser	Arg	Ser	Asp	Lys	Arg	Arg	Asn	Arg	Tyr	Arg	Thr
				245					250					255	
Arg	Ser	Thr	Ser	Ser	Ala	Gly	Ser	Asn	Asn	Ser	Ala	Glu	Gly	Ala	Gly
			260					265					270		
Leu	Thr	Asp	Asn	Gly	Cys	Arg	Arg	Arg	Gln	Asp	Arg	Thr	Lys	Glu	
		275					280					285			
Arg	Pro	Arg	Leu	Lys	Lys	Gln	Val	Ser	Val	Ser	Ser	Thr	Asp	Ser	Leu
	290					295					300				
Asp	Glu	Asp	Arg	Ile	Asp	Glu	Pro	Asp	Gly	Leu	Gly	Pro	Arg	Arg	Ser
305					310					315					320
Ser	Glu	Arg	Lys	Arg	His	Leu	Glu	Arg	Asn	Trp	Ser	Gly	Arg	Gly	Glu
				325					330					335	
Gly	Glu	Gln	Lys	Asn	Ser	Ala	Lys	Glu	Tyr	Arg	Gly	Thr	Leu	Arg	Val
			340					345					350		
Thr	Phe	Asp	Ala	Glu	Ala	Met	Asn	Lys	Glu	Ser	Pro	Met	Val	Arg	Ser
		355					360					365			
Ala	Arg	Asp	Asp	Met	Asp	Arg	Gly	Lys	Pro	Asp	Lys	Gly	Leu	Ser	Ser
	370					375					380				
Gly	Gly	Lys	Gly	Ser	Glu	Lys	Gln	Glu	Ser	Lys	Asn	Pro	Lys	Gln	Glu
385					390					395					400
Leu	Arg	Gly	Arg	Gly	Arg	Gly	Ile	Leu	Ile	Leu	Pro	Ala	His	Thr	Thr
				405				410					415		
Leu	Ser	Val	Asn	Ser	Ala	Gly	Ser	Pro	Glu	Ser	Ala	Pro	Leu	Gly	Pro
			420					425					430		
Arg	Leu	Leu	Phe	Gly	Ser	Gly	Ser	Lys	Gly	Ser	Arg	Ser	Trp	Gly	Arg
		435					440					445			
Gly	Gly	Thr	Thr	Arg	Arg	Leu	Trp	Asp	Pro	Asn	Asn	Pro	Asp	Gln	Lys
	450					455					460				
Pro	Ala	Leu	Lys	Thr	Gln	Thr	Pro	Gln	Leu	His	Phe	Leu	Asp	Thr	Asp
465					470					475					480
Asp	Glu	Val	Ser	Pro	Thr	Ser	Trp	Gly	Asp	Ser	Arg	Gln	Ala	Gln	Ala
				485					490					495	
Ser	Tyr	Tyr	Lys	Phe	Gln	Asn	Ser	Asp	Asn	Pro	Tyr	Tyr	Tyr	Pro	Arg
			500					505					510		
Thr	Pro	Gly	Pro	Ala	Ser	Gln	Tyr	Pro	Tyr	Thr	Gly	Tyr	Asn	Pro	Leu
		515					520					525			
Gln	Tyr	Pro	Val	Gly	Pro	Thr	Asn	Gly	Val	Tyr	Pro	Gly	Pro	Tyr	Tyr
	530					535					540				
Pro	Gly	Tyr	Pro	Thr	Pro	Ser	Gly	Gln	Tyr	Val	Cys	Ser	Pro	Leu	Pro
545					550					555					560
Thr	Ser	Thr	Met	Ser	Pro	Glu	Glu	Val	Glu	Gln	His	Met	Arg	Asn	Leu
				565					570					575	
Gln	Gln	Gln	Glu	Leu	His	Arg	Leu	Leu	Arg	Val	Ala	Asp	Asn	Gln	Glu
			580					585					590		
Leu	Gln	Leu	Ser	Asn	Leu	Leu	Ser	Arg	Asp	Arg	Ile	Ser	Pro	Glu	Gly
		595					600					605			
Leu	Glu	Lys	Met	Ala	Gln	Leu	Arg	Ala	Glu	Leu	Leu	Gln	Leu	Tyr	Glu
	610					615					620				
Arg	Cys	Ile	Leu	Leu	Asp	Ile	Glu	Phe	Ser	Asp	Asn	Gln	Asn	Val	Asp
625					630					635					640
Gln	Ile	Leu	Trp	Lys	Asn	Ala	Phe	Tyr	Gln	Val	Ile	Glu	Lys	Phe	Arg
				645					650					655	
Gln	Leu	Val	Lys	Asp	Pro	Asn	Val	Glu	Asn	Pro	Glu	Gln	Ile	Arg	Asn
			660					665					670		
Arg	Leu	Leu	Glu	Leu	Leu	Asp	Glu	Gly	Ser	Asp	Phe	Phe	Asp	Ser	Leu
		675					680					685			
Leu	Gln	Lys	Leu	Gln	Val	Thr	Tyr	Lys	Phe	Lys	Leu	Glu	Asp	Tyr	Met
	690					695					700				
Asp	Gly	Leu	Ala	Ile	Arg	Ser	Lys	Pro	Leu	Arg	Lys	Thr	Val	Lys	Tyr
705					710					715					720
Ala	Leu	Ile	Ser	Ala	Gln	Arg	Cys	Met	Ile	Cys	Gln	Gly	Asp	Ile	Ala
				725					730					735	
Arg	Tyr	Arg	Glu	Gln	Ala	Ser	Asp	Thr	Ala	Asn	Tyr	Gly	Lys	Ala	Arg
			740					745					750		

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Ser	Trp	Tyr	Leu	Lys	Ala	Gln	His	Ile	Ala	Pro	Lys	Asn	Gly	Arg	Pro
		755					760					765			
Tyr	Asn	Gln	Leu	Ala	Leu	Leu	Ala	Val	Tyr	Thr	Arg	Arg	Lys	Leu	Asp
	770					775					780				
Ala	Val	Tyr	Tyr	Tyr	Met	Arg	Ser	Leu	Ala	Ala	Ser	Asn	Pro	Ile	Leu
785					790				795						800
Thr	Ala	Lys	Glu	Ser	Leu	Met	Ser	Leu	Phe	Glu	Glu	Thr	Lys	Arg	Lys
				805					810					815	
Ala	Glu	Gln	Met	Glu	Lys	Lys	Gln	His	Glu	Glu	Phe	Asp	Leu	Ser	Pro
			820					825					830		
Asp	Gln	Trp	Arg	Lys	Gly	Lys	Lys	Ser	Thr	Phe	Arg	His	Val	Gly	Asp
	835						840					845			
Asp	Thr	Thr	Arg	Leu	Glu	Ile	Trp	Ile	His	Pro	Ser	His	Pro	Arg	Ser
	850					855					860				
Ser	Gln	Gly	Thr	Glu	Ser	Gly	Lys	Asp	Ser	Glu	Gln	Glu	Asn	Gly	Leu
865					870					875					880
Gly	Ser	Leu	Ser	Pro	Ser	Asp	Leu	Asn	Lys	Arg	Phe	Ile	Leu	Ser	Phe
				885					890					895	
Leu	His	Ala	His	Gly	Lys	Leu	Phe	Thr	Arg	Ile	Gly	Met	Glu	Thr	Phe
			900					905					910		
Pro	Ala	Val	Ala	Glu	Lys	Val	Leu	Lys	Glu	Phe	Gln	Val	Leu	Leu	Gln
		915					920					925			
His	Ser	Pro	Ser	Pro	Ile	Gly	Ser	Thr	Arg	Met	Leu	Gln	Leu	Met	Thr
	930					935					940				
Ile	Asn	Met	Phe	Ala	Val	His	Asn	Ser	Gln	Leu	Lys	Asp	Cys	Phe	Ser
945					950					955					960
Glu	Glu	Cys	Arg	Ser	Val	Ile	Gln	Glu	Gln	Ala	Ala	Ala	Leu	Gly	Leu
				965					970					975	
Ala	Met	Phe	Ser	Leu	Leu	Val	Arg	Arg	Cys	Thr	Cys	Leu	Leu	Lys	Glu
			980					985					990		
Ser	Ala	Lys	Ala	Gln	Leu	Ser	Ser	Pro	Glu	Asp	Gln	Asp	Asp	Gln	Asp
		995					1000					1005			
Asp	Ile	Lys	Val	Ser	Ser	Phe	Val	Pro	Asp	Leu	Lys	Glu	Leu	Leu	Pro
	1010					1015					1020				
Ser	Val	Lys	Val	Trp	Ser	Asp	Trp	Met	Leu	Gly	Tyr	Pro	Asp	Thr	Trp
1025					1030					1035				1040	
Asn	Pro	Pro	Pro	Thr	Ser	Leu	Asp	Leu	Pro	Ser	His	Val	Ala	Val	Asp
				1045					1050					1055	
Val	Trp	Ser	Thr	Leu	Ala	Asp	Phe	Cys	Asn	Ile	Leu	Thr	Ala	Val	Asn
			1060				1065						1070		
Gln	Ser	Glu	Val	Pro	Leu	Tyr	Lys	Asp	Pro	Asp	Asp	Asp	Leu	Thr	Leu
		1075					1080					1085			
Leu	Ile	Leu	Glu	Glu	Asp	Arg	Leu	Leu	Ser	Gly	Phe	Val	Pro	Leu	Leu
	1090					1095					1100				
Ala	Ala	Pro	Gln	Asp	Pro	Cys	Tyr	Val	Glu	Lys	Thr	Ser	Asp	Lys	Val
1105					1110					1115					1120
Ile	Ala	Ala	Asp	Cys	Lys	Arg	Val	Thr	Val	Leu	Lys	Tyr	Phe	Leu	Glu
				1125					1130					1135	
Ala	Leu	Cys	Gly	Gln	Glu	Glu	Pro	Leu	Leu	Ala	Phe	Lys	Gly	Gly	Lys
			1140					1145					1150		
Tyr	Val	Ser	Val	Ala	Pro	Val	Pro	Asp	Thr	Met	Gly	Lys	Glu	Met	Gly
		1155					1160					1165			
Ser	Gln	Glu	Gly	Thr	Arg	Leu	Glu	Asp	Glu	Glu	Glu	Asp	Val	Val	Ile
	1170					1175					1180				
Glu	Asp	Phe	Glu	Glu	Asp	Ser	Glu	Ala	Glu	Gly	Ser	Gly	Gly	Glu	Asp
1185					1190					1195					1200
Asp	Ile	Arg	Glu	Leu	Arg	Ala	Lys	Lys	Leu	Ala	Leu	Ala	Arg	Lys	Ile
				1205					1210					1215	
Ala	Glu	Gln	Gln	Arg	Arg	Gln	Glu	Lys	Ile	Gln	Ala	Val	Leu	Glu	Asp
			1220					1225					1230		
His	Ser	Gln	Met	Arg	Gln	Met	Glu	Leu	Glu	Ile	Arg	Pro	Leu	Phe	Leu
		1235					1240					1245			
Val	Pro	Asp	Thr	Asn	Gly	Phe	Ile	Asp	His	Leu	Ala	Ser	Leu	Ala	Arg
	1250					1255					1260				
Leu	Leu	Glu	Ser	Arg	Lys	Tyr	Ile	Leu	Val	Val	Pro	Leu	Ile	Val	Ile
1265					1270					1275					1280
Asn	Glu	Leu	Asp	Gly	Leu	Ala	Lys	Gly	Gln	Glu	Thr	Asp	His	Arg	Ala
				1285					1290					1295	

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Gly Gly Tyr Ala Arg Val Val Gln Glu Lys Ala Arg Lys Ser Ile Glu
1300 1305 1310
Phe Leu Glu Gln Arg Phe Glu Ser Arg Asp Ser Cys Leu Arg Ala Leu
1315 1320 1325
Thr Ser Arg Gly Asn Glu Leu Glu Ser Ile Ala Phe Arg Ser Glu Asp
1330 1335 1340
Ile Thr Gly Gln Leu Gly Asn Asn Asp Asp Leu Ile Leu Ser Cys Cys
1345 1350 1355 1360
Leu His Tyr Cys Lys Asp Lys Ala Lys Asp Phe Met Pro Ala Ser Lys
1365 1370 1375
Glu Glu Pro Ile Arg Leu Leu Arg Glu Val Val Leu Leu Thr Asp Asp
1380 1385 1390
Arg Asn Leu Arg Val Lys Ala Leu Thr Arg Asn Val Pro Val Arg Asp
1395 1400 1405
Ile Pro Ala Phe Leu Thr Trp Ala Gln Val Gly
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<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> PIN domain

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Leu Ala Arg Leu Leu Glu Ser Arg Lys Tyr Ile Leu Val Val Pro Leu
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Ile Val Ile Asn Glu Leu Asp Gly Leu Ala Lys Gly Gln Glu Thr Asp
35 40 45
His Arg Ala Gly Gly Tyr Ala Arg Val Val Gln Glu Lys Ala Arg Lys
50 55 60
Ser Ile Glu Phe Leu Glu Gln Arg Phe Glu Ser Arg Asp Ser Cys Leu
65 70 75 80
Arg Ala Leu Thr Ser Arg Gly Asn Glu Leu Glu Ser Ile Ala Phe Arg
85 90 95
Ser Glu Asp Ile Thr Gly Gln Leu Gly Asn Asn Asp Asp Leu Ile Leu
100 105 110
Ser Cys Cys Leu His Tyr Cys Lys Asp Lys Ala Lys Asp Phe Met Pro
115 120 125
Ala Ser Lys Glu Glu Pro Ile Arg Leu Leu Arg Glu Val Val Leu Leu
130 135 140
Thr Asp Asp Arg Asn Leu Arg Val
145 150

<210> 36
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN linker

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Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser
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<210> 37
<211> 1600
<212> PRT
<213> Artificial Sequence

<220>

UCSD097001WOSEQUENCELISTING

<223> PIN-XTEN-dCas9

<400> 37

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			20					25					30		
Arg	Lys	Tyr	Ile	Leu	Val	Val	Pro	Leu	Ile	Val	Ile	Asn	Glu	Leu	Asp
		35					40					45			
Gly	Leu	Ala	Lys	Gly	Gln	Glu	Thr	Asp	His	Arg	Ala	Gly	Gly	Tyr	Ala
	50				55						60				
Arg	Val	Val	Gln	Glu	Lys	Ala	Arg	Lys	Ser	Ile	Glu	Phe	Leu	Glu	Gln
65				70					75						80
Arg	Phe	Glu	Ser	Arg	Asp	Ser	Cys	Leu	Arg	Ala	Leu	Thr	Ser	Arg	Gly
				85					90					95	
Asn	Glu	Leu	Glu	Ser	Ile	Ala	Phe	Arg	Ser	Glu	Asp	Ile	Thr	Gly	Gln
			100					105					110		
Leu	Gly	Asn	Asn	Asp	Asp	Leu	Ile	Leu	Ser	Cys	Cys	Leu	His	Tyr	Cys
		115					120					125			
Lys	Asp	Lys	Ala	Lys	Asp	Phe	Met	Pro	Ala	Ser	Lys	Glu	Glu	Pro	Ile
	130					135					140				
Arg	Leu	Leu	Arg	Glu	Val	Val	Leu	Leu	Thr	Asp	Asp	Arg	Asn	Leu	Arg
145				150						155					160
Val	Lys	Ala	Leu	Thr	Arg	Asn	Val	Pro	Val	Arg	Asp	Ile	Pro	Ala	Phe
				165					170					175	
Leu	Thr	Trp	Ala	Gln	Val	Gly	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser
			180					185					190		
Glu	Ser	Ala	Thr	Pro	Glu	Ser	Asp	Lys	Lys	Tyr	Ser	Ile	Gly	Leu	Ala
		195					200					205			
Ile	Gly	Thr	Asn	Ser	Val	Gly	Trp	Ala	Val	Ile	Thr	Asp	Glu	Tyr	Lys
	210					215					220				
Val	Pro	Ser	Lys	Lys	Phe	Lys	Val	Leu	Gly	Asn	Thr	Asp	Arg	His	Ser
225					230					235					240
Ile	Lys	Lys	Asn	Leu	Ile	Gly	Ala	Leu	Leu	Phe	Asp	Ser	Gly	Glu	Thr
			245						250					255	
Ala	Glu	Ala	Thr	Arg	Leu	Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg
			260					265					270		
Arg	Lys	Asn	Arg	Ile	Cys	Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met
		275					280					285			
Ala	Lys	Val	Asp	Asp	Ser	Phe	Phe	His	Arg	Leu	Glu	Glu	Ser	Phe	Leu
	290					295					300				
Val	Glu	Glu	Asp	Lys	Lys	His	Glu	Arg	His	Pro	Ile	Phe	Gly	Asn	Ile
305					310					315					320
Val	Asp	Glu	Val	Ala	Tyr	His	Glu	Lys	Tyr	Pro	Thr	Ile	Tyr	His	Leu
				325					330					335	
Arg	Lys	Lys	Leu	Val	Asp	Ser	Thr	Asp	Lys	Ala	Asp	Leu	Arg	Leu	Ile
			340					345					350		
Tyr	Leu	Ala	Leu	Ala	His	Met	Ile	Lys	Phe	Arg	Gly	His	Phe	Leu	Ile
		355					360					365			
Glu	Gly	Asp	Leu	Asn	Pro	Asp	Asn	Ser	Asp	Val	Asp	Lys	Leu	Phe	Ile
	370					375					380				
Gln	Leu	Val	Gln	Thr	Tyr	Asn	Gln	Leu	Phe	Glu	Glu	Asn	Pro	Ile	Asn
385					390					395					400
Ala	Ser	Gly	Val	Asp	Ala	Lys	Ala	Ile	Leu	Ser	Ala	Arg	Leu	Ser	Lys
				405					410					415	
Ser	Arg	Arg	Leu	Glu	Asn	Leu	Ile	Ala	Gln	Leu	Pro	Gly	Glu	Lys	Lys
			420					425					430		
Asn	Gly	Leu	Phe	Gly	Asn	Leu	Ile	Ala	Leu	Ser	Leu	Gly	Leu	Thr	Pro
		435					440					445			
Asn	Phe	Lys	Ser	Asn	Phe	Asp	Leu	Ala	Glu	Asp	Ala	Lys	Leu	Gln	Leu
	450					455					460				
Ser	Lys	Asp	Thr	Tyr	Asp	Asp	Asp	Leu	Asp	Asn	Leu	Leu	Ala	Gln	Ile
465					470					475					480
Gly	Asp	Gln	Tyr	Ala	Asp	Leu	Phe	Leu	Ala	Ala	Lys	Asn	Leu	Ser	Asp
				485					490					495	
Ala	Ile	Leu	Leu	Ser	Asp	Ile	Leu	Arg	Val	Asn	Thr	Glu	Ile	Thr	Lys
			500					505					510		
Ala	Pro	Leu	Ser	Ala	Ser	Met	Ile	Lys	Arg	Tyr	Asp	Glu	His	His	Gln

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Asp	Leu	515	Thr	Leu	Leu	Lys	Ala	520	Leu	Val	Arg	Gln	Gln	525	Leu	Pro	Glu	Lys
530	Tyr	Lys	Glu	Ile	Phe	Phe	535	Asp	Gln	Ser	Lys	Asn	540	Gly	Tyr	Ala	Gly	Tyr
545	Ile	Asp	Gly	Gly	Ala	550	Ser	Gln	Glu	Glu	Phe	555	Tyr	Lys	Phe	Ile	Lys	Pro
					565	Met	Asp	Gly	Thr	Glu	570	Glu	Leu	Leu	Val	Lys	Leu	Asn
					580	Leu	Leu	Arg	Lys	Gln	585	Arg	Thr	Phe	Asp	Asn	Gly	Ser
					595	Gln	Ile	His	Leu	Gly	600	Glu	Leu	His	Ala	Ile	Leu	Arg
					610	His	Leu	His	Leu	Gly	615	Glu	Leu	His	Ala	Ile	Leu	Arg
					625	Asp	Phe	Tyr	Pro	Phe	630	Leu	Lys	Asp	Asn	Arg	Glu	Lys
					645	Arg	Ile	Pro	Tyr	Tyr	Val	Gly	Pro	Leu	Ala	Arg	Gly	Gly
					660	Phe	Ala	Trp	Met	Thr	Arg	Lys	Ser	Glu	Glu	Thr	Ile	Thr
					675	Asn	Phe	Glu	Glu	Val	Val	Asp	Lys	Gly	Ala	Ser	Ala	Gln
					690	Ile	Glu	Arg	Met	Thr	Asn	695	Phe	Asp	Lys	Asn	Leu	Pro
					710	Ser	Leu	Leu	Tyr	Glu	Tyr	715	Phe	Thr	Val	Tyr	Asn	Asn
					725	Lys	Val	Lys	Tyr	Val	Thr	Glu	Gly	Met	Arg	Lys	Pro	Ala
					740	Gly	Glu	Gln	Lys	Lys	Ala	745	Ile	Val	Asp	Leu	Leu	Phe
					755	Asn	Arg	Lys	Val	Thr	Val	Lys	Gln	Leu	Lys	Glu	Asp	Tyr
					770	Ile	Glu	Cys	Phe	Asp	Ser	775	Val	Glu	Ile	Ser	Gly	Val
					785	Asn	Ala	Ser	Leu	Gly	Thr	Tyr	His	Asp	Leu	Leu	Lys	Ile
					805	Lys	Asp	Phe	Leu	Asp	Asn	Glu	Glu	Asn	Glu	Asp	Ile	Leu
					820	Val	Leu	Thr	Leu	Phe	Glu	825	Asp	Arg	Glu	Met	Ile	Glu
					835	Leu	Lys	Thr	Tyr	Ala	His	Leu	840	Phe	Asp	Asp	Lys	Val
					850	Lys	Arg	Arg	Arg	Tyr	Thr	855	Gly	Trp	Gly	Arg	Leu	Ser
					865	Asn	Gly	Ile	Arg	Asp	Lys	Gln	Ser	Gly	Lys	Thr	Ile	Leu
					885	Lys	Ser	Asp	Gly	Phe	Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu
					900	Asp	Asp	Ser	Leu	Thr	Phe	Lys	Glu	Asp	Ile	Gln	Lys	Ala
					915	Gln	Gly	Asp	Ser	Leu	His	Glu	920	His	Ile	Ala	Asn	Leu
					930	Ala	Ile	Lys	Lys	Gly	Ile	Leu	Gln	Thr	Val	Lys	Val	Val
					945	Val	Lys	Val	Met	Gly	Arg	His	Lys	Pro	Glu	955	Asn	Ile
					965	Ala	Arg	Glu	Asn	Gln	Thr	Thr	Gln	Lys	Gly	Gln	Lys	Asn
					980	Arg	Met	Lys	Arg	Ile	Glu	Glu	Gly	Ile	Lys	Glu	Leu	Gly
					995	Leu	Lys	Glu	His	Pro	Val	Glu	1000	Asn	Thr	Gln	Leu	Gln
					1010	Tyr	Leu	Tyr	Tyr	Leu	Gln	Asn	Gly	Arg	Asp	Met	Tyr	Val
					1025	Leu	Asp	Ile	Asn	Arg	Leu	Ser	Asp	Tyr	Asp	Val	Asp	Ala
					1045	Gln	Ser	Phe	Leu	Lys	Asp	Asp	Ser	Ile	Asp	Asn	Lys	Val
					1050	Ser	Asp	Lys	Asn	Arg	Gly	Lys	Ser	Asp	Asn	Val	Pro	Ser

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Val	Val	Lys	Lys	Met	Lys	Asn	Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	
		1075														
Leu	Ile	Thr	Gln	Arg	Lys	Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	
		1090														
Gly	Leu	Ser	Glu	Leu	Asp	Lys	Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	
1105					1110					1115					1120	
Glu	Thr	Arg	Gln	Ile	Thr	Lys	His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	
				1125					1130						1135	
Met	Asn	Thr	Lys	Tyr	Asp	Glu	Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	
			1140						1145							
Val	Ile	Thr	Leu	Lys	Ser	Lys	Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	
			1155				1160					1165				
Gln	Phe	Tyr	Lys	Val	Arg	Glu	Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	
			1170			1175					1180					
Ala	Tyr	Leu	Asn	Ala	Val	Val	Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	
1185					1190					1195					1200	
Lys	Leu	Glu	Ser	Glu	Phe	Val	Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	
				1205					1210						1215	
Arg	Lys	Met	Ile	Ala	Lys	Ser	Glu	Gln	Glu	Ile	Gly	Lys	Ala	Thr	Ala	
			1220					1225					1230			
Lys	Tyr	Phe	Phe	Tyr	Ser	Asn	Ile	Met	Asn	Phe	Phe	Lys	Thr	Glu	Ile	
		1235					1240					1245				
Thr	Leu	Ala	Asn	Gly	Glu	Ile	Arg	Lys	Arg	Pro	Leu	Ile	Glu	Thr	Asn	
		1250				1255					1260					
Gly	Glu	Thr	Gly	Glu	Ile	Val	Trp	Asp	Lys	Gly	Arg	Asp	Phe	Ala	Thr	
1265					1270					1275					1280	
Val	Arg	Lys	Val	Leu	Ser	Met	Pro	Gln	Val	Asn	Ile	Val	Lys	Lys	Thr	
				1285				1290						1295		
Glu	Val	Gln	Thr	Gly	Gly	Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	Arg	
			1300					1305					1310			
Asn	Ser	Asp	Lys	Leu	Ile	Ala	Arg	Lys	Lys	Asp	Trp	Asp	Pro	Lys	Lys	
		1315					1320					1325				
Tyr	Gly	Gly	Phe	Asp	Ser	Pro	Thr	Val	Ala	Tyr	Ser	Val	Leu	Val	Val	
	1330					1335					1340					
Ala	Lys	Val	Glu	Lys	Gly	Lys	Ser	Lys	Lys	Leu	Lys	Ser	Val	Lys	Glu	
1345					1350					1355					1360	
Leu	Leu	Gly	Ile	Thr	Ile	Met	Glu	Arg	Ser	Ser	Phe	Glu	Lys	Asn	Pro	
				1365					1370					1375		
Ile	Asp	Phe	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Glu	Val	Lys	Lys	Asp	Leu	
			1380					1385					1390			
Ile	Ile	Lys	Leu	Pro	Lys	Tyr	Ser	Leu	Phe	Glu	Leu	Glu	Asn	Gly	Arg	
		1395	</													

UCSD097001WOSEQUENCELISTING

<210> 38
 <211> 1470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PIN-XTEN-dCas9(delta HNH)-2xNLS

<400> 38
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 1 5 10 15
 Gly Phe Ile Asp His Leu Ala Ser Leu Ala Arg Leu Leu Glu Ser Arg
 20 25 30
 Lys Tyr Ile Leu Val Val Pro Leu Ile Val Ile Asn Glu Leu Asp Gly
 35 40 45
 Leu Ala Lys Gly Gln Glu Thr Asp His Arg Ala Gly Gly Tyr Ala Arg
 50 55 60
 Val Val Gln Glu Lys Ala Arg Lys Ser Ile Glu Phe Leu Glu Gln Arg
 65 70 75 80
 Phe Glu Ser Arg Asp Ser Cys Leu Arg Ala Leu Thr Ser Arg Gly Asn
 85 90 95
 Glu Leu Glu Ser Ile Ala Phe Arg Ser Glu Asp Ile Thr Gly Gln Leu
 100 105 110
 Gly Asn Asn Asp Asp Leu Ile Leu Ser Cys Cys Leu His Tyr Cys Lys
 115 120 125
 Asp Lys Ala Lys Asp Phe Met Pro Ala Ser Lys Glu Glu Pro Ile Arg
 130 135 140
 Leu Leu Arg Glu Val Val Leu Leu Thr Asp Asp Arg Asn Leu Arg Val
 145 150 155 160
 Lys Ala Leu Thr Arg Asn Val Pro Val Arg Asp Ile Pro Ala Phe Leu
 165 170 175
 Thr Trp Ala Gln Val Gly Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
 180 185 190
 Ser Ala Thr Pro Glu Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile
 195 200 205
 Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val
 210 215 220
 Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile
 225 230 235 240
 Lys Lys Asn Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala
 245 250 255
 Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg
 260 265 270
 Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala
 275 280 285
 Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val
 290 295 300
 Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile Val
 305 310 315 320
 Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg
 325 330 335
 Lys Lys Leu Val Asp Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr
 340 345 350
 Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu
 355 360 365
 Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln
 370 375 380
 Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala
 385 390 395 400
 Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser
 405 410 415
 Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn
 420 425 430
 Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn
 435 440 445
 Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser
 450 455 460

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Lys 465	Asp	Thr	Tyr	Asp	Asp 470	Asp	Leu	Asp	Asn	Leu 475	Leu	Ala	Gln	Ile	Gly 480
Asp	Gln	Tyr	Ala	Asp 485	Leu	Phe	Leu	Ala	Ala 490	Lys	Asn	Leu	Ser	Asp 495	Ala
Ile	Leu	Leu	Ser 500	Asp	Ile	Leu	Arg	Val 505	Asn	Thr	Glu	Ile	Thr 510	Lys	Ala
Pro	Leu	Ser 515	Ala	Ser	Met	Ile	Lys 520	Arg	Tyr	Asp	Glu	His 525	His	Gln	Asp
Leu	Thr 530	Leu	Leu	Lys	Ala	Leu 535	Val	Arg	Gln	Gln	Leu 540	Pro	Glu	Lys	Tyr
Lys 545	Glu	Ile	Phe	Phe	Asp 550	Gln	Ser	Lys	Asn	Gly 555	Tyr	Ala	Gly	Tyr	Ile 560
Asp	Gly	Gly	Ala	Ser 565	Gln	Glu	Glu	Phe	Tyr 570	Lys	Phe	Ile	Lys	Pro 575	Ile
Leu	Glu	Lys	Met 580	Asp	Gly	Thr	Glu	Glu 585	Leu	Leu	Val	Lys	Leu 590	Asn	Arg
Glu	Asp	Leu 595	Leu	Arg	Lys	Gln	Arg 600	Thr	Phe	Asp	Asn	Gly 605	Ser	Ile	Pro
His	Gln 610	Ile	His	Leu	Gly	Glu 615	Leu	His	Ala	Ile	Leu 620	Arg	Arg	Gln	Glu
Asp 625	Phe	Tyr	Pro	Phe	Leu 630	Lys	Asp	Asn	Arg	Glu 635	Lys	Ile	Glu	Lys	Ile 640
Leu	Thr	Phe	Arg	Ile 645	Pro	Tyr	Tyr	Val	Gly 650	Pro	Leu	Ala	Arg	Gly 655	Asn
Ser	Arg	Phe	Ala 660	Trp	Met	Thr	Arg	Lys 665	Ser	Glu	Glu	Thr	Ile 670	Thr	Pro
Trp	Asn	Phe 675	Glu	Glu	Val	Val	Asp 680	Lys	Gly	Ala	Ser	Ala 685	Gln	Ser	Phe
Ile	Glu 690	Arg	Met	Thr	Asn	Phe 695	Asp	Lys	Asn	Leu	Pro 700	Asn	Glu	Lys	Val
Leu 705	Pro	Lys	His	Ser	Leu 710	Leu	Tyr	Glu	Tyr	Phe 715	Thr	Val	Tyr	Asn	Glu 720
Leu	Thr	Lys	Val	Lys 725	Tyr	Val	Thr	Glu	Gly 730	Met	Arg	Lys	Pro	Ala 735	Phe
Leu	Ser	Gly	Glu 740	Gln	Lys	Lys	Ala	Ile 745	Val	Asp	Leu	Leu	Phe 750	Lys	Thr
Asn	Arg	Lys 755	Val	Thr	Val	Lys	Gln 760	Leu	Lys	Glu	Asp	Tyr 765	Phe	Lys	Lys
Ile	Glu 770	Cys	Phe	Asp	Ser	Val 775	Glu	Ile	Ser	Gly	Val 780	Glu	Asp	Arg	Phe
Asn 785	Ala	Ser	Leu	Gly	Thr 790	Tyr	His	Asp	Leu	Leu 795	Lys	Ile	Ile	Lys	Asp 800
Lys	Asp	Phe	Leu	Asp 805	Asn	Glu	Glu	Asn	Glu 810	Asp	Ile	Leu	Glu	Asp 815	Ile
Val	Leu	Thr	Leu 820	Thr	Leu	Phe	Glu	Asp 825	Arg	Glu	Met	Ile	Glu 830	Glu	Arg
Leu	Lys	Thr 835	Tyr	Ala	His	Leu	Phe 840	Asp	Asp	Lys	Val 845	Met	Lys	Gln	Leu
Lys	Arg 850	Arg	Arg	Tyr	Thr	Gly 855	Trp	Gly	Arg	Leu	Ser 860	Arg	Lys	Leu	Ile
Asn 865	Gly	Ile	Arg	Asp	Lys 870	Gln	Ser	Gly	Lys	Thr 875	Ile	Leu	Asp	Phe	Leu 880
Lys	Ser	Asp	Gly	Phe 885	Ala	Asn	Arg	Asn	Phe 890	Met	Gln	Leu	Ile	His 895	Asp
Asp	Ser	Leu	Thr 900	Phe	Lys	Glu	Asp	Ile 905	Gln	Lys	Ala	Gln	Val 910	Ser	Gly
Gln	Gly	Asp 915	Ser	Leu	His	Glu	His 920	Ile	Ala	Asn	Leu	Ala 925	Gly	Ser	Pro
Ala	Ile 930	Lys	Lys	Gly	Ile	Leu 935	Gln	Thr	Val	Lys	Val 940	Val	Asp	Glu	Leu
Val 945	Lys	Val	Met	Gly	Arg 950	His	Lys	Pro	Glu	Asn 955	Ile	Val	Ile	Glu	Met 960
Ala	Arg	Glu	Asn	Gln 965	Thr	Thr	Gln	Lys	Gly 970	Gln	Lys	Asn	Gly	Ser 975	Gly
Ser	Gly	Leu	Asp 980	Lys	Ala	Gly	Phe	Ile 985	Lys	Arg	Gln	Leu	Val 990	Glu	Thr
Arg	Gln	Ile 995	Thr	Lys	His	Val	Ala 1000	Gln	Ile	Leu	Asp	Ser	Arg	Met	Asn

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Thr Lys Tyr Asp Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile
1010 1015 1020
Thr Leu Lys Ser Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe
1025 1030 1035 1040
Tyr Lys Val Arg Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr
1045 1050 1055
Leu Asn Ala Val Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu
1060 1065 1070
Glu Ser Glu Phe Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys
1075 1080 1085
Met Ile Ala Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr
1090 1095 1100
Phe Phe Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu
1105 1110 1115 1120
Ala Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1125 1130 1135
Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val Arg
1140 1145 1150
Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val
1155 1160 1165
Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser
1170 1175 1180
Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly
1185 1190 1195 1200
Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys
1205 1210 1215
Val Glu Lys Gly Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu
1220 1225 1230
Gly Ile Thr Ile Met Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp
1235 1240 1245
Phe Leu Glu Ala Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile
1250 1255 1260
Lys Leu Pro Lys Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg
1265 1270 1275 1280
Met Leu Ala Ser Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu
1285 1290 1295
Pro Ser Lys Tyr Val Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys
1300 1305 1310
Leu Lys Gly Ser Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu
1315 1320 1325
Gln His Lys His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe
1330 1335 1340
Ser Lys Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser
1345 1350 1355 1360
Ala Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
1365 1370 1375
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe
1380 1385 1390
Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys
1395 1400 1405
Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr
1410 1415 1420
Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp Ala Tyr Pro Tyr
1425 1430 1435 1440
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1445 1450 1455
Arg Lys Val Glu Asp Pro Lys Lys Lys Arg Lys Val Asp Val
1460 1465 1470

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<210> 39

<211> 1354

<212> PRT

<213> Artificial Sequence

<220>

<223> Streptococcus pyogenes dCas9 (D10A, H840A)

UCSD097001WSEQUENCELISTING

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			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

	Lys 545	Lys Val	Ala Gln	Ile Leu	Val Lys 565	Asp Glu	Leu Asp	Phe Tyr	Lys Phe 570	Thr Lys	Asn Ile	Arg Glu	Lys Cys	Val Phe 575	Thr Asp 580	
	Ser	Val	Glu	Ile 580	Ser	Gly	Val	Glu	Asp 585	Arg	Phe	Asn	Ala	Ser 590	Gly	
	Thr	Tyr	His 595	Asp	Leu	Leu	Lys	Ile 600	Ile	Lys	Asp	Lys	Asp 605	Phe	Leu	Asp
	Asn	Glu 610	Glu	Asn	Glu	Asp	Ile 615	Leu	Glu	Asp	Ile	Val 620	Leu	Thr	Leu	Thr
	Leu 625	Phe	Glu	Asp	Arg	Glu 630	Met	Ile	Glu	Glu	Arg 635	Leu	Lys	Thr	Tyr	Ala 640
	His	Leu	Phe	Asp	Asp 645	Lys	Val	Met	Lys	Gln 650	Leu	Lys	Arg	Arg	Arg 655	Tyr
	Thr	Gly	Trp	Gly 660	Arg	Leu	Ser	Arg	Lys 665	Leu	Ile	Asn	Gly	Ile 670	Arg	Asp
	Lys	Gln	Ser 675	Gly	Lys	Thr	Ile	Leu 680	Asp	Phe	Leu	Lys	Ser 685	Asp	Gly	Phe
	Ala	Asn 690	Arg	Asn	Phe	Met	Gln 695	Leu	Ile	His	Asp	Asp 700	Ser	Leu	Thr	Phe
	Lys 705	Glu	Asp	Ile	Gln	Lys 710	Ala	Gln	Val	Ser	Gly 715	Gln	Gly	Asp	Ser	Leu
	His	Glu	His	Ile	Ala 725	Asn	Leu	Ala	Gly	Ser 730	Pro	Ala	Ile	Lys	Lys 735	Gly
	Ile	Leu	Gln	Thr 740	Val	Lys	Val	Val	Asp 745	Glu	Leu	Val	Lys	Val 750	Met	Gly
	Arg	His	Lys 755	Pro	Glu	Asn	Ile	Val 760	Ile	Glu	Met	Ala	Arg 765	Glu	Asn	Gln
	Thr	Thr 770	Gln	Lys	Gly	Gln	Lys 775	Asn	Ser	Arg	Glu	Arg 780	Met	Lys	Arg	Ile
	Glu 785	Glu	Gly	Ile	Lys	Glu 790	Leu	Gly	Ser	Gln	Ile 795	Leu	Lys	Glu	His	Pro 800
	Val	Glu	Asn	Thr	Gln 805	Leu	Gln	Asn	Glu	Lys 810	Leu	Tyr	Leu	Tyr	Tyr 815	Leu
	Gln	Asn	Gly	Arg 820	Asp	Met	Tyr	Val	Asp 825	Gln	Glu	Leu	Asp	Ile 830	Asn	Arg
	Leu	Ser	Asp 835	Tyr	Asp	Val	Asp	Ala 840	Ile	Val	Pro	Gln	Ser 845	Phe	Leu	Lys
	Asp	Asp 850	Ser	Ile	Asp	Asn	Lys 855	Val	Leu	Thr	Arg	Ser 860	Asp	Lys	Asn	Arg
	Gly 865	Lys	Ser	Asp	Asn	Val 870	Pro	Ser	Glu	Glu	Val 875	Val	Lys	Lys	Met	Lys 880
	Asn	Tyr	Trp	Arg	Gln 885	Leu	Leu	Asn	Ala	Lys 890	Leu	Ile	Thr	Gln	Arg 895	Lys
	Phe	Asp	Asn	Leu 900	Thr	Lys	Ala	Glu	Arg 905	Gly	Gly	Leu	Ser	Glu 910	Leu	Asp
	Lys	Ala	Gly 915	Phe	Ile	Lys	Arg	Gln 920	Leu	Val	Glu	Thr	Arg 925	Gln	Ile	Thr
	Lys	His 930	Val	Ala	Gln	Ile	Leu 935	Asp	Ser	Arg	Met	Asn 940	Thr	Lys	Tyr	Asp
	Glu 945	Asn	Asp	Lys	Leu	Ile 950	Arg	Glu	Val	Lys	Val 955	Ile	Thr	Leu	Lys	Ser 960
	Lys	Leu	Val	Ser	Asp 965	Phe	Arg	Lys	Asp	Phe 970	Gln	Phe	Tyr	Lys	Val 975	Arg
	Glu	Ile	Asn	Asn 980	Tyr	His	His	Ala	His 985	Asp	Ala	Tyr	Leu	Asn 990	Ala	Val
	Val	Gly	Thr 995	Ala	Leu	Ile	Lys	Lys 1000	Tyr	Pro	Lys	Leu	Glu 1005	Ser	Glu	Phe
	Val	Tyr 1010	Gly	Asp	Tyr	Lys	Val 1015	Tyr	Asp	Val	Arg	Lys 1020	Met	Ile	Ala	Lys
	Ser 1025	Glu	Gln	Glu	Ile	Gly 1030	Lys	Ala	Thr	Ala	Lys 1035	Tyr	Phe	Phe	Tyr	Ser 1040
	Asn	Ile	Met	Asn	Phe 1045	Phe	Lys	Thr	Glu	Ile 1050	Thr	Leu	Ala	Asn	Gly 1055	Glu
	Ile	Arg	Lys	Arg 1060	Pro	Leu	Ile	Glu	Thr 1065	Asn	Gly	Glu	Thr	Gly 1070	Glu	Ile
	Val	Trp	Asp	Lys	Gly	Arg	Asp									

UCSD097001WSEQUENCELISTING

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      1075      1080      1085
Met Pro Gln Val Asn Ile Val Lys Lys Thr Glu Val Gln Thr Gly Gly
      1090      1095      1100
Phe Ser Lys Glu Ser Ile Leu Pro Lys Arg Asn Ser Asp Lys Leu Ile
1105      1110      1115      1120
Ala Arg Lys Lys Asp Trp Asp Pro Lys Lys Tyr Gly Gly Phe Asp Ser
      1125      1130      1135
Pro Thr Val Ala Tyr Ser Val Leu Val Val Ala Lys Val Glu Lys Gly
      1140      1145      1150
Lys Ser Lys Lys Leu Lys Ser Val Lys Glu Leu Leu Gly Ile Thr Ile
      1155      1160      1165
Met Glu Arg Ser Ser Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala
1170      1175      1180
Lys Gly Tyr Lys Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys
1185      1190      1195      1200
Tyr Ser Leu Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser
      1205      1210      1215
Ala Gly Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr
      1220      1225      1230
Val 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 His
1250      1255      1260
Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys Arg Val
1265      1270      1275      1280
Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys
      1285      1290      1295
His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile Ile His Leu
      1300      1305      1310
Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala Phe Lys Tyr Phe Asp
      1315      1320      1325
Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser Thr Lys Glu Val Leu Asp
1330      1335      1340
Ala Thr Leu Ile His Gln Ser Ile Thr Gly
1345      1350

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